UNIVERSITY of GREENWICH

Mechanisms underlying *Leishmania* parasites survival and dissemination at late stage of infection in human macrophages

Rajeev Rai (BSc Hons, MRes)

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DECLARATION

I certify that this work has not been accepted in substance for any degree, and is not concurrently being submitted for any degree other than that of Doctor of Philosophy being studied at the University of Greenwich. I also declare that this work is the result of my own investigations except where otherwise identified by references and that I have not plagiarized the work of others.

Candidate:

Rajeev Rai Date: 7/1/2016

Supervisor:

Dr. Giulia Getti Date: 7/1/2016

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ABSTRACT

Leishmania parasites are the causative agent of a wide range of human diseases known as leishmaniasis. The progression of disease pathogenesis is dependent on the ability of intracellular parasites to disseminate between human macrophages. It is assumed that parasites could exit macrophages following cell lysis. However, there is still a major gap in knowledge in understanding the exact mechanism pertaining to this critical step. This has been partially caused by the lack of reliable experimental models to study this stage of host-parasite interaction. This research aims to elucidate the mechanism behind cell-to-cell spreading of *Leishmania in vitro*.

A link between host cell apoptosis and *Leishmania* propagation was initially established by determining the effect of apoptotic induction on infection over a period of 96 hours. The result showed that 60-90% of cells were inoculated with *L. aethiopica* and *L. mexicana* within 72 and 96 hours infection. Although, the concentration of viable cells was greatly reduced as compared to non-induced samples, a heavily infected cell population was obtained with this approach. Hence, this population of *L. aethiopica* and *L. mexicana* infected cells at 72 hours was used to infect differentiated THP-1 macrophages and validated as a model for infection spreading. Amastigotes spreading was detected within 12 hours of co-culture as confirmed by flow cytometry and live cell imaging techniques. Interestingly, the live imaging revealed inter-cellular extrusion of *L. aethiopica* and *L. mexicana* from infected to a recipient cells without cell lysis. To address whether parasite extrusion is linked to apoptotic induction, this model was used to detect expression of several apoptotic markers. The results showed that *L. aethiopica* (but not *L. mexicana*) dissemination was correlated with host apoptotic induction, as there was a significant increase ($p<0.05$) in phosphatidyl serine (PS) externalization and active caspase-3 expression. In addition, western blot analysis demonstrated that *L. aethiopica* spread was associated with downregulation of three major apoptotic signaling pathways: AKT, NF-κB and PKC-δ. Further comparative proteomic analysis of this model supported these findings and showed that during *L. aethiopica* spreading, a number of host physiological processes were subverted. Specifically caspase-3 and caspase-9 activation strengthens the involvement of mitochondria in initiation of apoptosis. Interestingly, chitinase-3-like protein (inducer of IL-13 production) and butyrophilin (inhibitor of IFN-γ and IL-12) were markedly increased confirming the downregulation of inflammatory response. Finally, elevated increase in glutathione reductase and metallothionein-2 proteins, which are involved in scavenging free radicals, suggests that anti-microbial activity is also downregulated during *L. aethiopica* spreading.

In conclusion, by developing and validating for the first time a credible *in vitro* spreading model in human macrophages, this research has clarified the mechanism of *Leishmania* spreading. *L. aethiopica* promotes host cell apoptosis in order to disseminate from cell-to-cell without activating inflammatory and anti-microbial responses. In particular, apoptotic induction takes place via downregulation of AKT and NF-κB, release of cytochrome C and consequent activation of caspase-3 and PS exhibition, independently from PKC-δ. This model clearly fits with the silent spread of parasites that takes place in the first weeks (to months) of infection in mice model. Interestingly, the fact that *L. mexicana* utilizes a non-apoptotic strategy to spread suggests that alternative mechanisms of parasitic extrusion also exist underlying the necessity of species specific investigations. Understanding the molecular basis of *Leishmania* spreading contributes to filling a current gap in knowledge in the biology of *Leishmania* infection strategy of this very successful parasite. Moreover, it has the potential to open up a novel set of targets for drugs and vaccine development against this increasingly widespread neglected disease.

Table of Contents

Chapter 1 – Introduction……………………………………… 1

1.1 *Leishmania* parasites……………………………………………… 1

1.2 Life cycle of *Leishmania*………………………………………. 1

1.3 Leishmaniasis……………………………………………………….. 7

1.4 Expression of virulence factors in *Leishmania*…………………. 12

1.5 Interaction between *Leishmania* and host immune cells………. 16

1.5.1 T cells……………………………………………………….. 16

1.5.2 Natural Killer (NK) cells…………………………………… 17

1.5.3 Neutrophils…………………………………………………. 18

1.5.4 Macrophages………………………………………………… 18

1.6 Molecular interaction between *Leishmania* and macrophage…. 20

1.6.1 Phagocytic uptake of *Leishmania*………………………………. 20

1.6.2 Survival strategy for *Leishmania*…………………………… 22

1.6.3 Modulation of intracellular signaling pathways during *Leishmania* infection……………………………………………… 22

1.6.4 Dissemination of *Leishmania*…………………………… 26

1.7 Apoptosis……………………………………………………….. 28

1.8 Infection and Apoptosis………………………………………….. 33

1.9 Aims of the Thesis……………………………………………… 36

Chapter 2 – Materials and Methods…………………………. 38

2.1 Parasite culture…………………………………………………… 38

2.2 Human cell culture……………………………………………….. 38

2.3 Infection of differentiated THP-1 macrophage with GFP expressing *Leishmania*……………………………………………….. 39

2.3.1 Preparation of stationary phase metacyclic promastigotes….. 39

2.3.2 Preparation of differentiated THP-1 macrophages…………. 39

2.3.3 Parasite to cell ratio………………………………………… 40

2.4 Induction of apoptosis…………………………………………… 40

2.5 Infection of differentiated THP-1 macrophage with *Leishmania* infected cells………………………………………………………… 40

2.6 Inhibition of caspase-3 activity…… 42

2.7 Detection of apoptosis…….. 42

2.7.1 Annexin V / 7AAD assay…… 44

2.7.2 Caspase-3 enzymatic assay…….. 44

2.8 Flow cytometry…… 45

2.9 Real time lapse microscopy…… 48

2.10 Western blot…… 50

2.11 Quantitative proteomics by mass spectrometry…….. 52

2.11.1 Precipitation and enzymatic digestion of the protein samples……..... 52

2.11.2 Peptide labeling and mass spectrometry…… 53

2.12 Statistical Analysis…… 54

Chapter 3 – *Leishmania* infection and host cell apoptosis…... 55

3.1 Introduction…….. 55

3.2 Results and Discussion…… 56

3.2.1 Infection of differentiated THP-1 macrophages with *Leishmania* promastigotes…… 56

3.2.2 Effect of *Leishmania* promastigotes infection on the apoptosis of differentiated THP-1 macrophages…….. 60

3.2.3 Effect of apoptotic induction on *Leishmania* infection……... 63

3.2.3a Longer duration of treatment with camptothecin…….. 63

3.2.3b Time limited treatment with camptothecin…… 66

3.2.4 Assessment of viable cell concentration during *Leishmania* infection in the presence of camptothecin…… 71

3.3 Conclusions…… 71

Chapter 4 – The *in vitro* development of *Leishmania* dissemination model during late stage of macrophage infection…… 74

4.1 Introduction…… 74

4.2 Results and Discussion…… 76

4.2.1 Optimization of camptothecin treatment in *L. mexicana* (M5G) infected cells…… 76

4.2.2 Infection of differentiated THP-1 macrophage with L8G and M5G infected cells. …… 76

4.2.3 Live cell imaging of intracellular L8G and M5G amastigotes spreading…….. 81
4.2.4 Effect of *Leishmania* spreading on the apoptosis of host cells 84
4.2.5 Effect of caspase-3 inhibition on the apoptosis and infection spread…… 90

4.3 Conclusions…… 90

Chapter 5 – Regulation of apoptosis signaling pathways in human macrophage during *Leishmania* spreading…… 93
5.1 Introduction…… 93
5.2 Results and Discussion…… 96
5.2.1 Effect of L8G infected cells on AKT activation during cell-to-cell infection spread…… 96
5.2.2 Effect of AKT downregulation on the phosphorylation of BAD expression and cytochrome C release…… 98
5.2.3 Effect of L8G infected cells on NF-κB signaling pathways during cell-to-cell infection spread……... 100
5.2.4 Effect of L8G infected cells on PKC-δ signaling pathways during cell-to-cell infection spread……..... 103
5.3 Conclusions…… 105

Chapter 6 – Global protein response during late stage of *Leishmania* infection in human macrophage…… 107
6.1 Introduction…… 107
6.2 Results and Discussion…… 108
6.2.1 Identification and functional annotation of differentially expressed proteins…… 108
6.2.2 Proteins involved in apoptosis and cell death…….. 110
6.2.3 Proteins involved in immune response…… 114
6.2.4 Proteins involved in vesicular trafficking..…… 116
6.2.5 Proteins involved in metabolic pathways..……... 117
6.2.6 Proteins involved in gene expression…….. 118
6.3 Conclusions…… 119

Chapter 7 – Discussion…….. 120
7.1 Discussion…… 120

Chapter 8 – Conclusion and future works…… 128

8.1 Conclusions…… 128

8.2 Future works…… 129

Chapter 9 – References…….. 131

Chapter 10 – Appendices…… 144

List of Figures

Figure 1.1. Scanning electron microscope of two life stage of *Leishmania* parasites…… 3
Figure 1.2. Life cycle of *Leishmania* parasites between the Female sandfly (vector) and mammals (host) ……. 4
Figure 1.3. Developmental profile of various morphological forms of *Leishmania* inside the sandfly vector…… 6
Figure 1.4. Interaction of *Leishmania* parasites with the phagocytic pathway of host macrophages…… 8
Figure 1.5. Major clinical pathologies associated with human leishmaniasis. …… 10
Figure 1.6. Structural organization of *Leishmania* Lipophosphoglycan (LPG)…….. 14
Figure 1.7. Trojan horse model for neutrophils. …… 19
Figure 1.8. Two different types of receptor mediated approach undertaken by macrophage to phagocytize metacyclic promastigote……. 21
Figure 1.9. Schematic representation showing the differences in the molecular interaction of endosomal vesicles with the Wild type (Wt) and LPG defective (mutant) *Leishmania* promastigote…….. 23
Figure 1.10. Upstream and downstream effectors in NF- κB signaling pathway. …… 25
Figure 1.11. Schematic diagram representing the disruption of macrophage signaling pathways during *Leishmania* infection……. 27
Figure 1.12. Evolution of dermal lesions in C57BL/6 mice during *Leishmania* infection…… 29
Figure 1.13. Mechanism of apoptosis is comprised of extrinsic and intrinsic pathways…… 31
Figure 2.1. Schematic diagram representing the optimization strategy of camptothecin treatment on the percentage of infected cells……. 41
Figure 2.2. Flow cytometry analysis of PE-Annexin V / 7-AAD stained cells. ……. 46
Figure 2.3. Flow cytometry analysis of apoptosis in infected cultures…… 47

Figure 2.4. Flow cytometry analysis of PE-Caspase 3 stained cells…… 49
Figure 3.1. Time course of differentiated THP-1 macrophage infection with *Leishmania* promastigotes. …… 58
Figure 3.2. Measurement of viable cell concentration in the presence or absence of infection. …… 59
Figure 3.3. Effect of *Leishmania* promastigotes infection on the apoptosis of differentiated THP-1 macrophages. …… 61
Figure 3.4. Time course of differentiated THP-1 macrophage infection with *Leishmania* promastigotes. …… 62
Figure 3.5. Effect of longer exposure to camptothecin treatment on *Leishmania* infection…… 64
Figure 3.6. Effect of longer exposure to camptothecin treatment on the apoptosis of differentiated THP-1 macrophages infected with *Leishmania*. 65
Figure 3.7. Flow cytometry analysis of Annexin V versus 7-AAD dot plot. ……. 67
Figure 3.8. Flow cytometry analysis of Annexin V versus 7-AAD dot plot after washing protocol…….. 68
Figure 3.9. Effect of shorter exposure to camptothecin treatment on *Leishmania* infection…… 69
Figure 3.10. Effect of shorter exposure to camptothecin treatment on the apoptosis of differentiated THP-1 macrophages infected with *Leishmania*. 70
Figure 3.11. Effect of camptothecin on viable cell concentration in the presence or absence of infection. …… 72
Figure 4.1. Time course of differentiated THP-1 macrophage infection with *L. mexicana* (M5G) in the presence and/or absence of apoptotic induction…….. 77
Figure 4.2. Infection of THP-1 macrophages with *Leishmania* infected cells……... 79
Figure 4.3. Measurement of viable cell concentration during infection with *Leishmania* infected cells. …… 80
Figure 4.4. Live cell imaging of *L. aethiopica* (L8G) amastigotes spread from cell-to-cell. …….. 82

Figure 4.5. Live cell imaging of *L. mexicana* (M5G) amastigotes spread from cell-to-cell…… 83
Figure 4.6. Effect of L8G infection spreading on host cell apoptosis…….. 85
Figure 4.7. Effect of L8G infection spreading on the activation of caspase-3 in host cells. …… 87
Figure 4.8. Effect of M5G infection spreading on host cell apoptosis……. 88
Figure 4.9. Effect of M5G infection spreading on the activation of caspase-3 in host cells. …… 89
Figure 4.10. Effect of caspase-3 inhibition on the apoptosis and infection spread after infection with L8G infected cells…….. 91
Figure 5.1. Schematic diagram representing apoptotic signalling pathways in macrophages……..... 95
Figure 5.2. Effect of *L. aethiopica* (L8G) infected cells on AKT activation during infection spreading……... 97
Figure 5.3. Effect of AKT downregulation on BAD phosphorylation and cytochrome C release…….. 99
Figure 5.4. Effect of *L. aethiopica* (L8G) infected cells on NF-κB signaling during infection spreading……..... 102
Figure 5.5. Effect of *L. aethiopica* (L8G) infected cells on PKC-δ signaling during infection spreading. …….. 104
Figure 6.1. Pie-diagram showing functional annotation and relative distribution of the total proteins detected in differentiated THP-1 macrophages co-cultured with *L. aethiopica* infected cells……. 111
Figure 6.2. Functional distribution of differentially expressed proteins during *L. aethiopica* infected co-culture cells at 10 hours……... 112
Figure 7.1. Schematic diagram representing the complex nature of intracellular signaling pathways associated with apoptosis……. 124

List of Tables

Table 1.1. Classification of *Leishmania* parasites causing human disease into Old and New World species…….. 2

Table 1.2. Classification of human leishmaniasis……. 9

Table 1.3. Summary of the diverse range of virulence factors expressed by *Leishmania*……..... 13

Table 1.4. Summary of the diverse macrophage signaling pathways altered by *Leishmania*…… 24

Table 2.1. List of experiments designed for apoptosis and their time of analysis. …… 43

Table 2.2. List of antibodies and their appropriate dilution and appropriate blocking buffers used in western blot experiments. ……. 51

Table 6.1. List of differentially expressed proteins during late stage of *L. aethiopica* infection. …… 109

Table 7.1. Summary of the involvement of apoptotic signaling pathways concomitant with spreading of *L. aethiopica* infection……. 125

Abbreviations

APAF-1	Apoptotic Protease Activating Factor-1
APC	Antigen Presenting Cells
CL	Cutaneous Leishmaniasis
CP	Cysteine Peptidase
CR	Complement Receptor
CRD	Carbohydrate Recognition Domain
DAG	Di-Acyl Glycerol
DCL	Diffuse Cutaneous Leishmaniasis
DED	Death Effector Domain
DISC	Death Inducing Signaling Complex
ERK	Extracellular Signal Regulated Kinase
FADD	Fas-associated Death Domain
FCS	Fetal Calf Serum
FnR	Fibronectin Receptor
FSC	Forward Scatter
GFP	Green Fluorescent Protein
GIPL	Glycophosphatidylinositol Lipid
GP63	Glycoprotein 63
GPCR	G Protein Coupled Receptor
GPI	Glycosylphosphatidylinositol
IAP	Inhibitor of Apoptosis
ICS	Interconnecting Segment
iNOS	Inducible Nitric Oxide Synthase
JAK	Janus Kinase
JNK	c-Jun N terminal protein
LAMP	Lysosomal Associated Membrane Protein
LPG	Lipophosphogylcan
LPS	Lipopolysaccharide
LRR	Leucine Rich Repeat
MAC	Membrane Attack Complex
MAPK	Mitogen Activated Protein Kinase
MCL	Muco Cutaneous Leishmaniasis
MIP	Macrophage Inflammatory Protein
MR	Mannose Receptor
mRNA	Messenger RNA
NET	Neutrophil Extracellular Trap
NF	Nuclear Factor
NK	Natural Killer
NO	Nitric Oxide
PARP	Poly ADP Ribose Polymerase

PBS	Phosphate Buffer Saline
PCD	Programmed Cell Death
PE	Phycoerythrin
PH	Pleckstrin Homology
PI3K	Phosphatidylinositol 3 Kinase
PKDL	Post Kala Azar Leishmaniasis
PM	Peritrophic Matrix
PPG	Proteophosphoglycan
PS	Phosphatidyl Serine
PSA-2	Protein Surface Antigen-2
PSG	Promastigote Secretory Gel
PV	Parasitophorous Vacuole
RA	Retinoic Acid
RANTES	Regulated on Activation Normal T cell Expressed and Secreted
RAS	Rat Sarcoma
ROS	Reactive Oxygen Species
SHP-1	Src-homology-2 domain containing Phosphatase
SP	Serine Peptidase
SSC	Side Scatter
STAT	Signal Transducers and Activators of Transcription
TGF	Transforming Growth Factor
Th 1/2	T helper cells 1/2
TLR	Toll Like Receptor
TNF	Tumor Necrosis Factor
VL	Visceral Leishmaniasis
WASP	Wiscott Aldrich Syndrome Protein
WHO	World Health Organization

Chapter 1 – Introduction

1.1. *Leishmania* parasites

Unicellular protozoan parasites belonging to the genus *Leishmania* are the causative agent of a spectrum of human diseases known as leishmaniasis. Ever since the discovery of this parasite in 1903 (Leishman, 1903; Donovan, 1903; Bailey and Bishop, 1959), more than 30 species of *Leishmania* have been reported, out of which 12 species have been known to cause human leishmaniasis (Banuls et al., 2007). Depending on the location site of the disease, these species have been classified into Old World and New World and further sub-divided into *Leishmania* and *Viannia* sub-genus (Table 1.1). Affecting over 350 million people in 88 countries worldwide, the transmission of this parasite occurs through the bite of phlebotomine sandflies (Kedzierski, 2010).

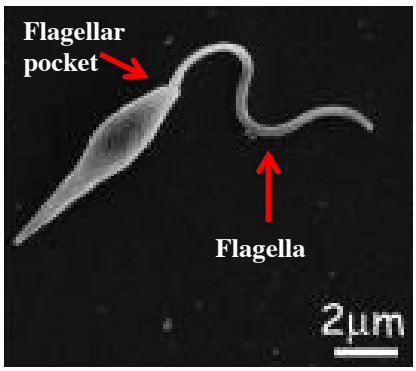
1.2. Life cycle of *Leishmania*

Leishmania undergoes structural and biochemical transformations throughout its life cycle. In sandfly, the parasite develops as flagellated and motile forms called promastigotes whereas a non-motile oval shaped amastigotes are found inside the mammalian host (Figure 1.1). The parasitic life cycle initiates when the sandfly ingests the amastigotes infected macrophages during its blood meal (Figure 1.2). After the first 12 hours post feeding, the increase in pH and reduced temperature triggers the differentiation of amastigotes into a non-infective procyclic promastigotes, which are relatively resistant against sandfly digestive enzymes (Bates, 2007). At this time point, the replicating promastigotes located in the endoperitrophic space are separated from the anterior midgut by a layer of protein and chitin mesh called peritrophic matrix (PM).

Old World (***Leishmania*** **sub-genus)**	**New World** (***Leishmania*** **sub-genus)**	**New World** (***Viannia*** **sub-genus)**
L. major	*L. mexicana*	*L. braziliensis*
L. tropica	*L. amazonensis*	*L. guyanensis*
L. aethiopica	*L. pifanoi*	*L. panamensis*
L. donovani		*L. peruviana*
L. infantum		

Table 1.1. Classification of *Leishmania* parasites causing human disease into Old and New World species. Species are further categorized into two different sub-genus, *Leishmania* and *Viannia*. Adapted from Kaye and Scott, 2011.

A



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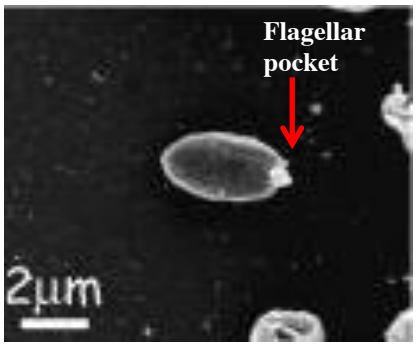


Figure 1.1. Scanning electron microscope images of two life cycle stage of *Leishmania* parasites. (A) Promastigote (motile and flagellated) and **(B)** Amastigote (oval shaped and non-motile). The flagellar pocket marks the anterior side of the parasites. Adapted from Besteiro et al., 2007.

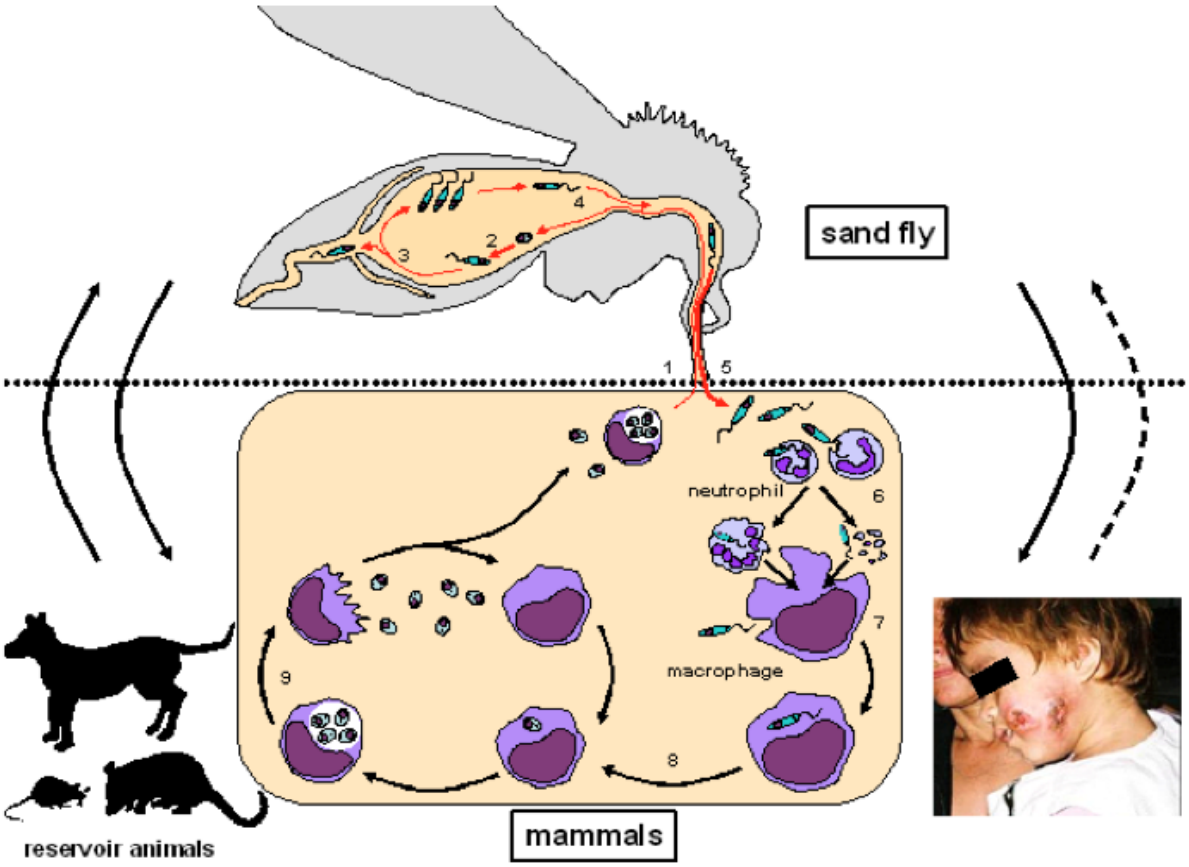


Figure 1.2. Life cycle of *Leishmania* parasites between the Female sandfly (vector) and mammals (host). During blood meal, the healthy sandfly consumes infected blood, containing amastigotes, from the host [1]. Changes in the pH and temperature inside the sandfly's midgut triggers differentiation of amastigotes into flagellated procyclic promastigotes [2]. Following replication and attachment on the peritrophic matrix of midgut, the parasites migrate towards the proboscis, where the procyclic differentiates into non-dividing and highly motile metacyclic promastigotes [3,4]. The infected sandfly then injects another healthy host during its next blood meal [5]. The metacyclic promastigotes is then phagocytized either directly by macrophages (definitive host cells) or indirectly through neutrophils (which then becomes a secondary meal for macrophage) [6]. Following its survival inside the phagolysosome of the macrophage, the promastigote differentiate into a non-motile amastigote [7, 8], which then undergoes replication and re-infection into other neighboring marcophages [9]. The life cycle is complete when infected macrophages are taken up by another healthy sandfly with the blood meal [1]. Adapted from Kato et al., 2010.

Within 2-3 post feeding, replication of procyclic form is reduced and differentiation into nectomonad promastigotes begins (Figure 1.3). This elongated and motile parasitic form secretes chitinase enzymes (PM degradation) and subsequently migrates to the anterior midgut in order to avoid expulsion during blood defecation (Rogers et al., 2008). As the nectomonads reaches the stomodeal valve, the parasite undergoes further differentiation into replicating leptomonads, which secrete promastigote secretory gel (PSG) (Rogers et al., 2002). The significance of PSG, which is composed of filamentous proteophoshoglycans, is not only linked to effective transmission via the sandfly proboscis but is also involved in dampening down the mammalian host immune response during the inoculation phase (Rogers et al., 2009; Rogers, 2012). From day five onwards, some leptomonads differentiates into haptomonads, whose primary role is to form a ball shaped mass in order to impede the blood flow into the midgut. The remaining leptomonads transform into the non-dividing infectious metacyclics promastigotes, which possess long flagella and are highly motile to migrate towards the pharynx and proboscis, ready for inoculation (Bates, 2007).

During blood meal, the infected sandfly transmits metacyclic promastigotes into the skin of the mammalian host, where the parasites become phagocytized either by macrophages or by neutrophils. Neutrophils, which are generally the first cells to be recruited to the site of infection, have an extremely short half-life and undergo spontaneous apoptosis within 24 hours of infiltration from the blood stream. However, during this early infection period, promastigote delays neutrophil apoptosis for further 24 hours (Aga et al., 2002). After this interruption, the promastigote infected neutrophils then become phagocytized by macrophages (Kaye and Scott, 2011), as discussed in more detail later (section 1.5.3).

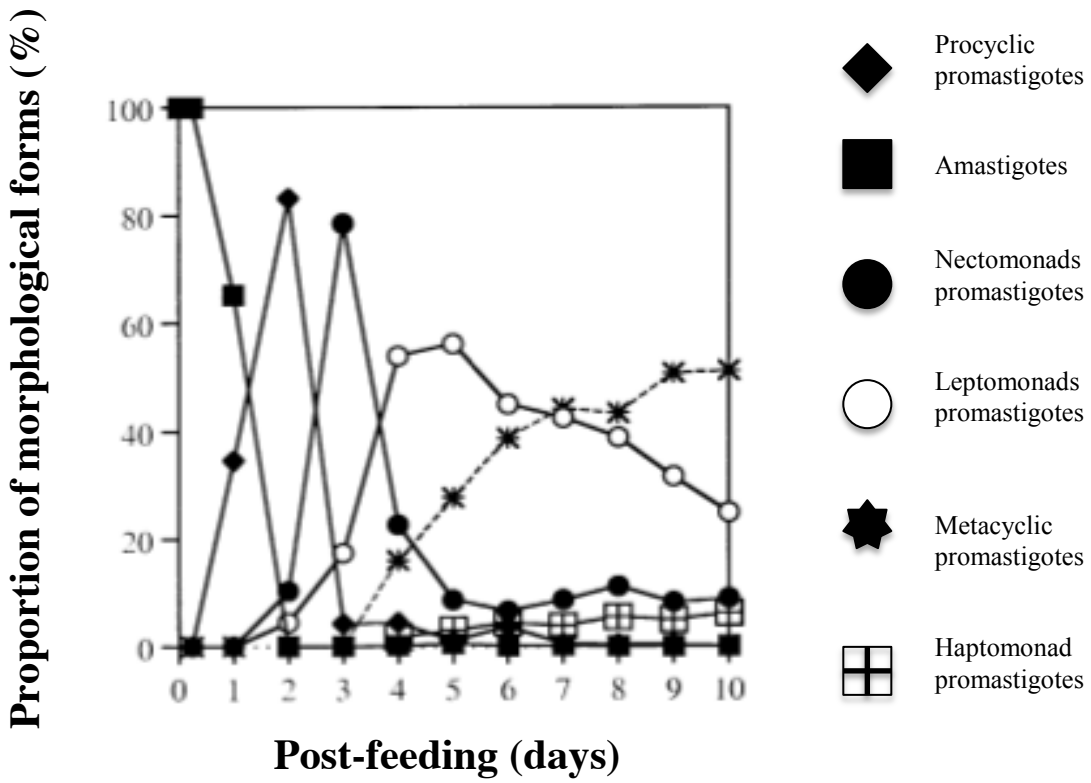


Figure 1.3. Developmental profile of various morphological forms of *Leishmania* inside the sandfly vector. Amastigotes undergoes complete transformation into procyclic within day 2 of post infection. From day 2, nectomonad and leptomonads are observed at low prevalence for the first time. Procyclic then begins to decrease rapidly, which is coincident with an increase in the number of nectomonad and leptomonad promastigotes. From day 5, the proportion of leptomonad slowly drops while the nectomonad already persist at a very low level. Within the same day, two forms begin to make their appearance; haptomonad and metacyclic promastigotes. Although the haptomonad fails to increase in number, the metacyclic gradually increases and becomes the predominant parasite population by day 10, at the expense of leptomonad promastigotes. Adapted from Rogers et al., 2002.

Immediately after phagocytosis, the promastigotes are located inside macrophage derived phagosomes (Figure 1.4). Interestingly, the lipophoshpoglycan (LPG) of metacylic promastigotes delays the fusion between phagosome containing parasites and acidic enzyme containing lysosomes hence preventing the formation of phagolysosomal vesicles (Lodge and Descoteaux, 2005). This sudden delay in phagosome biogenesis, which is referred to as pre-pregnant pause, is thought to allow promastigote sufficient time to differentiate into amastigote (Swanson and Fernandez-Moreira, 2002). After the release from pre-pregnant pause, the acidic environment within the phago-lysosome causes the maturation and replication of amastigotes. During the late stage of infection, replication is followed by virulent exit of intracellular amastigotes to re-infect other phagocytic cells (macrophages or dendritic cells). The mechanism of this spreading is not fully understood. It has been assumed that cell lysis of macrophage results in the release of free amastigotes. The transmission cycle is complete once the infected phagocytes and free amastigotes are consumed by a sandfly during the next blood meal.

1.3. Leishmaniasis

The interaction between amastigotes and macrophages is a key determinant for the clinical manifestation of leishmaniasis. The disease can be categorized into two main forms, cutaneous and visceral leishmaniasis (Table 1.2). Cutaneous leishmaniasis (CL) can further develop into Localized cutaneous leishmaniasis (LCL), Diffuse cutaneous leishmaniasis (DCL) and Muco cutaneous leishmanisis (MCL). LCL is the most common form of cutaneous disease and results in ulcerative lesions on the site of sandfly bite (Figure 1.5.A). The main species responsible for LCL are *L. aethiopica*, *L. major*, *L. tropica L. mexicana*, *L. amazonensis* and *L. braziliensis*.

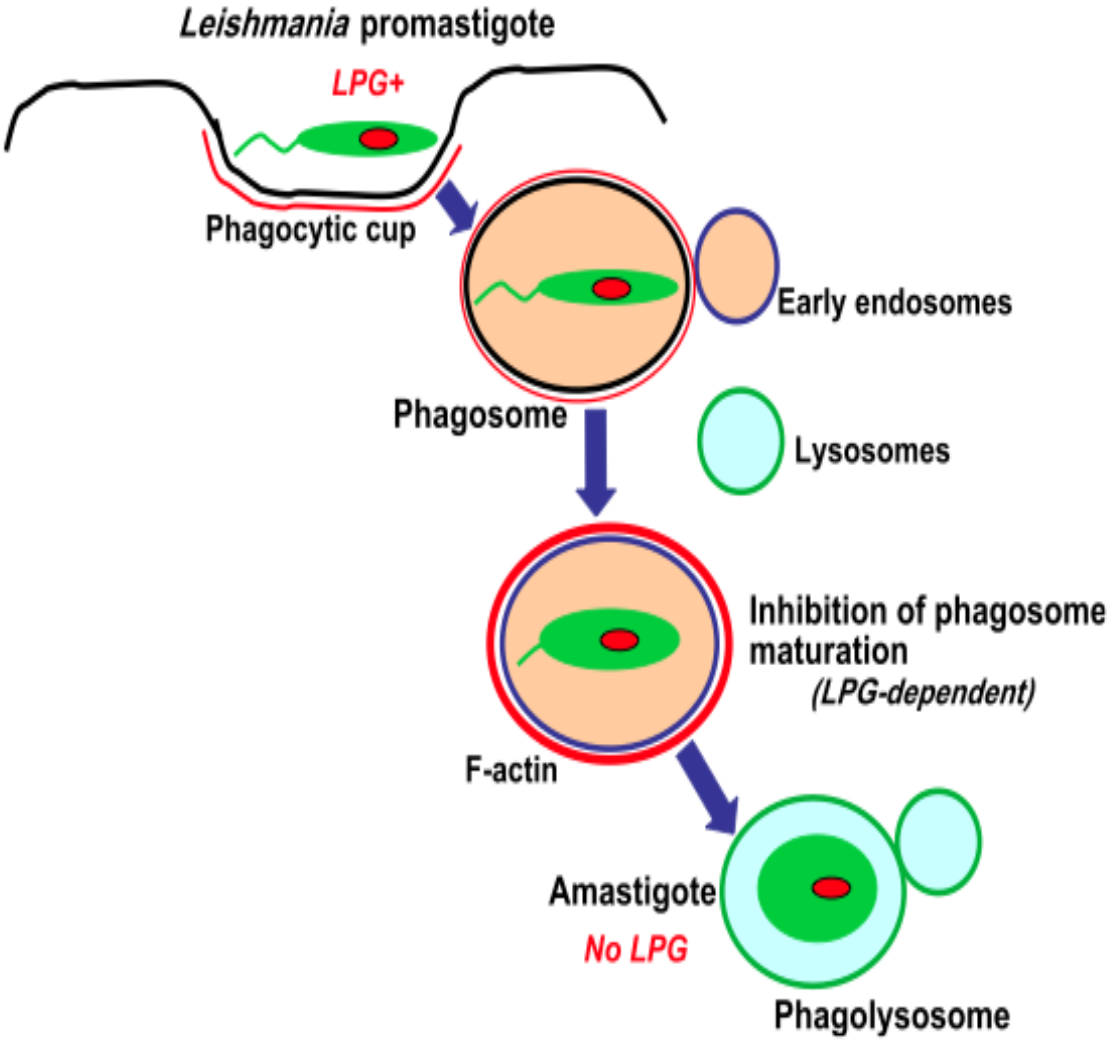


Figure 1.4. Interaction of *Leishmania* parasites with the phagocytic pathway of host macrophages. Following phagocytosis by macrophages, the promastigote is surrounded by the phagosome with additional accumulation of F-actin (red ring). Although the phagosome containing the parasite fuses with the early endosomes, the phagosome does not interact with the lysosomes until the promastigote differentiates into mature form of amastigote. Adapted from Lodge and Descoteaux, 2005.

	Disease	*Leishmania* species	Geographical distribution
Old world	Cutaneous	*L. aethiopica*	Ethiopia, Kenya
		L. major	North Africa, Middle east and Central Asia, Sub-saharan Africa and Sahel Belt
		L. tropica	Mediterranean coast
	Visceral	*L. donovani*	Indian subcontinent and Sudan
New world	Cutaneous	*L. mexicana*	Central America
		L. amazonensis	South America, North of Amazon
		L. panamensis	Panama and Colombia
		L. guyanensis	Pacific coast of South America
		L. braziliensis	South and Central America
	Visceral	*L. infantum*	Mediterranean basin, Middle east and Central Asia to Pakistan, China, Central and South America

Table 1.2. Classification of human leishmaniasis. Based upon clinical symptoms and pathology, the disease is mainly categorized into cutaneous (skin lesions) and visceral disease (organ failure and death). *Leishmania* species responsible for cutaneous and visceral leishmaniasis are linked with their geographical location. Adapted from Dawit et al., 2013.

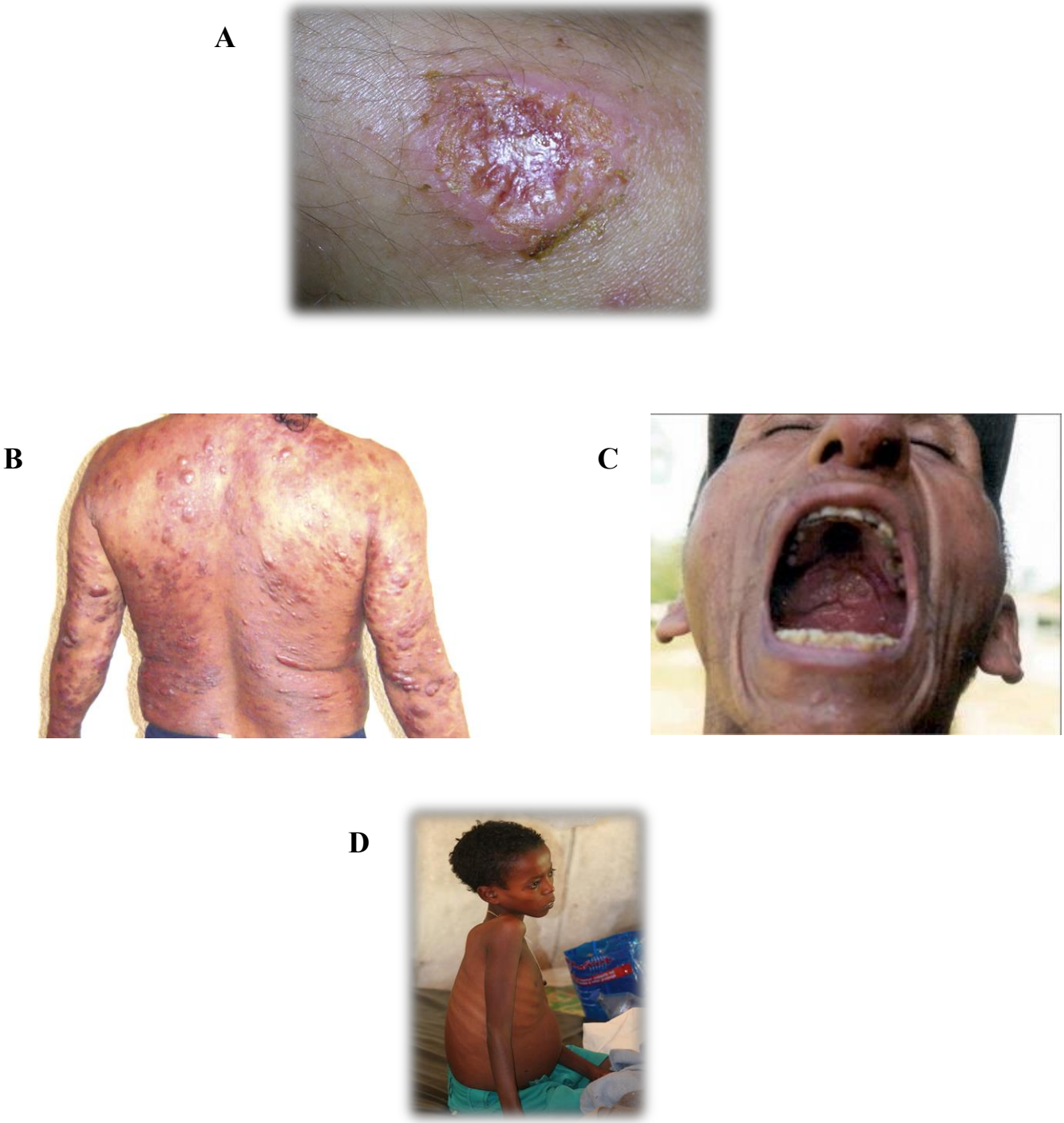


Figure 1.5. Major clinical pathologies associated with human leishmaniasis. (**A**) Localized cutaneous leishmaniasis. (**B**) Diffuse cutaneous leishmaniasis. (**C**) Muco cutaneous leishmaniasis. (**D**) Visceral leishmaniasis. Pictures for A and D were adapted from WHO, 2012 (www.who.int/leishmaniasis/clinical_forms_leishmaniasis). Pictures for B and D were adapted from Calvopina et al., 2006 and Reithinger et al., 2007, respectively.

DCL is an extensive and chronic form of CL, whereby multiple non-ulcerative nodules are found throughout the body (Figure 1.5.B). This is largely linked to an inefficient cell-mediated immune response against the leishmanial antigen (Desjeux, 1996). It is caused mainly by *L. aethiopica*, *L. mexicana* and *L. amazonensis* and is untreatable. MCL is characterized by the development of sores on the oronasal and pharyngeal mucosal membranes (Figure 1.5.C). This leads to facial mutilation and disfigurement and is mainly caused by *L. guyanensis*, *L. panamensis* and *L. braziliensis* and *L. aethiopica*.

Visceral leishmaniasis (VL), commonly referred to as "Kala azar", is the most severe form of the disease (Figure 1.5.D). The infected patient is more than likely to die (99% probability), if left untreated (Kumar and Nylen, 2012). Symptoms for VL include fever, extreme weight loss, anaemia, hepatosplenomegaly, pancytopenia and hypergammaglobulinaemia (Assimina et al., 2008). The main species responsible for VL are *L. donovani* (Indian subcontinent and Eastern Africa) and *L. infantum* (Mediterranean region and Latin America). Interestingly treatment of VL infected patients with antimonial drugs can lead to a dermal sequel of this specific disease called Post-Kala-azar Dermal Leishmaniasis (PKDL). PKDL appears to be caused by the host immune response against the latent parasites in the skin, which may have migrated from the VL infected organs (Ganguly et al., 2010). The disease is endemic in the Indian subcontinent and Sudan. Although, *L. donovani* is the major culprit in both regions, there are striking differences in the time intervals between VL cure and the onset of PKDL. The Indian PKDL occurs after 1-7 years (or even 20-30 years) after VL treatment, whereas the Sudanese PKDL arises concomitantly along with VL (Ganguly et al., 2010).

1.4. Expression of virulence factors in *Leishmania*

In order for the disease development, *Leishmania* needs to continually survive and replicate in hostile environments inside the mammalian host. This influences the parasite to express a number of specific virulence factors (Table 1.3). The unicellular membrane of *Leishmania* promastigotes consist of a densely coated glycocalyx that acts as an interface between the parasite and the extracellular environment (Smith and Rangarajan, 1995). Covering the entire surface of parasite, including flagellum, this complex coat is rich in lipophosphoglycan (LPG), proteophosphoglycan (PPG), glycoprotein 63 (GP63) and low molecular weight glycophosphatidylinositol lipids (GIPLs). These molecules are covalently attached towards the surface of the parasite via the glycosylphosphatidylinositol (GPI) lipid (Descoteaux and Turco, 1999).

LPG is the major surface glycoconjugate of promastigote and is expressed at approximately 5 x 10^6 molecules per cell (Franco et al., 2012). LPG consists of a terminal oligosaccharide chain cap, phosphoglycan polymer (6-Gal[β1,4]Man[α1]-PO_4) and glycan core region inserted into the membrane via a GPI lipid anchor (Figure 1.6). During promastigote to amastigote differentiation, LPG expression becomes downregulated by at least three orders of magnitude (Sacks, 1992). Analysis of LPG mutant parasite indicates that this molecule plays a critical role in establishing infection in macrophage through counteracting free radical production and complement mediated lysis, delays phagolysosome fusion and promoting an early non-protective IL-4 host response (Spath et al., 2003; Lodge et al., 2006; Liu et al., 2009; Moradin and Descoteaux, 2012).

Interestingly, the fact that LPG mutant promastigotes are still able to infect and replicate within phagocytes suggests the existence of LPG independent survival mechanism (McNeely and Turco 1990; Spath et al., 2003).

Virulence factor	Parasite stage expression	Functions
LPG	Promastigote (Pro/Met)	Protection against complement mediated lysis (Spath et al., 2003); Impairment in phagosome maturation (Moradin and Descoteaux, 2012); Inhibition of ROS production (Lodge et al., 2006)
GP63	Promastigote (Pro/Met) and Amastigote	Protection against complement mediated lysis (Brittingham et al., 1995); Degradation of anti-microbial peptides (Kulkarni et al., 2006); Initiates receptor mediated phagocytosis (Ueno et al., 2012); Alteration of various intracellular signaling pathways (e.g. PKC, MAPK, JAK-STAT, TLR-IRAK and mTOR) (Isnard et al., 2012)
PPG	Promastigote (Pro/Met)	Induction of arginase-1 expression to promote polyamine synthesis for parasite survival (Rogers, 2012)
CP	Promastigote (Met) and Amastigote	Cleavage of MHC class II gene product to inhibit antigen presentation (De Souza et al., 1995); Inhibition of IL-12 and NO production via NF-κb and STAT-1 degradation (Cameron et al., 2004; Abu-Dayyeh et al., 2010)
SP	Amastigote	Associated with downregulation of TLR and TNF receptors in macrophages (Swenerton et al., 2011)
PSA-2	Promastigote/Amastigote	Protection against complement mediated lysis (Lincoln et al., 2004)

Table 1.3. Summary of the diverse range of virulence factors expressed by *Leishmania*. LPG, Lipophosphoglycan; GP63, Glycoprotein 63; PPG, Proteophosphoglycan; CP; Cysteine Protease; SP, Serine Protease; PSA-2, Protein Surface Antigen; Pro, Procyclic; Met, Metacyclic; NO, Nitric oxide; ROS, Reactive Oxygen Species.

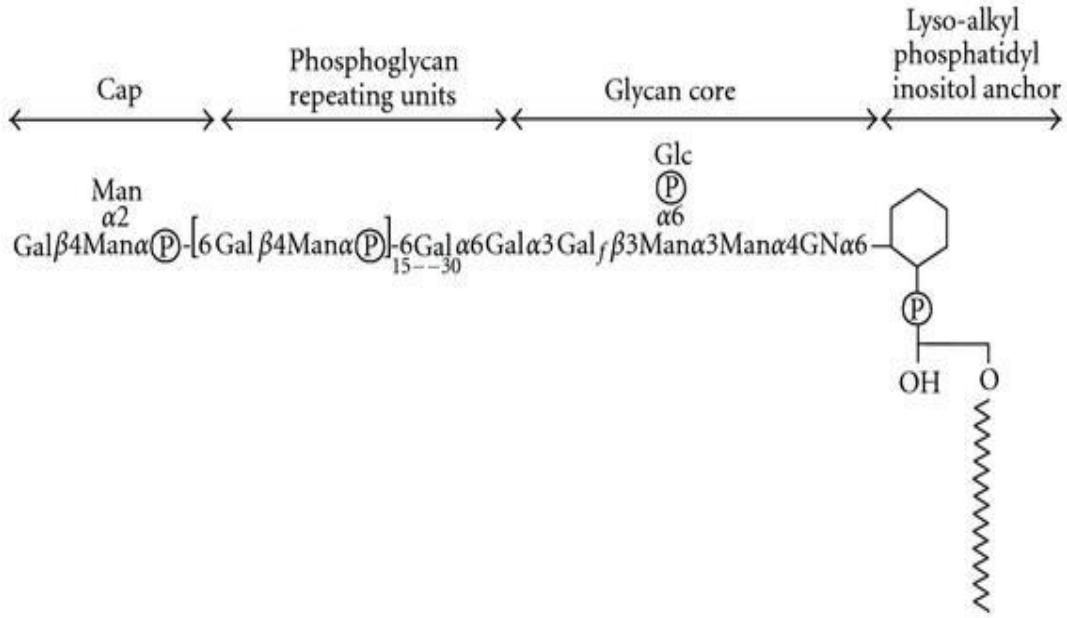


Figure 1.6. Structural organization of *Leishmania* Lipophosphoglycan (LPG). In general, LPG is composed of four domains (terminal cap, phosphoglycan repeating units, glycan core and GPI lipid anchor). In different species of *Leishmania*, the glycan core and lipid anchor remains conserved, whereas the cap structure and number of repeating phosphoglycan units becomes variable. Gal, galactose; Man, mannose; GN, glucosamine; Glc; glucose. Adapted from Franco et al., 2012.

This led to the identification of a zinc containing metalloprotease called GP63. One of the critical functions of GP63 is to prolong the parasite survival inside the phagolysosomes by altering the host macrophage signaling pathways such as JAK/STAT, MAP kinase and NF-κβ pathways (Isnard et al., 2012). Although GP63 is present both in promastigotes and amastigotes (Medina-Acosta et al., 1989), its expression is ten times higher in former than latter. Localized mainly at the parasite surface via the GPI anchor, this protein can also be secreted either through auto-proteolytic N terminal cleavage of GPI or direct release from the parasite vesicular trafficking (Ellis et al., 2002).

Similarly to GP63, another protein family called Cysteine peptidase (CP) is responsible for subverting NF-κβ signaling pathway. This resulted in the inhibition of IL-12 cytokine expression and nitric oxide production (Cameron et al., 2004; Abu-Dayyeh et al., 2010). The CP is grouped into five clans, of which clan CA family members (CPA, CPB and CPC) are the most studied due to their role in establishing host infection (Mottram et al., 2004). Expressed only in amastigotes, CPB has been clearly identified as the main virulence factor as its deletion alone caused reduced infection and fewer lesions in BALB/c mice, compared with wild type, CPA and CPC mutant parasites (Alexander et al., 1998).

Overall, the effect of the above *Leishmania* virulence factors is to disarm the microbicidal activity within macrophages. Interestingly, this effect also influences the generation of cytokines and chemokines from various other immune cells. Hence, it is very important to consider the interaction between parasite and other host immune cells.

1.5. Interaction between *Leishmania* and host immune cells

1.5.1. T cells

The involvement of T cells in regulating host immune response during leishmaniasis has been known since the late 19th century (Heinzel et al., 1989). Nevertheless, there are still contrasting views on the role of different T cells subset during *Leishmania* infection in humans (Alexander and Brombacher, 2012). This is due to large number of cases whereby patients with diverse genetic background are infected with various parasitic species, which can lead to a range of host clinical symptoms. T cells are mainly categorized into two different subsets, CD4+ and CD8+; with the former further divided into T helper 1 (Th1) and T helper 2 (Th2) cells.

Th1 cells are involved in the resolution and complete elimination of *Leishmania* (Sacks and Noben-Trauth, 2002). During infection, the binding between CD40 ligand of Th1 with CD40 receptor of macrophages causes IL-12 release from infected macrophages. The secreted IL-12 then stimulates the production of IFN-γ (from Th1 cells), which in turn activates macrophage mediated nitric oxide production to initiate parasite killing (Sacks and Noben-Trauth, 2002). These pathways are mainly observed on resistant C57BL/6 mice, where the infection site of *Leishmania* is rapidly healed. However, the parasite exposure in susceptible BALB/c mice leads to a non-healing chronic infection, which is supported by Th2 activation (Sacks and Noben-Trauth, 2002). Th2 cells are characterized as producing IL-4, IL-10 and IL-13 cytokines in response to Vβ4Vα8CD4+ T cells activation. From the above three secreted cytokines, IL-4 is of particular importance because it downregulates the expression of IL-12β2 receptor of Th1 cells during *L. major* infection of BALB/c mice, hence disabling IL-12 mediated Th1 response (Himmelrich et al., 1998).

Similarly, there appears to be a multifaceted role of CD8+ T cells during the

course of *Leishmania* infection (Stager and Rafati, 2012). Primed to kill any invading pathogenic microorganisms, CD8+ T cells display cytotoxicity towards infected cells via mechanisms involving secretion of toxic granules and TNF/Fas ligand induced apoptosis (Zhang and Bevan, 2011). In the context of *L. major* infection in mice, INF-γ production from CD8+ T cells were directly responsible for activating Th1 mediated healing response (Uzonna et al., 2004). However, this phenomenon appeared to be dependent on parasite inoculation as high concentration of *L. major* promastigotes had no impact on CD8+ T cell activation, even though the lesion healed via Th1 response (Uzonna et al., 2004). During visceral leishmaniasis in mice, the CD8+ T cells induced cytotoxic activity towards infected cells through FasL/Fas mediated apoptosis, followed by INF-γ and TNF-α secretions (Tsagozis et al., 2003). However, the authors also observed secretion of pro-inflammatory chemokines, such as MIP-1α (Macrophage Inflammatory Protein-1) and RANTES (Regulated on Activation Normal T cell Expressed and Secreted) from CD8+ T cells in response to *L. infantum* infection, which severely questions the protective nature of CD8+ T cells.

1.5.2. Natural Killer (NK) cells

During *Leishmania* infection, NK cells are activated in response to various cytokines such as IL-12 (from myeloid dendritic cells), IL-2 (from Th1 cells), IFN-α/β and IL-18 (from macrophages) (Bogdan, 2012). NK cells are engaged in protective immune response against *Leishmania* parasites. For example, in cutaneous leishmaniasis in mice, NK cells depletion prevented the elimination of *L. amazonensis* (Laurenti et al., 1999; Sanabria et al., 2008). As for visceral disease, it was shown that mice NK cells activated by IL-12/IL-18 released INF-γ and TNF-α, which in turn led to the nitric oxide production in *L. infantum* infected macrophages and subsequent parasite death (Prajeeth et al., 2011).

1.5.3. Neutrophils

Neutrophils are the first immune cells involved in the phagocytosis of *Leishmania* (Peters et al., 2008). In addition to hosting the parasite, neutrophils are thought to act as a Trojan horse for the transfer of *Leishmania* into macrophages (Figure 1.7). The model suggest that promastigotes delay spontaneous apoptosis of infected neutrophils for 2-3 days after which the infiltrating macrophages are able to phagocytize the apoptotic neutrophil harboring promastigotes (Laskay et al., 2003). However, conflicting evidence have been emerging that challenge this model. For example, NET released by human neutrophils was found to be effective in direct killing of *L. amazonensis* promastigotes (Guimaraes-Costa et al., 2009). Similarly, *L. major* was susceptible to neutrophil elastase mediated activation of macrophage in C57BL/6 mice (Ribeiro-Gomez et al., 2007). In summary, the exact role of neutrophils on *Leishmania* infection needs future investigation.

1.5.4. Macrophages

Macrophages are the definitive host cells for *Leishmania* survival and replication. With a distinctive pseudopodia membrane structure, macrophages are involved in the phagocytosis and subsequent killing of foreign microbes (Dale et al., 2008). However, intracellular pathogens such as *Leishmania* have evolved strategies to counteract the microbicidal activity of macrophages. In order to understand how such potent killing ability is inactivated, the precise molecular events that take place in the early, intermediate and late phase of *Leishmania* infection will be discussed in the following section.

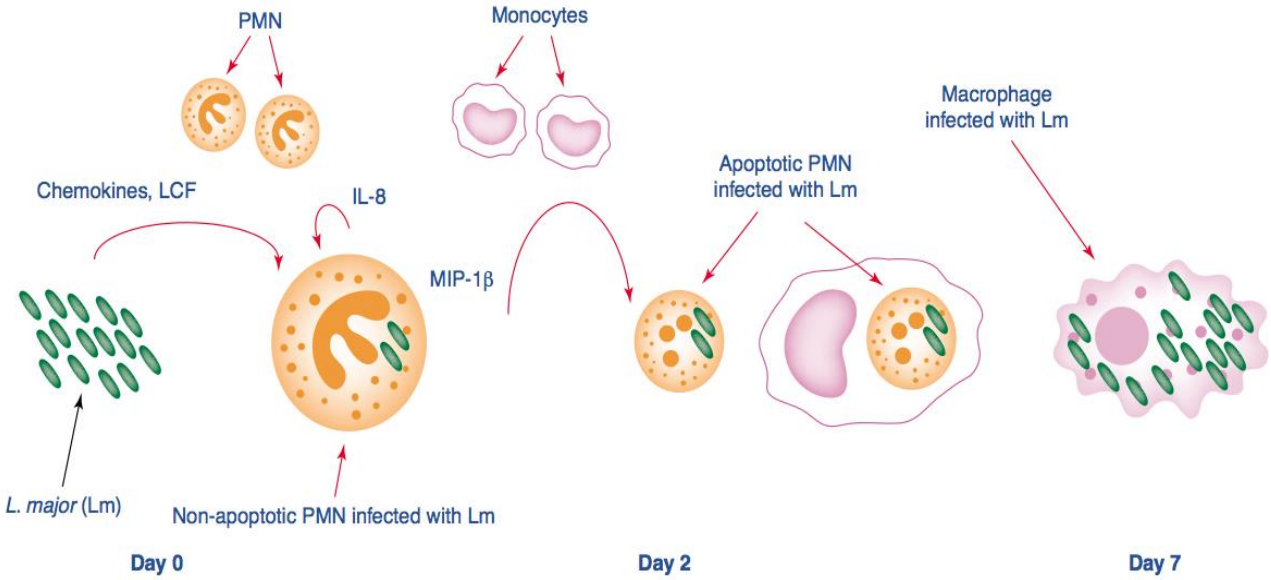


Figure 1.7. Trojan horse model for neutrophils. *Leishmania* promastigotes, which are inoculated by the sandfly, are primarily phagocytized by neutrophil (PMN). The promastigotes delays apoptosis of the infected neutrophils for 2 days, giving monocytes/macrophages enough time to enter the site of infection. After 2 days, the apoptotic neutrophils (containing promastigotes) are phagocytized by macrophages. In this way, promastigotes silently enter and replicate within macrophages without activating its microbicidal activity. Adapted from Laksay et al., 2003.

1.6. Molecular interaction between *Leishmania* and macrophage

1.6.1. Phagocytic uptake of *Leishmania*

The primary survival mechanism for metacyclic promastigote is to be engulfed by macrophages through receptor mediated phagocytosis (Ueno and Wilson, 2012). Receptors that are known to facilitate the phagocytosis of metacyclic promastigote include the complement receptor family (CR3 and CR1) and fibronectin receptor (FnR) (Figure 1.8); all of which will be discussed below.

CR3 is an integrin, which is comprised of complement and lectin binding sites (Quinton-Leslie, 2001). Localized on the surface of macrophage and neutrophil, the function of CR3 ranges from binding to inactivated complement (iC3b) and pathogen ligands to assisting phagocyte migration and actin cytoskeletal rearrangement. The promastigotes GP63 is responsible for binding with CR3 either directly on the lectin domain or indirectly to the complement binding sites via iC3b opsonin (Blackwell et al., 1985; Mosser and Wilson, 1985). The iC3b is generated following CR1 mediated cleavage of C3b opsonin (Sutterwala et al., 1996; Rosenthal et al., 1996).

Similar to CR3, the FnR can either bind directly or indirectly (via fibronectin opsonin) to the GP63 ligand of promastigote (Brittingham et al., 1999). FnR is an integrin comprised of alpha and beta subunits, which is found in immune (e.g. monocytes and macrophages, neutrophils) and non-immune (e.g. fibroblast) cells. Interestingly, GP63 is responsible for the degradation of fibronectin opsonin to generate ICS (Interconnecting Segment) fragment (Kulkarni et al., 2008). This resulted in the binding between GP63 and ICS that prevented the superoxide production while still allowing FnR mediated phagocytosis (Kulkarni et al., 2008).

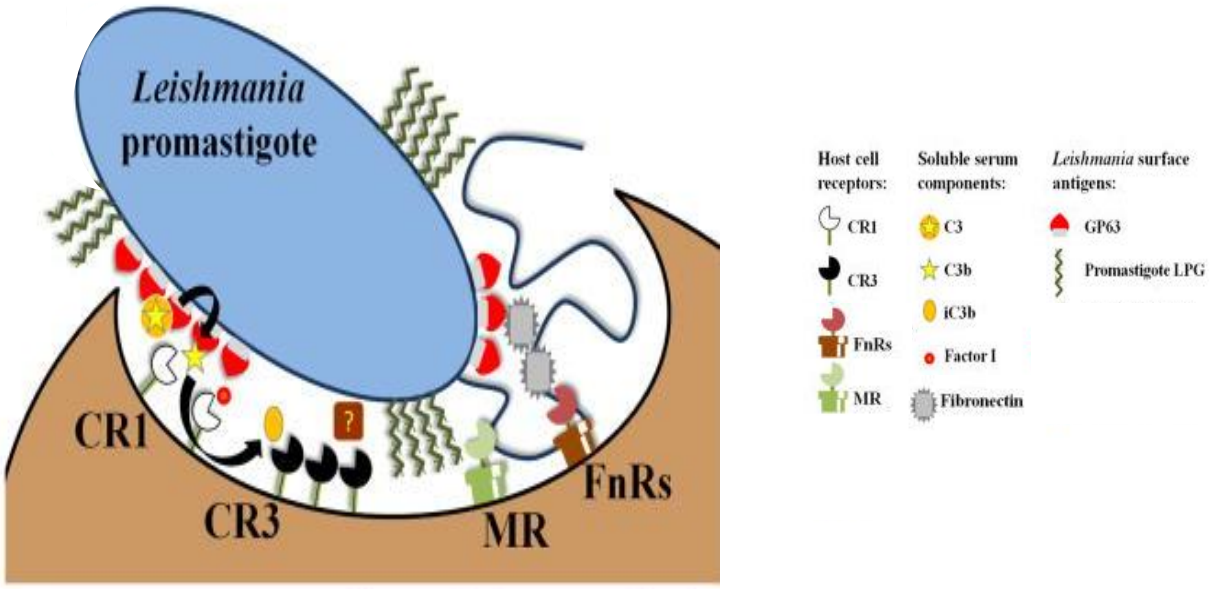


Figure 1.8. Two different types of receptor mediated approach undertaken by macrophage to phagocytize metacyclic promastigote. The GP63 expressed in promastigotes convert C3 opsonins into C3b, the natural ligand for Complement Receptor 1 (CR1). CR1 (with factor I) cleaves C3b into iC3b, which acts as a bridge between GP63 and CR3. CR3 may also mediate direct binding to promastigotes via a yet unknown surface epitope on promastigotes, possibly Protein Surface Antigen (PSA-2). GP63 also binds fibronectin, which then bridges the parasite to Fibronectin Receptor (FnR) for phagocytosis. It should be noted that Mannose Receptor (MR) is only involved in phagocytosis of procyclic promastigotes. Adapted from Ueno and Wilson, 2012.

1.6.2. Survival strategy for *Leishmania*

Following phagocytosis, *Leishmania* promastigote builds a safe niche within the infected macrophages. In order to achieve this, the LPG of promastigote delays the fusion of endosomes and lysosomes (Dermine et al., 2000; Rodriguez et al., 2011). In addition, the promastigote induces the accumulation of various actin polymerisation molecule including F-actin, Arp2/3, WASP and α-actinin around the phagosomes. Similarly, families of Rho GTPase, such as RhoA, cdc42 and Rac-1 have also been retained within the phagosome during phagocytosis (Lodge and Descoteaux, 2008). Although the reason behind the accumulation of these various molecules is unclear, it may block the recruitment of vesicle trafficking proteins required for phagolysosome formation, hence contributing to the survival of parasites (Figure 1.9).

1.6.3. Modulation of intracellular signaling pathways during *Leishmania* infection

Successful inhibition of lysosome fusion represents the earliest survival strategy of *Leishmania*. However, in order to further evade the host immune response, the parasite interferes with many signaling pathways of the macrophages (Table 1.4). The Nuclear Factor (NF)-κβ transcription factor, which is the master regulator of innate immunity, is one of the targets for *Leishmania*. The family of NF-κβ is comprised of five subunit members including: Rel-A (p65), c-Rel, Rel-B, p50 and p52, of which the first three possess higher transactivation domain activity than the latter two. In un-stimulated cells, the subunit dimer (mainly p65-p50) is bound to an inhibitor IκBα. Following stimulation, the degradation of inhibitor releases the dimer, which translocate into the nucleus to induce gene expression of various inflammatory cytokines and chemokines (Figure 1.10).

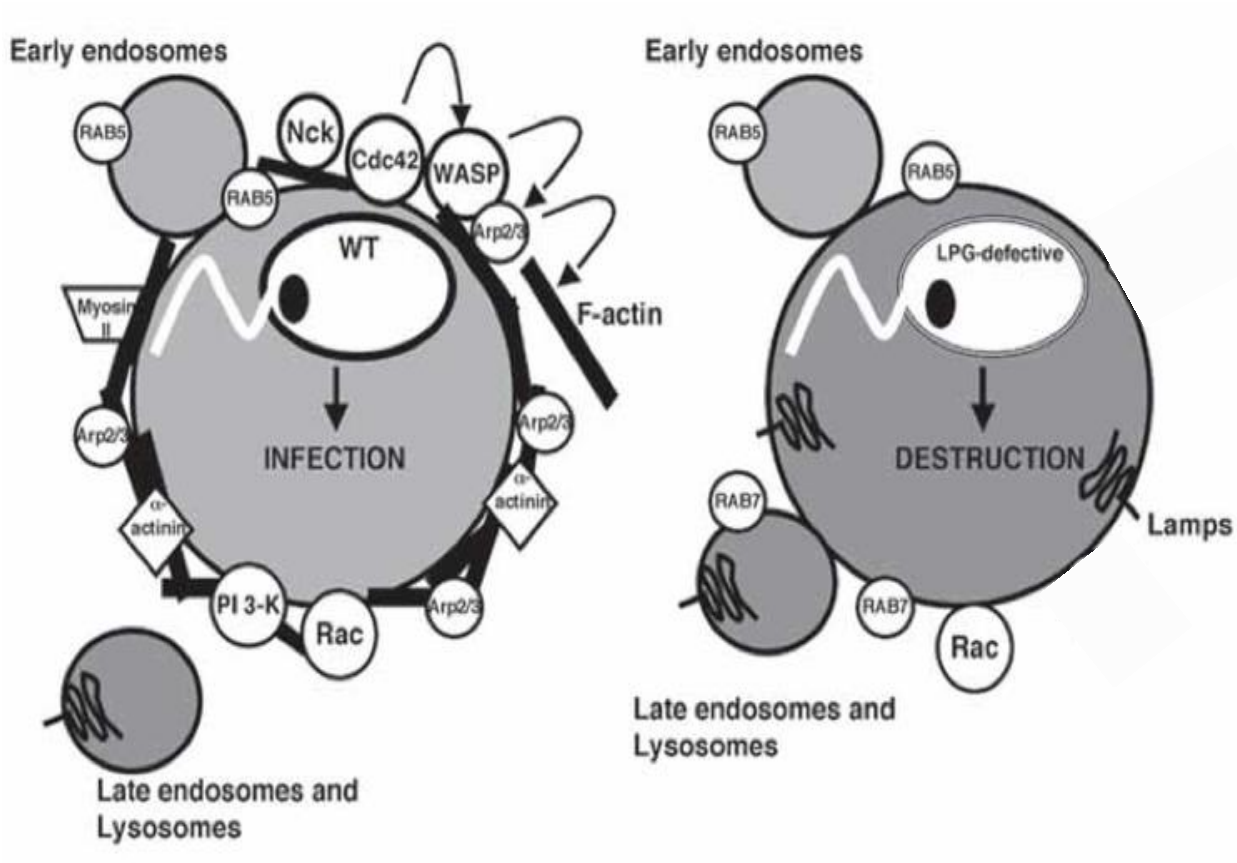


Figure 1.9. Schematic representation showing the differences in the molecular interaction of endosomal vesicles with the Wild type (Wt) and LPG defective (mutant) *Leishmania* promastigote. Within minutes from phagocytosis, both Wt and mutant parasites are localized inside the phagosome and interacts with the early endosomes. However, in contrast to mutant, the Wt induces F-actin accumulation through recruitment of Cdc42, WASP and Arp2/3. It is thought that accumulation of the above molecules around the phagosome may delay the recruitment of LAMP and RAB7 (markers for late endosomes and lysosomes), subsequently delaying the fusion between phagosome and acid hydrolase containing lysosomes. This inhibition of lysosome fusion would allow the virulent promastigote to survive. As for mutant form, there is a rapid recruitment of LAMP and RAB7 associated lysosomes resulting in the destruction of the parasites. Adapted from Lodge and Descoteaux, 2008. WASP, Wiskott-Aldrich Syndrome Protein; LAMP, Lysosome-associated membrane glycoprotein; Nck, Non-catalytic region of tyrosine kinase adaptor protein 1; PI3-K, Phoshpoinositide 3- kinase

Signaling pathways	Macrophage function	*Leishmania* mediated alteration
Protein Kinase C (PKC)	Production of reactive oxygen species (ROS)	Downregulation of PKC expression, which reduces phosphorylation of p67 and p47 subunits of NADPH oxidase (Bhattacharya et al., 2001). This leads to inhibition of ROS production.
JAK/STAT	Production of nitric oxide (NO)	De-phosphorylation of JAK (via phophatase activation) and/or proteasome mediated STAT degradation causes reduced translocation of transcription factors necessary for NO production (Blanchette et al., 1999; Forget et al., 2005).
ERK1/2 and p38 MAPK	Induction of inflammatory cytokines	Downregulation of p38 MAPK leads to IL-12 inhibition whereas activation of ERK1/2 leads to IL-10 secretion (Mathur et al., 2004; Yang et al., 2007).
NF-κB	Induction of inflammatory cytokine and NO production	Degradation of p65 NF-κB subunit results in IL-10 expression and inhibits IL-12 and NO production (Cameron et al., 2004; Guizane-Tabbane et al., 2004; Calgeri-Silva et al., 2009).

Table 1.4. Summary of the diverse macrophage signaling pathways altered by *Leishmania*. JAK/STAT, Janus Kinase/Signal Transducer and Activation of Transcription; ERK, Extracellular Regulated Kinase; MAPK, Mitogen Activated Protein Kinase; NF-κB, Nuclear Factor kappa B; SHP-1,

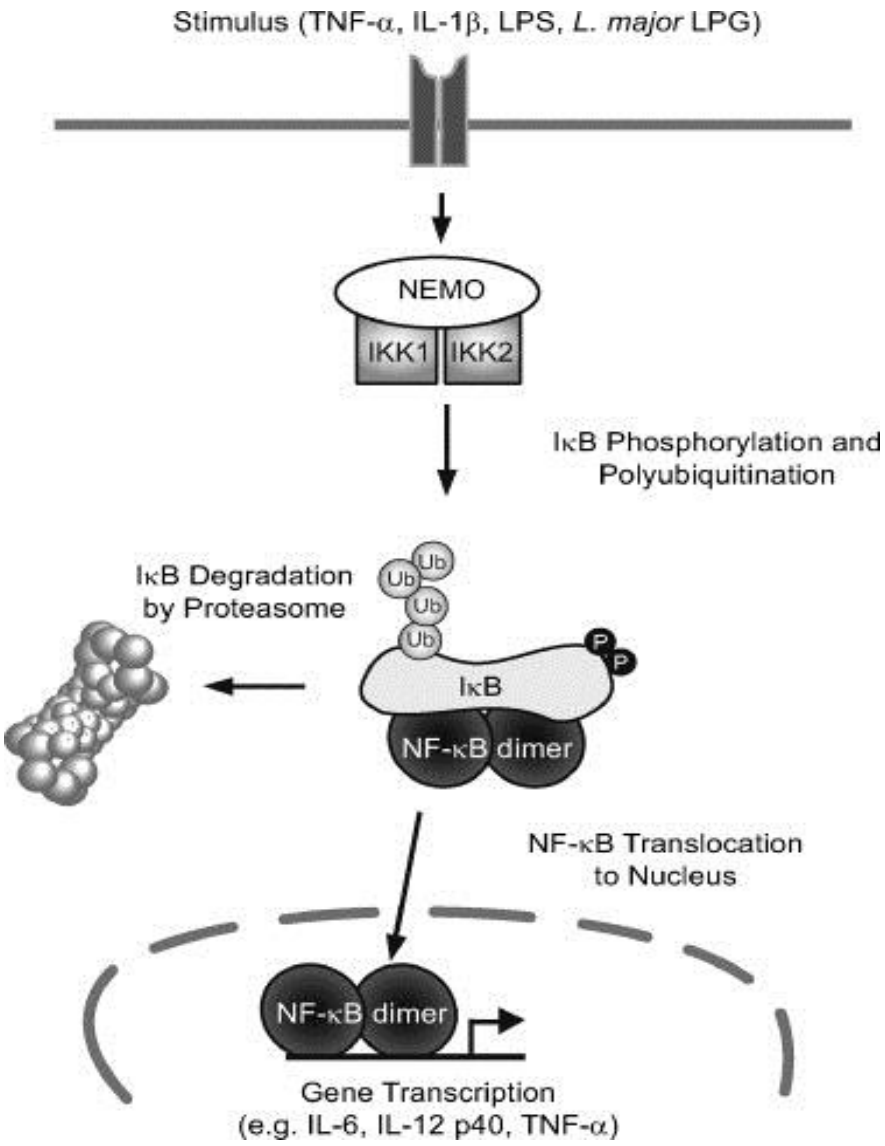


Figure 1.10. Upstream and downstream effectors in NF- κB signaling pathway. Initially, NF- κB dimer is inactivated due to its binding with an inhibitory IκB protein in un-stimulated cells. In the presence of diverse range of stimuli including, TNF-α, IL-1β, LPS and LPG, the activated receptor transduces the signal towards the IKK complex (NEMO, IKK1 and IKK2). The complex phosphorylates two serine residues of IκB, which targets IκB for ubiquitination and subsequent proteosomal degradation. This causes the release of NF- κB dimer, which translocate to the nucleus to induce the transcription of various gene targets. NF- κB, Nuclear Factor-kappa B; TNF, Tumor Necrosis Factor; IL-1, Interleukin-1; LPS, Lipopolysaccharide; LPG, Lipophosphoglycan. Adapted from Reinhard et al., 2012.

Both promastigotes and amastigotes form of *Leishmania* modulate NF-κβ signaling response. For example, *L. amazonensis* promastigotes were shown to activate the p50-p50 dimer (repressor complex) while causing degradation of p65 proteins at the same time of infection, hence resulting in reduced iNOS genes expression required for NO production (Calegari-Silva et al., 2009). Similarly, a study involving wider range of promastigote species including *L. major*, *L. mexicana*, *L. donovani* and *L. braziliensis* found that all parasites cleaved p65 into p35 subunit, which in turn dimerized with p50 (Gregory et al., 2008). This heterodimer induces various chemokines (examples: MIP-1α, MIP-1β and MCP-1) that cause recruitment of phagocytes (without activating iNOS genes) and eventual tissue destruction (Gregory et al., 2008). In another study, degradation of p65 was also observed during *L. major* and *L. mexicana* amastigotes infection resulting in the induction of IL-10 (Guizane-Tabbane et al., 2004) and inhibition of LPS induced IL-12 production (Cameron et al., 2004), respectively.

In summary, the above findings have provided substantial evidence of *Leishmania* capability to manipulate the signaling pathways of host macrophages. Both promastigotes and amastigotes survive by downregulating of pro-inflammatory cytokines, NO production and upregulating anti-inflammatory cytokines (Summarized in Figure 1.11).

1.6.4. Dissemination of *Leishmania*

Following the intracellular survival and replication of amastigotes, *Leishmania* parasite must disseminate from infected to neighboring uninfected macrophages. This process of cell-to-cell spreading is a critical step for the development of leishmaniasis pathogenesis.

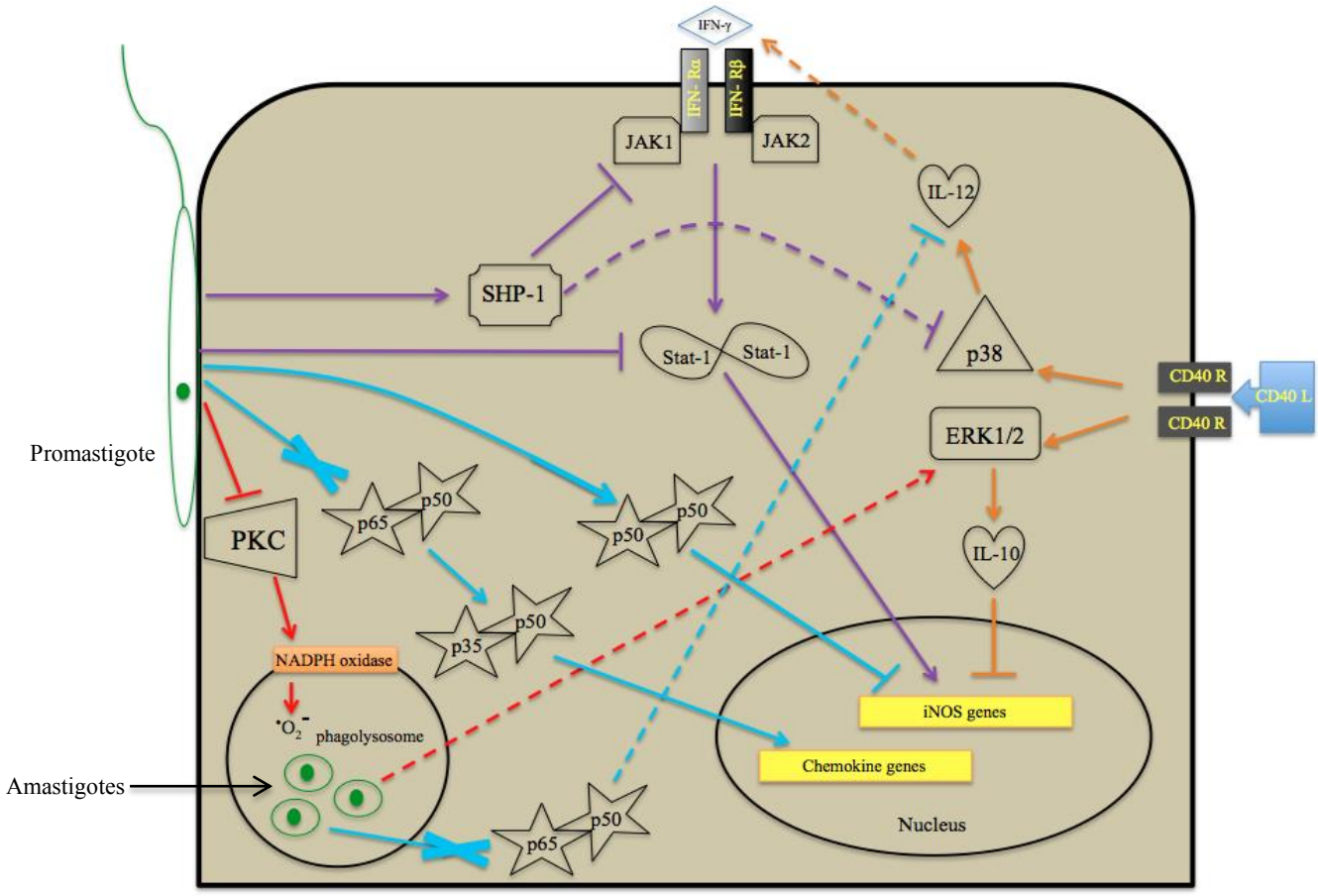


Figure 1.11. Schematic diagram representing the disruption of macrophage signaling pathways during *Leishmania* infection. The promastigotes and amastigotes modulates various signaling molecules associated with inflammatory pathways including PKC (red line), JAK-STAT (purple line), MAPK (orange line) and NF-κβ (blue line). Briefly, the promastigote inhibits PKC, resulting in the defective formation of NADPH oxidase and blocking superoxide radical production, which leads to survival of replicating amastigotes inside phagolysosome. Similarly, the promastigote can directly or indirectly (via SHP-1 activation) prevent IFN-γ stimulated Stat-1 dimer translocation that leads to repression of iNOS genes required for NO production. Moreover, SHP-1 activation is responsible for the de-phosphorylation of p38 (member of MAPK). This inhibits IL-12 production which in turn reduces IFN-γ release from T cells. Interestingly, amastigotes induces ERK1/2 mediated IL-10 production, which suppress iNOS gene expression. Finally, both forms of *Leishmania* degrade p65 subunit of NF-κB to induce chemokine genes expression and suppress the IL-12 production. Additionally, the promastigote also activate the p50-p50 dimer in order to inhibit iNOS gene expression. Dotted lines represent cross talk between two signaling pathways. PKC, Protein Kinase C; JAK-STAT, Janus Kinase – Signal Transduction of Activated Transcription; MAPK, Mitogen Activated Protein Kinase; NF, Nuclear Factor; SHP-1, Src-homology 2 domain containing Phosphatase -1; IFN, Interferron; IL, Interleukin.

It has been generally assumed that parasitic egress occurs via host cell lysis following amastigote replication. However, a recent study showed that the released *L. amazonensis* amastigotes remained surrounded by host membranes until engulfed by uninfected macrophages (Real et al., 2014). This finding was linked with an *in vivo* study from Belkaid and colleagues (Belkaid et al., 2000). By infecting C57BL/6 mice with low dose of *L. major* promastigotes, the authors detected a sharp increase in parasite number for first four weeks after infection without accompanying any inflammatory lesions (Figure 1.12). This silent phase could be representative of apoptotic mediated parasite spreading. Apoptotic cell death is the removal of damaged or dying cells without eliciting host immune response. Hence, it is be possible to speculate that the parasite could hijack the mechanism of apoptosis of infected macrophage and hide inside the apoptotic bodies without alerting the host adaptive immunity.

Therefore the physiological significance of apoptosis (section 1.7) and its current role during pathogenic infection (section 1.8) will be discussed before exploring the relationship between *Leishmani*a infection and host cell apoptosis (section 1.9).

1.7. Apoptosis

Apoptosis is an evolutionary conserved process of cell death, which occurs in a controlled manner. Apoptosis allows the elimination of dead cells without causing any damage to the surrounding cells, therefore avoiding inflammation and any consequent immune response (Danial and Korsmeyer, 2003).

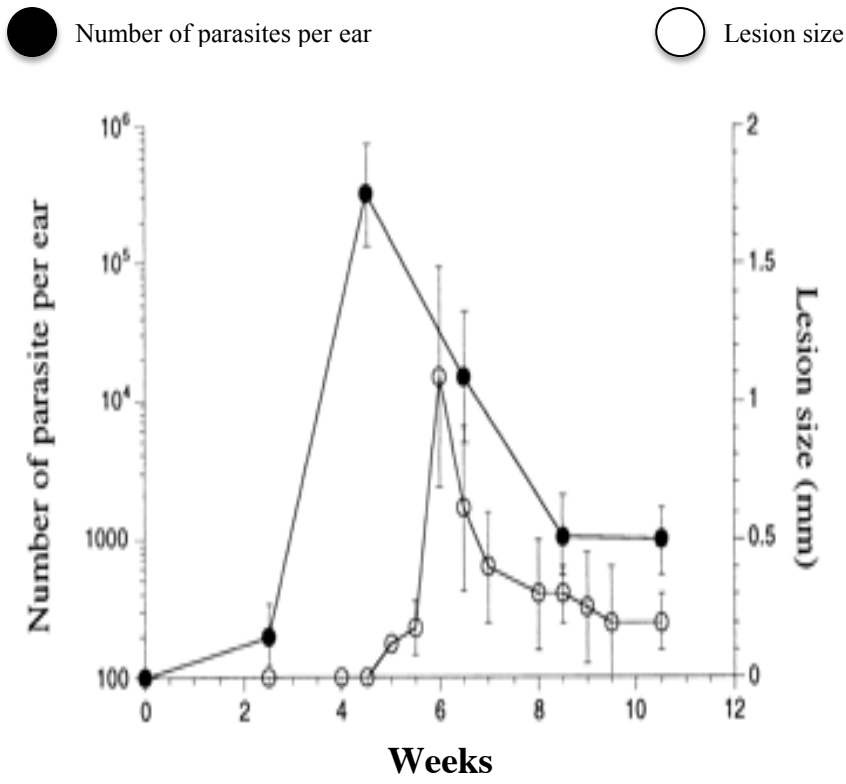


Figure 1.12. Evolution of dermal lesions in C57BL/6 mice during *Leishmania* infection. Intradermal inoculations with *L. major* metacyclic promastigotes (~100) were carried out on both ears of C57BL/6 mice. The numbers of parasites and lesion size were monitored and examined every 2 and once a week, respectively, over a period of 10.5 weeks. From week 2 to 4, a dramatic rise in the parasitic load per ear was observed without accompanied by any lesion development. The first appearance of lesion (1±0.5mm) was detected at week 6 and was coincident with a dramatic reduction (~95%) in parasite number from week 4 to 9. The lesion development was resolved before week 12. Adapted from Belkaid et al., 2000.

The characteristic features of apoptotic cells include plasma membrane blebbing, changes in the distribution of membrane lipids and enzymatic fragmentation of chromosomal DNA (Green, 2005). The significance of apoptosis has been well characterized in the development of mammalian homeostasis from removal of tissue cells between the developing finger digit of the fetus to removal of self-reactive T and B-lymphocytes (Jacobson et al., 1997).

There are two main signaling pathways, which participate in the induction of apoptosis. These are extrinsic and intrinsic pathways (Figure 1.13). The extrinsic pathway involves the activation of death receptors whereas the intrinsic pathway is activated intracellularly in response to cellular stress such as UV radiation and DNA damage. Although the source of activation is distinct, both pathways utilize specialized mediators of cysteine proteases called caspases, which are synthesized as inactive pro-caspase (Siegel, 2006). There are two groups of caspases involved in apoptosis; initiator and executioner caspases (Kumar, 2007). As their name suggest, the initiator caspases (e.g. caspase 2, 8, 9, 10 in humans) are the first caspase to be generated from the proteolytic cascade, whose role is to cleave and activate other pro-caspase, i.e. executioner caspases. The executioner caspases (e.g. caspase 3, 6 and 7 in humans) then cleave varieties of target proteins associated with the structure and integrity of cell membrane and DNA (Kumar, 2007). The engagement of caspases during extrinsic and intrinsic pathways will be discussed below.

The extrinsic pathway is initiated following the activation of death receptors. Homo-trimer in nature, this type of receptors is a member of large TNF receptor super family, which includes Fas and TNF receptor itself (Aggarwal, 2003).

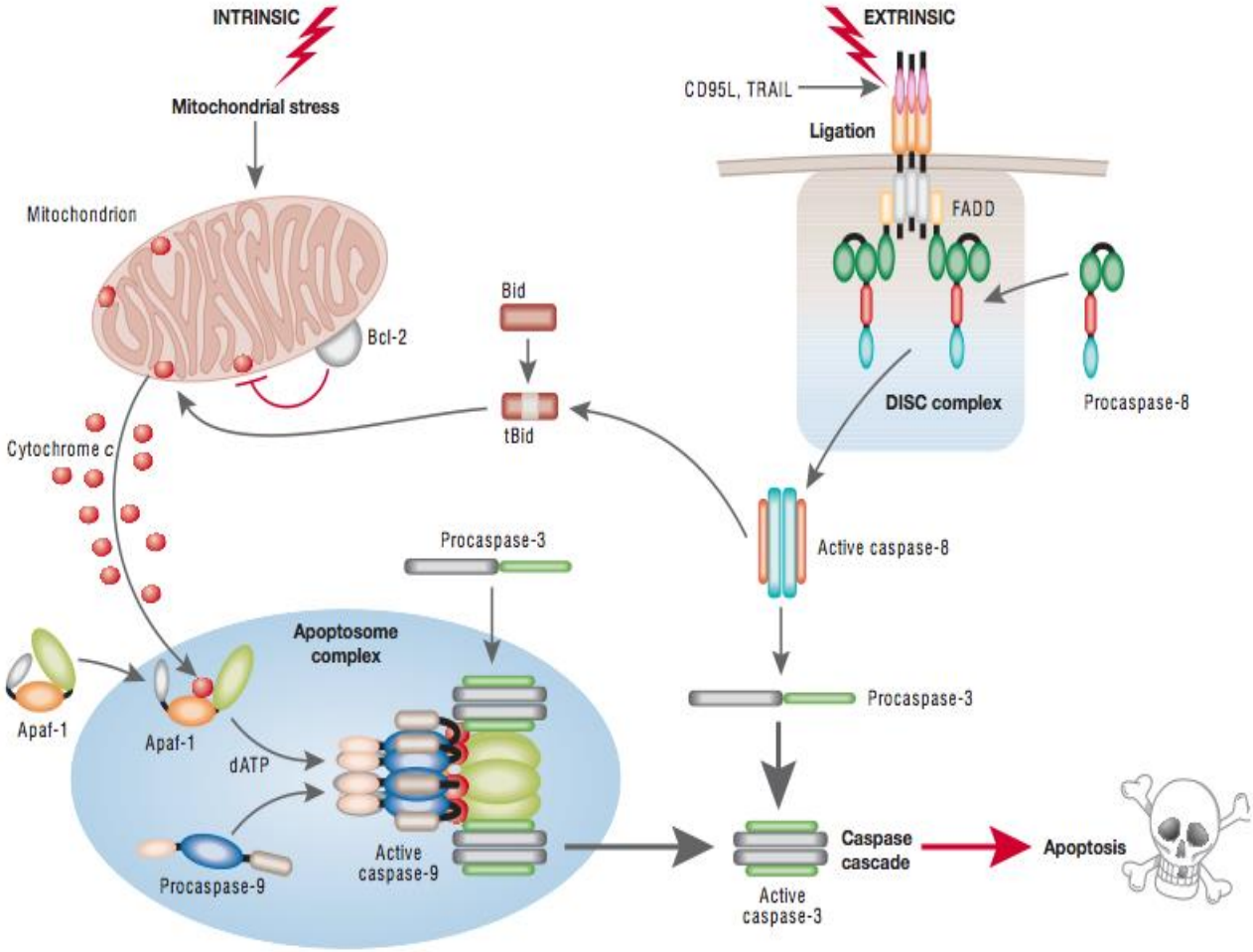


Figure 1.13. Mechanism of apoptosis is comprised of extrinsic and intrinsic pathways. Extrinsic and intrinsic pathways are activated by death receptors and stress-inducing stimuli, respectively. Briefly, triggering of death receptors, i.e. TNF and TRAIL receptors, initially causes rapid activation of the initiator caspase-8 following the DISC formation. Similarly, in the intrinsic pathway, stress induced apoptosis results in perturbation of mitochondria, releasing cytochrome c from the inner mitochondrial membrane space. The cytochrome c, which is regulated by anti-apoptotic Bcl-2 and pro-apoptotic Bax family members, binds to Apaf-1 resulting in the formation of Apaf1-caspase 9 apoptosome complex and activation of caspase-9. The activated initiator caspases 8 and 9 then activate effector caspases 3, 6 and 7, which are responsible for the cleavage of cellular substrates resulting in the classical biochemical and morphological changes associated with apoptotic phenotype. Adapted from Macfarlane and Williams, 2004.

For example, in Fas mediated apoptosis, trimers of Fas ligand binds to Fas receptor and results in clustering of death domain (MacFarlane and Williams, 2004). This allows the death domain to recruit a specific type of adaptor protein called FADD (Fas-associated via death domain), which comprises of death domain and death effector domain (DED). The death receptor and FADD bind via the death domain, leaving DED to recruit the initiator pro-caspase-8 (Figure 1.13). The resulting formation of complex between death receptor, adaptor protein and caspase is called Death Inducing Signaling Complex (DISC). Within the DISC, the initiator pro-caspase-8 molecules are brought into close proximity, resulting in self-activation. Once activated, the initiator caspase 8 is released from the DISC and leads to downstream activation of executioner pro-caspases (Macfarlane and Williams, 2004).

In contrast, the activation of the intrinsic pathway depends upon the release of mitochondrial protein known as cytochrome C (Jiang and Wang, 2004). During cellular stress, cytochrome C is released from the inter-membrane space of mitochondria to the cytoplasm and binds to an adaptor protein called Apaf-1 (apoptotic protease activating factor-1). Each Apaf-1 (bound with cytochrome C) then oligomerizes with the remaining six Apaf-1 proteins to form a wheel like heptamer called an apoptosome (Figure 1.13). The Apaf-1 in the apoptosome then recruits initiator pro-caspase-9, which are activated by close proximity in the apoptosome. The activated caspase-9 then cleaves and further activates the downstream executioner caspases (Kumar, 2007).

Similar to various biological processes, the intrinsic pathway of apoptosis is tightly regulated to ensure that a cell death occurs only when there is an apoptotic stimulus. There are two major regulators of intracellular proteins, which include: Bcl-2 family and IAP (Inhibitors of Apoptosis). The Bcl-2 family comprise of pro-apoptotic (e.g. Bax, Bak, Bad, Bid, Bim) and anti-apoptotic (e.g. bcl-2 and bcl-xl)

members. In addition, the pro-apoptotic group is further divided into two classes; BH123 (e.g. Bax and Bak) and BH-3 only proteins (e.g. Bad, Bim, Bid, Puma and Noxa). The inactive forms of BH123, which are membrane bound, aggregates and oligomerize to form a pore in the presence of an apoptotic stimulus, resulting in cytochrome C release (Danial, 2007). In the absence of an apoptotic stimulus, the anti-apoptotic bcl-2 proteins, which are located in the cytosol, directly inhibit the BH123 proteins (Danials, 2007). It has been proposed that an apoptotic stimulus activates the BH3-only protein and directly inhibits the anti-apoptotic bcl-2 protein by binding via the BH3 domain. Since the inhibition effect of bcl-2 protein is removed, the BH123 protein becomes activated, thereby releasing cytochrome C and inducing apoptosis (Shamas-Din et al., 2011). Finally, IAP is a group of cytosolic protein that provides further regulation in the intrinsic pathway. The mechanism of inhibition by IAP is either through direct binding or marking caspases with ubiquitin for proteasome degradation (Wei et al., 2008). However, in the presence of an apoptotic stimulus, anti-IAP (e.g. Smac/Diablo and Omi) is also released from mitochondria via the oligomeric pore of BH123 protein (Wei et al., 2008). These anti-IAP proteins bind and block the inhibitory activity of IAP, triggering caspase activation and apoptosis.

1.8. Infection and Apoptosis

The innate immune effector cells such as macrophages kill foreign microbes through phagocytosis and helps to prime the development of adaptive immunity, leading to the prevention of excessive tissue damage. In failure to eliminate infecting pathogens, macrophages will be programmed to undergo apoptosis as a last resort to resolve the infection. However, intracellular pathogens have evolved strategies to regulate host apoptosis (Thi et al., 2012). Depending upon the source and stage of infection, intracellular pathogens can either block apoptosis to protect its intracellular

niche or induce apoptosis to disseminate its progeny and evade the immune system (Swanson and Fernandez-Moreira, 2002; Thi et al., 2012). The following section will include findings that have been reported for bacterial, viral and protozoan infection and eventually discuss the current insight of how *Leishmania* species subvert apoptosis.

Pathogenic bacterial species, including *Legionella*, *Helicobacter* and *Chlamydia* are known to inhibit apoptosis to facilitate intracellular replication, whereas, *Yersinia* is known to only promote host cell apoptosis (Ashida et al., 2011). Interestingly, *Mycobacterium tuberculosis* exerts two distinctive strategies during macrophage infection to control cell death; the pathogen postpones cell death during early infection (Miller et al., 2010) but induces cell death in the later stage of infection to promote bacterial egress (Aguilo et al., 2013).

Similarly the balance between survival and apoptosis is also found in viral infected cells. Adenovirus, which is responsible for upper tract respiratory infection in humans, utilizes its transcription factor E1b 19k protein (homologue of bcl-2 protein) to suppress FasL and TNF induced apoptosis by inhibiting the activation of caspase-3 and processing of caspase substrate called PARP (O'Brien, 1998). However, the virus also encodes pro-apoptotic death proteins, such as E311.6 K and E4orf4 during the later stage of infection, whose probable role is to promote efficient cell lysis and release from the infected cell (Tollefson et al., 1996; Shtrichman et al., 1999).

Depending on the genus, infection with protozoa also elicits either apoptotic induction or inhibition of the host. *Trypanasoma brucei*, which causes African sleeping sickness disease, has been recently reported to induce B cell apoptosis so as to deplete the antibody response of the host (Bockstal et al., 2011). In addition, malaria causing Plasmodium species of *P. yeolli* prevented Fas mediated apoptosis of hepatocytes via Bcl-2 activation, which resulted in higher parasitic load and survival

rate (Kaushansky et al., 2013).

As for *Leishmania*, Moore and Mathlaskewski in 1994 were the first to report on the interaction between infection and apoptosis, where the authors found that *L. donovani* prevented the BALB/c mice macrophage from undergoing apoptosis in the absence of stimulating factors (Moore and Mathalaskewski, 1994). Since apoptotic detection from the above report was solely based upon DNA fragmentation, Akarid and colleagues demonstrated that the prevention of apoptosis by *L. major* was due to blockage in cytochrome C release and subsequent caspase-3 activation (Akarid et al., 2004). Further studies have now shown that various *Leishmania* species including *L. infantum*, *L. major*, *L. amazonensis*, *L. pifanoi* suppress the host cell apoptosis induced with various apoptotic inducers through intracellular mechanism such as PKC cleavage, NF-κβ, PI-3 kinase and Bcl-xL (Lisi et al., 2005; Ruhland et al., 2007; Donovan et al., 2009). Thus, from above findings it is clear the *Leishmania* parasites can interfere with the apoptotic process to protect its intracellular niche to allow survival and replication. In contrast, few studies have reported apoptotic induction during late stage of *Leishmania* infection (Getti et al., 2008; DaMata et al., 2015). However, these findings have not provided any evidence of an association between host cell apoptosis and *Leishmania* spreading.

Therefore, an urgent need is required to study the relation between *Leishmania* infection and apoptotic induction in order to consider the disease pathogenesis of leishmaniasis.

1.9. Aims of the Thesis

Although advances have been made in clarifying the infection mechanism behind human leishmaniasis, there is a major lack of understanding surrounding the late interaction between *Leishmania* and its mammalian host cells. One of such area in the field of *Leishmania* biology is the virulent strategy of amastigotes to disseminate from infected to uninfected healthy macrophages during late stage of infection in human cells. This is an exciting research area for parasitology and immunology because this process represents the basis for the development of disease pathogenesis. Although a number of studies have demonstrated a crucial link between *Leishmania* infection and host apoptosis, there is only one study that has provided evidence supporting a link between apoptosis and parasitic spreading (Real et al., 2014). However the infection model from this earlier study is based on macrophages derived from mice, which are not an ideal model for human *Leishmania* infection (Loria-Cervera and Andrada-Narvaez, 2014).

It is therefore an utmost importance to generate an *in vitro* infection model comprising of human macrophages to allow studies of late infection stages. To date, studies based on human cells are limited to early stages of infection. Such model will then form the basis for elucidating the mechanism behind cell-to-cell spreading of *Leishmania* parasites.

Hence, the five major aims of this project are:

1. To establish whether there is a link between *Leishmania* infection and human macrophages apoptosis *in vitro* using a current infection model.
2. To develop and validate *in vitro* infection model representative of the late stage of human macrophages infection to study the dissemination of *Leishmania*.

3. To use the above model to clarify whether there is a link between parasites spreading and host cell apoptosis. This will be carried out by determining the effect of spreading on two major markers of apoptosis: Phosphatidyl serine (PS) externalization and caspase-3 activation.
4. To define the mechanism by which *Leishmania* modulates human macrophage apoptotic pathways. Three major signaling pathways associated with apoptosis including AKT, PKC and NF-κB will be investigated.
5. To quantify and evaluate the global cellular response of human macrophages during *Leishmania* spreading. Through isotopic labeling coupled with tandem mass spectrometry (MS/MS) approach, comparative analysis will be performed to determine quantitative changes in protein between uninfected and infected cells.

Chapter 2 – Materials and Methods

2.1. Parasite culture

The promastigotes of four *Leishmania* species, *L. aethiopica* (MHOM/ET/72/L100), *L. major* (MHOM/SU/73/5ASKH), *L. mexicana* (MNYC/BZ/62/M379) and *L. tropica* (MHOM/SU/58/OD) were obtained from the London School of Hygiene and Tropical Medicine (LSHTM). A green fluorescent protein (GFP) reporter gene construct (pRib1.2αNeoαGFP) was transfected by Patel and colleagues in the above four species, which resulted in the constitutive expression of GFP throughout their life cycle, hence allowing flow cytometry and fluorescence microscopic analysis (Patel et al., 2014). For simplicity, the transgenic GFP expressing *Leishmania* clones were named as: L8G (*L. aethiopica*), S1G (*L. major*), M5G (*L. mexicana*) and O5G (*L. tropica*). The promastigotes were grown in Schneider's Drosophila Medium (Fisher Scientific, UK) supplemented with 23% Foetal Calf Serum (FCS) (Fisher Scientific) and 1× Penicillin-Streptomycin-Glutamine (Fisher Scientific) at neutral pH. The parasites were sub-cultured once a week at a concentration of 1×10^6 per ml, supplemented with 700 µg/ml of G418 (Sigma, UK), and were incubated at 24°C cooling incubator.

2.2. Human cell culture

Human THP-1 monocyte (ATCC) was sub-cultured, every 3 days, at a concentration of 2.5×10^5 per ml in complete RPMI 1640 medium (Fisher Scientific) and incubated at 37°C in a humidified CO_2 (5%) incubator. The medium was made complete following supplementation with 10% FCS and 1× Penicillin-Streptomycin-Glutamine. This lineage of human cell line was chosen to study infection as THP-1

cells are known to support the intracellular replication and growth of *Leishmania* parasites (Ogunkolade et al., 1990).

2.3. Infection of differentiated THP-1 macrophage with GFP expressing *Leishmania*

Differentiated THP-1 macrophages were infected with metacyclic promastigotes derived from all four species of *Leishmania* as described below.

2.3.1. Preparation of stationary phase metacyclic promastigotes

Initially, stationary phase promastigotes were obtained by culturing the parasites at 5×10^5 per ml, 96 hours prior to infection. The metacyclic promastigotes were isolated by peanut agglutination as previously described (Parbhu-Patel et al., 2013). Briefly, stationary phase parasite cultures were centrifuged at 1000 g for 10 minutes. Following agglutination with 50 µg/ml peanut lectin (Vector, UK) for 18 minutes, the parasites were further centrifuged at 500 g for 5 minutes. The resulting supernatant containing the metacyclic promastigotes was collected and subsequent concentration determined by microscopic counting. Metacyclic S1G parasites were not purified through the above technique due to low concentration after agglutination.

2.3.2. Preparation of differentiated THP-1 macrophages

THP-1 monocytes at a concentration of 2.5×10^5 per ml were treated with 1 µM of retinoic acid (RA) (Sigma) for 72 hours to induce differentiation of monocytes into non-replicating and non-adherent macrophages–like cells. Before infection with metacyclic promastigotes, the differentiated THP-1 macrophages were washed twice with 1× PBS (Sigma) to remove excess RA. After the final wash, the cells were re-suspended in complete RPMI 1640 medium and counted via Trypan blue staining

(Sigma). Cell viability greater than 80% was the threshold level to be used for subsequent infection experiments.

2.3.3. Parasite to cell ratio

Parasite concentration of 5×10^6 per ml was used to infect 5×10^5 per ml of differentiated THP-1 macrophage at a ratio of 10:1 (parasite to cell ratio). The infected cells were then incubated at 37°C in a humidified CO_2 (5%) incubator. The percentage of infection was determined via flow cytometry (section 2.7).

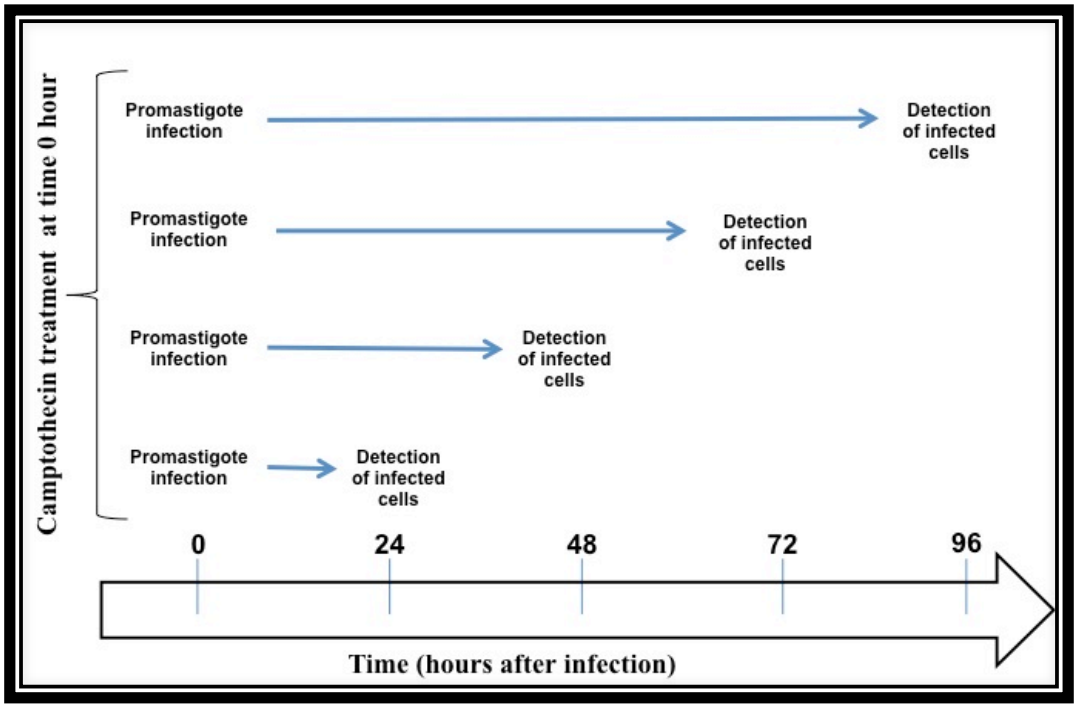
2.4. Induction of apoptosis

Following infection with all four species of promastigotes, the induction of apoptosis was carried out by treatment with 3 μM of camptothecin (Sigma). To determine the effect of camptothecin treatment on the percentage of infected cells, the length of treatment was optimized (Figure 2.1). The first optimization involved the addition of camptothecin at 0 hour after infection and continuously detecting the percentage of infection via flow cytometry at 24, 48, 72 and 96 hours (Figure 2.1.A). The second optimization involved camptothecin addition at 0 hour before washing away excess camptothecin from the culture medium with 1× PBS at 24 hours after infection and subsequently detecting the percentage of infection via flow cytometry at 24, 48, 72 and 96 hours (Figure 2.1.B). In the above experiments, both uninfected and infected cultures without camptothecin treatment were used as an appropriate control.

2.5. Infection of differentiated THP-1 macrophage with *Leishmania* infected cells

L. aethiopica (L8G) and *L. mexicana* (M5G) infected cells induced with 3 μM of camptothecin were seeded on 24 well plates.

A



B

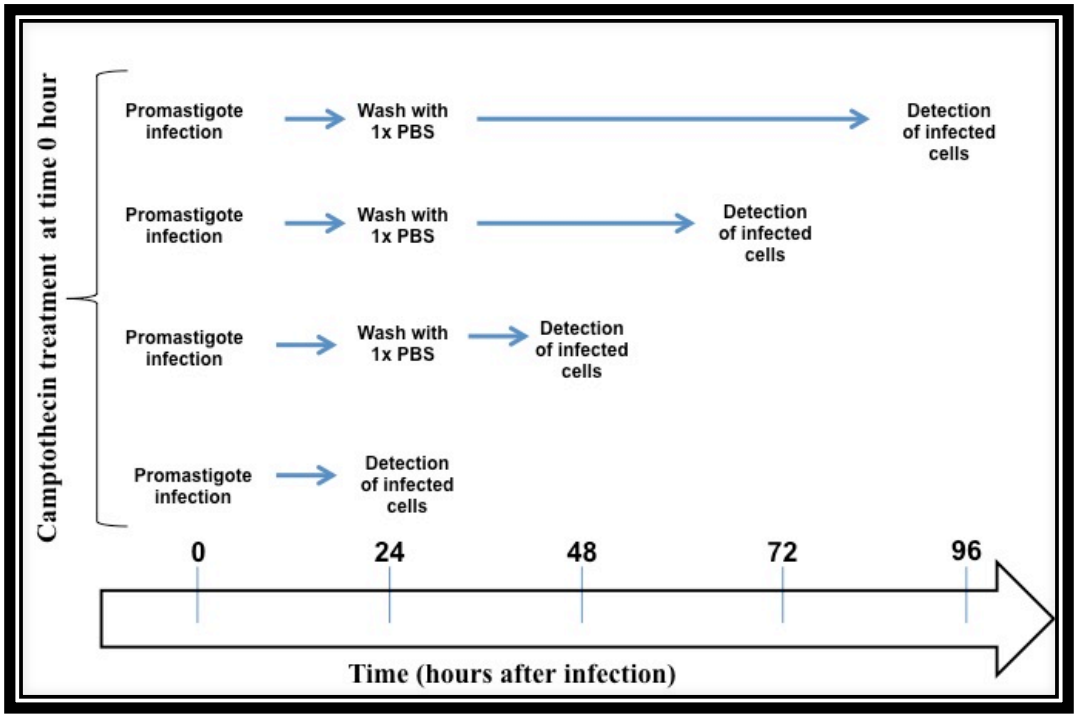


Figure 2.1. Schematic diagram representing the optimization strategy of camptothecin treatment on the percentage of infected cells. (**A**) Following promastigote infection, camptothecin was treated at 0 hour and the percentage of infected cells was detected from 24 to 96 hours. **(B)** Following promastigote infection, camptothecin was treated at 0 hour before washing excess drug at 24 hours after infection. The percentage of infected cells was detected from 24 to 96 hours.

Excess camptothecin from M5G and L8G infected culture were washed away with 1× PBS at 5 and 24 hours after infection respectively. After 72 hours of incubation at 37°C in a humidified CO_2 (5%) incubator, viable cell concentration from both infected culture was determined via Trypan blue staining. The infected cells were then centrifuged at 500 g for 10 minutes to remove the supernatant, before the addition of a freshly prepared batch of differentiated THP-1 macrophages. Three different infection ratios were tested including 10:1, 5:1 and 1:1 (infected cell per uninfected cell ratio). The percentage of infection was determined at 0, 12, 24 and 48 hours after co-culture via flow cytometry. In addition, live imaging of parasite transmission carried out through real time lapse microscopy (Section 2.8).

2.6. Inhibition of caspase-3 activity

L8G infected cells from 72 hours were pre-treated with 25 μM and 100 μM of Z-DEVD-FMK (BD Biosciences, UK) for 4 hours and incubated at 37°C in a humidified CO_2 (5%) incubator. After washing with 1× PBS, the infected cells were co-cultured with freshly prepared batch of differentiated THP-1 macrophages at 1:1 ratio (infected cell per uninfected cell ratio). The percentage of infection and caspase-3 expression were determined at 3 and 12 hours after co-culture. Untreated L8G infected cells were taken as a positive control.

2.7. Detection of apoptosis

Apoptosis assays were carried at different times after infection according to specific experiments (Table 2.1).

Type of experiments	Time of apoptotic assay
Promastigote infection of differentiated THP- macrophages	24, 48, 72 and 96 hours after infection
Camptothecin treatment of differentiated THP-1 macrophages infected with promastigote	24, 48, 72 and 96 hours after infection
Infection of differentiated THP-1 macrophages with infected cells (1 to 1 infection ratio)	0, 24 and 48 hours post infection

Table 2.1. List of experiments designed for apoptosis and their time of analysis.

2.7.1. Annexin V / 7AAD assay

PE Annexin V apoptosis kit I (BD Biosciences) was used to determine the externalization of phosphatidyl serine (PS) and membrane permeability of the cell. Annexin V protein binds to PS, which is externalized during early stages of apoptosis, whereas 7AAD intercalates with the cellular DNA if the membrane is damaged during late stage of apoptosis (necrosis). The kit was used according to manufacturer protocol. Briefly, the harvested cells were centrifuged at 500 g for 10 minutes and washed twice with ice-cold 1× PBS.

After re-suspension in 1× binding buffer at a cell concentration of 1×10^6 per ml, 100 µl of cells were then stained with 5 µl of PE Annexin V and 5 µl of 7AAD and incubated for 15 minutes in the dark at room temperature. Finally, 400 µl of 1× binding buffer was added to the stained cells and the percentage of Annexin V positive / 7AAD negative (early apoptosis) and Annexin V positive / 7AAD positive (late apoptosis or necrosis) cells were analysed through flow cytometry within 1 hour of staining.

2.7.2. Caspase-3 enzymatic assay

The PE Caspase-3 detection kit (BD Biosciences) was used to measure the activation level of caspase-3 enzyme of the cell. The kit was used according to the manufacturer protocol. Briefly, the harvested cells were centrifuged at 500 g for 10 minutes before washing twice with ice-cold 1× PBS. The cells were incubated at 0-4°C for 20 minutes with 1× Perm and Fix buffer at a cell concentration of 2×10^6 per ml. After incubation, the cells were washed twice with 1× washing buffer before staining with PE anti-caspase-3 antibody (20 µl per $1x10^6$ cells). Following 30 minutes incubation in dark, the stained cells were washed with 500 µl of 1× washing

buffer. After final re-suspension in 400 µl of 1× washing buffer, the percentage of caspase-3 positive cells were analysed through flow cytometry within 1 hour of staining.

2.8. Flow cytometry

The C6 flow cytometry (BD Accuri, UK) which is comprised of blue (excitation λ: 488 nm) and red (excitation λ: 640 nm) lasers, was used to detect the percentage of infected cells and apoptotic cells. In this flow cytometer, the FL-1, FL-2 and FL-3 optical filters detected emissions from blue lasers, whereas FL-4 filters detected emission from red lasers. The blue laser was used to excite different types of fluorochromes, specific to GFP (FL1), PE Annexin V and PE Caspase-3 (FL-2) and 7AAD (FL-3).

To measure the percentage of infection along with Annexin V and 7AAD stained cells, the cell populations were initially gated according to Forward scatter (FSC) and Side scatter (SSC) parameters (Figure 2.2.A), which defines cell size and cell granularity, respectively. After exclusion of doublet cells (Figure 2.2.B), two separate plots were designed. Figure 2.2.C.i shows a histogram plot of GFP versus count to determine the percentage of infection whereas Figure 2.2.C.ii represents a dot plot of Annexin V versus 7AAD to determine apoptosis. In this thesis, this plot will be referred as total population apoptosis. Each quadrant represents the percentage of live cells (Annexin V negative / 7AAD negative), early apoptotic cells (Annexin V positive / 7AAD negative), late apoptotic/necrotic cells (Annexin V positive / 7AAD positive) and dead cells (Annexin V negative / 7AAD positive). Furthermore, within infected cultures, the percentage of apoptosis from total population was sub-divided into infected only and uninfected only population (Figure 2.3).

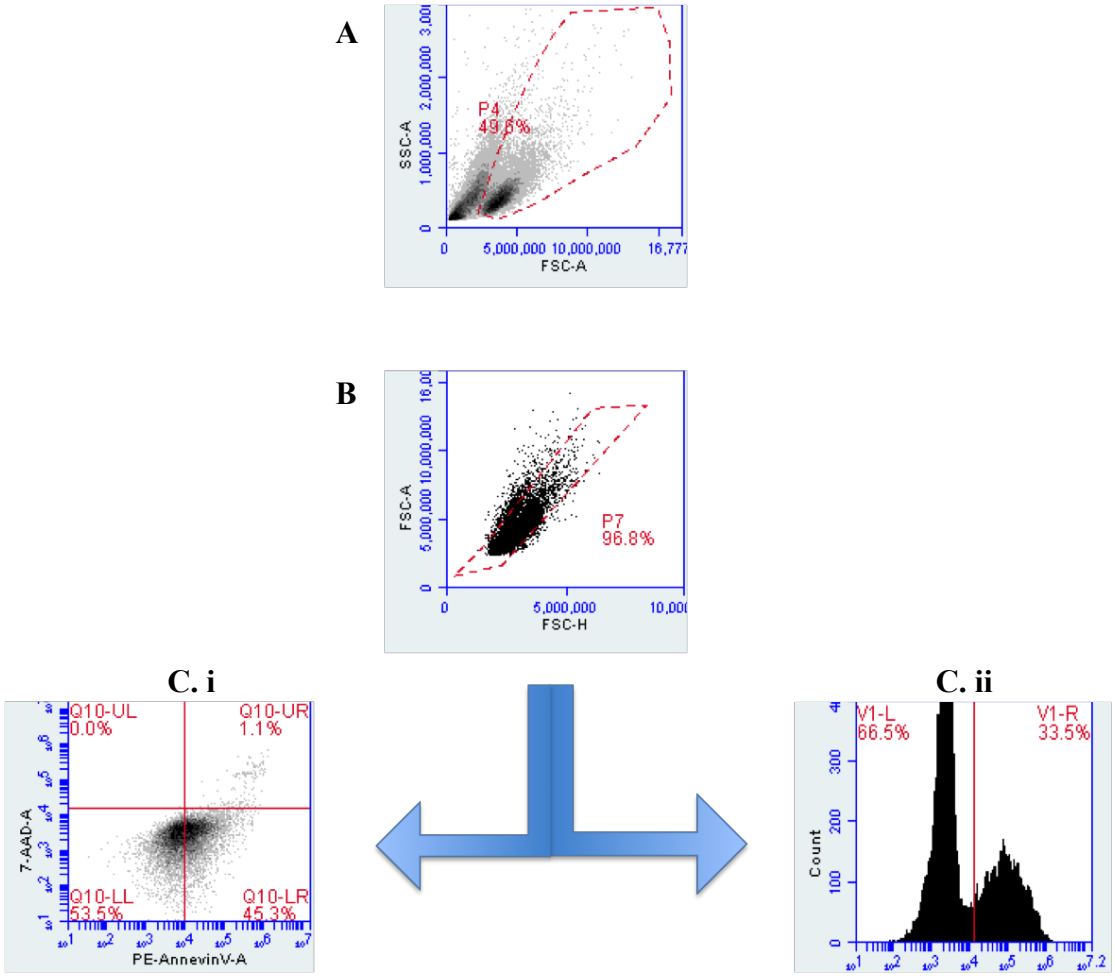


Figure 2.2. Flow cytometry analysis of PE-Annexin V / 7-AAD stained cells. **(A)** The total population of differentiated THP-1 macrophages (double stained with PE-Annexin V and 7AAD) were initially gated as P4, according to FSC-A and SSC-A parameters. **(B)** The doublet cells were excluded. **(C)** Following exclusion, two plots were created. **(C.i)** A dot plot comprising of PE-Annexin V (X-axis) versus 7-AAD (Y-axis) was created to isolate live (Q9-LL), early apoptotic (Q9-LR), late apoptotic (Q9-UR) and dead (Q9-UL) cells. **(C.ii)** A histogram plot comprising of GFP (X-axis) versus Count (Y-axis) was created to detect the percentage of infected cells in V1-R region from uninfected cells in V1-L region.

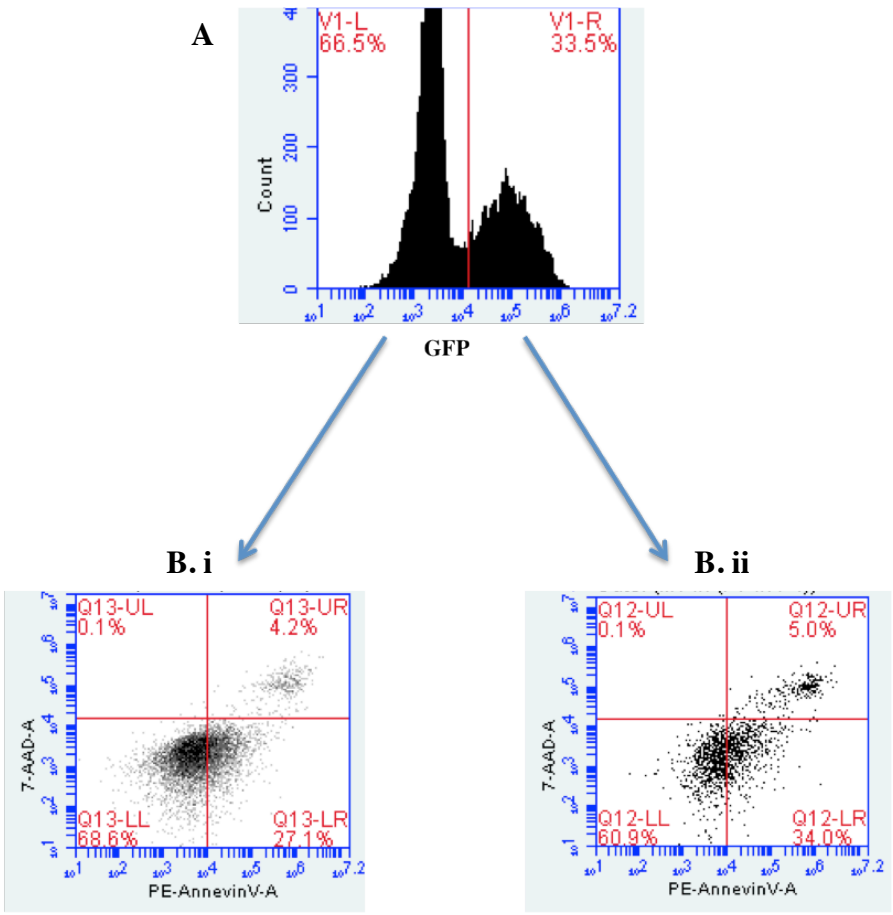


Figure 2.3. Flow cytometry analysis of apoptosis in infected cultures. (A) Representative histogram plot of infection based on GFP expression. **(B.i)** A dot plot comprising of PE-Annexin V (X-axis) versus 7AAD (Y-axis) was created from V1-L region. This apoptotic plot is called uninfected only population. **(B.ii)** Similarly, a dot plot comprising of PE-Annexin V (X-axis) versus 7AAD (Y-axis) was created from V1-R region. This apoptotic plot is called infected only population.

Similarly for caspase-3 activity, the stained cell populations were gated according to FSC and SSC (Figure 2.4.A) from which the doublet cells were excluded (Figure 2.4.B). Then, a histogram plot of caspase-3 versus count was created to measure the percentage of active caspase-3 cells (Figure 2.4.C). It should be noted that limits for the quadrants were always based upon positive and negative control.

2.9. Real time lapse microscopy

A fresh population of differentiated THP-1 macrophages at a concentration of 1×10^5 per ml was labelled with 0.5× CellMask^{TM} orange plasma membrane stain (Fisher Scientific) for 15 minutes at 37°C. After washing three times with 1× PBS the cells were re-suspended in RPMI medium and seeded in a 6 well culture plate containing 1×10^5 of either L8G or M5G infected cells (from 72 hour incubation). Immediately, the RPMI complete medium was removed from this co-culture and was replaced by RP buffer solution (1 mM Magnesium acetate (Sigma), 1 mM Calcium chloride (Sigma), 5 mM glucose (Sigma), 5 mM glutamate (Sigma), 10% FCS, 1× PBS). The 6 well culture plate was then mounted on 37°C hot plate connected to a fluorescent Eclipse Ti-S inverted microscope (Nikon, UK). Using an in built digital DS-Fi camera (Nikon), live images were acquired every 5 minutes with bright field and TRITC filters for a maximum period of 12 hours under 20× objectives. After acquisition, images were processed by NIS advanced version 4.2 software (Nikon), which allowed for the construction of multidimensional time-lapse videos.

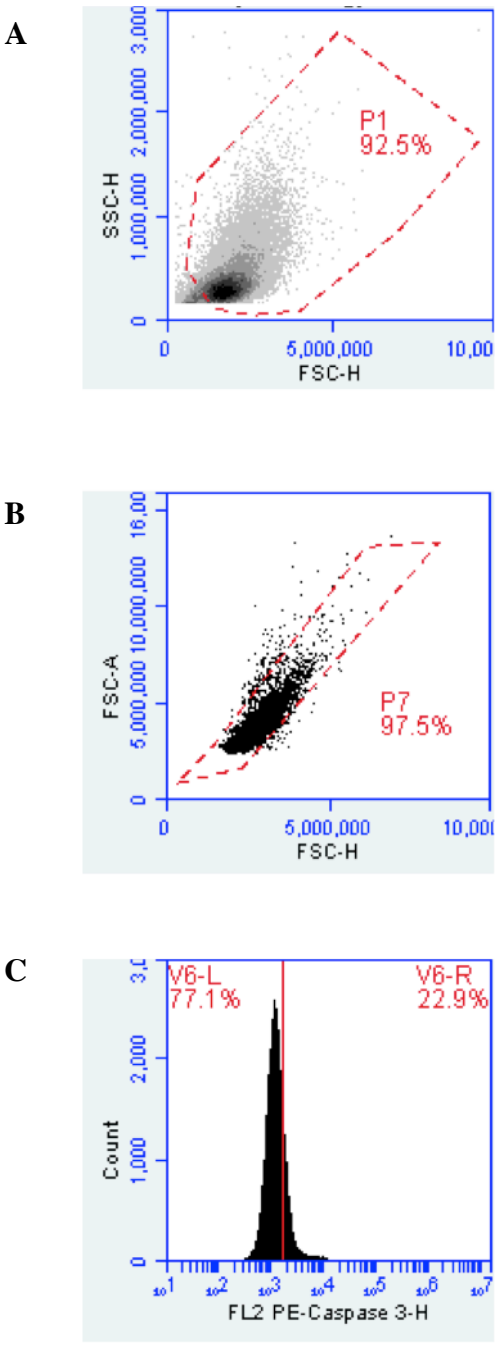


Figure 2.4. Flow cytometry analysis of PE-Caspase 3 stained cells. (A) The total population of differentiated THP-1 macrophages, which are stained with anti PE-Caspase 3 antibody is initially gated as P1, according to FSC-A and SSC-A parameters. **(B)** The doublet cells are excluded. **(C)** Following exclusion, a histogram plot comprising of PE-Caspase 3 (X-axis) versus Count (Y-axis) was created to detect the percentage of cells with activated caspase 3.

2.10. Western blot

Western blots were carried out to analyse the involvement of proteins associated with apoptotic pathways during L8G infection spreading specifically, AKT, PKC-δ and NF-κB. The lists of antibodies (Santa Cruz, UK) used in this experiment are listed in Table 2.2. Briefly, from each incubation time point, 1×10^6 cells were harvested by centrifugation at 500 g for 10 minutes. After removing the supernatant, the cell pellet was res-suspended in ice cold 1× PBS and centrifuged at 1000 g for 5 minutes. Then, 100 µl of 1× RIPA buffer (Abcam, UK), which was supplemented with 1× protease cocktail inhibitor (Fisher Scientific), was added to the pellet. After re-suspension, the samples were lysed on ice for 15 minutes with gentle shaking. The whole cell proteins were then collected from the supernatant through centrifugation at 10,000 g for 10 minutes at 4°C. For extracting cytosolic protein, the pellet was re-suspended in cell extraction buffer (Fisher Scientific) supplemented with 1× protease cocktail inhibitor.

The sample was lysed on ice for 30 minutes before collecting the supernatant through centrifugation at 10,000 g for 10 minutes at 4°C. The resulting protein concentration from a sample was determined through BCA absorbance assay kit (Fisher Scientific) according to the manufacturer protocol. To separate the proteins according to their sizes, 20 µg of proteins were run on a 10% Tris glycine SDS gels (Fisher Scientific) for 50 minutes under a constant 185 volts. The proteins were then transferred successfully onto a nitrocellulose membrane (BioRad, UK) before overnight blocking at 4°C with 5% non-fat dry milk TBS tween or 5% BSA TBS tween solution (BioRad).

List of antibodies	Dilution Factor	Blocking buffer
Anti-phospho (Thr 308) AKT	1 in 500	5% BSA in TBS tween
Anti-phospho (Ser 473) AKT	1 in 500	5% BSA in TBS tween
Anti-total AKT	1 in 1000	5% Milk in TBS tween
Anti-total PKC- δ	1 in 1000	5% Milk in TBS tween
Anti-total p65	1 in 1000	5% Milk in TBS tween
Anti-phospho (Ser 32/36) IκBα	1 in 500	5% BSA in TBS tween
Anti-total IκBα	1 in 500	5% Milk in TBS tween
Anti-Cytochrome C	1 in 500	5% Milk in TBS tween
Anti- phospho (Ser 136) BAD	1 in 250	5% BSA in TBS tween
Anti-total BAD	1 in 500	5% Milk in TBS tween
Anti- β actin	1 in 1000	5% Milk in TBS tween

Table 2.2. List of antibodies and their appropriate dilution and appropriate blocking buffers used in western blot experiments.

The membrane was then incubated with primary antibody at room temperature under gentle agitation for 1 hour. After three washes in TBS tween solution, the membrane was incubated with horse radish peroxidase conjugated secondary antibody for 1 hour at room temperature under gentle agitation. The membrane was further washed three times in TBS tween solution before applying an ECL reagent (Fisher Scientific) to detect the protein of interest under X ray film (Fisher Scientific). To re-probe for another protein, the membrane was washed two times in TBS solution before incubating with 1× stripping buffer (Fisher Scientific) for 40 minutes at room temperature. After further two washes in TBS solution, the membrane was ready for another round of blocking and subsequent antibody incubation.

2.11. Quantitative proteomics by mass spectrometry

The differentially expressed proteins during L8G infection spreading were analysed by Tandem Mass Tag^{TM} (TMT) 6-plex based liquid chromatography – tandem mass spectrometry (LC-MS/MS). The initial protein extraction was performed as described in section 2.9. The experimental procedures including isotopic protein labelling and mass spectrometry were performed by University of Bristol, UK using the TMT Mass Tagging Kits and Reagent (Fisher Scientific). For this thesis, only two samples (i.e. uninfected and L8G infected co-culture after 10 hours of co-culture) were chosen for labelling. The remaining four samples were designed for other researchers. According to the manufacturer protocol, the brief procedures are described below.

2.11.1. Precipitation and enzymatic digestion of the protein samples

Approximately, 100 µg of proteins from uninfected (control) and L8G infected co-culture samples at 10 hours after co-culture were transferred into a new micro-

centrifuge tube and its final volume was adjusted to 100 µl with 100 mM TEAB (Tri Ethyl Ammonium Bicarbonate) and 200 mM of TCEP (Tris 2-Carboxy Ethyl Phosphine). After incubating at 55°C for 1 hour, the samples were treated with 5 µl of 375 mM iodoacetamide and further incubated for 30 minutes in dark room temperature. Following overnight freezing (-20°C) in the presence of 600 µl of acetone, the samples were centrifuged at 8000 g for 10 minutes at 4°C. After careful removal of supernatant, the protein pellets were re-suspended with 100 µl of 100 mM TEAB. The protein digestion was completed by overnight incubation of the sample with 2.5 µl of trypsin at 37°C.

2.11.2. Peptide labelling and mass spectrometry

The peptides from the digested proteins were incubated with appropriate TMT label reagent (-129 and -130) for 1 hour at room temperature. The reaction was quenched following further incubation with 8 µl of 5% hydroxylamine for 15 minutes. These labelled samples were then combined together with the remaining four samples. The resulting mixture was then separated using liquid chromatography. Mass spectrometry of the column eluate was done using Velos Pros^{TM} ion trap mass spectrometer (Fisher Scientific). The peptide MS/MS data were analysed for protein identification and quantification using Proteome Discoverer ^{TM} 1.1 (Fisher Scientific). A false positive discovery rate (FDR) threshold of 5% was employed to ensure that there is at least 95% confidence that every peptide present was a genuine peptide from the database. By comparing the peak intensity of test sample with control, the relative fold change (RFC) was calculated. This allowed the identification of differentially expressed proteins with RFC > 1.5 and RFC < 0.5 considered as upregulated and downregulated, respectively.

2.12. Statistical Analysis

Data shown are representative of at least three independent experiments performed in triplicates wherever necessary. Data represents mean values with statistical error mean (SEM). Statistical analysis was performed using student *t* test provided by Graph pad prism and P values less than 0.05 ($p<0.05$) were considered significant differences between two independent samples.

Chapter 3 – *Leishmania* infection and host cell apoptosis

3.1. Introduction

Macrophages are the definitive host cell for the invasion by *Leishmania* parasites. The survival of *Leishmania* is due to the ability of the parasite to disable various host macrophages function such as cytokine production, reactive oxygen species and nitric oxide generation (Martinez and Gordon, 2014). Another virulent strategy utilized by *Leishmania* is to prevent the induction of macrophage apoptosis during early stage of infection (Akarid et al., 2004; Lisi et al., 2005; Ruhland et al., 2007). It has been suggested that this would allow sufficient time for the parasite to replicate before spreading its progeny towards neighbouring macrophages. However, the exact mechanism of parasite dissemination is far from clear.

Natural transmission studies in mice have shown that early phase of infection propagation occurs silently for weeks to months, without immunological and pathological changes (Belkaid et al., 2000; Nylon and Eidsmo, 2012). Since apoptosis is the removal of damaged cells by macrophages without eliciting an inflammatory response, this led to speculate that *Leishmania* could utilize this form of host cell death in order to spread. Indeed, this unique process would offer selective advantage to the parasites, which could potentially exit the host cell within apoptotic bodies and subsequently evade the host immune defence system. Similar strategies of cell-to-cell spreading through host cell apoptosis have been reported in a number of infectious pathogens including *Mycobacterium tuberculosis* (Aguilo et al., 2013) and Adenovirus (Mi et al., 2001). Interestingly, *L. amazonensis* has been the only

protozoa that have recently been shown to spread from cell-to-cell via mechanism resembling apoptosis (Real et al., 2014).

In this chapter, the link between *Leishmania* infection progression and apoptosis of host macrophages *in vitro* was investigated. This relationship was determined via two routes. Firstly, the effect of four GFP expressing *Leishmania* promastigotes (*L. aethiopica*, *L. major*, *L. mexicana* and *L. tropica*) infection on the apoptosis of differentiated THP-1 macrophages from 24 to 96 hours was analysed. Secondly, the effect of apoptotic induction on the parasitic infection was evaluated. Flow cytometry was used to detect the percentage of GFP expressing *Leishmania* infected cells as well as percentage of apoptotic marker (i.e. Phosphatidyl Serine [PS] externalisation) during infection. In addition, for the very first time, the apoptosis level (PS externalization) within an infected sample was analysed separately into infected only and uninfected only population.

3.2. Results and Discussion

3.2.1. Infection of differentiated THP-1 macrophages with *Leishmania* promastigotes

In order to test the effect of *Leishmania* infection on apoptosis, the infectivity level and survival period of four promastigotes species in differentiated THP-1 macrophages were initially determined. Flow cytometry analysis was used to monitor the course of infection by measuring the percentage of macrophages containing GFP positive parasites at early (24 and 48 hours) and late (72 and 96 hours) incubation time point.

After 24 hours incubation, between 30 to 60% of cells were successfully infected by all four promastigote species (Figure 3.1). The percentage of infection was highest for L8G (57.1±0.8%), M5G (56.8±9.1%) and O5G (57.1±4.5%), whereas the lowest infection was observed for S1G, which only infected 31±2.2% of cells. The infection rate seemed to stabilize after two days (48 hours) of continuous incubation for all species. From 48 to 96 hours, a significant decrease ($p<0.05$) in the percentage of cells infected with L8G, M5G and O5G were observed before maintaining low infectivity level. To query this dramatic reduction, trypan blue assay was performed which showed a two-fold increase in the concentration of viable cells from 48 to 96 hours in both uninfected and infected cells (Figure 3.2). This suggests that the inhibitory effect of retinoic acid on THP-1 replication terminated at 48 hours after which the monocytes underwent cellular replication.

Interestingly, the percentage of S1G infected cells remained low throughout the time period. This is likely due to loss of infectivity associated with high number of sub-culturing carried out on S1G (Segovia et al., 1992). In contrast, M5G and O5G were recently obtained and L8G has been reverted to axenic amastigote several times (personal communication), hence these species showed higher infective capacity (Getti et al., 2008).

In summary, all species (except S1G) displayed maximum infective level within the first 48 hours. However, the spreading of parasite was not detected partially due to intense replication of uninfected THP-1 cells. In terms of parasite survival, the infection remained existent till 96 hours, although significantly lower than 48 hours, indicating the survival of parasites within cell.

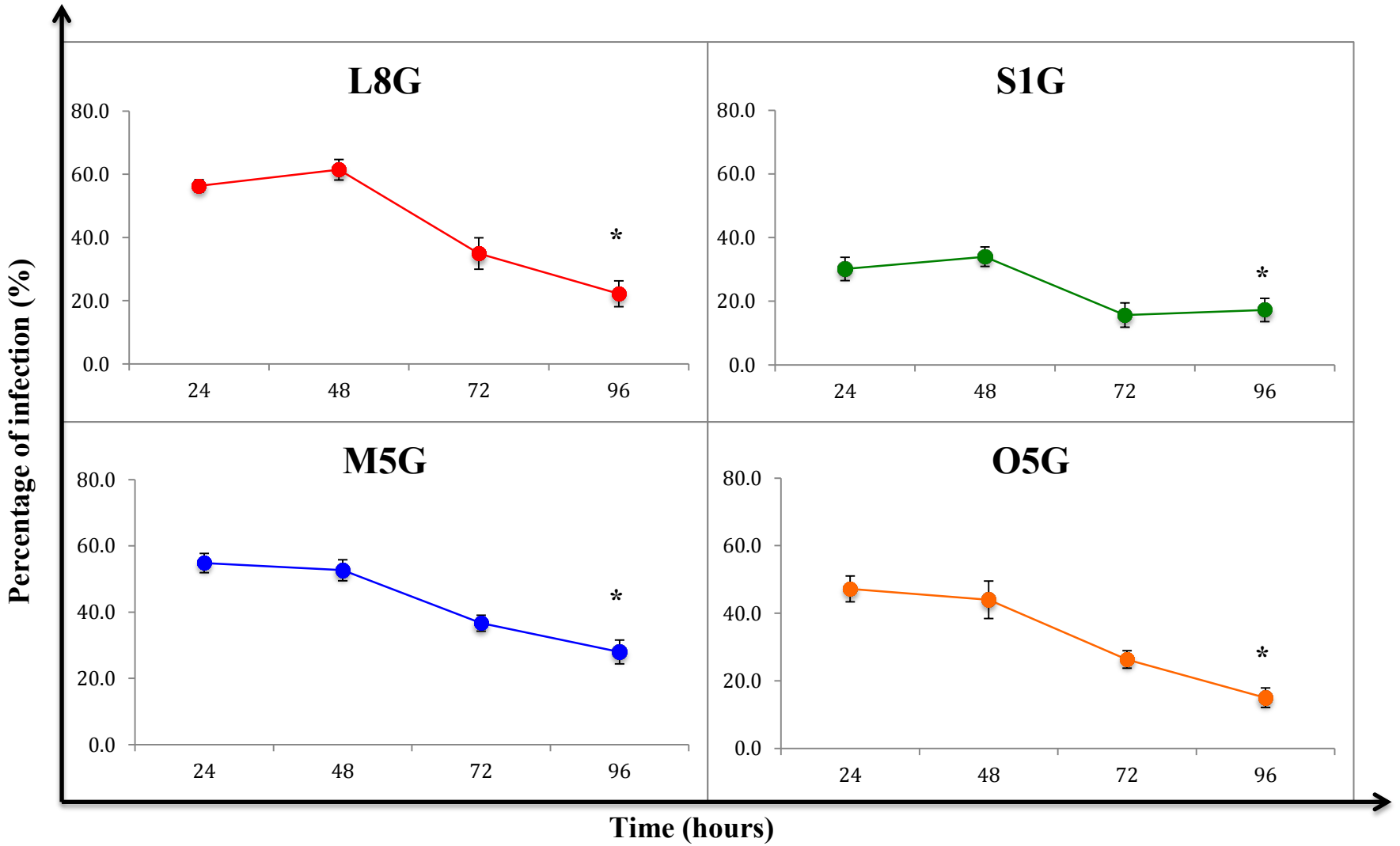


Figure 3.1. Time course of differentiated THP-1 macrophage infection with *Leishmania* promastigotes. Differentiated THP-1 macrophages were infected with four GFP expressing promastigotes species, *L. aethiopica* (L8G), *L. major* (S1G) and *L. mexicana* (M5G) and *L. tropica* (O5G) at 10:1 ratio (parasites to cell ratio). The percentage of infection was determined through flow cytometry at 24, 48, 72 and 96 hours. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$

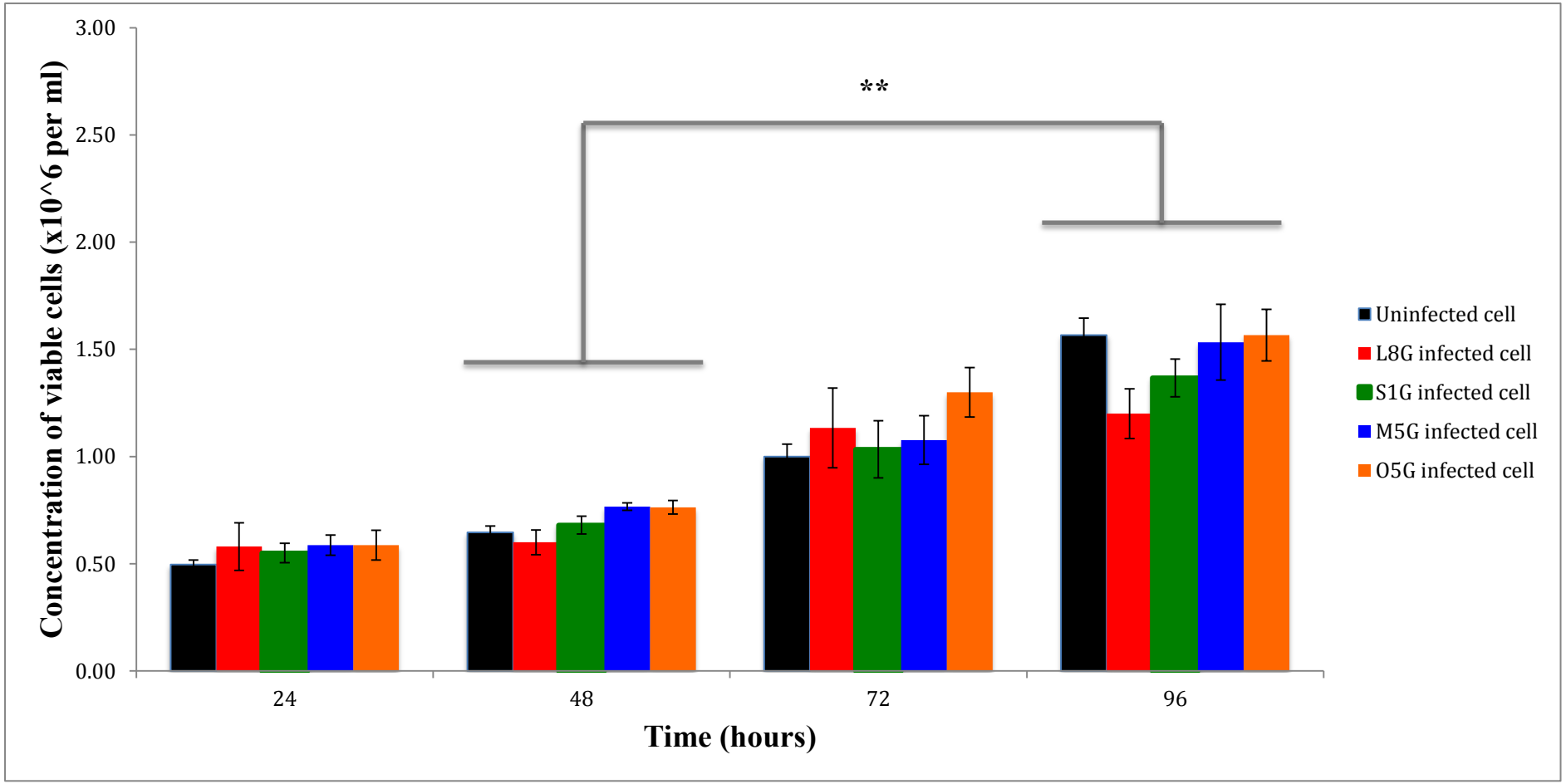


Figure 3.2. Measurement of viable cell concentration in the presence or absence of infection. Uninfected or infected cell by L8G, S1G, M5G and O5G were stained with trypan blue solution at 24, 48, 72 and 96 hours. The data represents mean concentration of viable cells (mean±SEM) from three independent experiments. ** = $p<0.01$.

3.2.2. Effect of *Leishmania* promastigotes infection on the apoptosis of differentiated THP-1 macrophages

Since the above results showed that parasites persisted till 96 hours, the next aim was to test the impact of host cell apoptosis during *Leishmania* promastigotes infection. Through Annexin V / 7-AAD assay, flow cytometry analysis of apoptosis in *Leishmania* infected cells was performed. In this experiment, cells undergoing early apoptosis (Annexin V positive / 7-AAD negative) and late apoptosis (Annexin V negative / 7-AAD negative) were termed apoptotic and necrotic, respectively. Due to the constitutive GFP expression of the parasites, comparison between the percentage of apoptosis (Figure 3.3) and infection (Figure 3.4) was analysed together. Furthermore, the apoptosis in the infected culture (total population) were divided into infected only and uninfected only populations.

As illustrated in figure 3.3, 29±2.3% of the uninfected control cells (black line) underwent apoptosis at 24 hours. In the infected only population, approximately 60% of L8G, M5G and O5G infected cells (Figure 3.4) showed significantly higher percentage ($p<0.05$) of apoptosis at 24 hours compared to the control (Figure 3.3 A[ii], C[ii] and D[ii]). As for S1G, the induction of apoptosis in the infected only cells was observed from 48 hours after infection (Figure 3.3 B[ii]). Interestingly, this increased level of apoptosis for all four species was maintained till 96 hours, despite the fact that infection rate decreased dramatically from 48 hours (Figure 3.4). This finding is in agreement with studies whereby infection with promastigotes of *L. aethiopica*, *L. tropica*, *L. major* and *L. amazonensis* induced apoptotic cell death in human and mice macrophages (Getti et al., 2008; Filardi et al., 2014; DaMata et al., 2015).

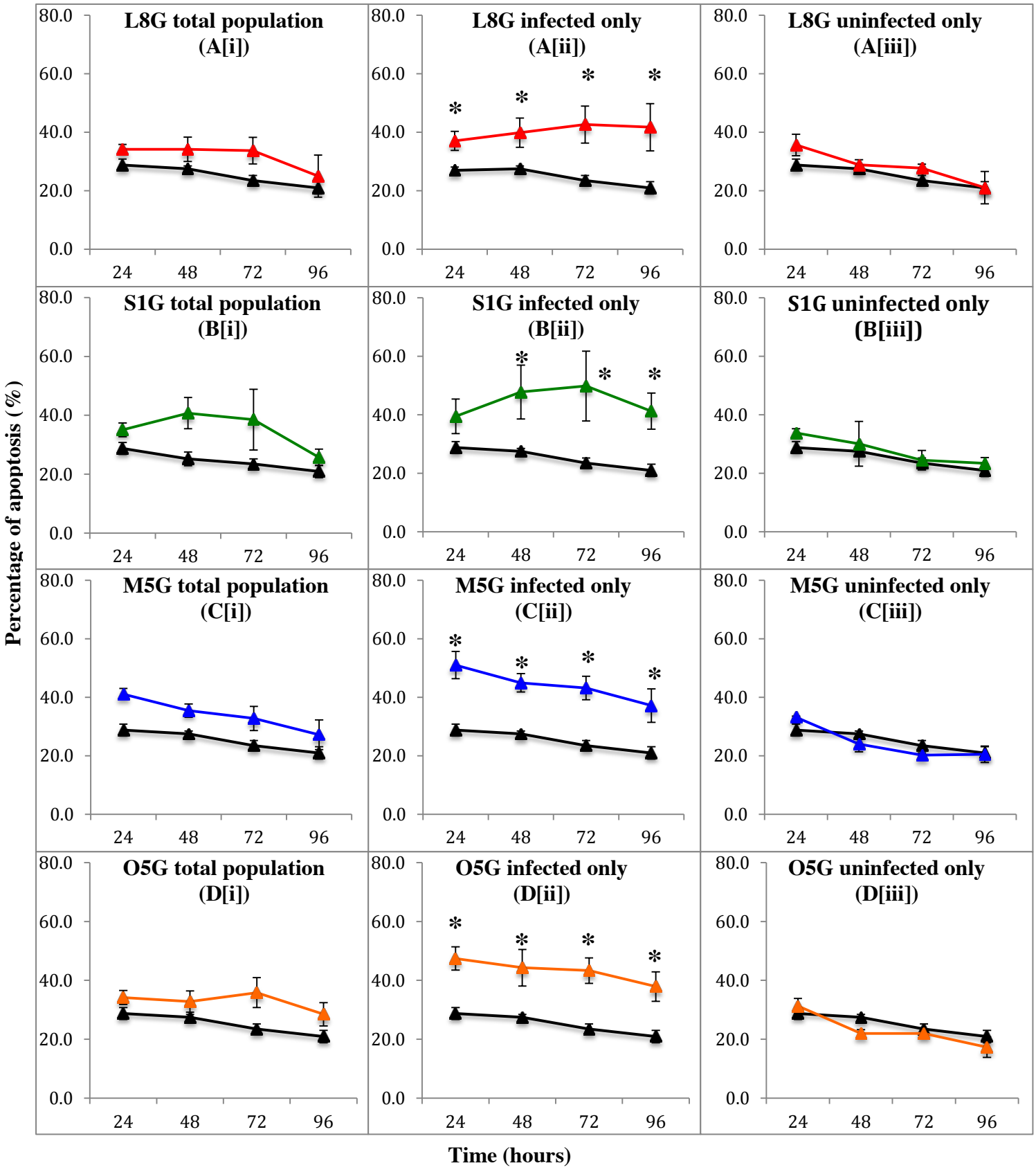


Figure 3.3. Effect of *Leishmania* promastigotes infection on the apoptosis of differentiated THP-1 macrophages. Following infection (10 parasites per 1 cell ratio), the percentage of apoptosis in L8G (A[i]), S1G (B[i]), M5G (C[i]) and O5G (D[i]) infected cells were detected at 24, 48, 72 and 96 hours. This data was divided into infected only [ii] and uninfected only [iii] populations. In the graph, the black line refers to uninfected cell (control). The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$.

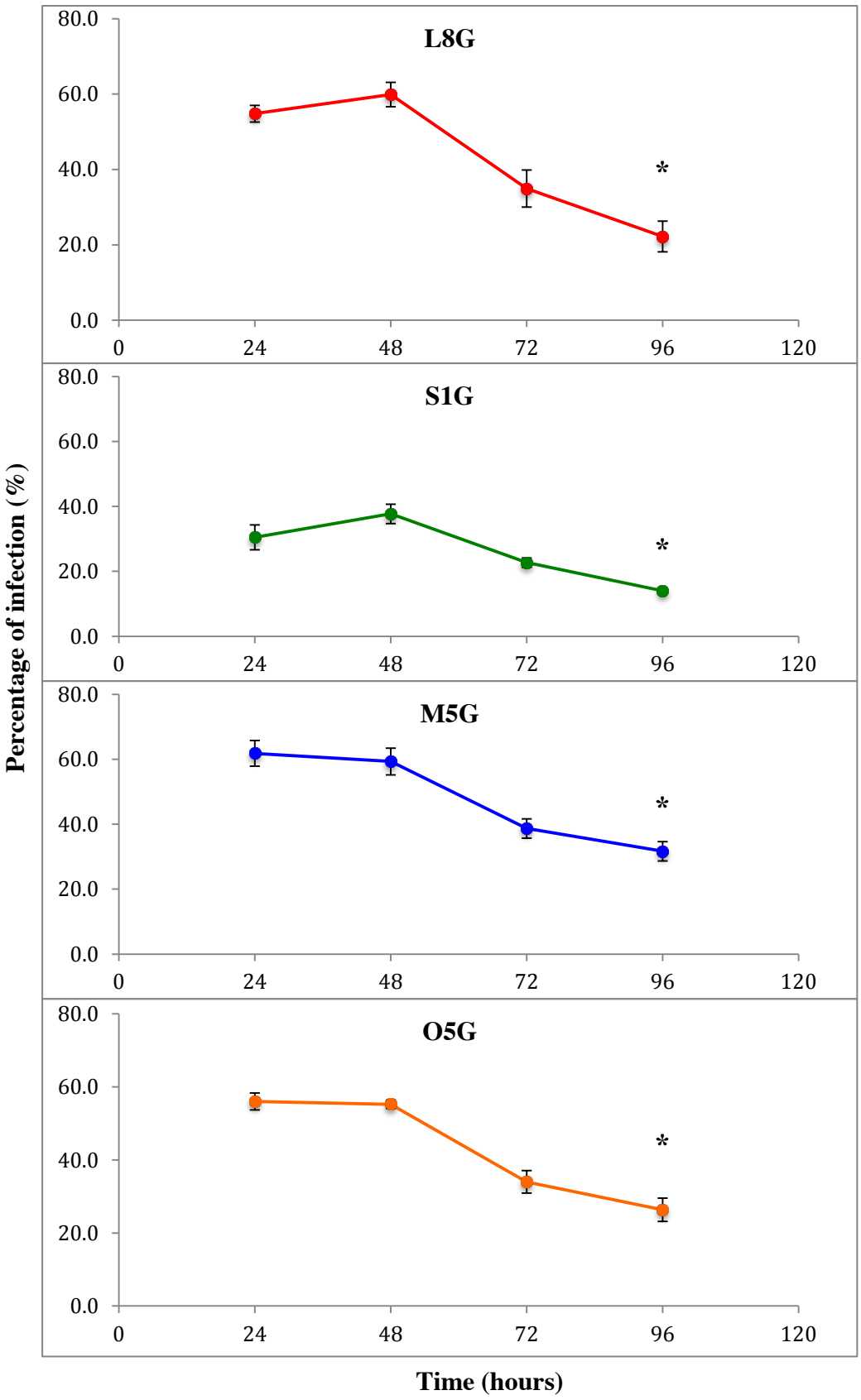


Figure 3.4. Time course of differentiated THP-1 macrophage infection with *Leishmania* promastigotes. In addition to the assessment of apoptosis during infection in Figure 3.3, information regarding the percentage of cells infected with L8G, S1G, M5G and O5G were also extracted and determined at 24, 48, 72 and 96 hours through flow cytometry. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$.

Overall, the above results suggest that *Leishmania* induces spontaneous host apoptosis within infected only cells. Although this experiment showed a correlation between infection and apoptosis, whether such induction in cell death leads to parasitic spreading could not be extrapolated.

3.2.3. Effect of apoptotic induction on *Leishmania* infection

As the above result was unable to clarify the link between infection propagation and host cell apoptosis, the next step was to determine the effect of apoptotic induction on parasite infection. By treating infected cells with camptothecin (an intrinsic apoptosis inducing drug), the infection outcome and apoptosis were analysed. In order to achieve this, an optimisation was needed to determine the effect of the camptothecin treatment on the percentage of infection over a period of 96 hours.

3.2.3a. Longer duration of treatment with camptothecin

Infected and uninfected cells were treated with (or without) 3μM camptothecin at the start of infection (0 hour) and subsequent infection and apoptosis were detected by flow cytometry every 24 hours (Chapter 2, Figure 2.1.A). Interestingly after 48 hours, there was a significant increase ($p<0.05$) in the percentage of L8G infected cells, which reached a maximum of 65.1±4% by 96 hours (Figure 3.5). For S1G, a gradual non-significant elevation in infection rate was observed. In contrast, camptothecin appeared to have an adverse effect on O5G infected cells, as the percentage of infection was lower than non-induced O5G infected cells at 48, 72 and 96 hours (Figure 3.5). Despite the increase in L8G infection, no significant increase in the percentage of apoptosis was detected in infected only population (Figure 3.6 A[ii]).

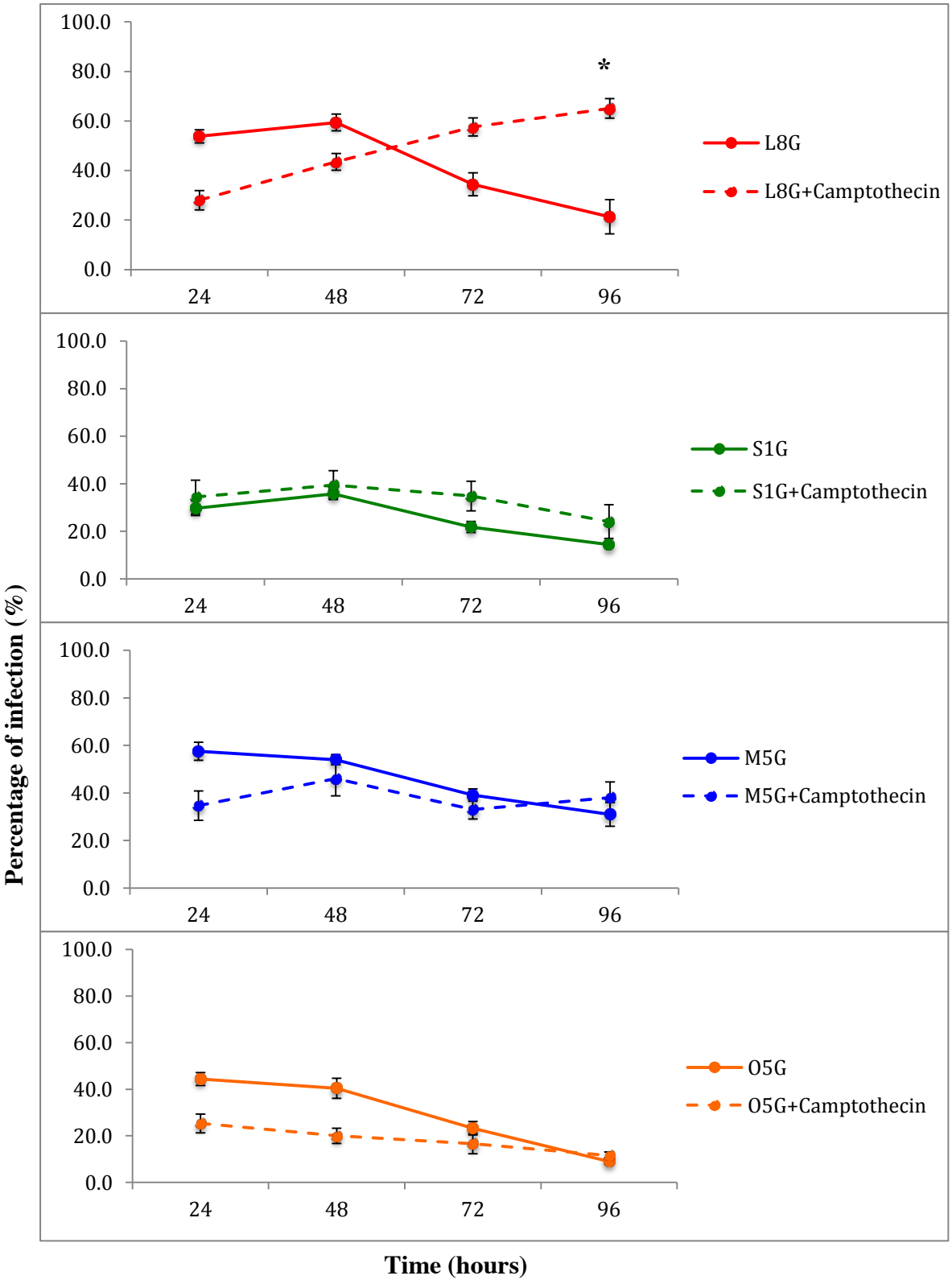


Figure 3.5. Effect of longer exposure to camptothecin treatment on *Leishmania* infection. Following infection (10 parasites per 1 cell ratio) with L8G, S1G, M5G and O5G, the infected cells were treated with or without camptothecin. The percentage of infection was determined at 24, 48, 72 and 96 hours through flow cytometry. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$.

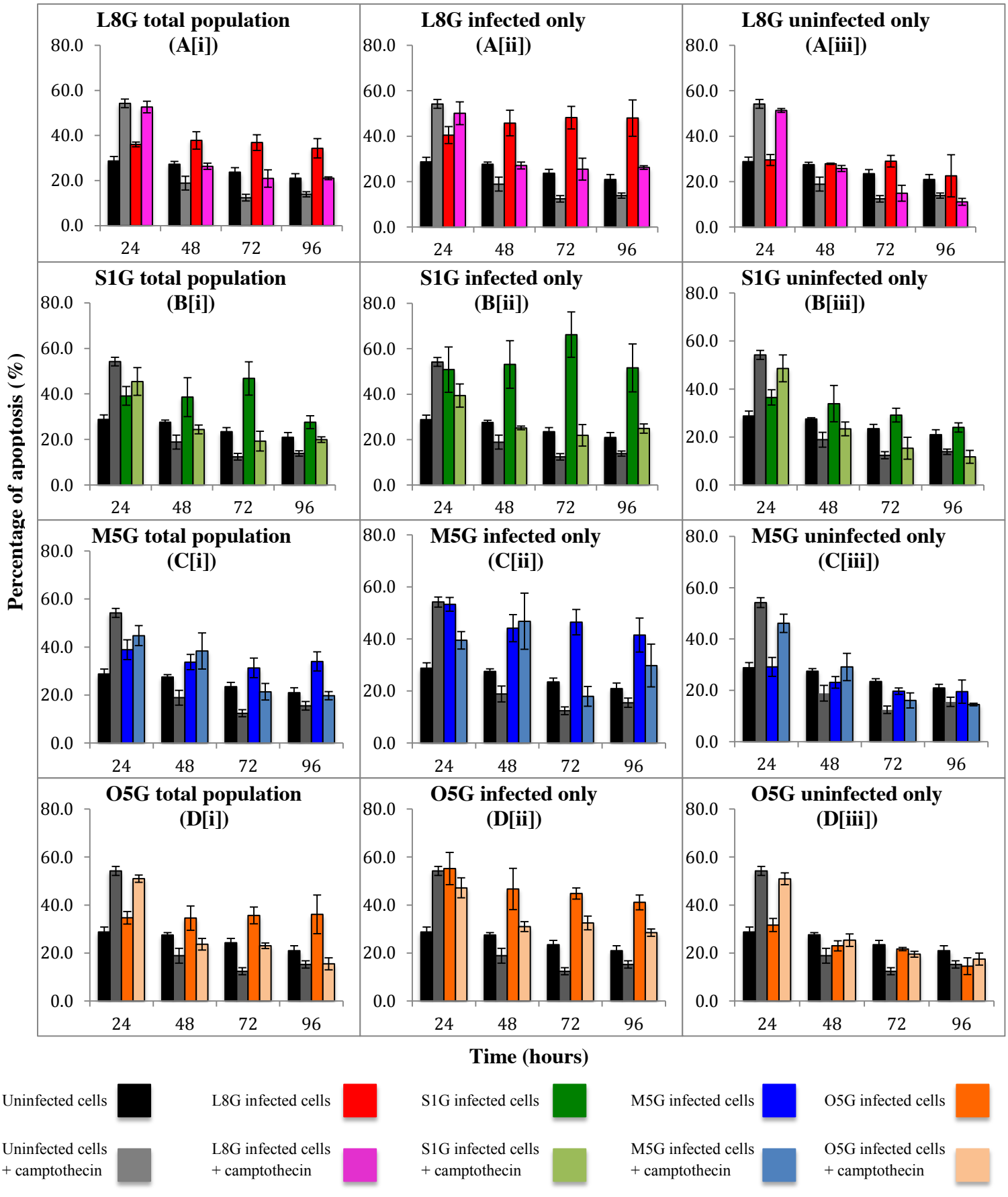


Figure 3.6. Effect of longer exposure to camptothecin treatment on the apoptosis of differentiated THP-1 macrophages infected with *Leishmania*. Following infection (10 parasites per 1 cell ratio) with L8G, S1G, M5G and O5G, the infected cells were treated with or without camptothecin. The percentage of apoptosis in total population was detected at 24, 48, 72 and 96 hours [i]. The data was divided into infected only [ii] and uninfected only [iii] populations. The data represents mean percentage (mean ± SEM) from three independent experiments.

This finding suggested two possibilities. 1) There is no correlation between apoptotic induction and infection. 2) The longer duration of camptothecin treatment led to necrosis. Examination of Annexin V/ 7-AAD dot plot supported the latter notion, as significant proportions of cells were undergoing necrosis in the uninfected and L8G infected culture post 24 hours (Figure 3.7). This clearly indicates that L8G infection rise was not due to parasite spreading, but instead caused by the death of uninfected bystander cells. Hence this optimization approach was not suitable to further investigate infection spreading.

3.2.3b. Time limited treatment with camptothecin

In order to minimise camptothecin induced necrosis, the exposure time of apoptotic inducer in both infected and uninfected cultures was decreased. Excess camptothecin was removed from the culture media after 24 hours of infection. The subsequent percentage of apoptosis and infection were determined at 24, 48, 72 and 96 hours through flow cytometry (Chapter 2, Figure 2.1.B). This method clearly reduced the percentage of necrotic cells post 24 hours, as indicated from Annexin V/ 7-AAD dot plot (Figure 3.8).

Similar to the previous experiment, the camptothecin induction showed a significant increase in the percentage of cells infected with L8G from 48 hours, reaching a maximum of 73.1±6.3% at 96 hours (Figure 3.9). However, such effects were not detected for S1G, M5G and O5G infected cell (Figure 3.9). Interestingly, in the presence of camptothecin, the percentage of apoptosis in L8G infected only population also markedly increased from 48 to 96 hours (Figure 3.10 A[ii]). This finding suggests a link between apoptotic induction and potential spreading of L8G parasites.

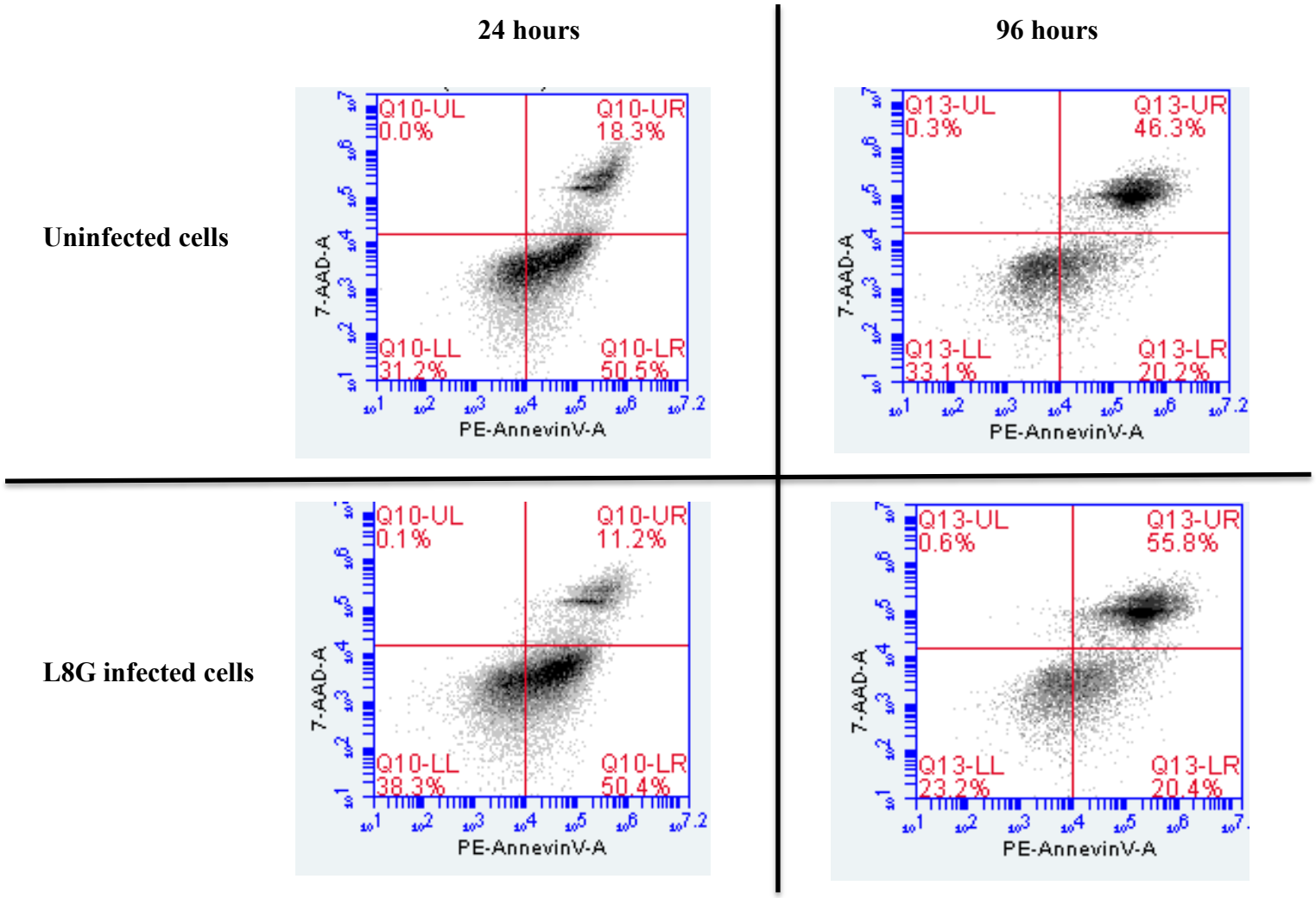


Figure 3.7. Flow cytometry analysis of Annexin V versus 7-AAD dot plot. Infected (e.g. L8G) and uninfected cells were treated with camptothecin and analysed for apoptosis from 24 to 96 hours. Without the removal of camptothecin, uninfected and L8G infected cells at 96 hours incubation showed an extreme level of necrosis (Q13-UR), compared with 24 hours. Moreover, this characteristic was also maintained at 48 and 72 hours from infection as well in all fours species examined.

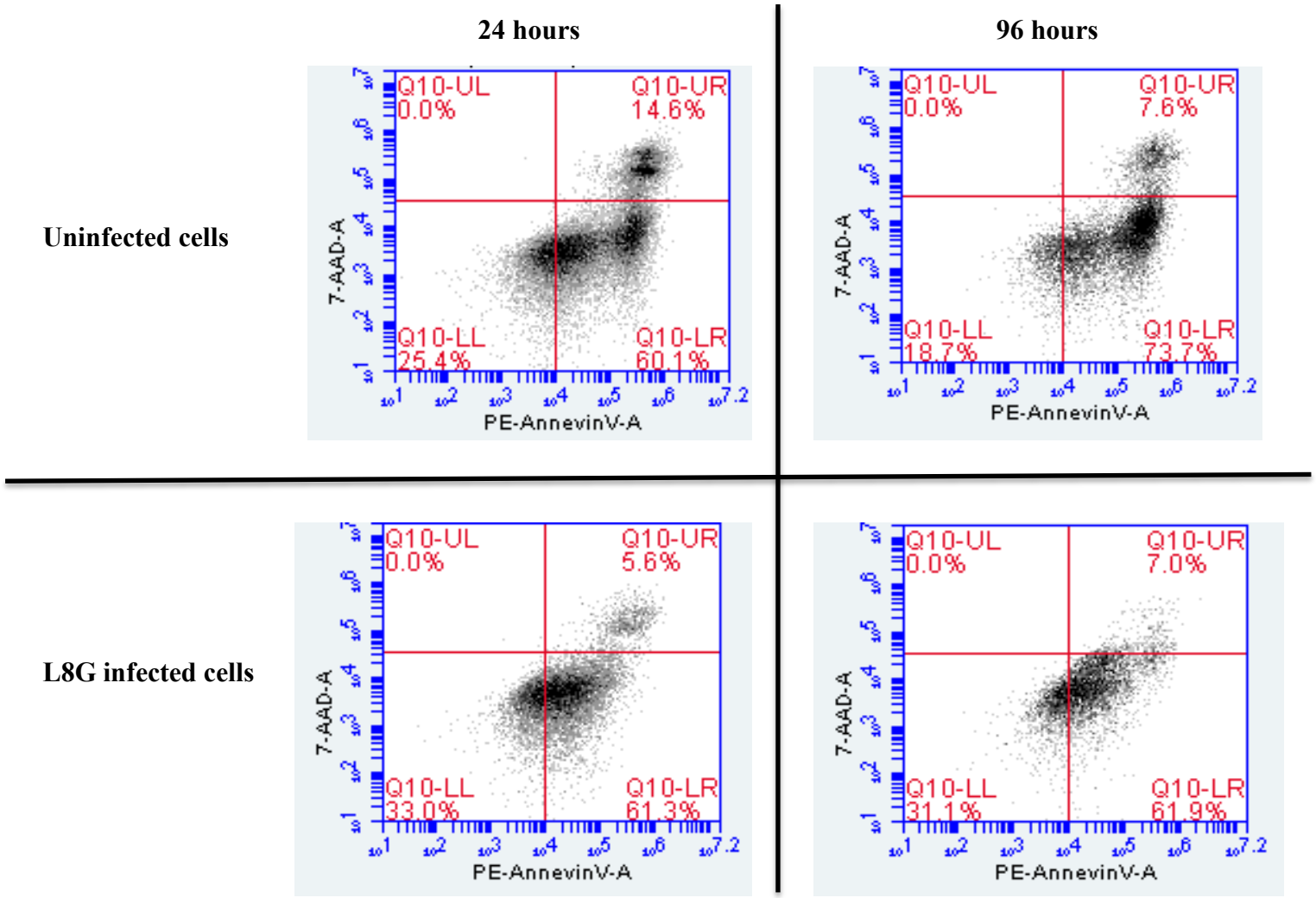


Figure 3.8. Flow cytometry analysis of Annexin V versus 7-AAD dot plot after washing protocol. Infected (e.g. L8G) and uninfected cells were treated with camptothecin and washed after 24 hours before analysing for apoptosis from 24 to 96 hours. By removing excess camptothecin (after 24 hours incubation), uninfected and L8G infected cells at 96 hours incubation showed comparable levels of necrosis in relative to 24 hours. Moreover, this characteristic was maintained at 24 and 72 hours from infection as well in all fours species examined.

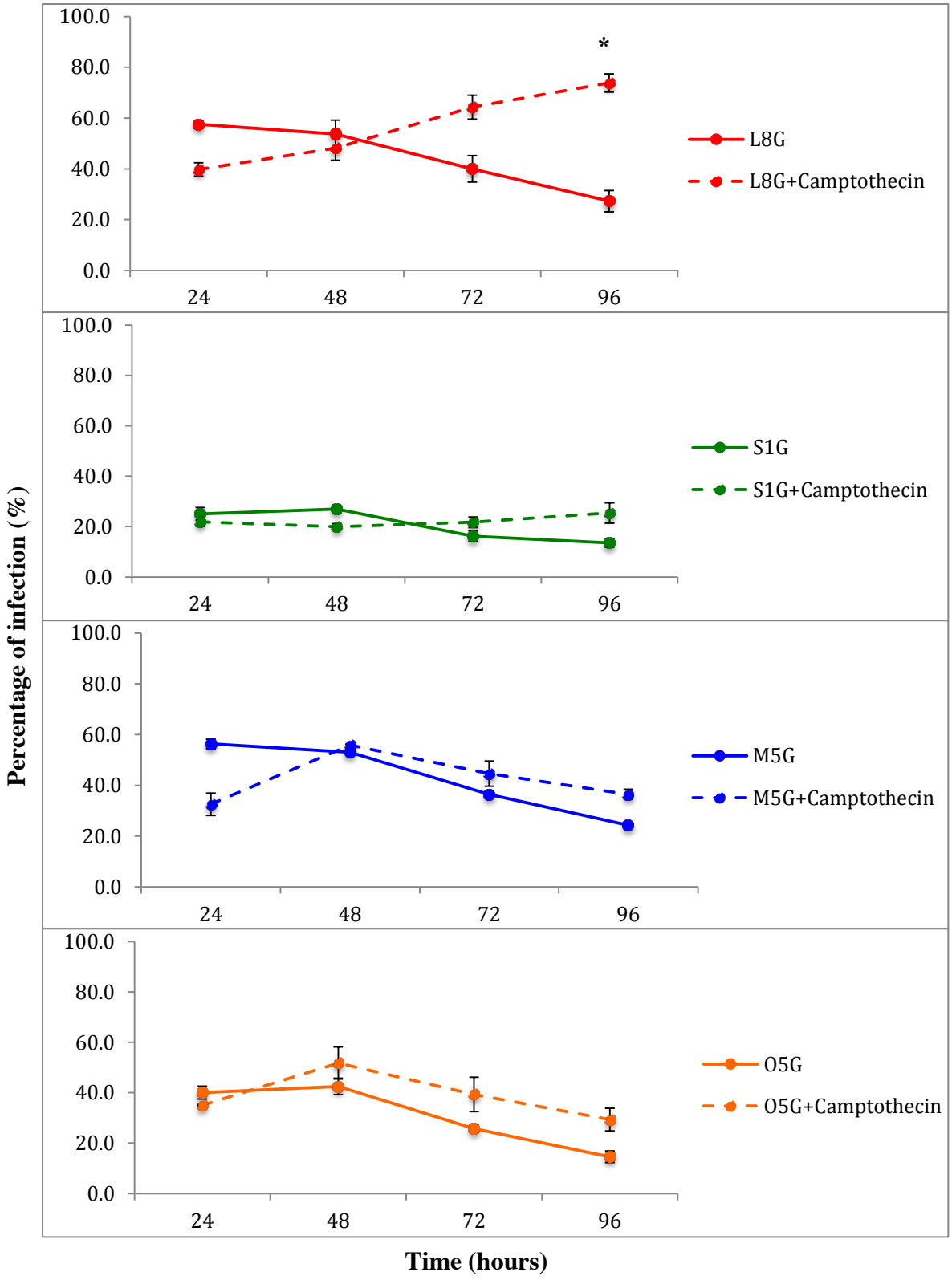


Figure 3.9. Effect of shorter exposure to camptothecin treatment on *Leishmania* infection. Following infection (10 parasites per 1 cell ratio) with L8G, S1G, M5G and O5G, the infected cells were treated with or without camptothecin. After 24 hours of infection, excess drug was washed away. The percentage of infection was then determined at 24, 48, 72 and 96 hours through flow cytometry. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$.

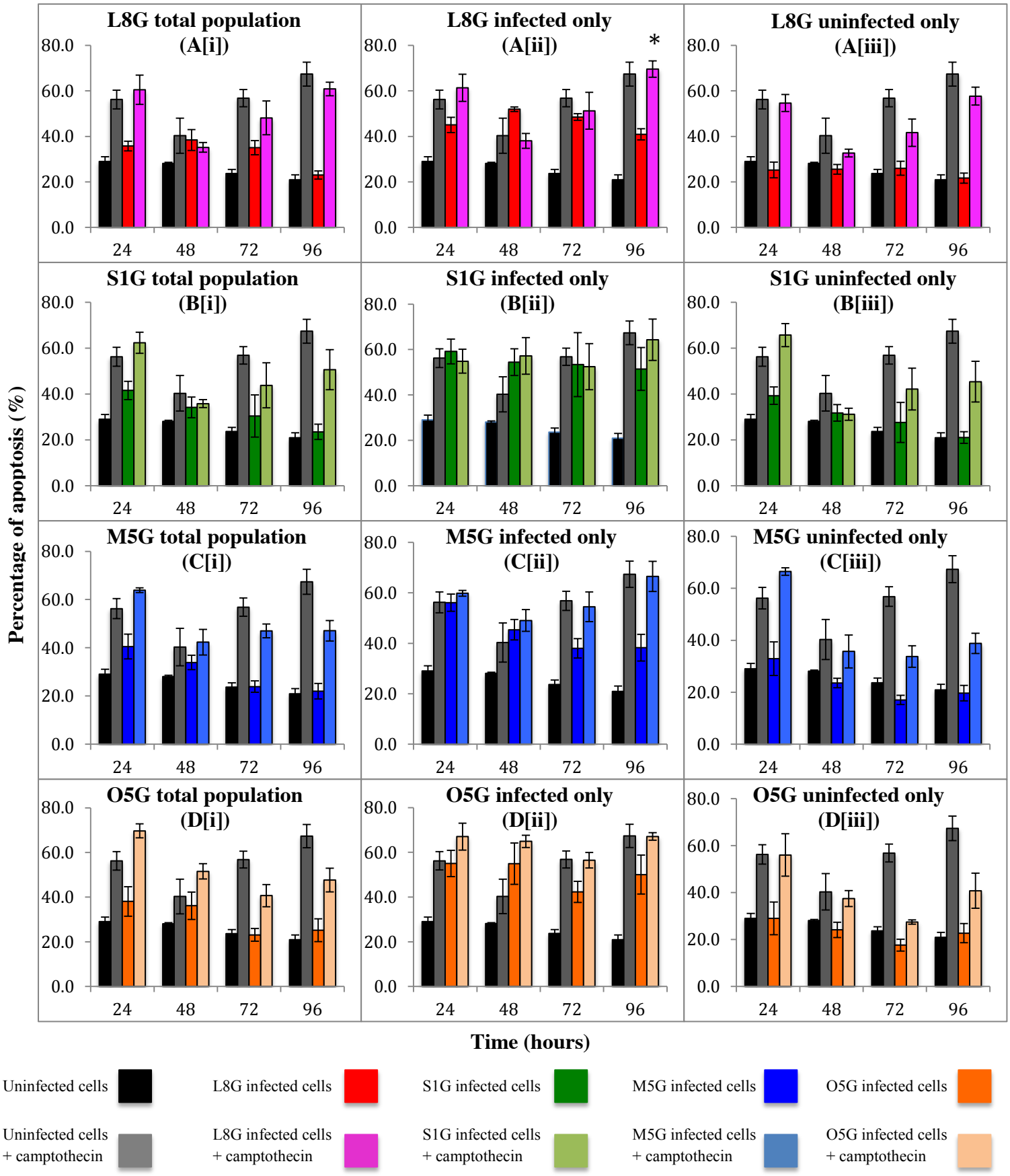


Figure 3.10. Effect of shorter exposure to camptothecin treatment on the apoptosis of differentiated THP-1 macrophages infected with *Leishmania*. Following infection (10 parasites per 1 cell ratio) with L8G, S1G, M5G and O5G, the infected cells were treated with or without camptothecin. After 24 hours of infection, excess drug was washed away. The percentage of apoptosis in total population was detected at 24, 48, 72 and 96 hours [i]. The data was divided into infected only [ii] and uninfected only [iii] populations. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$

3.2.4. Assessment of viable cell concentration during *Leishmania* infection in the presence of camptothecin

According to the above data, camptothecin treatment caused a significant rise in L8G infection, which was correlated with an increase in host cell apoptosis. To confirm whether this increase could be due to parasite spreading or loss of viable cells, trypan blue assay was performed. The result showed no significant difference in the concentration of viable cells in L8G infected cells from 24 to 96 hours in the presence of camptothecin (Figure 3.11). This indicates that parasite dissemination must be occurring within this time frame.

However, when the above result is compared against non-treated samples, there is a marked reduction in the concentration of viable cells in L8G infected culture throughout the time point (Figure 3.11). This suggests that the recipient cells within the infected culture may not be healthy and do not represent an effective model to study cell-to-cell spread.

3.3. Conclusions

In conclusion, this chapter demonstrated a clear link between *Leishmania* infection spreading and host cell apoptosis. This was confirmed through two experimental approaches. Firstly, promastigotes infection with *L. aethiopica*, *L. major*, *L. mexicana* and *L. tropica* caused an induction of apoptosis in differentiated THP-1 macrophages till 96 hours. However, as a result of uninfected THP-1 cells replication, there was a significant decrease in the percentage of infection in all four species.

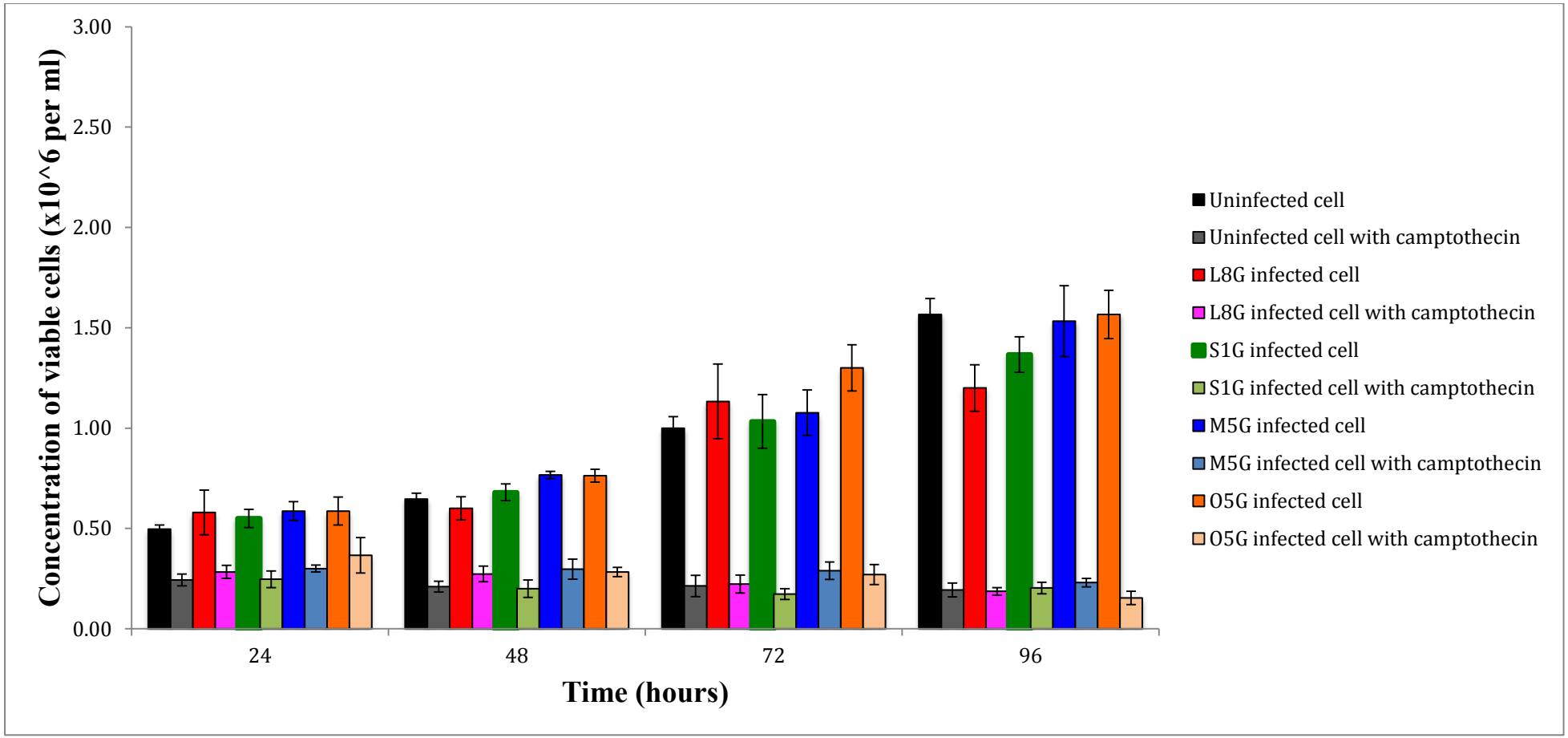


Figure 3.11. Effect of camptothecin on viable cell concentration in the presence or absence of infection. Uninfected or infected cells (L8G, S1G, M5G and O5G) treated with or without camptothecin were stained with trypan blue solution at 24, 48, 72 and 96 hours. The data represents mean concentration of viable cells (mean±SEM) from three independent experiments.

This made it difficult to detect infection and parasite dissemination from 48 hours onwards. This led to a second approach whereby infected cells were treated with apoptotic inducer to determine whether apoptotic induction had an effect on the outcome of infection. By optimizing the length of camptothecin treatment, a time dependent increase in the percentage of *L. aethiopica* infected cells was detected from 48 to 96 hours. As this effect was correlated with increased percentage of apoptosis, a positive link between infection spreading and apoptotic cell death was suggested. However, since the trypan blue assay revealed a marked reduction in the concentration of viable cells when compared to non-treated samples, this raised major doubts on whether the recipient cells are physiologically healthy to represent a cell-to-cell spreading model. Therefore, a novel *in vitro Leishmania* infection model needs to be optimized if infection spreading is to be carried out for further investigation.

Chapter 4 – The *in vitro* development of *Leishmania* dissemination model during late stage of macrophage infection

4.1. Introduction

The dissemination of infectious progeny from cell-to-cell is of vital importance for disease establishment by intracellular human pathogens. Various *in vitro* models have been successfully used to study cell-to-cell spreading for a number of human pathogens such as, *Listeria monocytogenesis* (Czuczman et al., 2014), *Shigella flexneri* (Fukumatsu et al., 2012), *Legionella pneumophila* (Chen et al., 2004), Human Immunodeficiency Virus (HIV) (Sattentau, 2010) and *Cryptococcus neoformans* fungus (Ma et al., 2007). Although these studies highlighted the diverse mechanism of pathogen spreading, whether such process is also reflected in natural infection transmission requires the use of *in vivo* animal models.

However, animal models designed to address infection spreading have various limitations, which are: 1) The approach is labor intensive and time consuming as it requires large number of animals to be sacrificed to obtain convincing data; 2) Dissection of animal at each set of time point means it would be impossible to monitor the progress of infection for an individual animal over time; 3) The approach is dependent on researcher's knowledge of the infected organs, as dissemination to unexpected anatomical sites or even to particular sub-compartments of the organ being examined may easily be missed. Due to these constraints, *in vitro* model represent a more suitable experimental system to investigate the spreading of human pathogens, including *Leishmania* parasites.

Unfortunately, *in vitro* studies associated with *Leishmania* spreading are very scarce due to experimental difficulty to model late stage of parasite-host interaction. Nevertheless, through live video microscopy, a recent study was able to show the transfer of amastigotes from 20 days *L. amazonensis* infected mice BMDM to RAW mice macrophages within 24 hours of cell-to-cell infection (Real et al., 2014). However, since mice are not the natural host for *Leishmania*, it is difficult to extrapolate the above findings from mice to human macrophage. Interestingly, another study successfully demonstrated *L. infantum chagasi* spreading in human U937 macrophages within 72 hours of infection (Hsiao et al., 2011). However, such phenomena were not observed in primary human monocyte derived macrophages (MDM), thereby underlying the importance of selecting a suitable cell line for *Leishmania* infection.

The present chapter, which is an extension of the work from chapter 3, is aimed at developing a novel *in vitro* model to study the dissemination of two *Leishmania* species, *L. aethiopica* and *L. mexicana*. By employing a cell associated infection strategy, the late stages of *L. aethiopica* and *L. mexicana* infected population were used as a donor cells to re-infect freshly differentiated THP-1 macrophages. Such co-culture system was optimized to identify the time frame behind amastigote spreading, which was confirmed via flow cytometry and real time lapse microscopy analysis. Moreover, to gain an understanding of the possible mechanism behind parasite spreading, two apoptotic markers including phosphatidyl serine (PS) externalization and caspase-3 activation within this time frame was assessed.

4.2. Results and Discussion

4.2.1. Optimization of camptothecin treatment in *L. mexicana* (M5G) infected cells

In order to optimize spreading, population of highly infected cells need to be isolated. As previously reported (Chapter 3, section 3.2.3), the largest proportion of *L. aethiopica* (L8G) infected cells was found at 72 and 96 hours from infection, following 24 hours camptothecin treatment. However, such effects were not detected during M5G infection. Based on a well-known notion that species-specific difference occurs in *Leishmania* parasites (Ilg, 2000), M5G infected cells were treated with camptothecin for only 5 hours from infection.

At 24 hours, there was no significant difference in the percentage of M5G infection between camptothecin treated and non-treated samples (Figure 4.1). Interestingly, the percentage of M5G infected cells increased significantly ($p<0.05$) from 24 hours, reaching a maximum of 90% by 72 hours in the presence of camptothecin. As expected, M5G infection in the absence of camptothecin stabilized at 48 hours, before dramatic reduction occurred at 72 and 96 hours. However, in camptothecin treated samples, the percentage of M5G infected cells remained high and plateaued till 96 hours. Hence, by reducing the exposure time of apoptotic induction, M5G was clearly able to maintain higher percentage of infected cells during the late stage of infection, similarly to what had been described for L8G in chapter 3.

4.2.2. Infection of differentiated THP-1 macrophage with L8G and M5G infected cells

Since the effect of camptothecin led to an increase in the percentage of L8G and M5G infected cells, this population was isolated and used to infect a freshly prepared culture of differentiated THP-1 macrophages.

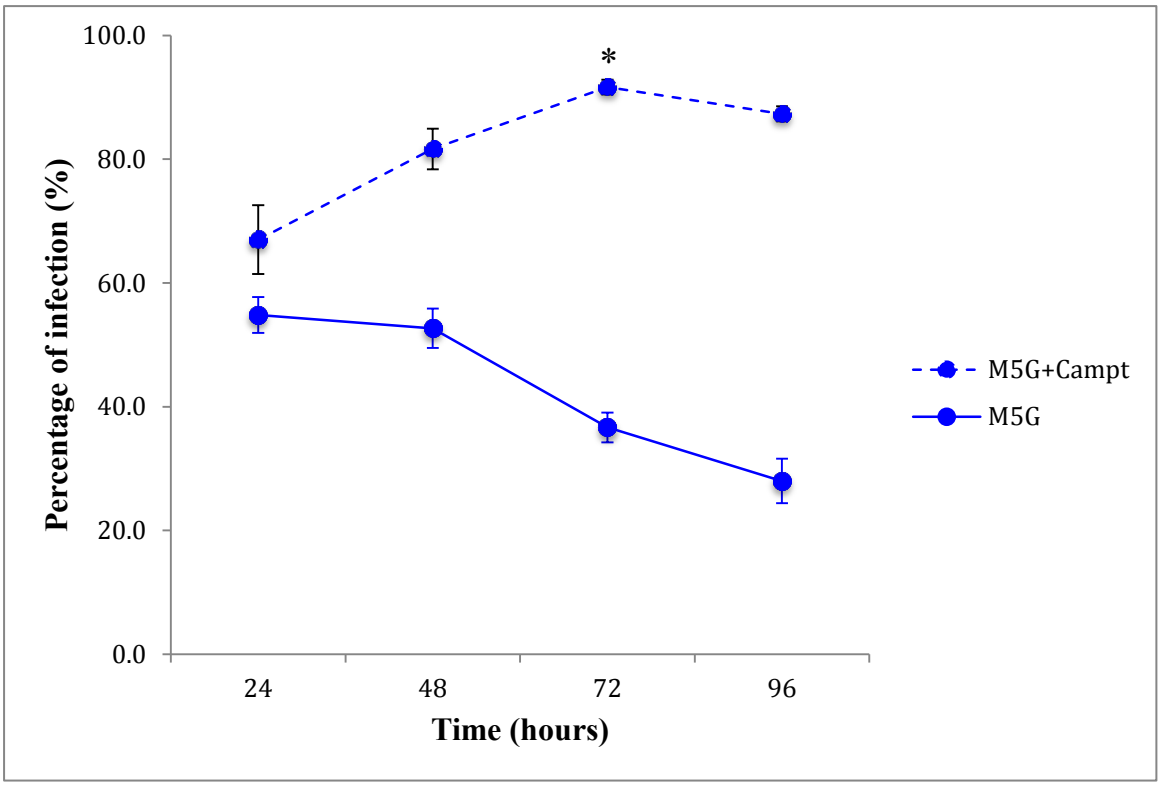


Figure 4.1. Time course of differentiated THP-1 macrophage infection with *L. mexicana* (M5G) in the presence and/or absence of apoptotic induction. Differentiated THP-1 macrophages were infected M5G promastigotes at 10:1 ratio (parasite to cell ratio) and treated with (or without) camptothecin to induce apoptosis. Excess camptothecin was washed away from culture medium at 5 hours after infection. The percentage of infection was determined through flow cytometry at 24, 48, 72 and 96 hours. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$

To initiate cell-to-cell infection, L8G and M5G infected cells from 72 hours were used as the donor population. Different infection ratios were tested (1:1, 5:1 and 10:1 [infected per healthy cell ratio]) and the course of infection was detected at 0, 12, 24 and 48 hours after co-culture through flow cytometry. At 0 hour after co-culture between infected and uninfected cells, a dilution effect on the percentage of infection for both L8G and M5G was detected (Figure 4.2.A and 4.2.C). Since a higher proportion of uninfected cells were incorporated with GFP positive infected cells at 1:1 infection ratio, this specific ratio generated a more pronounced decrease in infection than 5:1 and 10:1 ratio at 0 hour after co-culture. Strikingly, after 12 hours of co-culture, the percentage of L8G infected cells significantly increased ($p<0.05$) from 35±2.6 to 60±2.1% for 1:1, 54±2.4 to 69±2.9% for 5:1 and 58±4.1 to 74±0.8% for 10:1 infection ratios (Figure 4.2.B). Such significant increase in infection was also observed during co-culture with M5G infected cells; 51±2.3 to 76±5.5% for 1:1, 71±3.5 to 88±0.6% for 5:1 and 80±2.1 to 90±2.3% for 10:1 infection ratios (Figure 4.2.D).

The significance of the above findings is strengthened by the viability count, which showed no significant differences in the concentration of viable cells between 0 and 12 hours post infection (Figure 4.3). This strongly suggested that the infection increase from 0 to 12 hours time frame was due to spreading of L8G and M5G amastigotes from the 72 hours donor infected cells to healthy cells and not caused by the reduction of uninfected viable cells. However, there were no further increase in the percentage of L8G and M5G infected cells from 12 to 24 hours after co-culture (Figure 4.2.B and 4.2.D). This suggests that the transferred amastigotes in its new macrophage niche were unable to replicate within this time frame to continue next round of cell-to-cell spreading.

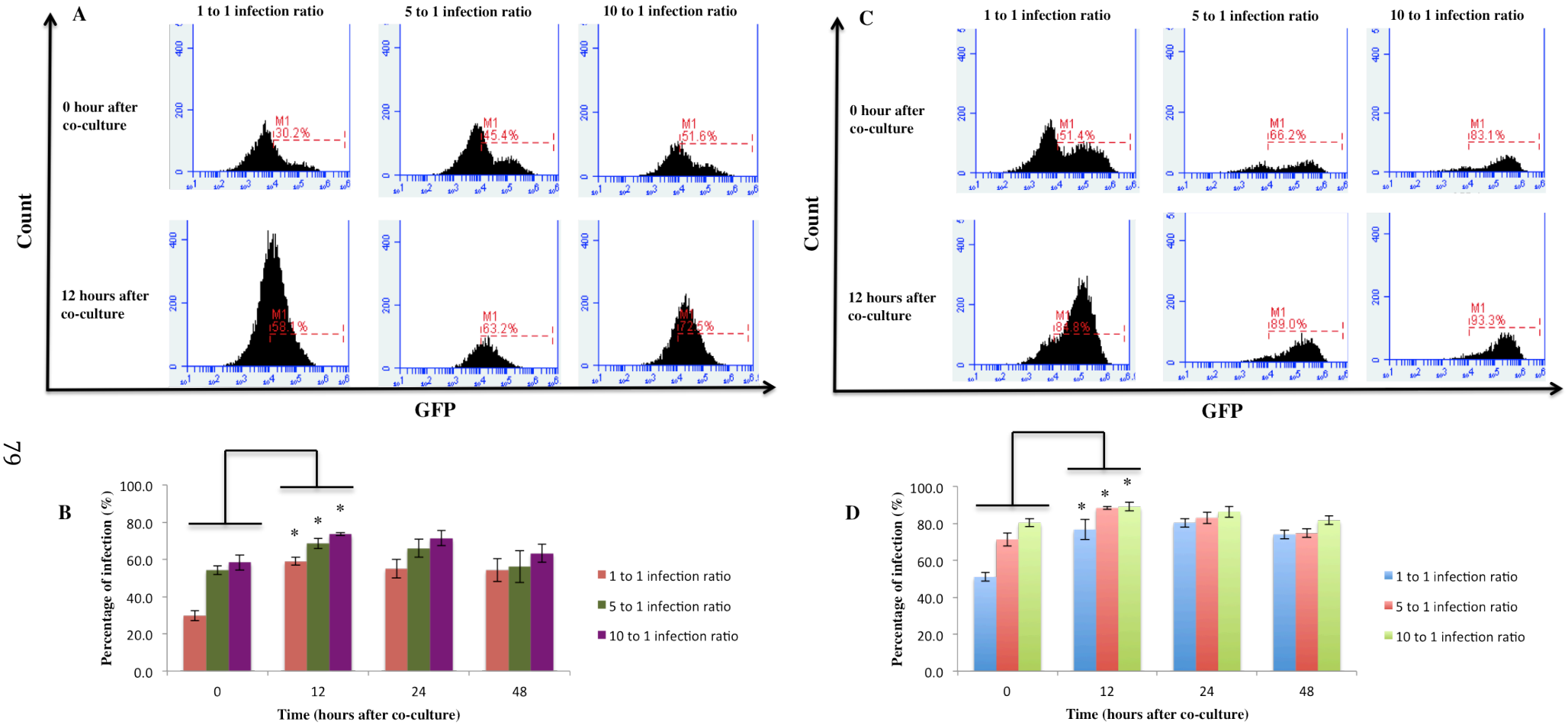


Figure 4.2. Infection of THP-1 macrophages with *Leishmania* infected cells. After 72 hours of infection, L8G and/or M5G infected cells were co-cultured with a fresh population of differentiated THP-1 macrophage at different infection ratios, 1:1, 5:1 and 10:1 (infected to uninfected cell ratio). (**A**) Flow cytometry histogram plot representative of L8G infected cells M1 at 0 and 12 hours after co-culture. (**B**) A bar graph representative of the percentage of L8G infection (mean ± SEM) at 0, 12, 24 and 48 hours after co-culture. (**C**) Flow cytometry histogram plot representative of M5G infected cells M1 at 0 and 12 hours after co-culture. (**D**) A bar graph representative of the percentage of M5G infection (mean ± SEM) at 0, 12, 24 and 48 hours after co-culture. * = $p<0.05$

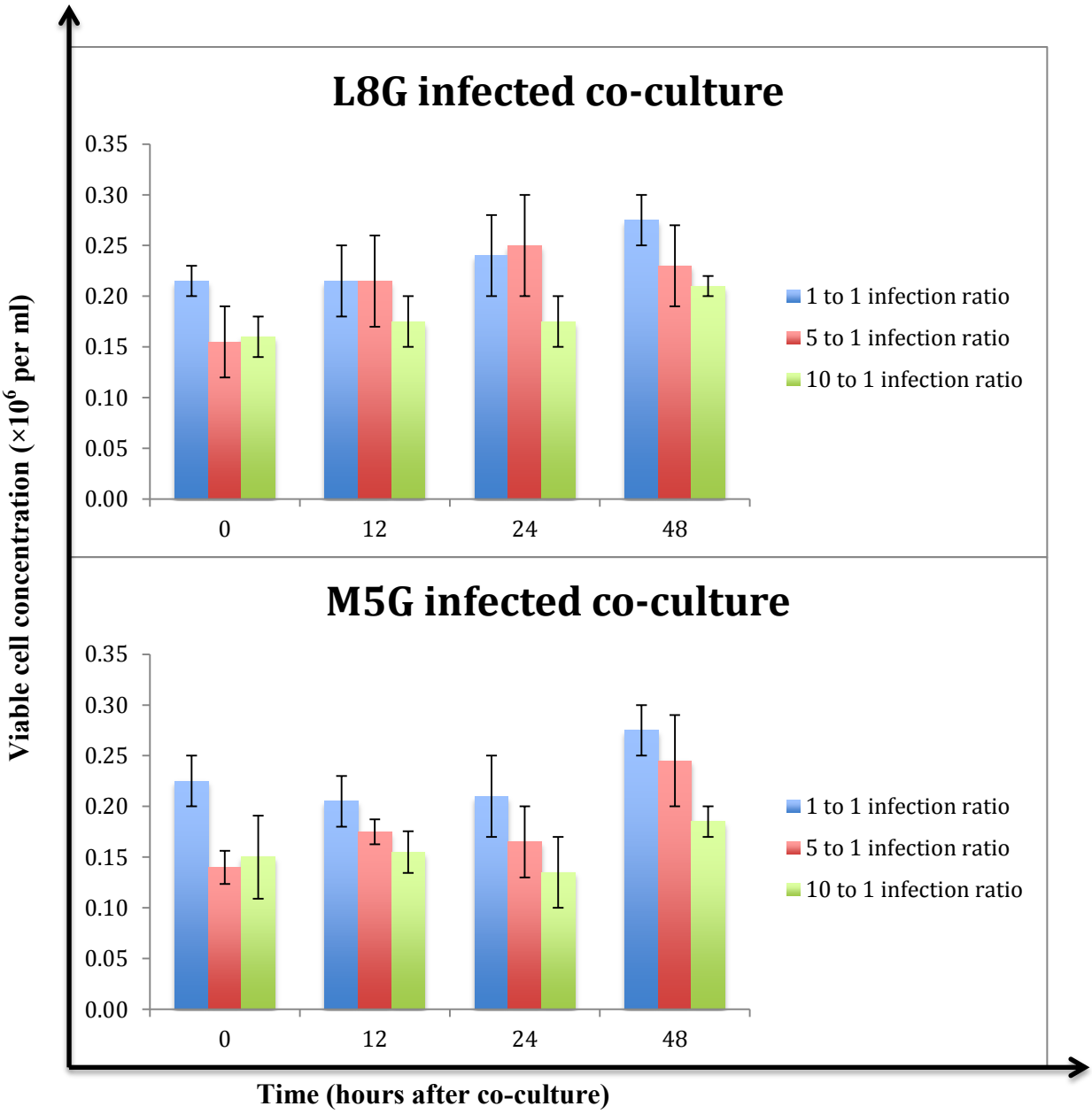


Figure 4.3. Measurement of viable cell concentration during infection with *Leishmania* infected cells. L8G infected and M5G infected co-culture cells at different infection ratios were stained with trypan blue solution at 0, 12, 24 and 48 hours after co-culture. The data represents mean concentration of viable cells (mean ± SEM) from three independent experiments.

Overall, the above results provided a quantitative evidence for L8G and M5G amastigotes spreading from 0 to 12 hours after co-culture. This *in vitro* spreading model provides an initial platform to address the cellular mechanism behind the 12 hours spreading time period.

4.2.3. Live cell imaging of intracellular L8G and M5G amastigotes spreading

During cell-to-cell infection spreading, intracellular pathogens within the donor cells can trigger either a lytic or a non-lytic release (Sattentau, 2010). To verify whether such process might occur during L8G and M5G release, real time lapse microscopy was performed using the newly developed *in vitro* spreading model comprising of 1:1 infection ratio. An advantage of 1:1 infection ratio over 5:1 and 10:1 was to ensure that there would be sufficient numbers of recipient host cells to harbor the released amastigotes.

Initially, differentiated THP-1 macrophages (pre-stained with membrane dye) were co-cultured with L8G and/or M5G infected cells and live cell imaged over 12 hours. Figure 4.4 shows time lapse events from 8 hours, in which L8G amastigotes (pointed with red arrow) begins to migrate towards the peripheral membrane of the donor cells, before completely transferring into the already infected recipient stained cells within 20 minutes of recording. This phenomenon was also visualized in M5G infected co-culture after 6 hours whereby an amastigote (pointed with red arrow) appeared to be extruded into the recipient stained cells (Figure 4.5). Since the donor cell membrane (in both scenarios) was not damaged during amastigote transfer, this suggests that *Leishmania* spread via non-lytic mode. It is not clear whether recipient macrophages selectively engulf L8G and M5G via recognition of parasite or host associated markers present in the donor cell.

L. aethiopica spreading

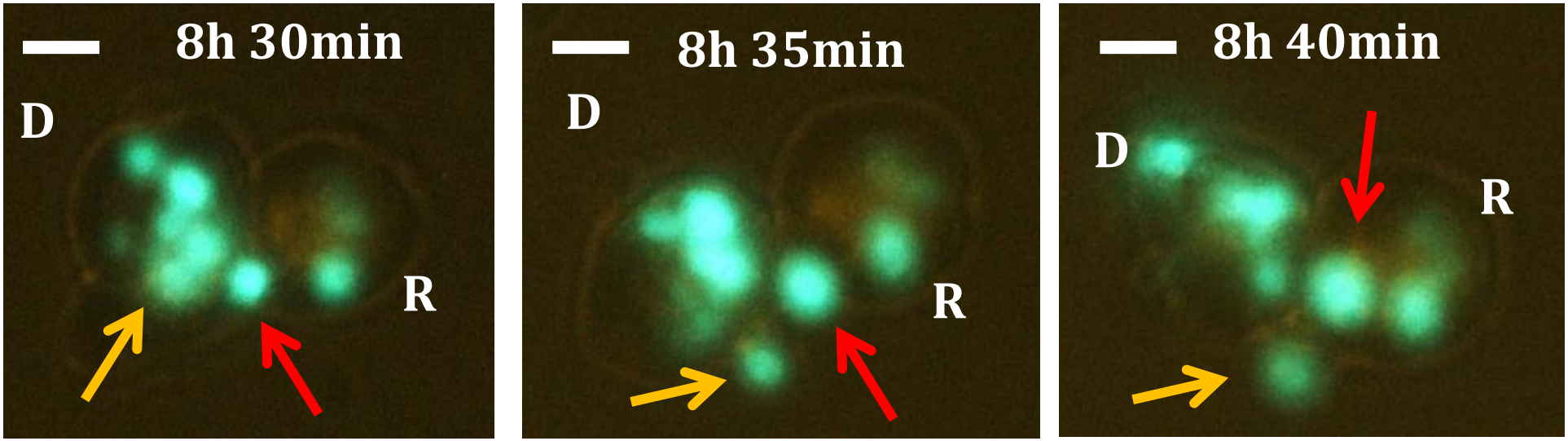


Figure 4.4. Live cell imaging of *L. aethiopica* (L8G) amastigotes spread from cell-to-cell. The differentiated THP-1 macrophage, which is the recipient uninfected cells (labeled as R), was pre-stained with CellMask^{TM} orange plasma membrane dye. The recipient cells were then co-cultured with L8G infected cells, which is the donor cells (labeled as D) as described in Chapter 2, section 2.8. The time of acquisition is represented by hours (h) and minutes (min). Image acquisition started at 8 hours after co-culture. Bar = 25 μm.

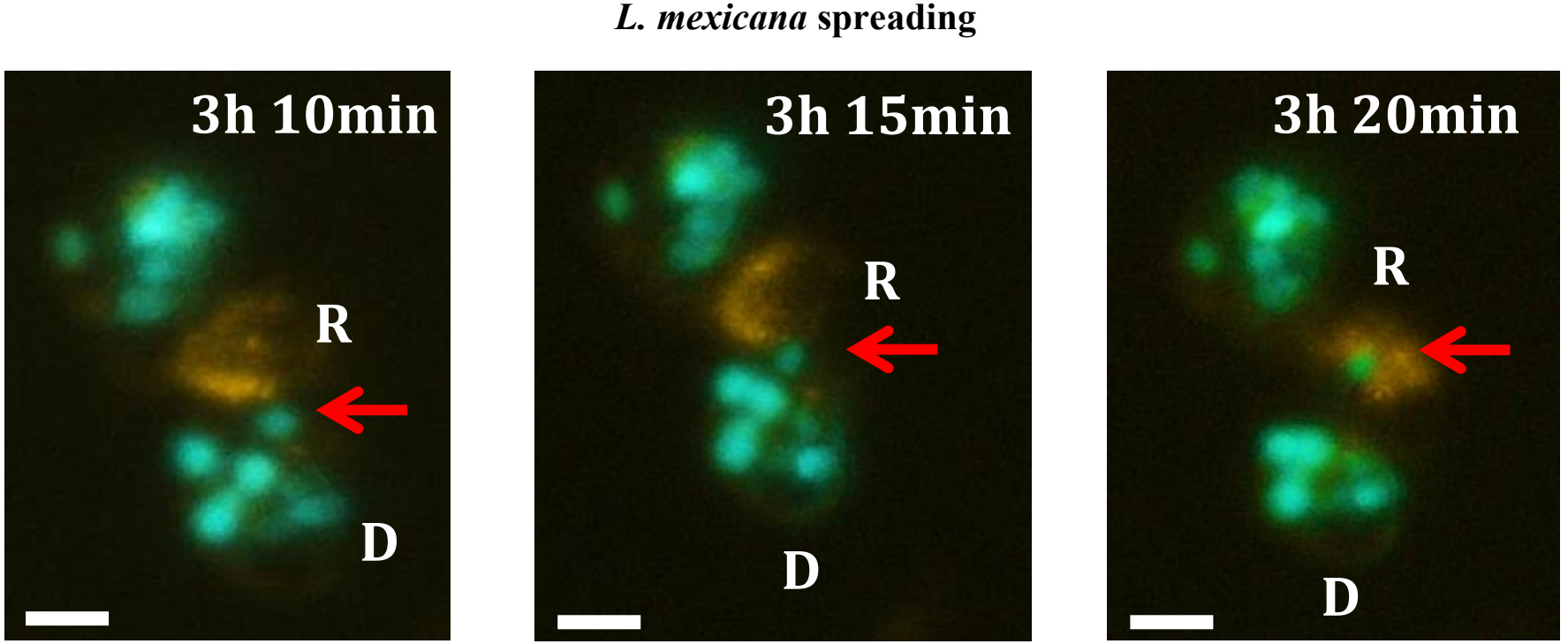


Figure 4.5. Live cell imaging of *L. mexicana* (M5G) amastigotes spread from cell-to-cell. The differentiated THP-1 macrophage, which is the recipient uninfected cells (labeled as R), was pre-stained with CellMask^{TM} orange plasma membrane dye. The recipient cells were then co-cultured with M5G infected cells, which is the donor cells (labeled as D) as described in Chapter 2, section 2.8. The time of acquisition is represented by hours (h) and minutes (min). Image acquisition started at 3 hours after co-culture. Bar = 25 μm.

In summary, the real time lapse microscopy revealed the non-lytic release of amastigotes from cell-to-cell and provided confirmation of a strong link with quantitative flow cytometry data on infection spreading. This has now opened up an avenue to further investigate the role of host cells in facilitating the spreading of *Leishmania* amastigotes.

4.2.4. Effect of *Leishmania* spreading on the apoptosis of host cells

A recent study revealed the non-lytic exit of *L. amazonensis* amastigotes from mice macrophage was correlated with apoptotic features such as zeiotic and blebbed membranes (Real et al., 2014). Therefore, in order to determine whether apoptosis could also be involved in the spreading of *L. aethiopica* and *L. mexicana*, the presence of host apoptotic markers, i.e. Phosphatidyl serine (PS) externalization and Caspase-3 activation, were tested using the newly developed model.

Initial assessment of PS externalization showed a time dependent increase in the percentage of apoptosis from 1 to 12 hours after co-culture with L8G infected cells (Figure 4.6.A). This effect appeared to be mediated solely by the intracellular L8G amastigotes since the uninfected cells co-culture displayed no significant changes in apoptosis within 12 hours. Interestingly, direct analysis of the L8G infected only population showed that the percentage of apoptosis was significantly higher ($p<0.05$) at 12 hours (55±3.5%) than at 1 hour (38±4.1%) (Figure 4.6.B). This clearly indicated a positive correlation between apoptotic induction and infection spreading. In contrast, there were no significant differences in the percentage of nerosis from 1 to 12 hours in L8G infected only population (Appendix I). This together with the fact that the necrosis in the uninfected only population was comparable with the control suggested that L8G infection spreading was independent with necrotic cell death (Appendix I).

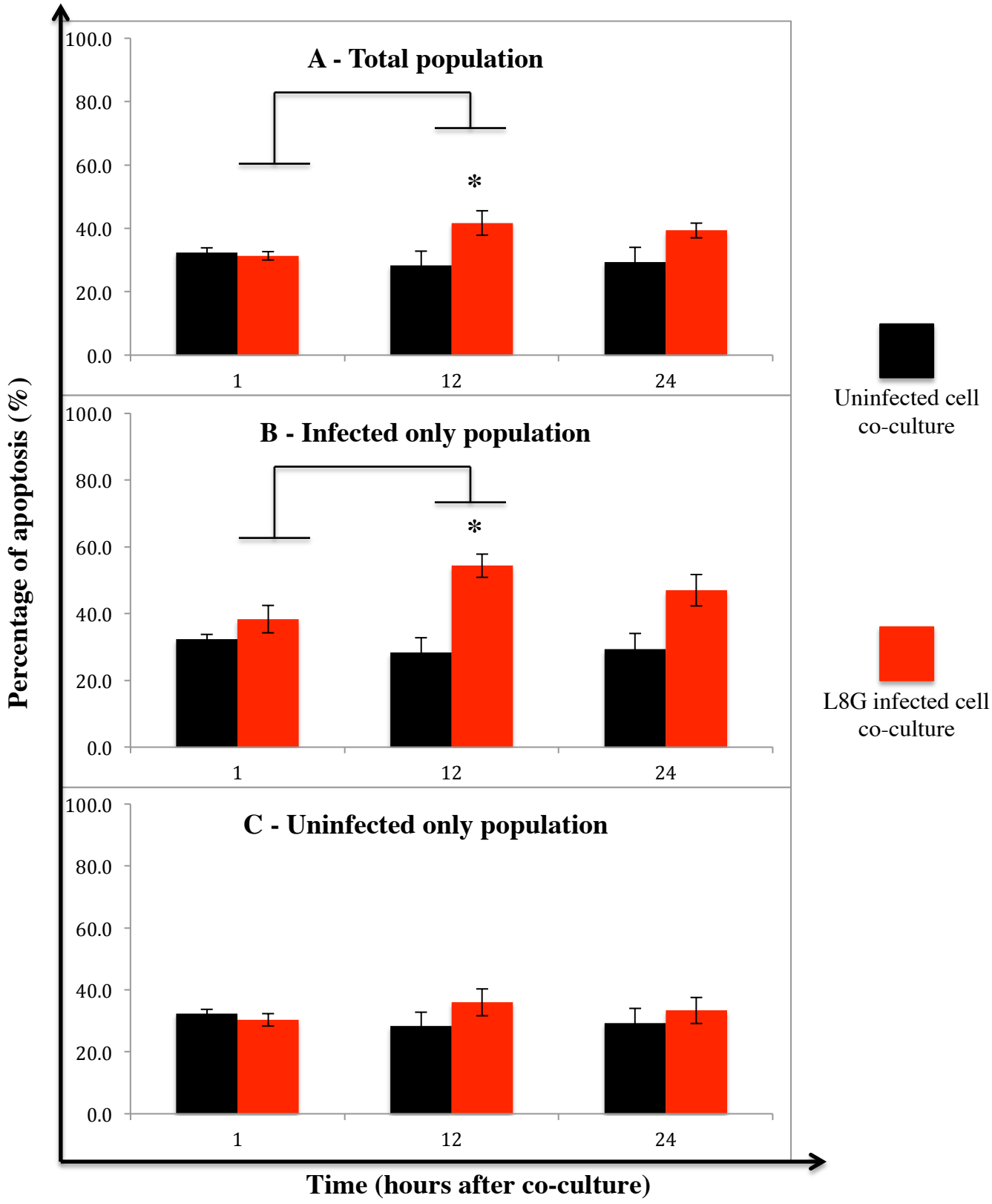


Figure 4.6. Effect of L8G infection spreading on host cell apoptosis. After infection of differentiated THP-1 macrophages with L8G infected cells, the co-culture were analyzed for the percentage of apoptosis (Annexin V+/7AAD-) through flow cytometry at 1, 12 and 24 hours after co-culture. Apoptosis from the total population **(A)** were divided into infected only **(B)** and uninfected only **(C)** populations. Uninfected cells co-cultured with differentiated THP-1 macrophages were taken as a positive control. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$

Next, the expression of active caspase-3 was detected at 1, 3 and 6 and 12 hours after co-culture with L8G infected cells. The percentage of active caspase-3 at 1 hour was comparable to uninfected controls (Figure 4.7). Interestingly, from 3 to 12 hours, the active caspase-3 expression remained significantly higher ($p<0.05$). This data along with PS externalization supports the notion that apoptotic induction is actively occurring during L8G spreading.

These findings were in stark contrast to M5G, as the parasitic spread was not associated with any markers of apoptosis. Firstly, there was no significant increase in the percentage of PS externalized cells from 1 to 12 hours after co-culture (Figure 4.8). Secondly, the percentage of active caspase-3 was comparable with the uninfected control at throughout the spreading time period (Figure 4.9). These suggest the involvement of non-apoptotic mechanism of infection spreading induced by M5G amastigotes.

Dissemination of human pathogens via non-apoptotic has been noted previously. The bacteria *Chlamydia* exit host cells after a non-lytic, actin-dependent extrusion from the host cell. In this process, the bacteria are extruded in a double-membrane vesicle generated from the bacterial intracellular vacuole and cytoplasmic membranes (Hybiske and Stephens, 2007). During *in vitro* cell-to-cell transmission, *M. marinum* is ejected from host cells through an F-actin-rich structure denominated ejectosome (Hagedorn et al., 2009); the bacteria also remain associated with membrane remnants in the process. The fungus *Cryptococcus neoformans* escape from host cells by an active, pathogen-driven extrusion process, apparently without damaging the host (Ma et al., 2007). Whether such mechanism exist during *L. mexicana* spread requires further investigation.

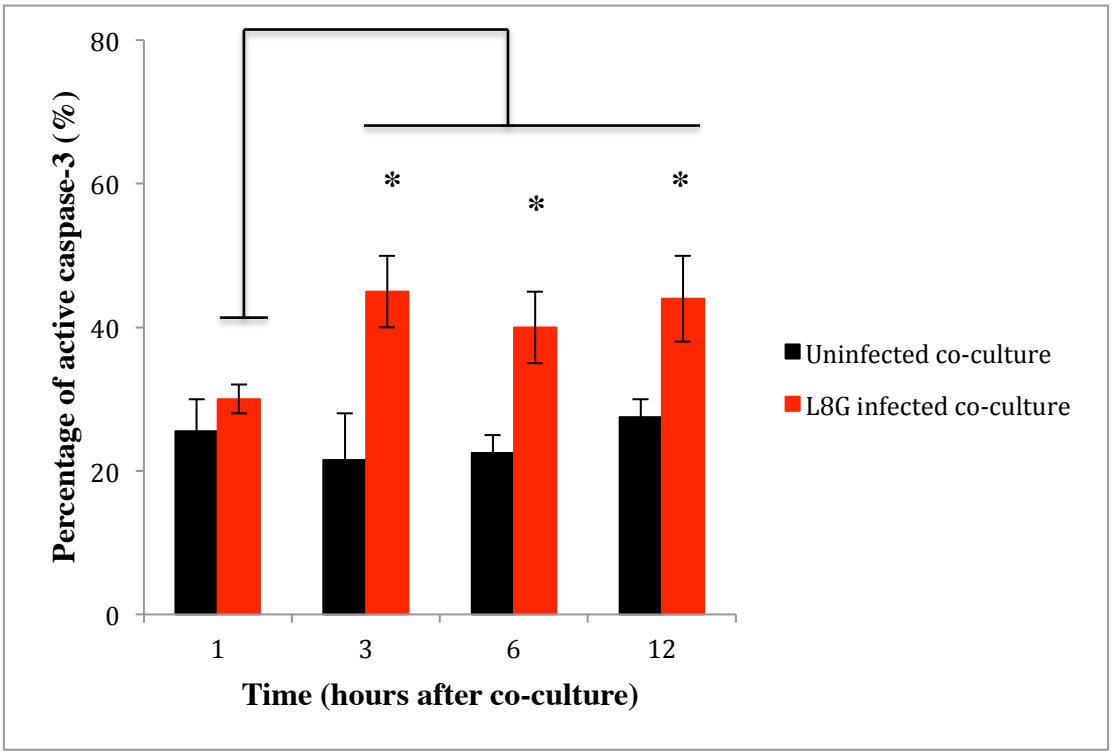


Figure 4.7. Effect of L8G infection spreading on the activation of caspase-3 in host cells. After re-infection of differentiated THP-1 macrophages with L8G infected cells, the co-culture were analyzed for the percentage of activated caspase-3 through flow cytometry at 1,3, 6 and 12 hours after co-culture. Uninfected cells co-cultured with differentiated THP-1 macrophages were taken as a positive control. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$

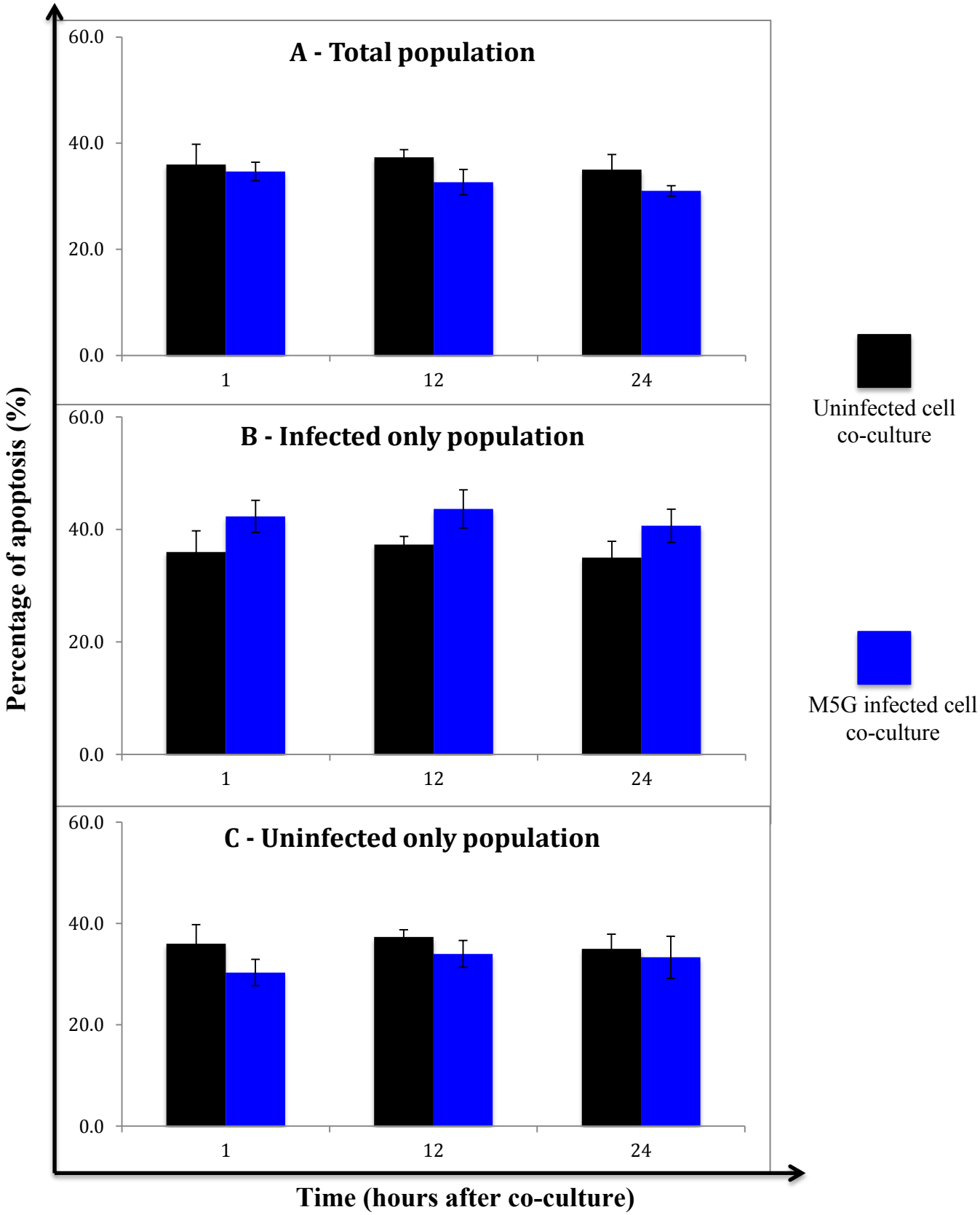


Figure 4.8. Effect of M5G infection spreading on host cell apoptosis. After infection of differentiated THP-1 macrophages with M5G infected cells, the co-culture were analyzed for the percentage of apoptosis (Annexin V+/7AAD-) through flow cytometry at 1, 12 and 24 hours after co-culture. Apoptosis from the total population **(A)** were divided into infected only **(B)** and uninfected only **(C)** populations. Uninfected cells co-cultured with differentiated THP-1 macrophages were taken as a positive control. The data represents mean percentage (mean ± SEM) from three independent experiments.

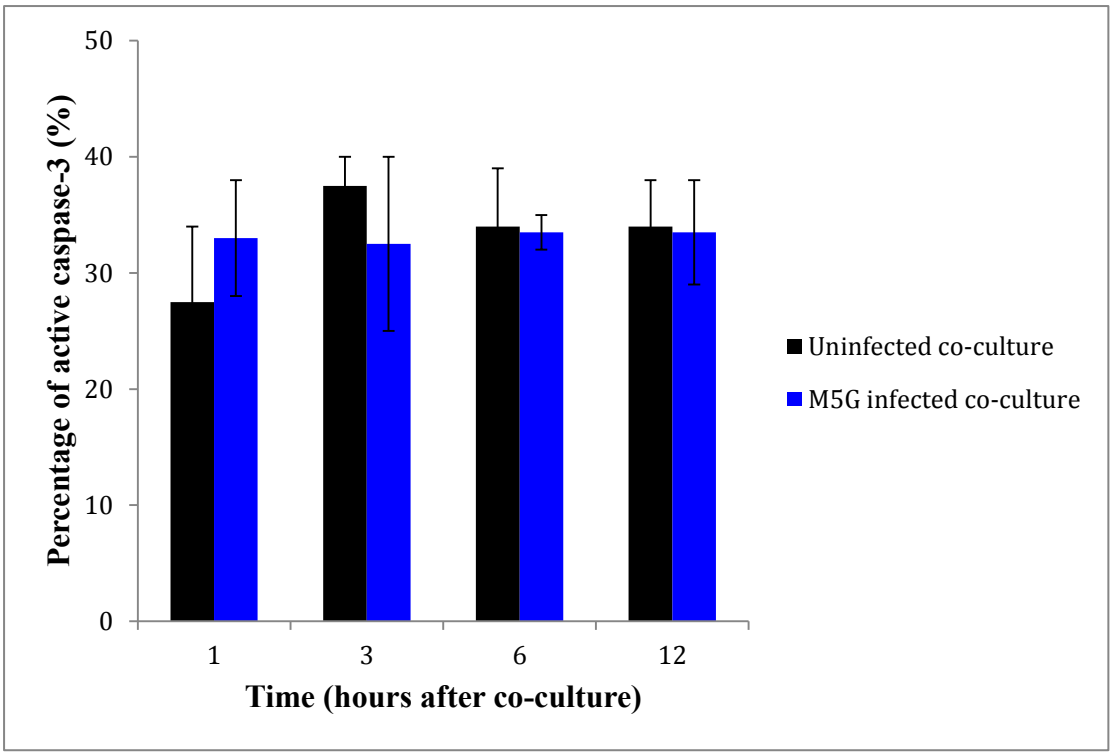


Figure 4.9. Effect of M5G infection spreading on the activation of caspase-3 in host cells. After re-infection of differentiated THP-1 macrophages with M5G infected cells, the co-culture were analyzed for the percentage of activated caspase-3 through flow cytometry at 1,3, 6 and 12 hours after co-culture. Uninfected cells co-cultured with differentiated THP-1 macrophages were taken as a positive control. The data represents mean percentage (mean ± SEM) from three independent experiments.

4.2.5. Effect of caspase-3 inhibition on the apoptosis and infection spread

Since the data suggested a clear link between L8G spreading and apoptosis, the next step was to test whether apoptotic induction is critically involved in infection spreading. The infected donor cells were treated with various concentration of Caspase-3 inhibitor (Z-DEVD-FMK) before infecting differentiated THP-1 macrophages. The co-culture was analyzed for infection rate and active caspase-3 expression at 3 and 12 hours. Infected co-culture without Z-DEVD-FMK treatment was taken as a positive control in this experiment.

The result showed that 25 μM of inhibitor was unable to reduce the percentage of active caspase-3 compared to non-treated samples (Figure 4.10.A). However, the pre-treatment with 100 μM significantly ($p<0.05$) reduced the percentage of active caspase-3 at 3 and 12 hours, compared to the non-treated infected co-culture (Figure 4.10.A). Interestingly, this effect of caspase-3 inhibition led to a marked decrease in the percentage of infection at 12 hours in comparison with positive control (Figure 4.10.B). Since the percentage of infection increase observed from 3 to 12 hours was not significant indicates that this inhibitory effect completely blocked, rather than delayed, the spreading of infection.

Together the above findings demonstrate that the L8G amastigotes induces apoptosis via caspase-3 dependent pathway in order to initiate the process of cell-to-cell spreading of infection.

4.3. Conclusions

In conclusion, for the first time, the development of a credible *in vitro* model representing the dissemination of *Leishmania* parasites during late stage of human macrophage infection was reported.

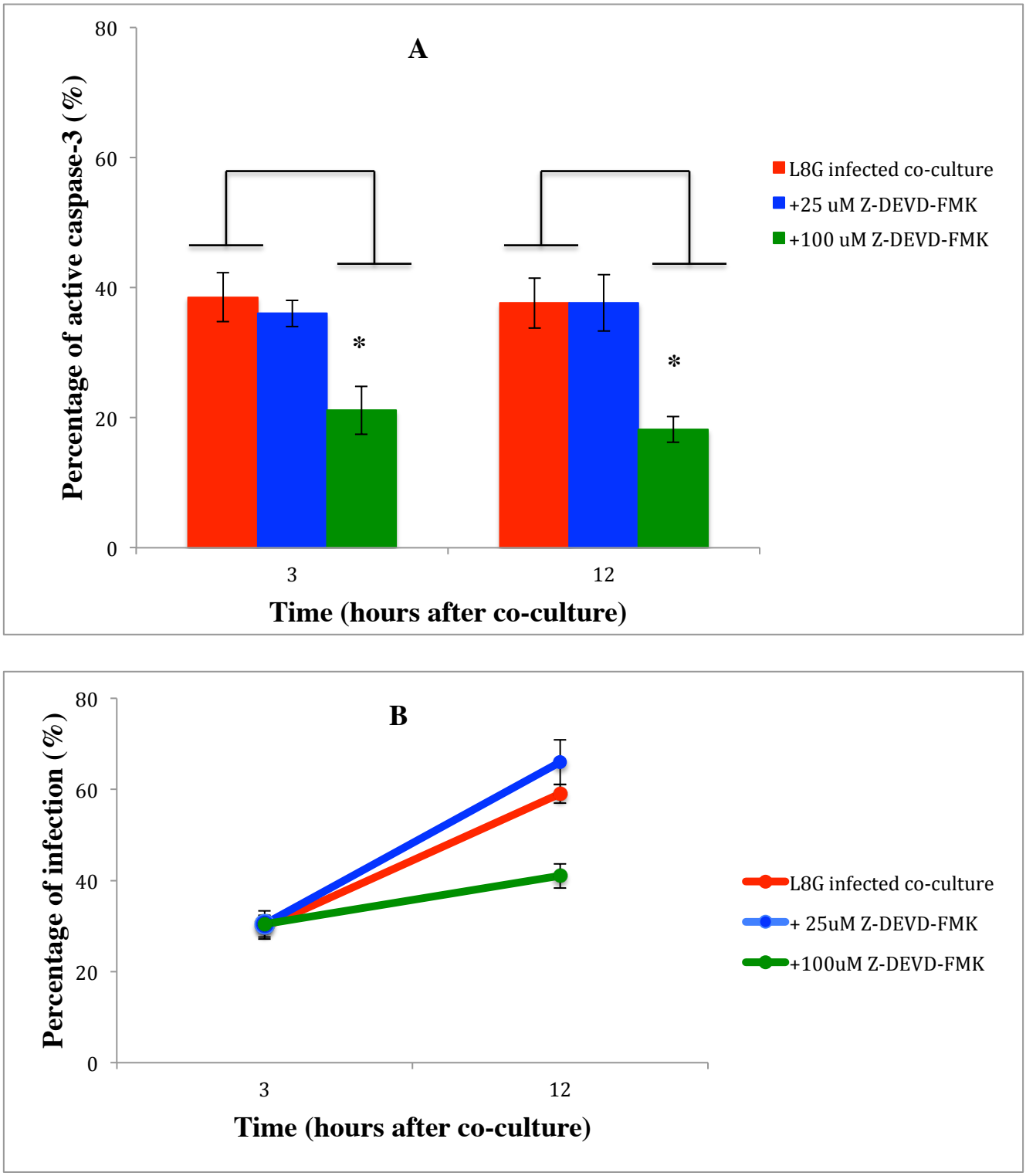


Figure 4.10. Effect of caspase-3 inhibition on the apoptosis and infection spread after infection with L8G infected cells. After L8G infected cell treatment with and/or without Z-DEVD-FMK for 4 hours, it was co-cultured with differentiated THP-1 macrophages. The co-culture was analyzed for the percentage of activated caspase-3 (**A**) and infection (**B**) through flow cytometry at 3 and 12 after co-culture. The data represents mean percentage (mean ± SEM) from three independent experiments. * = $p<0.05$

Initially, this model involved the co-culture of *L. aethiopica* and *L. mexicana* infected cells (apoptotic induced) with a healthy population of differentiated THP-1 macrophages. This experimental infection with infected cells led to an overall increase in the percentage of infection within 12 hours, demonstrating a potential cell-to-cell spreading of *L. aethiopica* and *L. mexicana* amastigotes. This was confirmed using real time lapse microscopy, which revealed extrusion and subsequent transfer of amastigotes from infected to a healthy macrophage in a non-lytic mode.

Interestingly, this form of cell-to-cell spreading of *L. aethiopica*, but not *L. mexicana*, appeared to be correlated with apoptotic induction as there was a significant increase in the PS externalization and active caspase-3 expression. Furthermore, the inhibition of apoptosis via caspase-3 inhibitor completely prevented an increase in the percentage of infection. This highlighted the critical involvement of *L. aethiopica* mediated apoptosis in driving parasitic spreading from the infected cells and maintain its virulent life cycle in a new macrophage niche.

Chapter 5 – Regulation of apoptosis signaling pathways in human macrophage during *Leishmania* spreading

5.1. Introduction

The promastigotes and amastigotes form of *Leishmania* have a remarkable ability to modulate the host macrophage signaling pathways, which includes; inhibition of lysosomal fusion, disruption of various inflammatory cytokine and chemokine production, downregulation of MHC class II expression and prevention of cell death (Cecilio et al., 2014). These virulent functions prolong the longevity of the parasites within the infected cells by providing sufficient time for promastigote to successfully differentiate into amastigote within the host phagolysosome niche. However, following amastigote replication, the ultimate objective for these intracellular parasites is to successfully disseminate and colonize its progeny into neighboring macrophages. The previous chapter revealed that *L. aethiopica* (L8G) amastigotes spreading from cell-to-cell was associated with host apoptosis induction *in vitro*. Unfortunately, the mechanistic insight into the cell signaling pathways for this type of cell-to-cell dissemination remains poorly understood.

Studies focused on early stage of infection with *Leishmania* promastigotes have shown that various host apoptosis signaling pathways are involved for parasite survival. For example, AKT signaling was found to play an important role in resisting induction of mice macrophage apoptosis during infection with *L. major*, *L. amazonensis* and *L. pifanoi* promastigotes (Ruhland et al., 2007). Similarly, the pro-apoptotic signaling pathway of PKC-δ was severely impaired by *L. infantum*, which resulted in inhibition of human U937 macrophage induced apoptosis (Lisi et al., 2005). Finally, engagement of NF-κB signaling pathways was responsible for the

survival of infected J774A.1 mice macrophage within 1 hour of *L. donovani* infection (Singh et al., 2004). These reports suggest that *Leishmania* employ a diverse set of mechanistic pathways to block apoptotic induction during the early stages of infection. Since many pathogenic microorganism, including *Mycobacteria* (Aguilo et al., 2014), *Chlamydia* (Byrne and Ojcius, 2004) and retroviruses (Sattentau et al., 2010) are known to subvert the host apoptotic signaling pathways depending on the stage of infection, it is of great interest to further investigate whether the regulation of these signaling pathways fluctuates at later stages of infection that might account for *Leishmania* spreading.

Therefore, this chapter aims to evaluate how the three signaling pathways associated with apoptosis, AKT, NF-κB and PKC-δ, are modulated by *L. aethiopica* (L8G) amastigotes during spreading (Figure 5.1). The *in vitro* spreading model developed in Chapter 4 was utilized firstly to investigate the protein expression of activated and total AKT through western blot. Further analysis of the downstream pathways of AKT signaling, including BAD phosphorylation and cytochrome C release, were determined. The involvement of NF-κB was also investigated by analyzing the presence of upstream IkB phosphorylated protein and downstream p65 total protein through western blot. Finally, the role of PKC-δ protein was assessed. This was implemented by detecting the accumulation of pro-apoptotic cleaved fragment of the protein during *L. aethiopica* (L8G) amastigotes spreading.

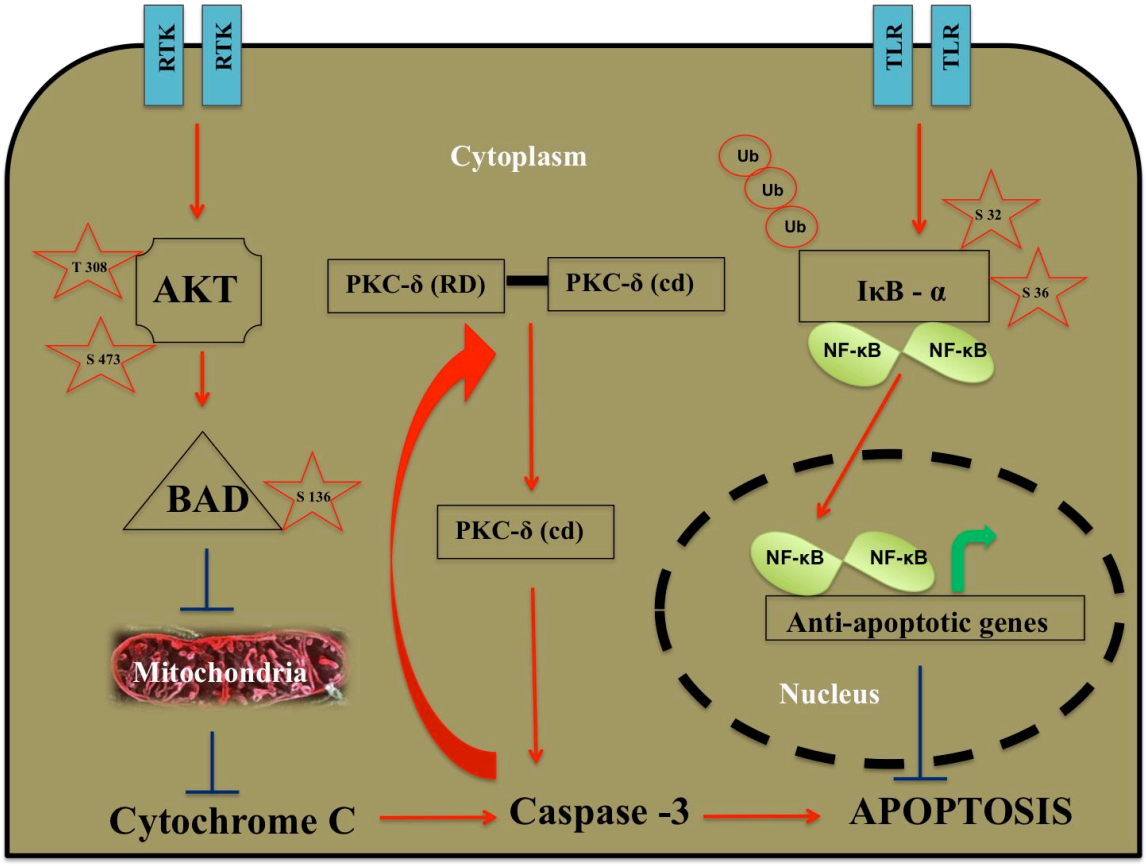


Figure 5.1. Schematic diagram representing apoptotic signalling pathways in macrophages. Upon Receptor Tyrosine Kinase (RTK) stimulation, AKT is phosphorylated at Threonine 308 (T 308) and Serine 473 (S 473). Fully activated AKT then phosphorylates BAD protein at Serine 136 (S 136), which inhibits the permeability of mitochondrial membrane. As cytochrome C is not released from mitochondria to cytoplasm, caspase-3 is not activated which otherwise leads to induction of apoptosis. One of the key targets of active caspase-3 is PKC-δ protein, which is composed of regulatory domain (RD) and catalytic domain (cd). Caspase-3 cleaves the hinge region (indicated by solid bar) of the full length PKC- δ. The released cd initiates the activation of caspase-3 in a positive feedback mechanism. Similarly, Toll Like Receptor (TLR) stimulation induces the phosphorylation at Serine 32 (S 32) and Serine 36 (S 36) of IκB. This is followed by ubiquitination and subsequent proteosomal degradation of IκB. This causes the release of NF- κβ dimers, which translocate to the nucleus to induce the transcription of anti-apoptotic genes.

5.2. Results and Discussions

5.2.1. Effect of L8G infected cells on AKT activation during infection spreading

The activation of AKT follows phosphorylation at Threonine (Thr) 308 and Serine (Ser) 473 residues (Garcia-Echeverria and Sellers, 2008). Hence, to determine activation of AKT during infection spreading, L8G infected co-culture was isolated at 1, 6, 12 and 24 hours and were immunoblotted against antibodies specific to Thr 308 and Ser 473 phosphorylation sites. The results were compared to the positive control of co-cultured uninfected cells.

After 1 hour of co-culture, there was a decrease in the band intensity at both Thr 308 and Ser 473 residues of AKT in L8G infected cells when compared to uninfected control (Figure 5.2.A and 5.2.B). The densitometry analysis further showed that this reduction in the expression of phosphorylated AKT at both residues was significant ($p<0.05$) not only at 1 hour, but also at 6, 12 and 24 hours after co-culture (Figure 5.2.A and 5.2.B). To verify whether this effect is solely caused by de-phosphorylation or low expression of the total protein, the membrane blot were stripped and re-probed with total AKT antibody. Surprisingly, from 6 hours onwards, there was approximately a two fold reduction of the total protein in infected co-culture when compared to control, suggesting lower AKT expression (Figure 5.2.C). Since the band intensity of β actin protein remained constant throughout the time period (Figure 5.2.D), this confirmed that the above effects were not due to unequal loading of the protein during SDS gel electrophoresis. Finally, to discount the fact that the L8G infected cells before co-culture was biased towards AKT reduction, the infected and uninfected cells from 72 hours were separately probed with all three antibodies. The result confirmed no significant differences in band intensity for phosphorylated and total protein between infected and uninfected cells (Appendix II).

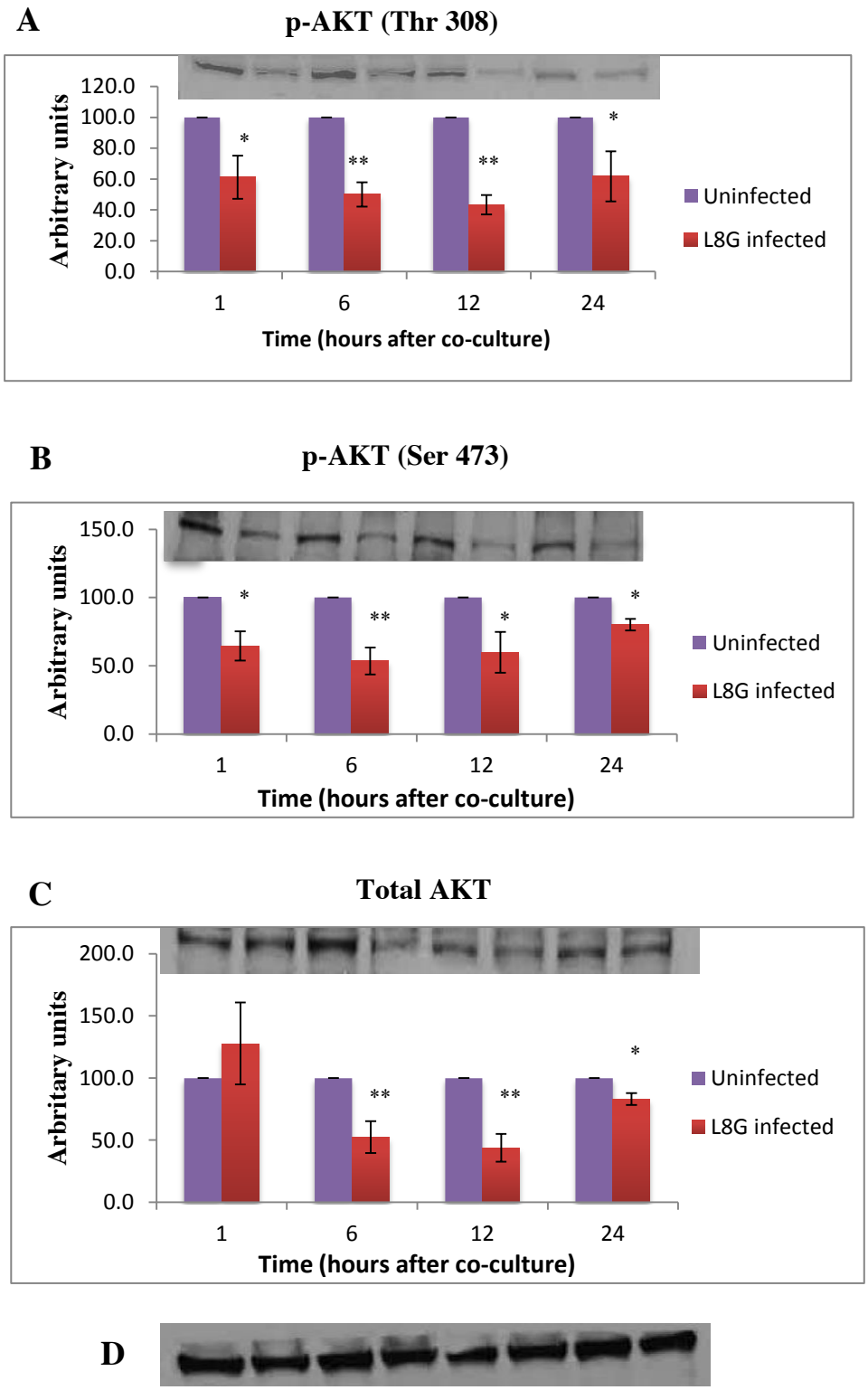


Figure 5.2. Effect of *L. aethiopica* (L8G) infected cells on AKT activation during infection spreading. Following infection of differentiated THP-1 macrophages with L8G infected cells, whole cell lysates were collected at 1, 6, 12 and 24 hours after co-culture. Equal amounts (30 µg) were resolved by SDS-PAGE and analysed through western blotting. (**A**) Representative blot of p-AKT (Thr 308) and its corresponding densitometry analysis. (**B**) Representative blot of p-AKT (Ser 473) and its corresponding densitometry analysis. (**C**) Representative blot of total AKT and its corresponding densitometry analysis. (**D**) Representative blot of β-actin. Co-culture between differentiated THP-1 macrophages and uninfected cells were taken as a positive control. * = $p<0.05$ and ** = $p<0.01$

This confirms that the above effects in AKT reduction were solely caused by L8G infected cells following co-culture experiment. Overall, the above results suggest a temporal double strategy of *L. aethiopica* amastigotes mediated AKT reduction. As *Leishmania* species induces the activation of host serine/threonine phosphatase (PSP) during infection (Kar et al., 2010), this could lead to AKT de-phosphorylation in both Thr 308 and Ser 473 residues within 1 hours of co-culture. Alternatively the secretion of parasite virulent factors such as cysteine/serine protease and GP63 could initiate total AKT degradation from 6 hours onwards, therefore disrupting AKT survival signaling pathways.

5.2.2. Effect of AKT downregulation on the phosphorylation of BAD expression and cytochrome C release

One of the downstream events that occur following AKT activation is the phosphorylation of BAD (Figure 5.1). The resulting phosphorylation at Ser 136 residues initiates binding of BAD with 14-3-3 molecular chaperone protein, thereby attenuating the downstream pro-apoptotic function of BAD (Datta et al., 1997). To confirm whether inactivated AKT during infection spreading has any consequential effect on the status of BAD phosphorylation, cell lysates from L8G infected co-culture were assessed for the expression of phosphorylated BAD at Ser 136 through western blot. The result showed a marked reduction in BAD phosphorylation in infected co-culture from 1 to 24 hours when compared to uninfected control (Figure 5.3.A). However, the expression of total BAD protein was very similar across the time period (Figure 5.3.A). These observations support the notion that BAD de-phosphorylation is dependent on L8G mediated AKT inactivation during *in vitro* spreading.

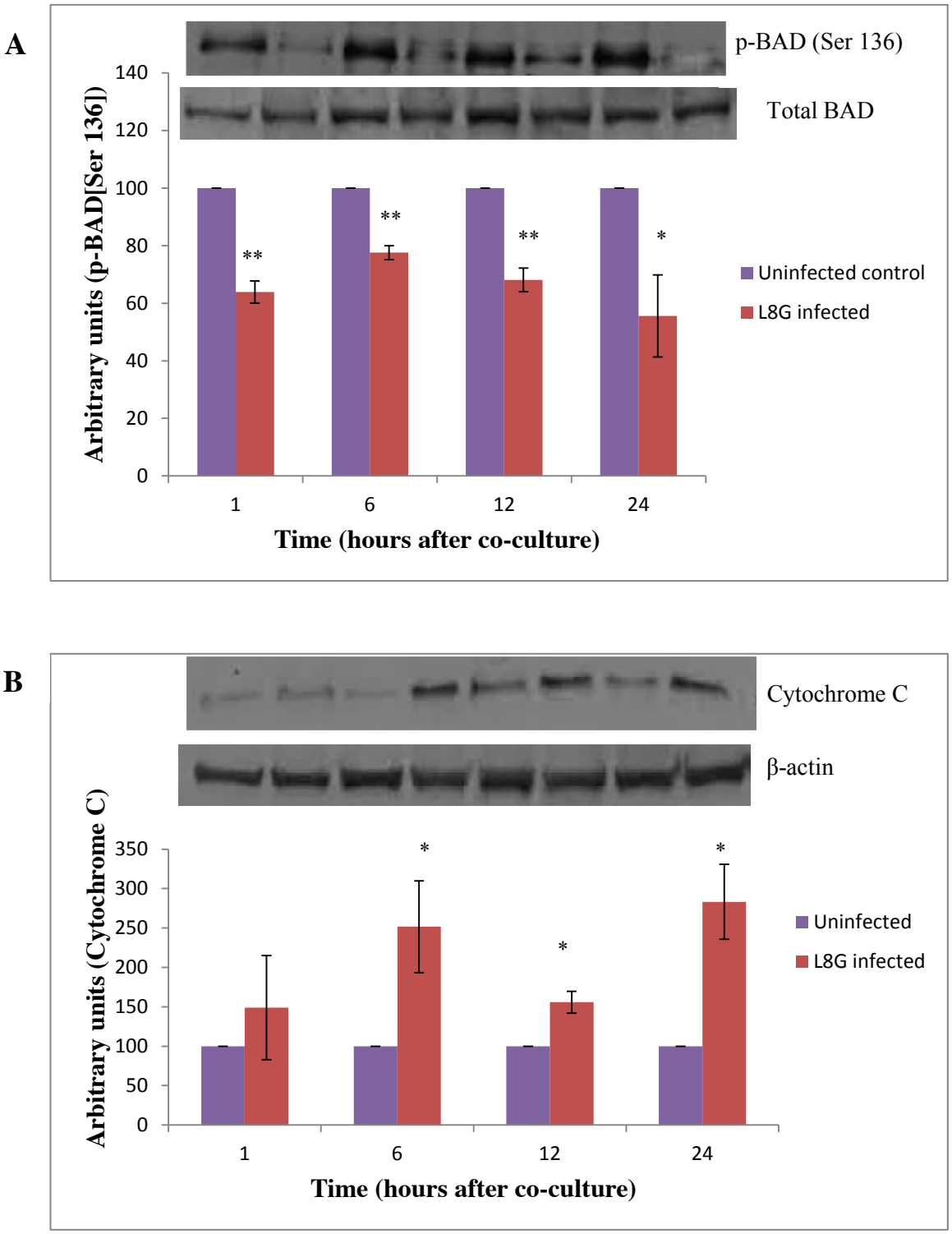


Figure 5.3. Effect of AKT downregulation on BAD phosphorylation and cytochrome C release. Following infection of differentiated THP-1 macrophages with L8G infected cells, whole cell and/or cytosolic lysates were collected at 1, 6, 12 and 24 hours after co-culture. Equal amounts (30 µg) of proteins were resolved by SDS-PAGE and analysed through western blotting. (**A**) Representative blot of p-Bad (Ser 136) from whole cell lysate and its corresponding densitometry analysis, with β-actin as loading control. (**B**) Representative blot of cytochrome C from cytosolic lysate and its corresponding densitometry analysis with β-actin as loading control. Co-culture between differentiated THP-1 macrophages and uninfected cells were taken as a positive control. * = $p<0.05$ and ** = $p<0.01$

The major pro-apoptotic function of de-phosphorylated BAD is induction of mitochondrial membrane permeability via the activation of BAX protein mediated oligomeric pores formation (Danials, 2007). This increase in permeability causes cytochrome C release which, subsequently binds with Apaf-1 protein to induce the activation of caspase-3 enzyme (Jiang and Wong, 2004). To test whether the de-phosphorylated BAD protein affects mitochondrial permeability, the presence of cytochrome C in the cytosolic extract from L8G infected co-culture was detected by western blot. Within 1 hour, there was no significant difference in cytosolic accumulation of cytochrome C between infected and uninfected co-culture (Figure 5.3.B). Interestingly, release of cytochrome C into cytosol increased by approximately two-fold from 6 hours onwards in the infected co-culture, which was maintained till 24 hours time point (Figure 5.3.B). This indicates that the effect of active BAD on cytochrome C release appears to be associated only after 6 hours of co-culture with L8G infected cells. This time delay, independent of AKT inactivation, could be explained by the lag phase associated with BAX oligomeric pores, which involves a slow and stepwise conformational change (Valentijn et al., 2003). Nevertheless, since elevated levels of active caspase-3 was found between 6 and 12 hours after cell-to-cell infection (Chapter 4), this suggest a positive correlation between active BAD mediated cytochrome C release and caspase-3 activation during L8G infection spreading.

5.2.3. Effect of L8G infected cells on NF-κB signaling during infection spreading

The importance of NF-κB regulation in stimulating immune response against intracellular pathogen including *Leishmania* has been well documented (Reinhard et al., 2012). As discussed in Chapter 1 (section 1.6.3), various stimuli including LPS,

TNF-α and IL-1 results in phosphorylation (Serine 32 and 36 residues), polyubiquitination and subsequent degradation of the inhibitory Iκ-Bα. This releases the NF-κB dimers, mainly p65-p50, which then migrates into the nucleus to induce transcription of inflammatory genes including, IL-6, IL-12 and NOS (Figure 5.1). Although anti-apoptotic gene upregulation is one of the vital function of NF-κB activation (Barket and Gilmore, 1999), its importance during *Leishmania* infection, particularly late stage has not been studied. Therefore, the next goal was to examine whether NF-κB signaling could be modulated during infection spreading.

Initially, the phosphorylation of Iκ-Bα (Ser 32/36) was assessed through western blot. From 1 to 24 hours, a significant ($p<0.01$) decrease in phosphorylation was detected within infected co-culture compared to uninfected control (Figure 5.4.A). Surprisingly, this effect was correlated to a lower expression of total Iκ-Bα (Figure 5.4.B). Furthermore, when the infected cell lysates were probed with p65 antibody, a marked reduction of total p65 protein was detected from 1 to 24 hours, as compared to control (Figure 5.4.C). The above result correlates with one study, where the authors found cysteine peptidase of *L. mexicana* amastigotes was responsible for complete degradation of Iκ-Bα and p65 subunit, resulting in an inhibition of IL-12 production during mice macrophage infection (Cameron et al., 2004).

This interesting finding implies that during L8G infection spreading, NF-κB signaling is negatively regulated due to degradation of Iκ-Bα and p65 subunit, which diminishes the expression of anti-apoptotic genes in the nucleus.

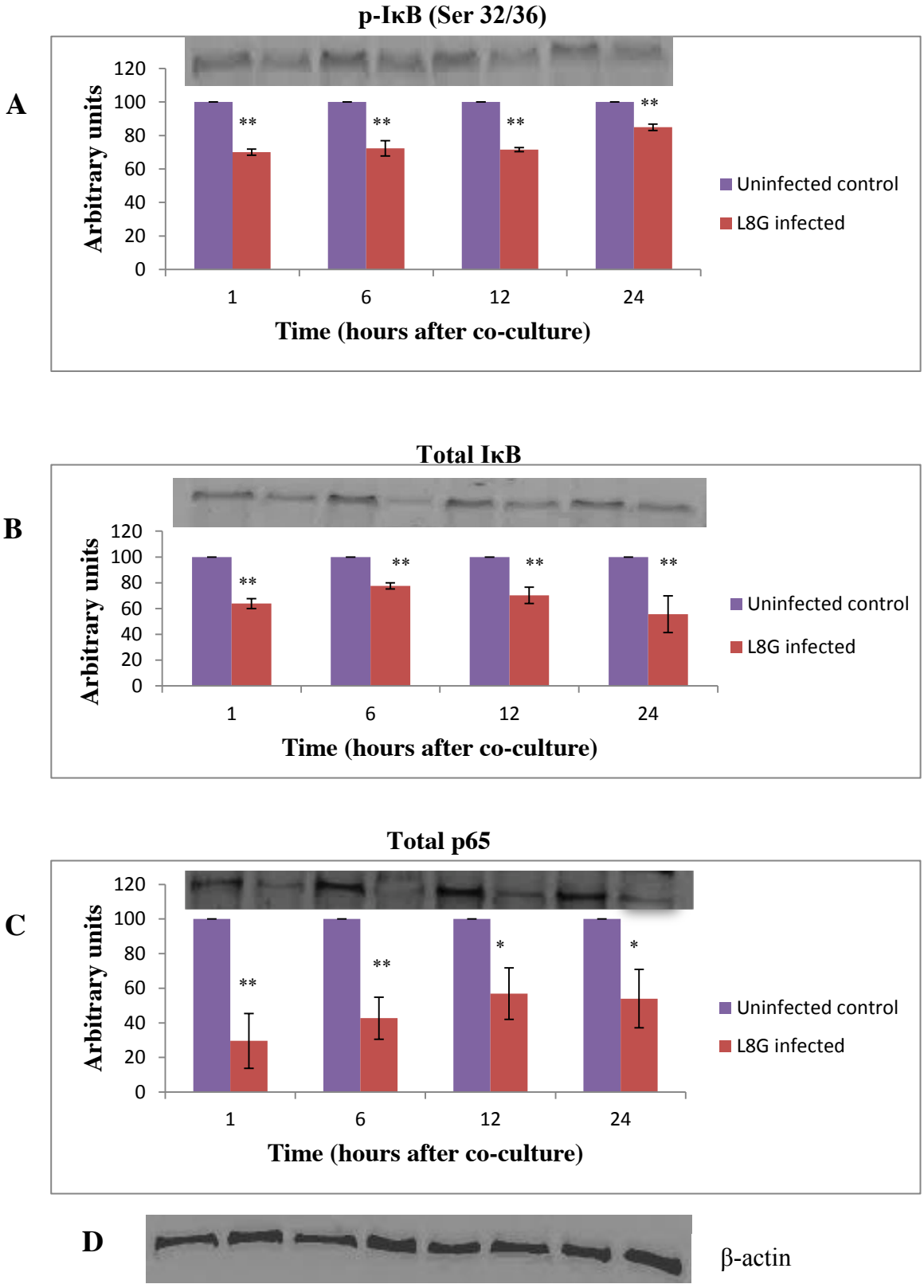


Figure 5.4. Effect of *L. aethiopica* (L8G) infected cells on NF-κB signaling during infection spreading. Following infection of differentiated THP-1 macrophages with L8G infected cells, whole cell lysates were collected at 1, 6, 12 and 24 hours after co-culture. Equal amounts (30 µg) of proteins were resolved by SDS-PAGE and analysed through western blotting. (**A**) Representative blot of p-IκB (Ser 32/36) and its corresponding densitometry analysis. (**B**) Representative blot of total IκB and its corresponding densitometry analysis. (**C**) Representative blot of p65 and its corresponding densitometry analysis. (**D**) Representative blot of β-actin. Co-culture between differentiated THP-1 macrophages and uninfected cells were taken as a positive control. * = $p<0.05$ and ** = $p<0.01$

5.2.4. Effect of L8G infected cells on PKC-δ signaling during infection spreading

Leishmania is known to severely alter the macrophage Protein kinase C (PKC) signaling pathways, which results in the disruption of reactive oxygen species production (Bhattacharya et al., 2001).

Although PKC subtypes are known to have either pro or anti-apoptotic function, only PKC-δ has been studied so far in the field of *Leishmania* infection and host cell death (Figure 5.1). Lisi and colleagues showed that early stage *L. infantum* infection prevents actinomycin D induced host apoptosis via PKC-δ inactivation (Lisi et al., 2005). This inactivation was due to the ability of LPG molecule to inhibit PKC-δ cleavage, which was further associated with reduced expression of activated caspase-3. As Chapter 4 revealed caspase-3 involvement in cell-to-cell infection, an investigation was carried out to assess whether there is a link between the activation of caspase-3 and PKC-δ (i.e. PKC-δ cleavage) during L8G infection spreading.

After isolating cell lysates at 1, 6, 12 and 24 hours, the infected co-culture was probed with PKC-δ antibodies before analyzing PKC-δ protein expression through western blot. A band of approximately 78 kDa representative of total PKC-δ protein was detected in uninfected control from 1 to 24 hour (Figure 5.5). However, throughout the time period, the PKC-δ intensity was significantly reduced ($p<0.01$) in infected co-culture (Figure 5.5). Interestingly, this effect was not due to accumulation of PKC-δ cleaved fragment (CF) as there was no protein band present at 45 kDa (expected size of CF). This observation clearly shows that caspase-3 activation during infection spreading is not linked to PKC-δ activation. Instead, parasite mediated downregulation of PKC-δ appeared to be one of the causal factors behind apoptotic mediated infection spreading.

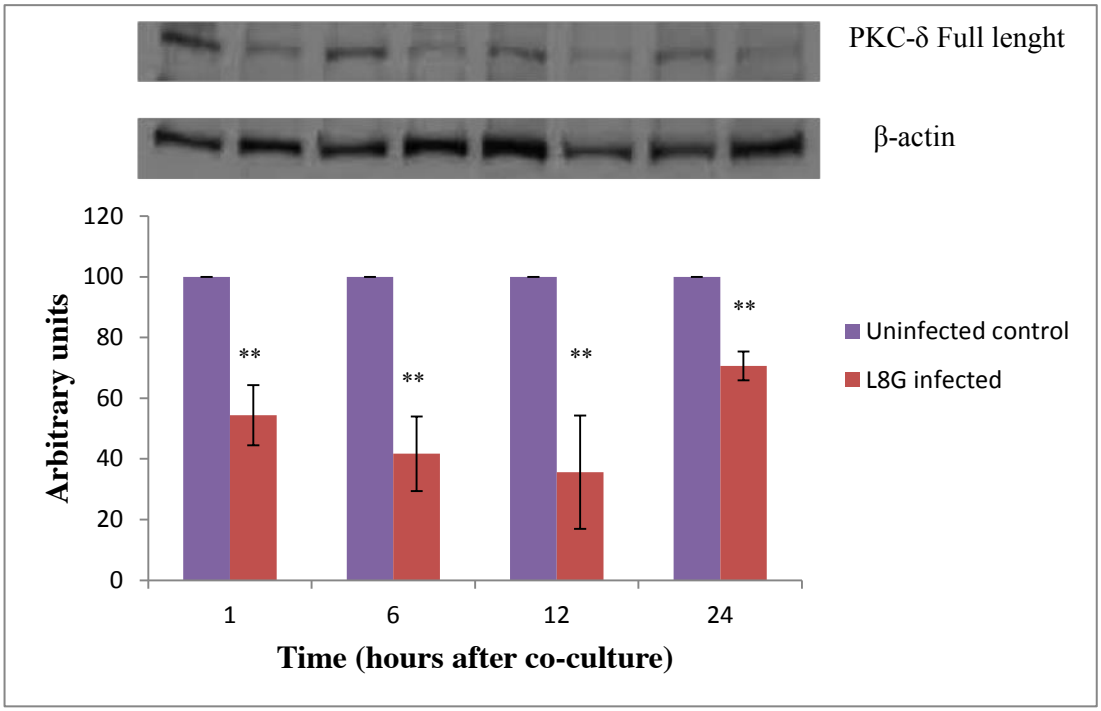


Figure 5.5. Effect of *L. aethiopica* (L8G) infected cells on PKC-δ signaling during infection spreading. Following re-infection of differentiated THP-1 macrophages with L8G infected cells, whole cell lysates were collected at 1, 6, 12 and 24 hours after co-culture. Equal amounts (30 µg) of proteins were resolved by SDS-PAGE and analysed by western blotting. Representative blot of PKC-δ and β-actin protein expression is shown. The graph represents densitometry analysis of PKC-δ. Co-culture between differentiated THP-1 macrophages and uninfected cells were taken as a positive control. ** = $p<0.01$

This surprising finding correlates to an *in vivo* study from Guler and colleagues, whereby PKC-δ knockout (-/-) mice exhibited rapid increase in the dissemination of *L. major* parasites from footpad to liver, as compared to wild type control (Guler et al., 2011). Although the above study did not extend the work in defining the apoptotic state of infected cells, it provides an initial platform to further investigate whether there is a link between PKC-δ downregulation and apoptotic induction during L8G infection spreading.

5.3. Conclusions

Experimental results from this chapter have clearly demonstrated the overall impact in host apoptotic signaling pathways during *L. aethiopica* dissemination. By employing an *in vitro* spreading model, significant levels of modulation were observed in three major signaling pathways, AKT, NF-κB and PKC-δ.

In the earliest stage of infection spread, there was a dramatic reduction in phosphorylation of AKT within *L. aethiopica* infected co-culture cells. Although this caused a decrease in phosphorylated BAD, there was no any effect on cytochrome C release from mitochondria. However, from 6 hours onwards, western blot analysis revealed an increase level of cytochrome C in cytosol when compared to uninfected co-culture cells. This strongly indicates the involvement of intrinsic mitochondrial apoptosis during *L. aethiopica* amastigote spreading. Similarly, the NF-κB signaling was downregulated during spreading as the infected co-culture cells illustrated a reduced expression of Iκ-Bα and p65 subunit. This defect in NF-κB might have a consequential effect on the downstream expression of a number of critical anti-apoptotic genes. Finally, PKC-δ protein was also downregulated instantaneously within 1 hours of infected cell co-culture. Interestingly, this negative effect was

consistent throughout the spreading of L8G infection with no clear evidence of PKC-δ CF accumulation. This rules out any possibility of a link between caspase-3 and PKC-δ activation during spreading of *L. aethiopica*.

In conclusion, a temporal based downregulation of apoptotic signaling pathways during *L. aethiopica* spreading in human macrophages have been revealed in this chapter. Engineering a genetic overexpression of AKT, NF-κB and PKC-δ proteins will be the next research goal to address whether these signaling pathways are critical during the *Leishmania* infection propagation.

Chapter 6 – Global protein response during late stage of *Leishmania* infection in human macrophage

6.1. Introduction

Parasitic mediated subversion of the macrophage signaling pathways is vital for intracellular survival of *Leishmania* species. Through DNA microarray analysis, efforts to understand such changes have been achieved by studying the modulation of global host gene expression during infection (Buates and Mattelawski, 2001; Chausabel et al., 2003; Rodriguez et al., 2004; Zhang et al., 2010). These studies have revealed the down-regulation of pro-inflammatory genes as a contributing factor behind anti-microbial suppression towards *Leishmania*. However, genomic studies and its associated techniques suffer from one critical limitation, as the final gene product does not necessarily correlate to the total levels of protein due to post-translational modification (Cox and Mann, 2007).

Since proteins are the effectors of biological and cellular functions, investigations have been shifted towards utilizing proteomic approaches to study the effect of *Leishmania* infection on host protein expression. Menezes and colleagues used a liquid chromatography tandem mass spectrometry technique to compare the expression of proteins involved in host cell metabolism during *L. major* and *L. amazonensis* infection in mouse macrophages (Menezes et al., 2013). Through the same approach, GP63 of *L. major* and *L. mexicana* was found to be responsible for degradation of mice macrophage nuclear proteins such as nucleoporins and nucelocytoskeleton (Isnard et al., 2015). Similarly, a study focusing on *L. donovani* infection of human THP-1 macrophage comprehensively identified differential expression of proteins ranging from cell death to immune response and metabolism

(Singh et al., 2015). Although the above studies highlighted modulation in global host signaling pathways by *Leishmania* during early phase of infection, no analysis has been carried out to address whether these critical change take place at later stages of infection.

Therefore, this chapter is aimed to fill the gap in knowledge in global proteomic expression of human macrophage during cell-to-cell *Leishmania* spreading. Using an isotopic labeling coupled with tandem mass spectrometry (MS/MS) approach, comparative analysis was performed to determine quantitative changes in specific sets of protein between uninfected and *L. aethiopica* infected cells.

6.2. Results and Discussion

6.2.1. Identification and functional annotation of differentially expressed protein

Quantitative analysis of protein expressions of *L. aethiopica* infected co-culture at 10 hours were compared with uninfected control and the relative fold change (RFC) was determined. Three independent biological experimental repeats (Set A, B and C) were performed to increase the significance and reliability of the total proteins identified. A total number of 6969, 7070, 5928 proteins were identified at Set A, B and C, respectively (Appendix III). Using RFC as a key indicator, any proteins that showed either upregulation (RFC > 1.5) or downregulation (RFC < 0.5) were classified as differentially expressed protein. Within 10 hours of co-culture, a total of 19 host proteins were differentially modulated during *L. aethiopica* spreading (Table 6.1). These proteins were categorized into 5 major functional groups using Gene Ontology (GO) annotations. These include: apoptosis and cell death; immune response, vesicles trafficking; metabolic pathways; gene expression.

Functional groups	Number	Accession ID	Name	Relative fold change
Apoptosis and cell death	1	H0Y6Y2	Caspase-9 p35	2.0
	2	P42574	Caspase-3 p17	1.8
	3	Q56A86	AKT	0.39
	4	Q01105	SET	0.15
	5	D3DT21	Selenoprotein K	0.30
	6	O95470	Sphingosine-1-phosphate lyase	2.6
Immune response	7	P36222	Chitinase-3-like protein	1.73
	8	B2R577	Protein S-100	0.23
	9	A0A024QZZ1	Butyrophillin	1.87
	10	H0YC68	Glutathione reductase	3.4
	11	P02795	Metallothionein-2	4.0
Vesicular trafficking	12	B8ZZT4	VAMP8	0.3
	13	Q9H1H9	Kinesin-3	4.0
Metabolism	14	P50336	Protoporphyrinogen oxidase	2.5
	15	P48047	ATP synthase subunit	3.8
	16	P31930	Cytochrome bc-1	2.5
Gene expression	17	E9PI38	p65 NF-κB	0.23
	18	Q1RMZ3	NCoA6	0.1
	19	Q9Y2W1	TRAP	0.43

Table 6.1. List of differentially expressed proteins during late stage of *L. aethiopica* infection. The identified proteins were categorized into 5 major functional groups including apoptotic cell death, immune response, vesicular trafficking, metabolism and gene expression.

The pie diagram shows the percentage distribution of functionally annotated proteins at 10 hours of cell-to-cell infection with *L. aethiopica* (Figure 6.1). The number of proteins that showed either increase and/or decrease in expression is shown in Figure 6.2. The following section will discuss on key proteins modulated from each category during infection spreading of *L. aethiopica*.

6.2.2. Proteins involved in apoptosis and cell death

Among five proteins identified as differentially expressed in apoptosis and cell death category, three proteins showed increased expression whereas the remaining two showed reduced expression under infected co-culture cells (Table 6.1). Initially, there was a two fold increase in expression of Caspase-9 p35. This pro-apoptotic protein, which is a cleaved form of pro-caspase-9, is involved in the downstream activation of caspase-3 (Chapter 1, Figure 1.13). During intrinsic apoptosis, cytochrome C binds to Apaf-1 (apoptotic protease activating factor -1) to form a wheel like heptamer called an apoptosome (Kumar, 2007). The Apaf-1 in the apoptosome then recruits initiator caspase-9 p35, which in turn causes the cleavage of pro-caspase-3 into active caspase-3 and subsequent induction of apoptosis (Twiddy and Cain, 2007). Active caspase-3, which is also known to cleave pro-caspase-9, was upregulated by 1.8 fold suggested a positive amplification of caspase-3 mediated apoptosis during *L. aethiopica* spreading. This result is consistent with the findings in Chapter 4, where caspase-3 was strongly expressed throughout spreading time frame. In addition, the fact that AKT protein expression (RFC = 0.39) was also downregulated confirms the notion that AKT mediated mitochondrial apoptotic response is occurring during late stage of infection.

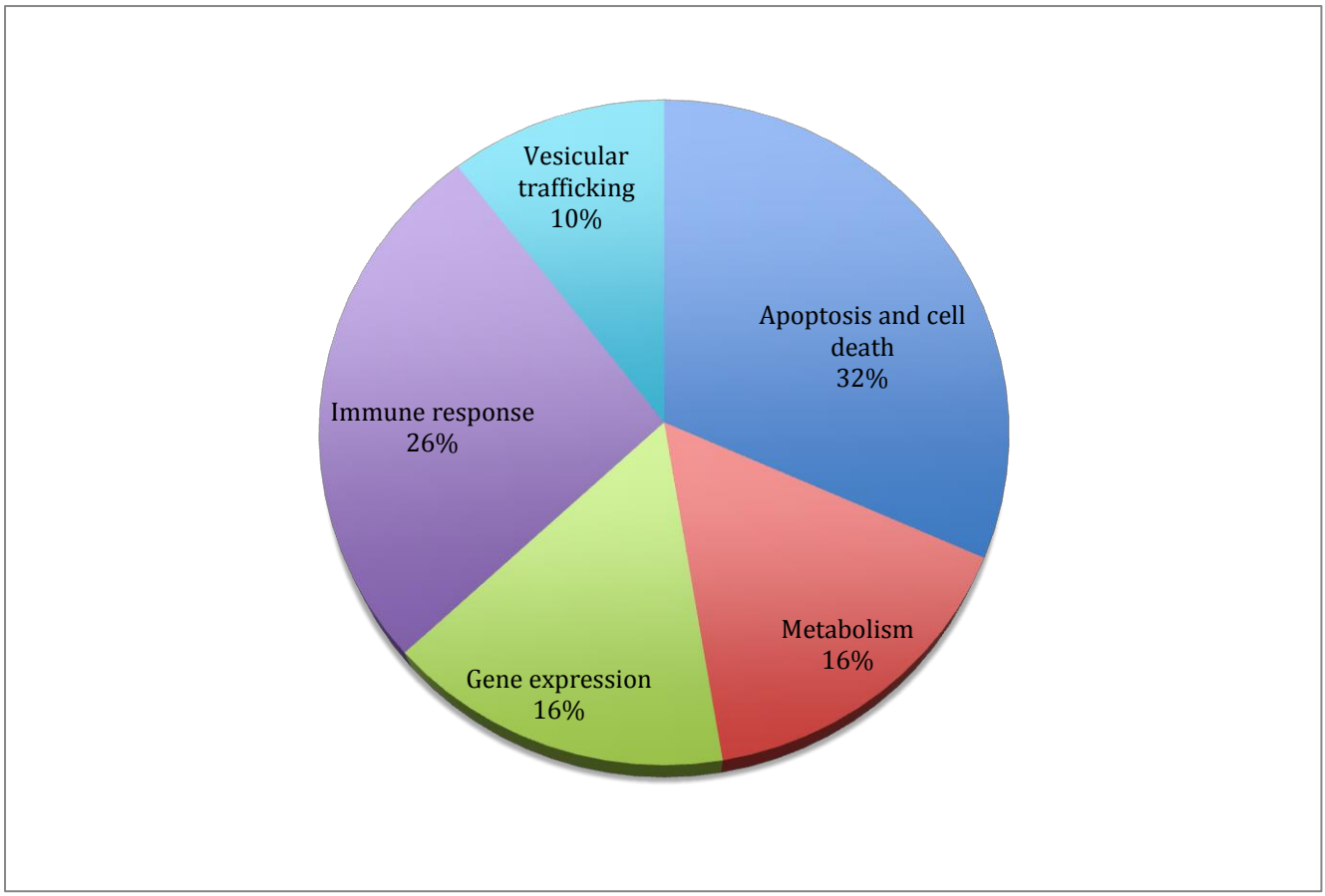


Figure 6.1. Pie-diagram showing functional annotation and relative distribution of the total proteins detected in differentiated THP-1 macrophages co-cultured with *L. aethiopica* infected cells. 5 major functional classes were identified depending on their cellular function using GO annotation.

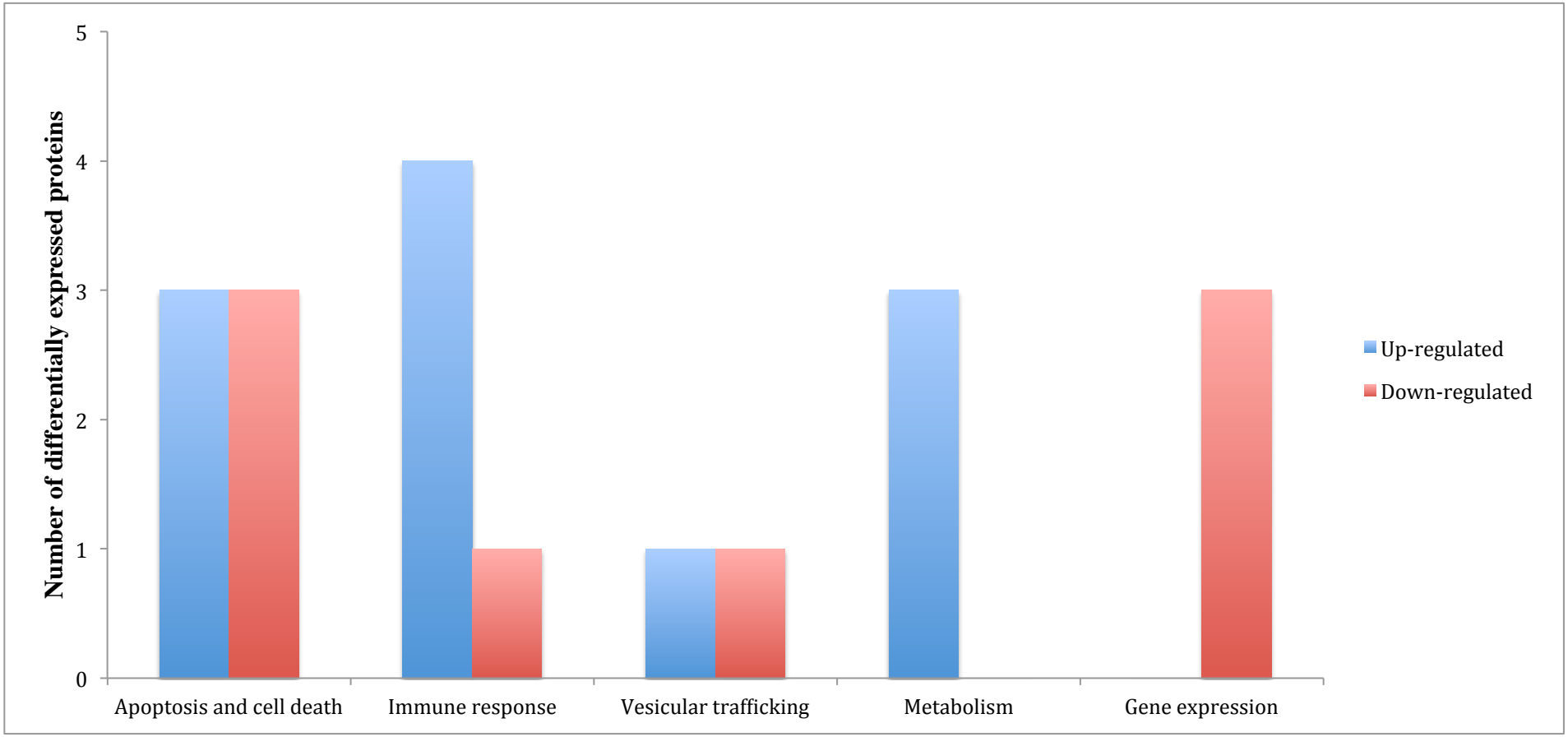


Figure 6.2. Functional distribution of differentially expressed proteins during *L. aethiopica* infected co-culture cells at 10 hours. Using releative fold change (RFC), proteins were assigned either up-regulated (RFC > 1.5) or down-regulated (RFC < 0.5).

Surprisingly, there was a marked decrease (RFC = 0.15) in the expression of SET protein. This 39 kDa phospho-protein is localized in the nucleus and plays an essential role in the inhibition of Granzyme A activated DNAase (GAAD). During T cell mediated macrophage apoptosis, granzyme A, which is a serine protease, cleaves SET protein along with other complex such as HMG2 and Ape1 protein to release GAAD, which then directly causes DNA degradation independent of caspase activity (Chakravarti and Hong, 2003). Since granzyme A activation was not observed in the proteomic data, this suggest that *L. aethiopica* might secrete serine protease, homolog of granzyme A, to degrade SET. Whether this causes caspase independent apoptosis is questionable since HMG2 and Ape1 expression were not reduced at 10 hours after co-culture. However, this does not necessarily rule out the possibility of caspase independent apoptosis during the early time periods of spreading. Similarly, another protein that showed reduced expression was Selenoprotein K (RFC = 0.3). The protein is part of a family of endoplasmic reticulum (ER) membrane protein, which regulates the calcium ion influx (Verma et al., 2011). Disruption in calcium ion regulation leads to ER stress, which is one of the causal factors behind cellular apoptosis (Szegezdi et al., 2006). This could imply that *L. aethiopica* might selectively target Selenoprotein K to impair the ER physiological function and induce apoptosis in the infected cells.

Finally, there was also an enrichment (RFC = 2.6) of Sphingosine-1-phosphate lyase (SPL). The enzyme is responsible for the irreversible cleavage of Sphinghosine-1-phosphate (S1P) molecule into fatty acids and phosphoethanolamine (Van Brocklyn and Williams, 2012). The involvement of S1P in apoptosis comes from the fact that this molecule is a well-known inhibitor apoptosis (Van Brocklyn and Williams, 2012). This suggests that *L. aethiopica* upregulation of SPL might be involved in reducing the pool of anti-apoptotic S1P molecule and enhancing apoptotic induction during parasite spreading.

During early stage of infection, *Leishmania* species confers protection to macrophage in the presence of apoptotic induction allowing sufficient time for parasite replication within phagolysosomes (Akarid et al., 2004; Ruhland et al., 2007). In addition, the above proteomic data has revealed that a pro-apoptotic response could be occurring to facilitate *L. aethiopica* infection dissemination, which supports the results from Chapter 4/5 and Real and collleagues (Real et al., 2014).

6.2.3. Proteins involved in immune response

One of the ways through which *Leishmania* averts the immune response is by altering cytokine production in infected cells. The proteomic screen identified five differentially expressed proteins involved in immune response during cell-to-cell infection (Table 6.1). Firstly, Chitinase-3-like (CH3L) protein was upregulated by 1.73 fold. CH3L is a 40 kDa human homolog protein of chitinase found in plants and insects that lacks the enzymatic activity towards chitin (Eurich et al., 2009). Importantly, CH3L is linked with the formation of alternatively activated macrophage and causes the secretion of IL-13 during several inflammatory diseases such as Gaucher disease and asthma (Eurich et al., 2009). Increased expression indicates that a protective Th2 response could be induced during infection spreading of *L. aethiopica*. Interestingly, such event appears to be correlated with a significant down-regulation of pro-inflammatory response.

This was evident from reduced expression of Protein S-100 (RFC = 0.23) and higher expression of Butyrophilin (RFC = 1.87). The calcium binding Protein S-100, which belongs to a group of damage associated molecular pattern protein (DAMP), is released by phagocytes during inflammation and induces the expression of pro-inflammatory cytokines such as TNF-α and IFN- γ (Foell et al., 2007). Similarly, Butyrophilin protein belonging to a family of B7 co-stimulatory molecule is known to

play an inhibitory role in T cell activation (Abeler-Dorner et al., 2012). Indeed, various independent studies have confirmed the ability of this protein to suppress CD3 induced secretion of IL-2 and IFN-γ from both mouse and human Th1 CD4+ and CD8+ T cells (Smith et al., 2010; Cubillos-Ruiz et al., 2010). By taking these into account, the above result suggests that *L. aethiopica* might reciprocally regulate Protein S-100 and Butyrophilin, respectively, in order to reduce the adaptive pro-inflammatory responses during infection spreading.

The reactive oxygen species (ROS) such as superoxide/hydroxyl radicals along with reactive nitric species (RNS) represent an anti-microbial function of macrophages. However, *Leishmania* is capable of preventing both ROS and RNS production by inactivating NADPH oxidase and JAK/STAT proteins, respectively (Lodge et al., 2006; Matte and Descoteaux, 2010). Although, the proteomic data did not show any reduction of NADPH oxidase and JAK/STAT, it detected a strong elevation in Glutathione reductase (RFC = 3.4) and Metallothionein-2 (RFC = 4). Glutathione reductase is an enzyme responsible for catalyzing the formation of reduced glutathione (GSH), which is considered as intracellular free radical scavengers. Various *in vitro* and *in vivo* studies have demonstrated the role of glutathione reductase and GSH in protecting *Leishmania* during macrophage infection in the presence of ROS and RNS treatment (Romao et al., 1999; Romao et al., 2006; Cruz et al., 2008). Similarly, free radical anti-oxidant properties have also been ascribed to Metallothionein-2, which is a 7 kDa metal binding protein (Viarengo et al., 2000). Two independent genomic studies have shown the induction of metallothionein-2 gene expression during *in vitro* infection with *L. major*, *L. donovani* and *L. panamenesis* (Gregory et al., 2008; Gomez et al., 2014). In particular, Gomez and colleagues showed that metallothionein-2 expression was heavily linked with survival of *L. panamenesis* within infected human macrophages in the presence of NO inducing drug

(Gomez et al., 2014). Cumulatively, the high protein expression of glutathione reductase and Metallothionein-2 in the proteomic data suggests that during cell-to-cell spreading, the released *L. aethiopica* might induce the expression of the two proteins in the recipient cell in order to prevent from ROS and NO exposure.

Overall, the above results shows that *L. aethiopica* spreading is associated with downregulation of inflammatory response and anti-microbial activity in order to favor the parasite survival during re-infection of uninfected macrophages.

6.2.4. Proteins involved in vesicular trafficking

Phagosome biogenesis involves a transition of early phagosome into phago-lysosomes with a stepwise fusion of endosomal and lysosomal vesicles (Hass, 2007). The formation of phago-lysosome is an important step for the killing of intracellular pathogens. However *Leishmania* have evolved mechanisms to delay phagosome maturation process, thus avoiding an encounter with the macrophage microbicidal machinery. The parasite is able to achieve this task by interfering with the vesicle docking proteins such as syntaxin, WASP and SNAP-25 (Lodge and Descoteaux, 2008).

In accordance, the proteomic results showed a reduced expression of VAMP8 [Vesicle Associated Membrane Protein] (RFC = 0.3) in *L. aethiopica* infected co-culture (Table 6.1). The 25 kDa protein belongs to a family of SNARE complex which is essential for the fusion of lysosome containing hydrolase enzymes into phagosomes (Behrendorff et al., 2011). This is consistent with a recent finding whereby GP63 of *L. donovani* was responsible for the cleavage of VAMP8, which led the prevention of NADPH oxidase assembly and led to parasite survival (Matheoud et al., 2013). Strikingly, there was a four fold elevation in kinesin-3 expression (Table 6.1). Composed of two heavy and two light chains, kinesin-3 protein engages in the plus end

directed transport of vesicular cargoes (Hirokawa et al., 2009). This might suggest that during parasitic exit from the donor cells, there could be an increase activity of kinesin-3 mediated transport of vacuole containing *L. aethiopica* amastigotes towards the peripheral region of the cell. Although this unique process has not been documented in protozoan species, it has already been reported for the transfer of vesicles containing *Salmonella typhimurium* from juxtanuclear position to the HeLa cell periphery (Szeto et al., 2009). The authors noted that bacterial type 3 secretion system effectors, PipB2 and SifA were responsible for the recruitment and subsequent activation of kinesin-1 (similar to kinesin-3) in order to promote the movement of *S. typhimurium* along the micro-tubule for its dissemination (Szeto et al., 2009). Whether such virulent mechanism is exhibited by *Leishmania* is not known.

6.2.5. Proteins involved in metabolic pathways

Leishmania amastigotes successfully reside and replicate within the host phagolysosomes. Although these vacuoles provide a safe niche, there is a limiting source of nutrients such as, purines, vitamins, heme and amino acid within the phagolysosome lumen (Naderer et al., 2008). Therefore scavenging these essential nutrients becomes a top priority for parasites to supplement energy in order to survive during the late stage of infection. The proteomic data showed a 2.5 fold increase in the expression of Protoporphyrinogen oxidase during infected co-culture cells (Table 6.1). This enzyme is responsible for catalyzing the oxidation of protoporphyrogen to protoporphyrin, which is a precursor for heme group. Since heme is important component for mitochondrial electron transport, this indicates the active involvement of mitochondrial machinery of oxidative phosphorylation during *L. aethiopica* spread. This is further strengthened by the fact that there were also subsequent increase in expression of ATP synthase subunit (RFC = 3.8) and cytochrome bc-1 complex (RFC

= 2.5) (Table 6.1). This was consistent with the finding from a study, which reported upregulation of various host mitochondrial proteins within 24 hours of *L. donovani* infection (Singh et al., 2015). However, this study reported expression of other host enzymes involved in glycolysis and citric acid cycle metabolic pathways. This discrepancy could be due to species specific differences or could be linked to different stage of infection studied.

6.2.6. Proteins involved in gene expression

Infection with *Leishmania* is well known to inhibit the host expression of a wide range of genes involved in cytokine, chemokine and NO production (Buates and Mattelawski, 2001). This occurs as a direct consequence of parasite mediated suppression of transcription factors such as STAT, NF-κB and AP-1 (Forget et al., 2005; Cameron et al., 2004; Conteras et al., 2010). Consistent with the western blot result in chapter 4, the proteomic data showed a reduce expression of p65 NF-κB (RFC = 0.23) domain (Table 6.1). Although the expression of inhibitory p50 domain was not affected, the possibility of p50/p50 dimer formation could not be ruled out. Whether this inhibitory dimer activation leads to *Leishmania* induced Th2 cytokine (TGF-beta and IL-10) production and reduced iNOS gene expression would require further investigation (Calegari-Silva et al., 2009). Remarkably, the proteomic data showed a severe reduction in NCoA6 [Nuclear Receptor Co-activator 6] (RFC = 0.1) and TRAP [Thyroid Receptor Associated Protein] (RFC = 0.43) proteins in the presence of *L. aethiopica* infected co-culture (Table 6.1). These two proteins represent a multi-functional co-activator for transcription factors including STAT, NF-κB and AP-1 (Mahajan and Samuels, 2008). Since this has not been reported during *Leishmania*, this might indicate one of the novel strategies employed by *L. aethiopica* where the parasite

could target the co-activator protein in order to additively lower the effect of transcription factor induced gene expression.

6.3. Conclusions

In conclusion, for the first time, this chapter has evaluated changes in global proteome expression profiles of human macrophages during the late stage of *Leishmania* infection. Using an isotopic labeling proteomic approach, the result showed modulation of diverse range of host proteins ranging from apoptotic cell death and immune response to metabolism and vesicular trafficking during the virulent periods of *L. aethiopica* spreading. Close examination of 19 differentially expressed proteins revealed two major changes at late stage of infection. Firstly, the apoptotic induction was actively involved during parasitic spread, which is consistent with chapter 4 and 5 of this thesis. Secondly, a significant downregulation of pro-inflammatory and anti-microbial activity and upregulation of anti-inflammatory response was involved; both of which are well known strategy utilized by *Leishmania* to promote its survival in macrophage. As very little is known on *L. aethiopica* specific regulation, future work involves validating these differentially expressed proteins through western blot and comparing these data with similar proteomic experiments conducted in different *Leishmania* species over a larger sets of time periods. This will provide a broader picture of global differences in host cell proteome that might be targeted by species specific parasites for their spreading during the establishment of cutaneous and visceral leishmaniasis.

Chapter 7 – Discussion

7.1. Discussion

Cell-to-cell spreading of intracellular amastigotes not only represents an important survival strategy for *Leishmania* parasites but is also forms the basis for pathogenic development of human leishmaniasis. This is emphasized by the fact that majority of promastigotes inoculated by the sandfly are killed by the host complement system (Dominguez et al., 2003). Hence, a selective pressure is exerted on surviving intracellular amastigotes to replicate and disseminate its progeny for disease development. Studies conducted on *Leishmania* infection of mice macrophages have provided indication that parasitic egress could occur via apoptotic cell death and not through host cell lysis as previously assumed (Rittig et al., 1998; Real et al., 2014). Despite this assumption, there is a major gap in knowledge pertaining the mechanism of *Leishmania* spreading in human cells. This has been largely caused by the lack of reliable experimental model to study the late stage of parasite-host interaction.

To preliminary assess the correlation between *Leishmania* infection spread and apoptosis, two experimental approaches were carried out (Chapter 3). These include: (i) determining the effect of *Leishmania* infection on cell apoptosis; (ii) determining the effect of apoptotic induction on parasites infection. Differentiated THP-1 macrophages were chosen as a host cell line for infection as it has been reported to support growth and replication of *Leishmania* (Ogunkolade et al., 1990). *In vitro* studies on *Leishmania* infection have used different cell line lineage to model parasite-host interaction such as U937, PMA treated THP-1 and RAW 26.4 macrophages (Lisi et al., 2005; Ruhland et al., 2007; Getti et al., 2008). The selection of THP-1 in our model stems from the fact that it is non-adherent in nature, which makes them ideal for flow cytometry studies. The use of adherent cell lines requires

detachment through harsh trypsin treatment that might damage cell membrane causing subsequent parasite release, leading to inconsistent data. The result showed significant increase in apoptotic induction during infection with four species of promastigotes including *L. aethiopica*, *L. major*, *L. mexicana* and *L. tropica*. This was consistent with recent experiments involving mice peritoneal macrophage infection with *L. major* (Filardy et al., 2014) and *L. amazonensis* (DaMata et al., 2015) as well as U937 infection with *L. aethiopica*, *L. major*, *L. tropica* (Getti et al., 2008). This suggests that apoptotic response was not due to specific choice of system but rather due to the interaction between parasite and host. However, an intense level of THP-1 replication after 48 hours of infection made it impossible to further study infection as replicating uninfected cells effectively masked infection spreading. The link between infection spread and apoptosis was further confirmed by testing the effect of apoptotic induction on *Leishmania* infection. Such effect was particularly evident for *L. aethiopica* and *L. mexicana* infection. However, this model cannot be considered as an effective system to study cell-to-cell spreading since the treatment with camptothecin affected uninfected bystander cells in both *L. aethiopica* and *L. mexicana* infected samples.

Interestingly, camptothecin treatment generated a population of heavily infected cells at 72 and 96 hours after infection. Therefore, it was possible to use *L. aethiopica* and *L. mexicana* infected cells from 72 hours to set up co-cultures with uninfected differentiated THP-1 macrophages for analysing parasite spreading (Chapter 4). This form of cell-to-cell infection has been successfully utilized in studies of other infectious agents such as HIV-1 (Gropelli et al., 2015), *Mycobacterium* (Hagedorn et al., 2009) and *L. amazonensis* (Real et al., 2014), but never in *Leishmania* infection of human cells. Results from flow cytometry and trypan blue assay confirmed that increase in percentage of infection from 1 to 12 hours was due to intracellular

amastigote dissemination and not caused by a decrease in viable cell number. Moreover, real time lapse microscopy clearly showed that both species of *Leishmania* exit the host cell via non-lytic mode. This is in line with a previous report by Real and colleagues, where the authors observed that *L. amazonensis* amastigotes were surrounded by host membrane during its egress from mice marcophages (Real et al., 2014). Collectively, the above findings support the *in vivo* model of *Leishmania* infection in mice, where an increase in parasite number was detected from 2 to 4 weeks post infection without inflammatory response (Belkaid et al., 2000). The existence feature of this silent phase together with the evidence of non-lytic amastigote release suggested the involvement of apoptosis. This was confirmed during *L. aethiopica* infection as high expression of Phosphatidyl serine (PS) externalization and caspase-3 activation were detected concomitantly with cell-to-cell spreading. This data suggest that apoptosis could be an infectious mechanism that allows *L. aethiopica* to colonize new cells and ensure a safe replication niche. The role of apoptotic induction in facilitating microbial propagation has also been documented for other intracellular pathogens. The secreted ESAT-6 virulent protein of *M. tuberculosis* was responsible for successful replication and dissemination between mice alveolar macrophages (Aguilo et al., 2013). Similarly, TNF-α secreted during adenovirus infection caused the replicated virions inside the metastatic tumours to spread via apoptotic bodies (Mi et al., 2001).

Remarkably, a non-apoptotic response was associated with *L. mexicana* transmission. Several apoptotic independent mechanisms can be proposed for *L. mexicana* spread when other pathogenic exit strategies are considered. For example, *Chlamydia* exit host cells after a non-lytic, actin-dependent extrusion from the host cell. In this process, the bacteria are extruded in a double-membrane vesicle generated from the bacterial intracellular vacuole and cytoplasmic membranes (Hybiske and

Stephens, 2007). Similarly, during *in vitro* cell-to-cell transmission, *M. marinum* are ejected from host cells through an F-actin-rich structure denominated ejectosome (Hagedorn et al., 2009); the bacteria also remain associated with membrane remnants in the process. Finally, HIV-1 has also developed non-lytic strategies to egress from host cells either through virological synapses (Jolly and Sattentau, 2005).

As *L. aethiopica* spread was linked to apoptosis, further analysis was carried out to identify which of the apoptotic signalling pathways are involved and regulated by intracellular amastigotes (Chapter 5). Induction of apoptosis involves a very complex and sophisticated signalling pathway that is tightly regulated at multiple points (Figure 7.1). Current literature reports *Leishmania* promastigotes regulation of host apoptotic induction via three major signalling pathways: AKT, NF-κB and PKC-δ during the initial stage of infection (Akarid et al., 2004; Ruhland et al., 2007; Singh et al., 2004; Lisi et al., 2005). However, such studies are limited to early stages of promastigotes infection and provide no information on the effect of amastigotes on host apoptosis. This research showed for the first time how *L. aethiopica* amastigotes disrupts the pro-survival pathways of human macrophages in order to promote apoptosis (Table 7.1).

Firstly, a significant reduction in AKT was detected, which led to BAD activation and cytochrome C release from mitochondria. This decrease could be due to the action of parasite mediated host proteasome activation as a recent study showed that *Legionella pneumophilla* stimulated the ubiquitination and subsequent degradation of AKT through proteasome activity in mice macrophages (Ivanov and Roy, 2013). Further analysis showed that p65 subunit, which is the main transactivation domain of NF-κB responsible for mediating anti-apoptotic gene expression, was also significantly reduced throughout the spreading time period.

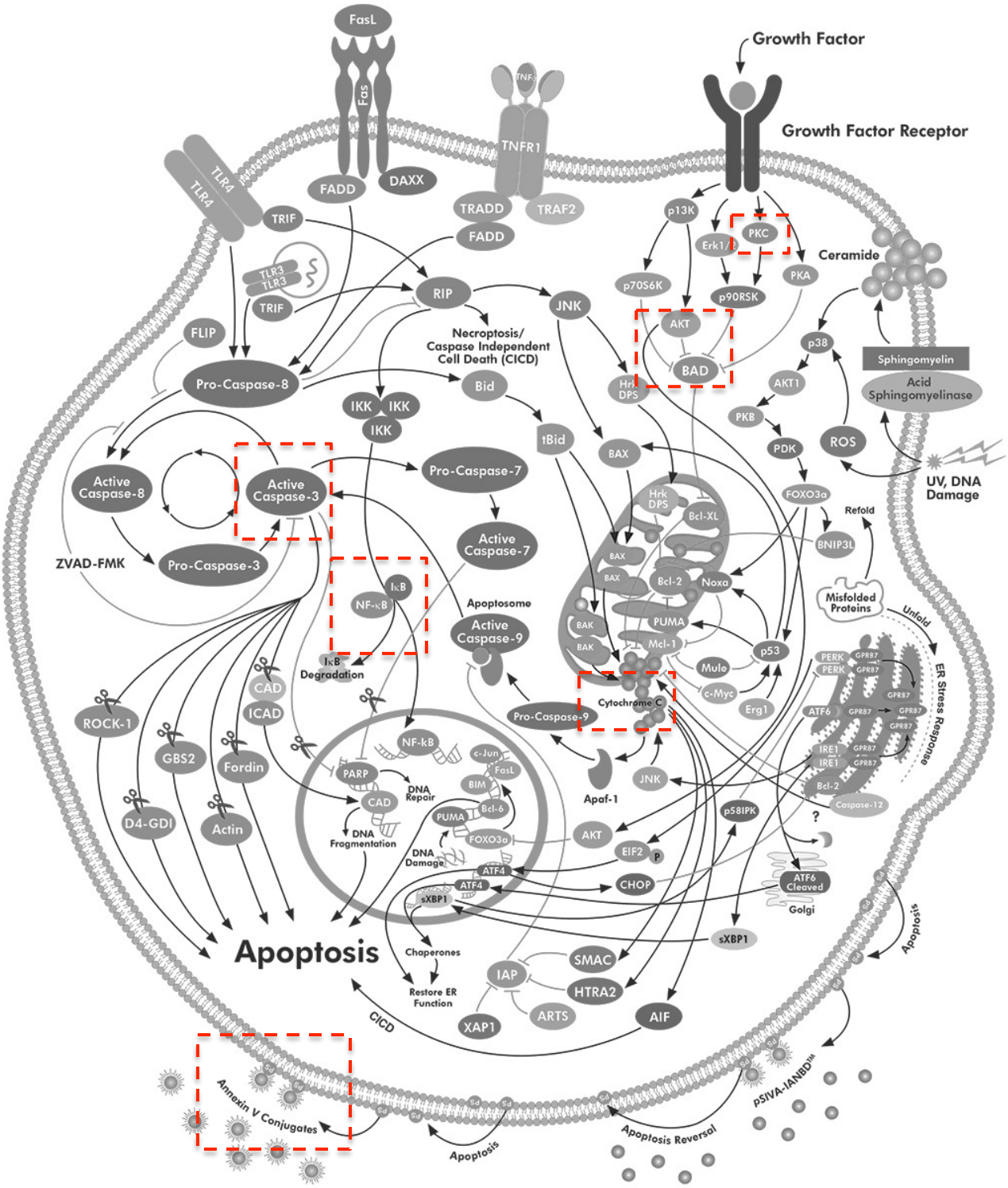


Figure 7.1. Schematic diagram representing the complex nature of intracellular signaling pathways associated with apoptosis. Induction of apoptosis stems from various stimuli that is tightly regulated at multiple points. In the above diagram, dotted red box refers to the specific molecule investigated in this research. Adapted from Novus Biological (www.novusbio.com).

Time (hours after co-culture)	Apoptotic assays		Western blot								
	PS externalization	Active caspase-3	p-AKT	Total AKT	p-BAD	Total BAD	Cytochrome C release	p-IκBα	Total IκBα	p65 NF-κB	PKCδ
1	+/–	+/–	–	+/–	–	+/–	+/–	–	–	–	–
6	n/a	+	–	–	–	+/–	+	–	–	–	–
12	+	+	–	–	–	+/–	+	–	–	–	–
24	+	n/a	–	–	–	+/–	+	–	–	–	–

Table 7.1. Summary of the involvement of apoptotic signaling pathways concomitant with spreading of *L. aethiopica* infection. +/–, similar expression with uninfected control; +, increase in protein expression; –, decrease in protein expression; n/a, data not recorded; PS, Phosphatidyl serine; p-, phosphorylated

Such mechanism of NF-κB downregulation has been previously reported as, cysteine peptidase from *L. mexicana* amastigotes was accountable for the degradation of p65 in infected mice macrophages (Cameron et al., 2004). Similar effects were also observed in poliovirus infection where the viral protease C degraded p65 in HeLa cell (Neznanov et al., 2005). However, it is interesting to note that other human pathogens have evolved diverse strategies to counteract NF-κB signalling mediated apoptosis. *Yersinia* secretes YopJ effector to supress the phosphorylation and degradation of IκB inhibitor, which prevents the release and nuclear migration of p65 causing apoptotic induction of epithelial cells (Schesser et al., 1998). Whereas, type 3 secretion protein VP1686 of *Vibrio* interacted with p65 in order to block the DNA binding activity of NF-κB that resulted in apoptosis of RAW macrophage (Bhattacharjee et al., 2006).

Interestingly, the pro-apoptotic protein PKC-δ was not associated with spreading, as there was no presence of catalytic fragment (CF) at the expected 42 kDa region of the western blot. During apoptosis, the catalytic fragment (CF) of PKC-δ is generated following caspase-3 mediated cleavage of full-length protein. The formation of CF is responsible for the activation of pro-apoptotic Bax, cytochrome C release, inhibition of DNA repairing enzyme DNApk, destruction of nuclear lamin and activating caspase-3 activation (Reyland, 2007). This indicates that *L. aethiopica* does not utilize PKC- δ cleavage as one of the contributing factor for initiating apoptosis.

The mechanism by which *L. aethiopica* selectively targeted the above three pathways suggest that this parasitic species could exploit other apoptotic signalling pathways, which have not been explored yet. It was therefore interesting to determine whether intracellular amastigotes could subvert physiological processes in host cells during parasite transmission. To address this question, a proteomic study was conducted to identify differentially expressed proteins of macrophages involved in

apoptosis, immune response, vesicular trafficking, metabolism and gene expression during *L. aethiopica* spreading (Chapter 6). This was achieved via the use of tandem mass tag (TMT) labelling coupled with tandem mass spectrometry technique. One of the main advantages of this approach over traditional non-labelling methods is its ability to combine and analyse several samples (i.e. uninfected versus *L. aethiopica* infected co-cultures with 3 biological replicates) within one experiment. This eliminates the need to compare multiple mass spectrometry data sets, thereby reducing run-to-run variation and overall analytical time (Rauniyar and Yates, 2014). The proteomic data supported the finding from chapter 4 and 5 where caspase-3 upregulation and AKT/p65 NF-κB protein downregulation was observed. Furthermore, the activation of caspase-9 and casaspe-3 strengthened the involvement of mitochondrial mediated apoptosis.

Finally, identified proteins from immune response and gene expression showed that *L. aethiopica* induces the generation of an anti-inflammatory responses. This is evident from the fact that Chitinase-3-like protein (induces IL-13 production) and butyrophilin (reduces INF-γ and IL-12 response) were strongly upregulated. In particular, elevated increase in the protein expression of glutathione reductase and metallothionein-2, which are very important for scavenging free radicals, suggest that the anti-microbial activity during spreading is disarmed by *L. aethiopica* amastigotes for effective cell-to-cell spreading.

Chapter 8 – Conclusion and future works

8.1. Conclusion

In conclusion, this research has provided for the first time a clear understanding of the mechanism of *Leishmania* spreading between human macrophages, an issue extensively neglected in the study of these parasites. Preliminary experiments showed that apoptotic induction increased the percentage of *L. aethiopica* and *L. mexicana* infected cells during late stage of infection. Although this led to the establishment of a link between host apoptosis and *Leishmania* infection spreading (Aim 1), the viable cell concentration was significantly lower than non-induced cells. Nevertheless, such approach led to the accumulation of heavily infected cells. This provided a platform to develop a novel *in vitro* model to illustrate cell-to-cell spreading of *L. aethiopica* and *L. mexicana* in human macrophage (Aim 2). Through flow cytometry, parasite spreading was detected within 12 hours of co-culture. Interestingly, the live imaging revealed inter-cellular extrusion of *L. aethiopica* and *L. mexicana* from infected to a recipient cells without cell lysis. Interestingly, *L. aethiopica* (but not *L. mexicana*) dissemination was correlated with host apoptotic induction, as there was a significant increase in the phosphatidyl serine (PS) externalization and active caspase-3 expression (Aim 3). In addition, western blot analysis demonstrated that *L. aethiopica* spread was associated with modulation of three major apoptotic signaling pathways: AKT, NF-κB and PKC-δ (Aim 4). Specifically, the parasite was able to initiate apoptosis by reducing the expression of pro-survival AKT and p65 NF-κB proteins as well as by inducing cytochrome C release. These selective alterations by *L. aethiopica* prompted a global proteomic study to evaluate the expression of differentially regulated proteins of human macrophages during spreading. Through liquid

chromatography coupled with tandem mass spectrometry, 19 differentially expressed proteins were identified that were either involved in apoptosis, immune response, metabolism, vesicular trafficking and gene transcription (Aim 5). Further examination of these proteins collectively showed that *L. aethiopica* is involved in disarming various inflammatory and anti-microbial responses of human macrophages in order to spread effectively from cell-to-cell.

Infection with *L. aethiopica* is responsible for all forms of cutaneous leishmaniasis (CL) including muco and diffuse CL. Despite such clinical variation, very little is known about the biology and pathogenesis of *L. aethiopica* at the molecular level compared to other *Leishmania* species. This study has greatly contributed to understanding how *L. aethiopica* amastigotes manipulates the host signalling pathways in order to disseminate effectively and promote survival of its infectious progeny in a new macrophage niche, both of which are essential criteria for disease pathogenesis.

8.2. Future works

There are several research questions that can be investigated in future which will aim to further enhance our knowledge into the mechanism of *Leishmania* infection spreading.

1. Critical importance of AKT and NF-κB signalling pathways

Although the western blot data highlighted that *L. aethiopica* spreading correlated with AKT and NF-κB inactivation, whether any of these deficient proteins is the underlying factor behind apoptotic induced dissemination is not known. To address this question, transient overexpression of AKT and p65 NF-κB in the infected cells

will have to be performed. This will indicate whether or not both proteins are the major targets of *L. aethiopica* amastigotes in order to spread from infected to uninfected cells.

2. Involvement of virulence factors in *Leishmania* spreading

   If the above host proteins are instrumental for apoptosis, it will be interesting to find whether such effects are influenced by the virulence factors of *L. aethiopica*. To test this proposal, amastigotes mutant for various virulent proteins such as GP63 and Serine/Cysteine peptidase have to be designed. Then, using the spreading model, experiments will be performed to address two key questions. Is there a difference in the protein level of AKT and p65 NF-κB between wild type and mutant parasites? If the mutant parasite is unable to degrade both proteins, does it have an effect on the percentage of infection and host apoptosis? These would provide a link between virulence factors, host apoptotic response and infection outcome.

3. Elucidate the mechanism for *L. mexicana* spread

   This research clearly showed that L. Mexicana dissemination mechanism involves extrusion of parasites without cell lysis. But the mechanism behind such behaviour is unclear. Intracellular pathogens such as *Chlmaydia*, *Shigella* and *Listeria* have evolved mechanism to recruit the host actin cytoskeleton in order to protrude across the uninfected cells (Ireton, 2013). To determine whether similar process is also utilized by *L. mexicana*, two critical experiments needs to be carried out. First, the infected donor cells can be stained with F-actin before co-culturing with uninfected cells and live cell imaged. This will indicate whether F-actin is concentrated around the region of exiting amastigotes. Secondly, inhibitors designed to block actin polymerization and nucleation can be used to completely prove that molecular networks of cytoskeleton are involved in facilitating *L. mexicana* spreading.

Chapter 9 – References

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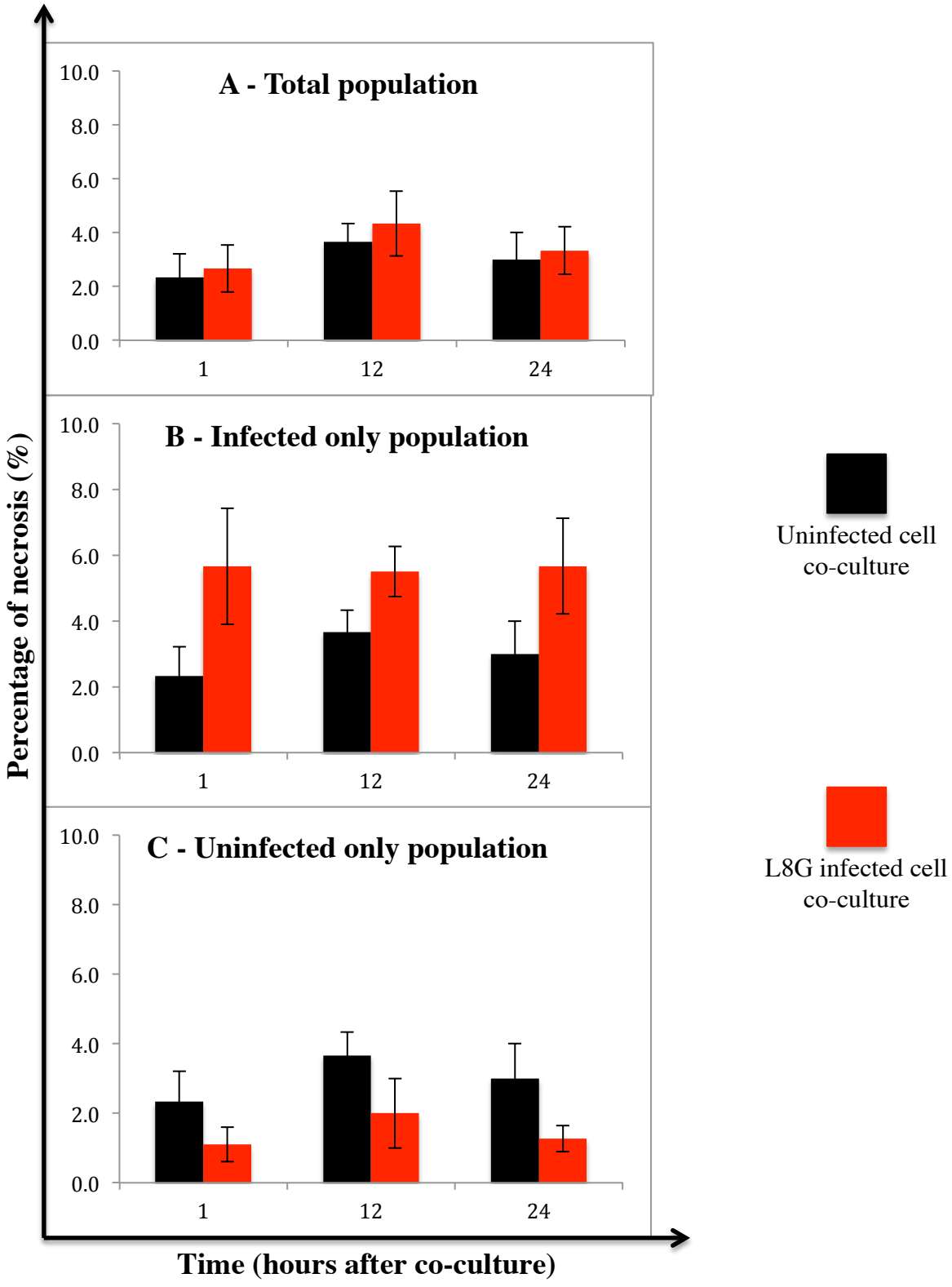
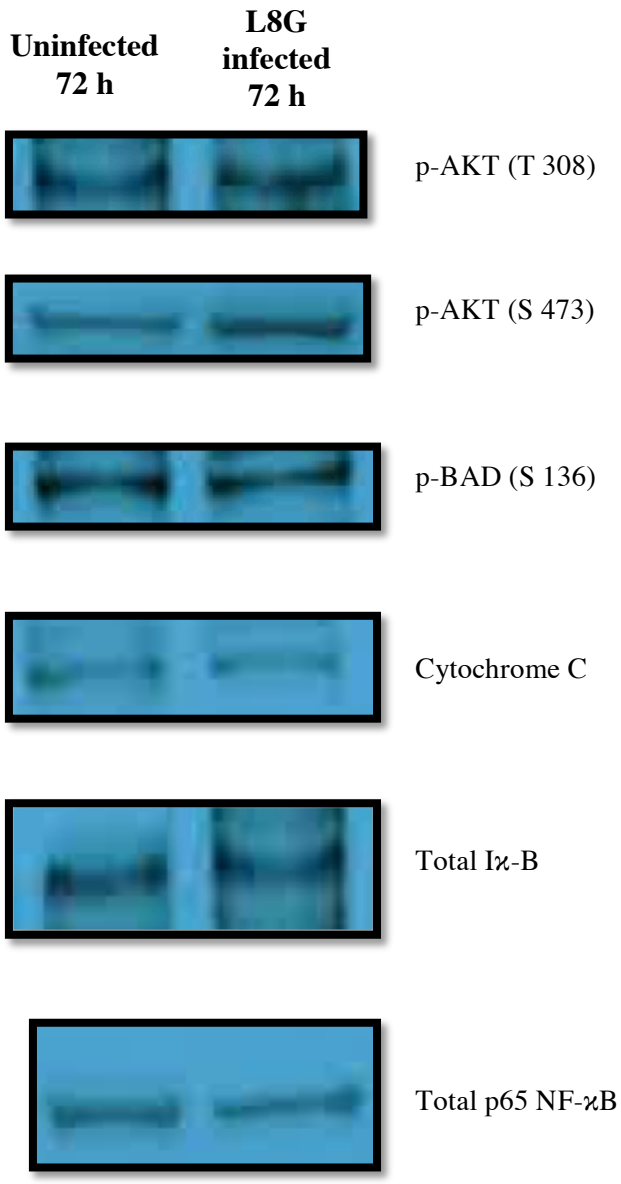


Appendix I – Effect of L8G infection spreading on host cell necrosis. After infection of differentiated THP-1 macrophages with L8G infected cells, the co-culture were analyzed for the percentage of necrosis (Annexin V+/7AAD+) through flow cytometry at 1, 12 and 24 hours after co-culture. Necrosis from the total population **(A)** were divided into infected only **(B)** and uninfected only **(C)** populations. Uninfected cells co-cultured with differentiated THP-1 macrophages were taken as a positive control. The data represents mean percentage (mean ± SEM) from three independent experiments.



Appendix II – Representative western blot of six different proteins in uninfected and L8G infected cells at 72 hours prior to co-culture. Whole cell and/or cytosolic lysates were collected at 72 hours from uninfected and L8G infected cells. Equal amounts (30 µg) were resolved by SDS-PAGE. The presence of p-AKT (Ser and Thr), total AKT, p-BAD (Ser), cytochrome C, total Iκ-B and total p65 were analyzed by western blot.

Appendix III – Representative example of protein expression from Set A following tandem mass spectrometry

Accession	Description	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	130/129	130/129 Count	130/129 Variability [%]	Score	# AAs	MW [kDa]
B7Z6P1	cDNA FLJ53662, highly similar to Actin, alpha skeletal muscle OS=Homo sapiens PE=2 SV=1 - [B7Z6P1_HUMAN]	33.53	54	1	14	1027	1.000	17	0.000	2707.879	343	38.554
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	51.8	15	23	41	917	1.000	329	7.692	2548.425	724	83.212
B4DW52	cDNA FLJ55253, highly similar to Actin, cytoplasmic 1 OS=Homo sapiens PE=2 SV=1 - [B4DW52_HUMAN]	51.59	59	1	16	878	1.000	2	0.000	2359.053	347	38.608
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	43.03	16	17	36	761	1.000	232	2.192	2109.981	732	84.607
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	55.11	27	13	39	787	1.000	243	9.332	2099.080	646	70.854
B2RDY9	Adenylyl cyclase-associated protein OS=Homo sapiens PE=2 SV=1 - [B2RDY9_HUMAN]	64.42	19	26	28	770	1.000	697	11.145	1976.859	475	51.583
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	46.02	18	89	109	748	1.000	565	11.299	1917.881	1960	226.392
E7EVS6	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens GN=ACTB PE=1 SV=3 - [E7EVS6_HUMAN]	51.83	16	1	9	574	1.000	1		1740.229	164	17.964
K7EM38	Actin, cytoplasmic 2, N-terminally processed (Fragment) OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [K7EM38_HUMAN]	58.65	15	1	9	574	1.000	1		1738.508	133	14.513
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]	43.72	9	89	109	641	1.000	524	8.653	1736.700	2541	269.599
V9HVZ7	Epididymis luminal protein 176 OS=Homo sapiens GN=HEL-176 PE=2 SV=1 - [V9HVZ7_HUMAN]	54.71	33	1	12	490	1.000	11	0.000	1389.859	223	25.020
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	49.31	22	20	22	517	1.000	443	8.949	1374.317	434	47.139
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	53.52	5	29	36	532	1.000	376	7.863	1354.465	654	72.288
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3 - [PDIA1_HUMAN]	51.18	20	15	34	506	1.000	186	9.514	1280.098	508	57.081
I3L4N8	Actin, cytoplasmic 2 (Fragment) OS=Homo sapiens GN=ACTG1 PE=1 SV=3 - [I3L4N8_HUMAN]	43.8	45	1	10	478	1.000	1		1254.509	242	26.917
Q5CAQ5	Tumor rejection antigen (Gp96) 1 OS=Homo sapiens GN=TRA1 PE=2 SV=1 - [Q5CAQ5_HUMAN]	43.52	12	39	40	420	1.000	335	7.375	1141.490	802	92.282
B3GQS7	Mitochondrial heat shock 60kD protein 1 variant 1 OS=Homo sapiens GN=HSPD1 PE=2 SV=1 - [B3GQS7_HUMAN]	45.87	18	23	24	396	1.000	363	7.697	1078.888	569	60.642
P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2 - [H14_HUMAN]	53.88	7	7	18	368	1.000	84	11.091	1067.153	219	21.852
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	55.18	43	2	30	398	1.000	9	4.603	1058.131	531	57.900
B4DRT3	Pyruvate kinase OS=Homo sapiens PE=2 SV=1 - [B4DRT3_HUMAN]	52.64	42	1	29	391	1.144	3	6.155	1035.127	511	55.891
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	38.32	8	14	16	376	1.000	315	4.624	1014.110	334	36.615
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	50	11	16	21	362	1.000	286	10.413	1001.410	364	39.395
E9PN89	Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [E9PN89_HUMAN]	58.97	2	1	19	358	0.756	2	43.216	983.109	312	34.797
B7Z4V2	cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z4V2_HUMAN]	48.42	12	35	37	373	1.000	325	3.205	964.727	665	72.356
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	39.83	37	4	21	454	0.997	82	13.269	955.071	462	50.109
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]	48.48	12	24	30	401	1.000	267	4.876	947.082	627	70.244
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	51.17	4	5	15	321	0.942	56	10.193	942.017	213	21.352
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	35.81	32	1	16	353	1.000	3	10.773	928.133	444	49.639
P68371	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]	35.73	31	2	16	352	1.000	52	4.498	908.099	445	49.799
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	39.04	13	33	37	353	1.000	313	6.126	900.070	858	95.277
B3KQT9	Protein disulfide-isomerase OS=Homo sapiens PE=2 SV=1 - [B3KQT9_HUMAN]	43.96	8	19	26	331	1.000	210	7.657	894.435	480	54.068
P02545	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 - [LMNA_HUMAN]	61.45	10	41	43	310	1.000	287	11.696	861.924	664	74.095
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	40.7	10	45	47	360	1.000	347	10.563	860.177	710	76.568
P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2 - [H13_HUMAN]	42.53	4	8	16	294	0.977	63	12.592	852.784	221	22.336
Q75MT9	Malate dehydrogenase (Fragment) OS=Homo sapiens GN=MDH2 PE=3 SV=1 - [Q75MT9_HUMAN]	53.48	6	15	15	314	1.000	308	8.988	848.312	316	33.208
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	61.87	6	22	26	296	1.000	214	1.538	808.234	417	44.586
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	55.46	5	24	45	328	1.000	145	7.834	798.275	577	67.778
Q6LC01	MRNA encoding beta-tubulin. (from clone D-beta-1) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6LC01_HUMAN]	31.81	10	1	15	322	1.143	2	19.960	792.056	437	48.848
H0Y3Z3	Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4HB PE=1 SV=1 - [H0Y3Z3_HUMAN]	50.36	2	1	19	320	1.105	14	13.884	779.495	274	31.523
B2RDE1	cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDE1_HUMAN]	68.55	15	13	27	270	1.000	122	6.823	744.881	248	29.000
Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2 - [SAMH1_HUMAN]	46.96	4	30	30	287	1.000	272	6.421	721.561	626	72.155
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	45.67	9	14	15	302	1.000	280	10.534	717.125	335	36.030
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]	54.64	18	41	43	275	1.000	249	7.733	703.591	840	94.271
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	48.82	4	12	30	259	1.000	82	9.956	701.418	553	59.714
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	21.25	11	36	36	266	1.000	251	4.766	692.530	1675	191.493
P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	46.02	4	13	18	259	1.116	171	16.416	673.664	226	22.566
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	22	4	88	88	242	1.000	233	9.114	659.493	4128	468.788
P09525	Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 - [ANXA4_HUMAN]	53.92	9	20	22	242	1.000	217	3.098	646.589	319	35.860
B8ZZQ6	Uncharacterized protein OS=Homo sapiens GN=PTMA PE=1 SV=1 - [B8ZZQ6_HUMAN]	24.3	20	5	5	202	1.000	180	0.000	644.365	107	11.752
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	59.23	38	24	31	242	1.000	174	0.000	635.417	466	53.619
Q0QEN7	ATP synthase subunit beta (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1 - [Q0QEN7_HUMAN]	42.02	6	13	14	220	1.000	189	0.000	631.959	445	48.083
P80723	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2 - [BASP1_HUMAN]	89.87	2	19	19	214	1.000	204	7.512	625.232	227	22.680
B4DNE0	cDNA FLJ52573, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B4DNE0_HUMAN]	39.24	13	1	16	324	1.000	3	0.000	620.343	395	42.569
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	70	3	10	10	215	1.000	208	5.977	611.572	140	15.045
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	59.61	11	13	16	222	1.000	140	6.819	603.899	255	29.155
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	69.28	8	3	16	224	0.996	38	11.415	602.256	166	18.491
Q96C96	P4HB protein (Fragment) OS=Homo sapiens GN=P4HB PE=2 SV=2 - [Q96C96_HUMAN]	43.22	1	1	17	251	0.991	2	6.690	600.853	273	31.443
A7BI36	p180/ribosome receptor OS=Homo sapiens GN=RRBP1 PE=2 SV=2 - [A7BI36_HUMAN]	52.92	11	5	61	214	1.073	8	15.233	598.980	1540	165.649
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	35.86	25	3	14	242	1.000	21	7.174	598.234	449	49.863
F6KPG5	Albumin (Fragment) OS=Homo sapiens PE=2 SV=1 - [F6KPG5_HUMAN]	35.04	14	22	22	238	1.039	229	13.067	586.308	585	66.488
Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN]	48.01	9	1	57	208	1.000	3	0.000	585.763	1410	152.381
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	50.14	5	14	16	230	1.000	190	0.595	576.881	353	37.407
B4DJI1	L-lactate dehydrogenase OS=Homo sapiens PE=2 SV=1 - [B4DJI1_HUMAN]	45.57	26	16	18	212	1.000	148	9.150	566.858	305	33.572
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]	55.13	41	3	9	208	1.000	14	0.000	566.023	156	17.953
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	52.63	4	10	15	224	1.000	73	0.953	565.423	247	28.285
Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 - [EF1A2_HUMAN]	21.81	5	3	12	272	1.044	4	12.341	563.988	463	50.438
E9B3L2	Heat shock protein 83-1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_0312 PE=3 SV=1 - [E9B3L2_LEIMU]	36.09	1	27	28	198	1.000	119	11.615	563.674	701	80.521
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	45.43	7	31	32	276	1.000	229	7.358	561.181	645	72.887
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]	46.53	12	7	13	238	1.000	120	6.022	555.141	245	27.728
Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	34.87	17	94	97	236	1.000	212	7.455	549.544	5890	628.699
B5BU24	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=2 SV=1 - [B5BU24_HUMAN]	51.22	5	6	14	230	1.000	45	12.161	530.479	246	28.095
P61158	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 - [ARP3_HUMAN]	40.19	16	18	18	180	1.000	170	7.272	530.164	418	47.341
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPQ_HUMAN]	52.74	5	28	28	226	1.000	216	8.321	524.462	548	59.583
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	35.47	16	27	27	192	1.000	184	8.595	518.073	592	67.526
P62987	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]	49.22	40	1	7	194	0.932	1		514.394	128	14.719
P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	38.39	15	22	25	228	1.000	204	8.026	510.637	461	50.994
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	29.64	21	7	22	204	1.102	27	14.466	509.902	641	70.009
B3KX72	cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens PE=2 SV=1 - [B3KX72_HUMAN]	30.67	6	3	30	214	1.000	38	23.595	507.350	750	83.033
V9HWK1	Triosephosphate isomerase OS=Homo sapiens GN=HEL-S-49 PE=2 SV=1 - [V9HWK1_HUMAN]	49.8	8	11	11	160	1.000	152	0.000	502.445	249	26.653
F5H3P3	Rho GDP-dissociation inhibitor 2 (Fragment) OS=Homo sapiens GN=ARHGDIB PE=1 SV=3 - [F5H3P3_HUMAN]	54.72	7	9	9	172	1.000	166	7.517	502.036	159	17.925
P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	58.52	2	8	8	182	1.000	175	7.102	500.524	135	14.706
E9ATD2	Putative polyubiquitin (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3530 PE=4 SV=1 - [E9ATD2_LEIMU]	73.75	7	2	7	186	1.000	5	0.000	494.423	80	8.860
B4DUQ1	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1 - [B4DUQ1_HUMAN]	37.13	12	17	17	203	1.000	196	10.860	490.540	439	48.480
E9B099	Putative heat-shock protein hsp70 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2770 PE=3 SV=1 - [E9B099_LEIMU]	34.25	3	9	24	206	1.000	47	0.000	489.988	654	71.197
E9PQB7	Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=1 - [E9PQB7_HUMAN]	72.13	2	1	13	183	1.267	1		485.574	122	13.914
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	64.32	2	10	13	222	1.000	162	8.914	485.096	199	22.096
A0A024RC87	Ribonuclease/angiogenin inhibitor 1, isoform CRA_a OS=Homo sapiens GN=RNH1 PE=4 SV=1 - [A0A024RC87_HUMAN]	36.18	8	9	16	174	1.000	86	0.000	475.087	456	49.385
B4DLR3	cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens PE=2 SV=1 - [B4DLR3_HUMAN]	27.55	4	2	29	195	1.000	19	0.000	468.627	784	86.806
P67809	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 - [YBOX1_HUMAN]	49.69	12	9	12	171	1.000	127	0.000	467.869	324	35.903
A8K486	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1 - [A8K486_HUMAN]	53.33	15	8	11	226	1.000	193	11.687	455.227	165	18.002
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	48.98	7	7	14	189	1.000	51	3.856	453.374	245	27.747
B2RCQ9	cDNA, FLJ96225, highly similar to Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RCQ9_HUMAN]	21.37	5	1	16	171	1.000	1		439.217	641	70.332
P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	53.63	9	5	21	163	1.000	37	15.827	436.370	248	28.504
K7EK77	ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [K7EK77_HUMAN]	75.85	4	1	17	161	1.000	2	0.000	435.650	207	22.186
A8K690	cDNA FLJ76863, highly similar to Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA OS=Homo sapiens PE=2 SV=1 - [A	51.57	5	41	41	186	1.000	181	9.265	432.118	543	62.615
P52209	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 - [6PGD_HUMAN]	32.51	10	16	16	153	1.000	144	4.471	431.543	483	53.106
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	62.14	17	16	16	164	1.000	157	5.678	428.552	243	26.671
P20700	Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2 - [LMNB1_HUMAN]	49.83	4	29	33	164	1.000	141	9.553	427.832	586	66.368
A4QPB0	IQ motif containing GTPase activating protein 1 OS=Homo sapiens GN=IQGAP1 PE=2 SV=1 - [A4QPB0_HUMAN]	29.21	13	39	46	155	1.000	132	6.833	426.034	1657	189.162
Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	18.13	17	85	90	162	1.000	144	13.941	414.551	4684	531.466
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	41.85	10	7	12	133	1.000	44	6.969	413.851	356	37.474
P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	30.49	19	9	14	138	1.000	54	1.635	399.223	364	39.431
P12956	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 - [XRCC6_HUMAN]	36.45	15	23	23	146	1.000	140	6.009	398.990	609	69.799
Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN]	32.67	12	21	22	137	1.000	58	6.669	398.124	704	80.060
P07814	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	29.63	7	42	43	157	1.000	151	4.396	397.743	1512	170.483
P06396	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1 - [GELS_HUMAN]	24.68	14	25	25	154	1.000	144	10.151	397.293	782	85.644
P05023	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 - [AT1A1_HUMAN]	35.87	31	24	34	135	1.000	85	9.442	395.534	1023	112.824
P06753	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 - [TPM3_HUMAN]	39.65	6	2	19	156	1.000	5	2.168	394.023	285	32.930
B2R6J2	cDNA, FLJ92973, highly similar to Homo sapiens villin 2 (ezrin) (VIL2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6J2_HUMAN]	44.54	17	23	36	182	1.000	80	10.811	392.793	586	69.358
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	46.34	6	9	13	160	1.000	53	14.464	386.947	246	28.201
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	38.17	10	18	19	190	1.000	163	9.651	377.052	427	47.667
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]	51.22	4	12	12	140	1.000	137	11.065	376.197	205	22.768
P51858	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1 - [HDGF_HUMAN]	67.08	7	1	18	132	1.000	10	13.451	375.544	240	26.772
H7BZJ3	Protein disulfide-isomerase A3 (Fragment) OS=Homo sapiens GN=PDIA3 PE=1 SV=1 - [H7BZJ3_HUMAN]	56.91	1	1	8	133	1.000	15	0.000	374.521	123	13.511
E9ARD0	Elongation factor 1-alpha OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0080 PE=3 SV=1 - [E9ARD0_LEIMU]	40.53	5	15	19	190	1.585	64	77.129	371.758	449	49.175
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN]	30.58	16	3	13	179	0.918	4	42.413	371.468	448	49.892
B2RDE8	cDNA, FLJ96580, highly similar to Homo sapiens hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA OS=Homo sapiens PE=2 SV=1 - [B	67.08	4	1	18	125	0.835	4	8.463	368.385	240	26.789
Q53G71	Calreticulin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G71_HUMAN]	34.24	6	17	17	173	1.000	167	8.030	359.942	406	46.890
P61604	10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2 - [CH10_HUMAN]	57.84	5	4	7	142	1.102	81	14.421	351.760	102	10.925
P08133	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	36.7	12	9	29	150	1.020	41	13.927	349.752	673	75.826
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	34.62	18	24	30	143	1.000	105	4.352	349.509	806	89.266
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	14.18	6	70	71	138	1.000	137	7.673	349.218	4646	532.072
P07355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN]	48.38	27	19	19	129	1.000	120	1.771	348.757	339	38.580
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	30.88	6	1	36	141	1.000	28	0.000	345.833	1101	120.762
E9AP62	Alpha tubulin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0280 PE=3 SV=1 - [E9AP62_LEIMU]	11.86	4	2	7	141	5.467	2	2018.696	343.166	548	60.146
O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 - [FLNB_HUMAN]	26.06	14	61	67	136	0.947	128	12.839	342.472	2602	277.990
P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LPPRC_HUMAN]	26.97	4	44	44	138	1.000	136	9.808	340.782	1394	157.805
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	37.01	13	10	10	130	1.000	121	5.484	340.119	254	28.786
Q562Z4	Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=3 SV=1 - [Q562Z4_HUMAN]	40.78	43	2	4	116	1.000	9	0.000	339.927	103	11.548
H3BRU6	Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [H3BRU6_HUMAN]	32.56	20	1	9	107	1.000	1		339.593	301	31.690
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN]	26.37	14	28	28	126	1.000	122	4.514	337.121	1058	117.774
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	35.68	2	16	16	127	1.000	121	6.893	335.059	440	48.091
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	35.24	7	20	21	150	1.000	143	8.604	333.729	437	50.087
B3KX11	T-complex protein 1 subunit gamma OS=Homo sapiens PE=2 SV=1 - [B3KX11_HUMAN]	36.97	12	22	22	133	1.000	124	18.955	331.655	522	57.909
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]	21.51	5	47	49	125	0.995	119	13.672	330.507	2511	273.254
A8K3C3	T-complex protein 1 subunit delta OS=Homo sapiens PE=2 SV=1 - [A8K3C3_HUMAN]	40.82	5	21	21	122	1.000	117	5.405	329.759	539	57.916
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	20.55	7	6	20	128	1.000	54	18.248	328.133	944	106.807
P07602	Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	21.18	8	12	12	136	1.195	135	23.688	326.425	524	58.074
P46777	60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 - [RL5_HUMAN]	37.71	7	14	14	133	1.000	118	10.844	324.838	297	34.341
Q562L9	Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=3 SV=1 - [Q562L9_HUMAN]	30.1	43	1	3	108	0.954	1		324.474	103	11.549
A0A087WTP3	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=4 SV=1 - [A0A087WTP3_HUMAN]	37.27	14	22	28	122	1.000	97	5.082	321.136	711	72.982
V9HWC6	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=HEL-S-39 PE=2 SV=1 - [V9HWC6_HUMAN]	63.46	8	14	15	145	1.000	135	11.054	320.649	208	22.728
F8W1R7	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=4 SV=1 - [F8W1R7_HUMAN]	51.72	16	6	8	112	1.000	59	0.000	320.243	145	16.280
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	32.99	31	4	13	129	1.000	25	16.694	319.533	394	44.732
P49588	Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 - [SYAC_HUMAN]	26.24	3	28	28	117	1.000	115	10.461	314.654	968	106.743
E9PFP8	Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 PE=4 SV=1 - [E9PFP8_HUMAN]	21.61	13	0	7	97				313.609	361	38.163
A0A024R895	SET translocation (Myeloid leukemia-associated), isoform CRA_b OS=Homo sapiens GN=SET PE=3 SV=1 - [A0A024R895_HUMAN]	31.41	4	1	8	103	1.000	5	0.000	312.343	277	32.084
J3KTA4	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [J3KTA4_HUMAN]	38.44	15	19	26	143	1.000	71	5.655	310.615	614	69.044
Q16891	MICOS complex subunit MIC60 OS=Homo sapiens GN=IMMT PE=1 SV=1 - [MIC60_HUMAN]	37.86	15	15	32	114	1.000	58	8.050	310.549	758	83.626
P62328	Thymosin beta-4 OS=Homo sapiens GN=TMSB4X PE=1 SV=2 - [TYB4_HUMAN]	45.45	8	2	5	119	0.996	7	10.098	309.659	44	5.050
P12270	Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN]	24.08	9	58	59	110	1.000	106	7.561	309.338	2363	267.131
B7Z4C7	cDNA FLJ57321, moderately similar to Moesin OS=Homo sapiens PE=2 SV=1 - [B7Z4C7_HUMAN]	61.76	1	1	13	127	1.032	1		309.125	204	23.899
P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 - [TAGL2_HUMAN]	59.3	5	12	12	123	1.000	118	6.778	308.925	199	22.377
A0A024QZJ6	Myosin, heavy polypeptide 11, smooth muscle, isoform CRA_b OS=Homo sapiens GN=MYH11 PE=4 SV=1 - [A0A024QZJ6_HUMAN]	7.64	20	2	17	112	0.998	5	34.468	303.523	1938	223.439
Q53HV2	Chaperonin containing TCP1, subunit 7 (Eta) variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HV2_HUMAN]	37.38	7	20	21	116	1.000	107	6.834	302.903	543	59.303
B2R5U1	cDNA, FLJ92620, highly similar to Homo sapiens staphylococcal nuclease domain containing 1 (SND1),mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5U1_HUMAN]	29.94	8	28	28	115	1.000	109	6.914	301.397	885	99.609
Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	34.83	4	2	9	100	0.654	2	41.836	298.996	290	33.469
P63313	Thymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2 - [TYB10_HUMAN]	34.09	3	1	4	114	0.953	2	7.174	300.010	44	5.023
P23381	Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 - [SYWC_HUMAN]	28.24	24	13	13	108	1.000	104	10.391	299.596	471	53.132
Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	34.83	4	2	9	100	0.654	2	41.836	298.996	290	33.469
D6R9P3	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=1 - [D6R9P3_HUMAN]	34.29	7	8	11	113	1.000	57	0.000	293.263	280	30.284
P12814	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN]	29.6	31	15	25	132	1.000	81	11.762	292.385	892	102.993
P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 - [ERP29_HUMAN]	37.93	3	10	10	103	1.000	97	11.550	291.270	261	28.975
P07339	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	35.68	6	12	12	108	1.086	96	15.144	290.628	412	44.524
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	35.14	5	20	20	106	1.000	99	1.883	290.448	535	57.452
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	32.21	3	3	12	126	1.008	20	4.295	289.564	298	32.831
E9B125	Putative heat shock 70-related protein 1, mitochondrial OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2550 PE=3 SV=1 - [E9B125_LEIMU]	35.07	8	19	22	112	1.876	42	117.793	289.182	653	70.823
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	47.62	18	14	14	126	1.000	115	8.422	288.204	294	32.555
F5H7S3	Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2 - [F5H7S3_HUMAN]	39.59	17	2	14	112	1.000	6	0.000	287.814	245	28.508
Q96HX3	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96HX3_HUMAN]	30.28	8	20	20	113	1.000	108	5.426	287.513	568	64.542
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	45.89	17	35	35	134	0.996	133	11.161	285.595	730	77.464
F8W6I7	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=2 - [F8W6I7_HUMAN]	43.32	16	9	12	111	1.000	70	6.200	284.935	307	33.135
A8K4W0	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=2 SV=1 - [A8K4W0_HUMAN]	47.35	16	17	17	121	1.000	119	6.285	284.570	264	29.936
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	30.23	24	29	29	114	1.000	111	10.762	281.326	999	111.266
B1AK87	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 - [B1AK87_HUMAN]	49.23	9	14	15	121	1.000	115	10.271	280.651	260	29.277
A0A024R1Y2	ATP citrate lyase, isoform CRA_a OS=Homo sapiens GN=ACLY PE=4 SV=1 - [A0A024R1Y2_HUMAN]	30.71	7	1	36	114	0.854	1		280.249	1091	119.695
B2R8R5	cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8R5_HUMAN]	29.58	5	21	21	113	1.000	103	2.264	279.569	835	88.503
Q58FG1	Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1 - [HS904_HUMAN]	8.85	1	1	4	103	1.000	8	0.000	279.015	418	47.682
B4DJQ5	cDNA FLJ59211, highly similar to Glucosidase 2 subunit beta OS=Homo sapiens PE=2 SV=1 - [B4DJQ5_HUMAN]	37.94	8	18	18	119	1.000	108	9.307	277.898	535	60.096
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]	37.57	3	21	21	102	1.000	97	11.670	277.762	527	59.719
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	37.01	5	20	20	105	0.994	102	13.117	275.326	408	44.938
Q6PJ75	Integrin beta (Fragment) OS=Homo sapiens GN=ITGB2 PE=2 SV=1 - [Q6PJ75_HUMAN]	42.74	32	26	28	119	1.000	106	5.224	275.305	758	83.605
Q9Y4G6	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4 - [TLN2_HUMAN]	7.91	8	2	23	101	1.000	4	0.000	273.718	2542	271.443
Q9BU08	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BU08_HUMAN]	29.87	16	20	21	117	1.000	113	11.316	273.138	539	59.431
B4DPW9	cDNA FLJ51929, highly similar to Plastin-3 OS=Homo sapiens PE=2 SV=1 - [B4DPW9_HUMAN]	15.42	13	4	10	130	1.006	8	36.084	272.142	603	67.557
B4DU58	cDNA FLJ51488, highly similar to Macrophage capping protein OS=Homo sapiens PE=2 SV=1 - [B4DU58_HUMAN]	29.97	7	10	10	98	1.000	94	14.401	271.669	327	36.225
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	34.54	4	11	12	103	1.000	91	12.819	271.659	249	28.663
D9YZV5	Tropomyosin 1 (Alpha) isoform 4 OS=Homo sapiens GN=TPM1 PE=3 SV=1 - [D9YZV5_HUMAN]	31.34	19	1	14	108	0.361	1		271.506	284	32.856

E5RK69	Annexin OS=Homo sapiens GN=ANXA6 PE=1 SV=1 - [E5RK69_HUMAN]	38.48	4	1	21	115	1.000	6	0.000	270.580	460	51.744
C9J9K3	40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=3 - [C9J9K3_HUMAN]	32.58	10	7	9	94	1.000	82	0.000	269.934	264	29.487
B4E0X8	cDNA FLJ61021, highly similar to Far upstream element-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E0X8_HUMAN]	38.63	12	7	24	106	1.000	34	8.143	267.879	629	66.191
P49321	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 - [NASP_HUMAN]	39.59	15	29	29	95	1.000	90	11.782	263.833	788	85.186
P53999	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3 - [TCP4_HUMAN]	55.12	7	9	9	102	1.000	100	12.006	263.174	127	14.386
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	27.78	8	5	6	87	1.000	85	12.884	262.554	216	24.408
Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	22.1	12	24	25	91	1.000	87	14.737	262.434	1086	113.823
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	37.75	4	6	6	77	1.000	75	0.000	261.525	151	16.263
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 - [SFPQ_HUMAN]	27.02	6	20	21	113	1.000	105	12.702	261.232	707	76.102
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 - [GDIB_HUMAN]	38.2	10	13	16	101	1.000	78	1.079	260.645	445	50.631
A0A087WTT1	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=4 SV=1 - [A0A087WTT1_HUMAN]	36.78	25	15	20	119	1.000	76	0.000	259.588	522	58.499
O75844	CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2 - [FACE1_HUMAN]	18.11	3	9	9	103	1.000	83	3.080	258.614	475	54.778
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]	42.97	6	13	13	88	1.000	79	3.354	257.931	263	29.537
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	34.29	5	14	21	112	1.000	39	12.898	257.252	729	80.222
P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 - [FETUA_HUMAN]	10.9	4	6	6	110	1.095	97	13.520	256.517	367	39.300
A8K7F6	cDNA FLJ78244, highly similar to Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K7F6_HUMAN	41.38	31	7	18	114	1.000	40	10.420	255.085	406	46.093
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	48.12	4	16	17	95	0.987	92	18.615	253.696	266	29.977
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	29.68	12	16	16	104	1.000	99	2.606	252.660	556	60.306
P29350	Tyrosine-protein phosphatase non-receptor type 6 OS=Homo sapiens GN=PTPN6 PE=1 SV=1 - [PTN6_HUMAN]	35.13	13	23	23	93	1.000	93	5.322	251.880	595	67.519
B4DHK9	cDNA FLJ51656, highly similar to Actin-like protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DHK9_HUMAN]	30.99	31	1	10	105	1.000	4	0.000	250.771	342	39.004
B3KSI4	Transketolase OS=Homo sapiens PE=2 SV=1 - [B3KSI4_HUMAN]	31.11	11	16	16	101	1.000	92	7.187	249.928	540	58.944
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	48.66	6	18	19	99	0.999	96	13.088	249.577	337	37.516
E7EUU4	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 - [E7EUU4_HUMAN]	18.08	11	18	34	111	1.000	52	11.199	249.217	1560	171.535
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 - [MDHC_HUMAN]	36.53	6	14	14	98	0.991	95	12.321	248.346	334	36.403
K7ENT6	Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 - [K7ENT6_HUMAN]	54.19	5	0	15	102				247.794	179	20.608
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	32.45	8	33	33	99	0.889	95	17.663	247.754	1014	113.012
Q86UE4	Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2 - [LYRIC_HUMAN]	34.02	5	19	19	79	1.000	75	13.502	246.906	582	63.799
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	39.52	8	7	15	116	1.000	47	8.781	245.711	248	29.207
P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 - [EFTU_HUMAN]	47.57	2	21	21	86	1.000	84	7.023	245.109	452	49.510
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	41.95	9	5	14	115	1.000	9	1.617	244.941	298	32.845
B4DMF5	Glutamate dehydrogenase OS=Homo sapiens PE=2 SV=1 - [B4DMF5_HUMAN]	36.15	12	7	18	93	1.000	51	1.436	244.899	509	56.568
O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN]	32.27	23	17	27	105	1.000	56	8.230	242.288	911	104.788
P54577	Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]	39.39	2	24	24	99	1.000	97	12.358	242.035	528	59.106
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	50.57	5	9	16	94	1.000	59	12.940	240.317	263	29.579
E9AMJ8	Beta tubulin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_1230 PE=3 SV=1 - [E9AMJ8_LEIMU]	10.39	5	1	5	72	8.353	2	14145.790	238.237	414	46.215
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	40.76	8	12	12	105	1.000	99	13.873	237.646	211	24.247
P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_HUMAN]	40.75	6	14	14	90	1.000	83	9.020	237.634	346	38.690
P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	16.53	1	1	5	103	1.000	1		236.366	248	27.757
B4DE36	Glucose-6-phosphate isomerase OS=Homo sapiens PE=2 SV=1 - [B4DE36_HUMAN]	28.11	15	16	17	101	1.000	98	9.551	233.696	530	60.148
P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 - [RADI_HUMAN]	33.96	15	14	27	119	0.989	20	21.028	233.688	583	68.521
P26640	Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4 - [SYVC_HUMAN]	23.1	19	25	26	85	1.000	80	5.589	233.246	1264	140.387
H0YCR7	Ribonuclease inhibitor (Fragment) OS=Homo sapiens GN=RNH1 PE=1 SV=1 - [H0YCR7_HUMAN]	24.91	1	1	7	80	1.000	6	0.000	232.457	285	30.430
Q53T09	Putative uncharacterized protein XRCC5 (Fragment) OS=Homo sapiens GN=XRCC5 PE=4 SV=1 - [Q53T09_HUMAN]	30.99	2	18	18	84	1.000	76	15.207	229.813	568	64.203
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN]	26.1	9	22	29	95	1.000	71	9.040	228.199	1042	114.683
Q6IQ30	PABPC4 protein OS=Homo sapiens GN=PABPC4 PE=2 SV=1 - [Q6IQ30_HUMAN]	30.76	17	6	23	87	1.000	23	12.097	227.733	660	72.315
B4DY08	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=1 - [B4DY08_HUMAN]	44.1	55	14	14	77	1.008	70	7.617	227.278	288	31.952
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	42.31	9	11	11	97	1.000	97	11.329	225.828	156	17.684
P51149	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [RAB7A_HUMAN]	58.45	10	4	12	83	1.000	21	6.566	225.612	207	23.475
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN]	44.88	4	9	10	78	1.000	72	6.702	223.612	283	30.754
Q2NKY5	TUBB6 protein OS=Homo sapiens GN=TUBB6 PE=2 SV=1 - [Q2NKY5_HUMAN]	28.86	5	1	13	112	1.000	1		223.556	447	50.058
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	55.03	3	11	11	91	1.000	84	4.818	223.333	189	19.878
E9PCY7	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 - [E9PCY7_HUMAN]	31.93	28	4	12	87	1.000	39	12.924	222.805	429	47.057
A0A024RDF4	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa), isoform CRA_e OS=Homo sapiens GN=HNRPD PE=4 SV=1 - [A0A024RDF	32.35	8	3	12	98	1.000	11	18.169	222.715	306	32.814
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	9.3	15	37	37	82	1.000	72	3.839	221.985	4374	481.589
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	46.37	24	14	14	82	1.000	82	0.000	221.721	317	35.055
B4DQ92	cDNA FLJ59379, highly similar to Hematopoietic lineage cell-specific protein OS=Homo sapiens PE=2 SV=1 - [B4DQ92_HUMAN]	41.2	10	2	17	83	1.000	13	15.356	220.948	449	49.586
B2R8Z8	cDNA, FLJ94136, highly similar to Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8	28.73	7	11	18	87	1.000	41	28.414	220.755	623	69.559
A8K0T9	cDNA FLJ75422, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K0T9_HUMAN]	31.82	2	7	8	85	1.000	75	2.498	220.433	286	32.888
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	45.86	5	21	21	82	1.000	79	9.583	219.926	519	56.131
Q12771	P37 AUF1 OS=Homo sapiens PE=2 SV=1 - [Q12771_HUMAN]	29.02	7	2	11	94	1.107	9	15.149	218.535	286	31.462
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]	54.77	2	10	10	83	1.000	75	4.934	218.324	241	26.906
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	38.94	4	16	16	76	1.000	73	9.993	217.785	434	47.046
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	67.27	5	10	10	85	1.000	79	7.323	217.259	165	17.808
P60953	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2 - [CDC42_HUMAN]	26.7	18	4	5	75	1.000	61	6.859	216.533	191	21.245
A0A024QZN4	Vinculin, isoform CRA_c OS=Homo sapiens GN=VCL PE=4 SV=1 - [A0A024QZN4_HUMAN]	35.93	6	38	38	85	1.000	82	7.707	215.441	1066	116.649
B4DZ08	cDNA FLJ51705, highly similar to Aconitate hydratase, mitochondrial (EC 4.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B4DZ08_HUMAN]	27.46	9	9	19	71	1.000	37	6.064	215.117	761	83.361
F8W1A4	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=1 - [F8W1A4_HUMAN]	37.93	7	9	9	84	1.000	80	4.201	212.579	232	25.614
M0QYM7	Tubulin beta-4A chain (Fragment) OS=Homo sapiens GN=TUBB4A PE=4 SV=3 - [M0QYM7_HUMAN]	32.3	6	1	4	68	1.322	1		212.048	161	17.823
P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 - [RBP2_HUMAN]	11.82	19	24	36	80	1.000	40	5.246	211.751	3224	357.974
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	38.57	18	6	13	97	1.000	44	13.824	211.472	293	31.305
B5BUB5	Autoantigen La (Fragment) OS=Homo sapiens GN=SSB PE=2 SV=1 - [B5BUB5_HUMAN]	40.2	10	21	21	90	1.000	90	11.086	211.424	408	46.838
A8K6Y1	cDNA FLJ75526, highly similar to Homo sapiens proliferation-associated 2G4, 38kDa (PA2G4), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K6Y1_HUMAN]	36.24	11	13	15	86	1.000	79	10.417	210.804	367	40.886
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2 - [ECH1_HUMAN]	32.01	7	11	11	83	1.000	80	8.107	210.328	328	35.793
Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=1 SV=1 - [Q32Q12_HUMAN]	48.97	8	4	10	104	0.975	12	11.186	209.042	292	32.621
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	49.76	42	6	12	80	1.000	33	10.226	208.706	205	22.663
B2RBR9	cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBR9_HUMAN]	21.35	9	19	19	84	1.000	84	11.037	208.645	876	97.122
D5H3T4	MHC class I antigen OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [D5H3T4_HUMAN]	43.84	751	2	13	74	1.000	8	15.539	207.599	365	40.882
B5BU83	Stathmin OS=Homo sapiens GN=STMN1 PE=2 SV=1 - [B5BU83_HUMAN]	65.1	17	13	13	85	0.936	76	9.885	206.338	149	17.320
Q4ZG57	Putative uncharacterized protein MCM6 (Fragment) OS=Homo sapiens GN=MCM6 PE=3 SV=1 - [Q4ZG57_HUMAN]	28.92	4	25	25	74	1.000	71	12.200	206.182	785	88.890
Q5JR95	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=1 - [Q5JR95_HUMAN]	37.77	3	6	6	76	1.000	74	6.804	204.867	188	21.866
G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens GN=APEX1 PE=1 SV=1 - [G3V3M6_HUMAN]	41.06	12	13	13	64	1.000	62	10.353	202.316	263	29.172
D2EAU0	Heat shock protein 70 (Fragment) OS=Leishmania aethiopica GN=hsp70 PE=3 SV=1 - [D2EAU0_9TRYP]	27.67	2	4	15	78	1.053	17	7.654	201.644	459	50.383
J9R021	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=eIF3a PE=2 SV=1 - [J9R021_HUMAN]	24.67	7	41	42	88	0.984	87	13.245	201.242	1382	166.381
A8K525	cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K525_HUMAN]	32.91	6	16	18	88	1.000	73	5.443	200.937	471	54.253
Q9Y266	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 - [NUDC_HUMAN]	50.76	7	18	20	79	0.994	75	12.672	200.758	331	38.219
B4DZ53	cDNA FLJ59643, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1 - [B4DZ53_HUMAN]	17.72	4	1	15	82	1.000	8	0.000	200.570	852	96.467
B2RDW0	cDNA, FLJ96792, highly similar to Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDW0_HUMAN]	46.98	14	3	8	83	1.000	56	1.900	200.135	149	16.767
O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	43	7	15	15	83	0.983	77	9.438	199.648	300	34.311
P51572	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3 - [BAP31_HUMAN]	45.93	10	16	17	86	1.000	82	11.247	198.280	246	27.974
P17812	CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2 - [PYRG1_HUMAN]	30.12	5	21	21	78	1.000	74	5.059	196.064	591	66.648
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	29.62	5	22	22	76	1.000	76	9.051	195.980	763	82.947
Q1ELT0	MHC class I antigen OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [Q1ELT0_HUMAN]	32.6	321	0	10	72				195.878	365	40.979
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	40.28	4	18	18	80	1.000	77	13.052	195.863	427	45.171
P15153	Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 - [RAC2_HUMAN]	38.54	15	3	7	77	1.000	15	14.777	194.626	192	21.415
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]	50.66	4	1	7	95	0.770	3	26.867	194.084	152	17.138
H6VRF8	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 - [H6VRF8_HUMAN]	34.78	11	19	22	73	0.365	59	41.814	193.378	644	66.013
P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 - [KINH_HUMAN]	37.28	30	28	37	77	1.000	57	13.973	192.559	963	109.617
A0A024RDQ0	Heat shock 105kDa/110kDa protein 1, isoform CRA_a OS=Homo sapiens GN=HSPH1 PE=3 SV=1 - [A0A024RDQ0_HUMAN]	27.64	8	20	24	80	1.000	64	8.603	191.424	814	92.057
E9PHY5	Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1 - [E9PHY5_HUMAN]	33.8	26	26	29	75	1.000	69	8.996	190.745	935	104.296
F8VQY6	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 - [F8VQY6_HUMAN]	52.82	17	7	7	75	1.000	75	7.705	189.920	142	15.803
Q03252	Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=3 - [LMNB2_HUMAN]	37.17	2	21	25	68	0.997	50	11.266	189.537	600	67.647
Q6NTA2	HNRNPL protein (Fragment) OS=Homo sapiens GN=HNRNPL PE=2 SV=2 - [Q6NTA2_HUMAN]	32.52	7	2	16	64	1.000	5	0.000	189.071	572	61.888
Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	19.81	39	42	44	71	0.979	63	12.251	188.597	2115	238.115
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	27.25	6	13	14	67	1.011	63	8.466	188.539	510	54.602
Q2TNB3	Cell migration-inducing protein 22 OS=Homo sapiens PE=2 SV=1 - [Q2TNB3_HUMAN]	38.49	8	10	10	77	1.000	74	14.792	188.141	239	27.331
B4DJV2	Citrate synthase OS=Homo sapiens GN=CS PE=1 SV=1 - [B4DJV2_HUMAN]	25.61	22	12	13	90	1.000	85	7.477	187.913	453	50.400
Q4W4Y1	Dopamine receptor interacting protein 4 OS=Homo sapiens GN=DRIP4 PE=2 SV=1 - [Q4W4Y1_HUMAN]	29.15	9	27	28	74	1.000	73	7.842	187.805	868	96.019
E7EPN9	Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=1 - [E7EPN9_HUMAN]	13.02	8	35	37	72	1.000	63	8.686	187.693	2819	308.589
P14317	Hematopoietic lineage cell-specific protein OS=Homo sapiens GN=HCLS1 PE=1 SV=3 - [HCLS1_HUMAN]	37.04	10	1	16	72	0.991	2	5.405	187.443	486	53.981
P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1 - [RAC1_HUMAN]	38.54	16	3	7	77	0.979	16	15.156	187.435	192	21.436
P38159	RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3 - [RBMX_HUMAN]	42.71	25	5	18	82	1.191	21	21.721	187.181	391	42.306
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 - [VDAC2_HUMAN]	29.25	6	8	8	62	1.000	60	4.705	186.609	294	31.547
B2R4K7	60S ribosomal protein L6 OS=Homo sapiens PE=2 SV=1 - [B2R4K7_HUMAN]	35.76	13	14	14	94	0.987	93	10.072	183.382	288	32.682
B2R959	cDNA, FLJ94229, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein L (HNRPL),mRNA OS=Homo sapiens PE=2 SV=1 - [B2R959_HUMAN]	32.08	4	1	15	61	1.000	2	0.000	182.751	558	60.211
Q99623	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	44.48	10	15	15	75	1.000	74	4.648	182.248	299	33.276
P50552	Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 - [VASP_HUMAN]	38.16	6	14	14	59	1.000	53	0.000	181.750	380	39.805
B4E1G2	Serine hydroxymethyltransferase OS=Homo sapiens PE=2 SV=1 - [B4E1G2_HUMAN]	35.75	23	17	18	80	1.000	74	8.711	180.465	442	49.230
P48735	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 - [IDHP_HUMAN]	32.96	5	12	15	74	1.000	62	3.843	180.341	452	50.877
A0A087WXM6	60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=4 SV=1 - [A0A087WXM6_HUMAN]	27.81	10	4	5	65	1.000	52	11.385	180.217	169	19.573
P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	23.48	6	24	24	71	1.000	69	13.716	180.209	971	110.346
P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3 - [IF2A_HUMAN]	42.54	8	12	14	68	1.000	58	2.255	180.139	315	36.089
B4E266	cDNA FLJ58466, highly similar to Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) OS=Homo sapiens PE=2 SV=1 - [B4E266_HUMAN]	19.91	17	24	24	66	1.000	64	6.656	178.234	1130	129.105
Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 - [TR150_HUMAN]	21.26	5	24	25	75	0.350	72	4.976	178.194	955	108.601
P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	21.84	26	24	24	78	1.000	74	5.308	177.538	847	94.565
H3BRG4	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=1 - [H3BRG4_HUMAN]	27.67	7	10	10	60	1.000	59	9.289	176.751	412	44.607
O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	29.83	9	13	13	70	1.000	64	10.005	176.317	533	56.614
Q9UJU6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]	35.12	15	3	13	66	1.000	15	6.355	176.044	430	48.178
P36222	Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2 - [CH3L1_HUMAN]	38.64	5	15	15	70	1.900	62	0.188	174.444	383	42.598
B4DQY1	cDNA FLJ56133, highly similar to Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens PE=2 SV=1 - [B4DQY1_HUMAI	28.29	13	15	18	71	0.998	60	8.329	173.651	555	61.482
Q15907	Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4 - [RB11B_HUMAN]	46.79	10	10	10	68	1.000	68	9.798	172.477	218	24.473
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	43.42	3	9	9	68	1.000	66	10.026	171.815	152	17.708
B4DP54	cDNA FLJ52712, highly similar to Tubulin beta-6 chain OS=Homo sapiens PE=2 SV=1 - [B4DP54_HUMAN]	33.73	15	3	13	92	0.935	7	11.002	171.489	418	46.672
C5IWY3	MHC class I antigen OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [C5IWY3_HUMAN]	27.67	200	0	8	61				170.930	365	40.861
Q86UP2	Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1 - [KTN1_HUMAN]	22.48	10	31	32	63	1.000	58	12.878	170.189	1357	156.179
X6R433	Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=1 - [X6R433_HUMAN]	19.13	12	20	21	62	1.000	56	2.597	169.485	1145	131.047
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	7.29	11	2	15	69	1.000	2	0.000	169.034	1976	228.858
O75083	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]	24.26	9	15	15	64	0.996	62	9.835	168.902	606	66.152
Q6FIG4	RAB1B protein OS=Homo sapiens GN=RAB1B PE=2 SV=1 - [Q6FIG4_HUMAN]	45.77	42	4	10	71	1.000	25	11.979	168.813	201	22.184
Q9BSQ6	RPL13A protein (Fragment) OS=Homo sapiens GN=RPL13A PE=2 SV=2 - [Q9BSQ6_HUMAN]	38.31	11	9	9	71	1.000	62	5.110	168.423	201	23.360
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	20.39	7	26	27	65	1.000	59	12.927	167.696	1270	140.869
Q59EZ3	Insulin-like growth factor 2 receptor variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EZ3_HUMAN]	14.13	4	32	32	68	1.000	67	11.927	166.917	2414	265.943
S4R3N1	Protein HSPE1-MOB4 OS=Homo sapiens GN=HSPE1-MOB4 PE=3 SV=1 - [S4R3N1_HUMAN]	23.37	5	3	6	69	1.006	8	33.402	166.828	261	29.718
Q68D08	Putative uncharacterized protein DKFZp686B04128 OS=Homo sapiens GN=DKFZp686B04128 PE=2 SV=1 - [Q68D08_HUMAN]	36.42	12	4	10	63	1.000	34	9.489	165.638	324	36.727
B2R5M8	Isocitrate dehydrogenase [NADP] OS=Homo sapiens PE=2 SV=1 - [B2R5M8_HUMAN]	34.78	11	16	17	63	1.000	61	10.695	165.508	414	46.619
P07205	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN]	12.47	2	2	6	67	1.013	4	8.302	165.344	417	44.767
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	21.65	3	5	5	66	1.000	63	14.193	164.528	194	22.113
B4DFL1	Dihydrolipoyl dehydrogenase OS=Homo sapiens PE=2 SV=1 - [B4DFL1_HUMAN]	23.75	6	11	11	58	1.000	56	16.657	164.357	459	48.868
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN]	50.6	5	13	13	73	1.000	70	11.403	164.236	249	28.705
A5Z217	Mutant desmin OS=Homo sapiens PE=2 SV=1 - [A5Z217_HUMAN]	13.4	25	2	9	64	0.936	2	9.875	163.207	470	53.563
Q59ET3	Chaperonin containing TCP1, subunit 6A isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59ET3_HUMAN]	28.92	8	18	18	72	1.000	71	13.083	162.204	529	57.725
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 - [COPA_HUMAN]	21.08	1	28	28	66	1.000	65	10.581	161.821	1224	138.258
B4DEP6	cDNA FLJ59206, highly similar to Eukaryotic translation initiation factor 4B OS=Homo sapiens PE=2 SV=1 - [B4DEP6_HUMAN]	30.32	13	22	22	76	1.000	66	1.132	160.875	587	66.089
Q14643	Inositol 1,4,5-trisphosphate receptor type 1 OS=Homo sapiens GN=ITPR1 PE=1 SV=3 - [ITPR1_HUMAN]	10.55	12	25	30	64	1.000	43	1.662	160.716	2758	313.729
B4DJI2	cDNA FLJ53342, highly similar to Granulins OS=Homo sapiens PE=2 SV=1 - [B4DJI2_HUMAN]	27.92	8	12	12	61	1.000	53	8.534	160.459	530	56.813
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	41.18	4	6	7	56	0.996	55	21.409	160.060	119	13.364
B3KY63	cDNA FLJ16830 fis, clone UTERU3022536, highly similar to Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KY63_HUM	15.64	14	23	25	61	1.000	53	0.000	159.585	1886	215.149
Q14444	Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2 - [CAPR1_HUMAN]	14.25	7	12	12	66	1.000	63	6.286	159.569	709	78.318
O95036	Similar to 60S ribosomal protein L7; similar to P18124 (PID:d133021) OS=Homo sapiens GN=WUGSC:H_RG054D04.1 PE=3 SV=1 - [O95036_HUMAN]	29.55	3	2	11	74	1.000	5	0.000	159.044	247	29.018
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 - [LRRF1_HUMAN]	25.99	3	8	20	49	1.000	22	15.042	158.791	808	89.199
E7EQG2	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=1 - [E7EQG2_HUMAN]	29.56	15	1	12	75	0.810	1		158.602	362	41.264
B4DP93	cDNA FLJ53437, highly similar to Major vault protein OS=Homo sapiens PE=2 SV=1 - [B4DP93_HUMAN]	23.83	19	17	17	63	1.000	60	6.401	158.297	789	87.491
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]	31.25	6	11	13	75	0.973	59	11.532	158.290	320	35.914
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	48.73	4	10	10	73	0.952	72	11.685	158.218	158	18.419
B7Z9I1	Medium-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [B7Z9I1_HUMAN]	37.14	11	14	14	53	1.000	52	8.309	157.967	385	42.399
C9IZZ0	Ras-related protein Rab-7a (Fragment) OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [C9IZZ0_HUMAN]	82.76	2	1	9	62	1.000	1		157.573	116	13.067
B2R7C5	cDNA, FLJ93378, highly similar to Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R	25.87	8	20	20	62	1.000	60	7.370	157.475	808	90.952
P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	36.33	9	18	18	60	1.000	59	10.407	157.404	501	57.100
P61224	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1 - [RAP1B_HUMAN]	38.59	21	4	8	73	1.000	19	18.436	157.116	184	20.812
A0A024R652	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase, isoform CRA_a OS=Homo	29.3	6	28	29	58	0.934	55	12.377	156.655	935	101.467
O75396	Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN]	39.07	4	8	8	51	1.000	48	8.331	156.546	215	24.578
E9AT99	14-3-3 protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3210 PE=4 SV=1 - [E9AT99_LEIMU]	24.03	1	5	6	59	3.012	10	361.185	156.398	258	29.668
E9ASX8	Chaperonin HSP60, mitochondrial OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2030 PE=3 SV=1 - [E9ASX8_LEIMU]	32.04	4	7	17	63	1.522	23	68.792	156.191	565	59.618
Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	15.94	10	18	19	61	1.000	57	0.868	154.776	1217	135.492
B2R7W4	cDNA, FLJ93632, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7W4_HUMAN]	22.91	10	9	16	59	1.000	16	17.286	154.705	633	70.858
B3KTJ9	cDNA FLJ38393 fis, clone FEBRA2007212 OS=Homo sapiens PE=2 SV=1 - [B3KTJ9_HUMAN]	25.46	12	20	20	62	1.000	61	8.813	154.488	923	102.866
Q0VD83	Apolipoprotein B receptor OS=Homo sapiens GN=APOBR PE=1 SV=2 - [APOBR_HUMAN]	26.65	2	22	23	53	1.000	50	5.270	153.839	1088	114.805
P20042	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2 - [IF2B_HUMAN]	37.84	5	11	11	66	1.000	64	2.540	153.749	333	38.364
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	50.34	7	10	10	72	1.000	70	8.597	153.649	145	16.051
Q59FU3	Far upstream element-binding protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FU3_HUMAN]	29.82	6	1	17	68	1.000	2	0.000	153.279	493	52.032
Q9BXP5	Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1 - [SRRT_HUMAN]	18.26	6	18	18	64	1.000	63	5.048	153.172	876	100.604
B4DL49	cDNA FLJ58073, moderately similar to Cathepsin B (EC 3.4.22.1) OS=Homo sapiens PE=2 SV=1 - [B4DL49_HUMAN]	27.11	18	6	6	52	1.010	51	16.157	153.076	273	30.748
F8VZJ2	Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1 - [F8VZJ2_HUMAN]	30.88	8	3	3	55	1.000	51	0.000	153.075	136	15.007
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	29.63	7	14	14	64	1.000	58	9.113	152.970	378	44.440
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN]	43.52	15	3	9	57	1.000	25	14.135	152.798	193	21.754
Q7L014	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2 - [DDX46_HUMAN]	26.67	8	29	30	65	1.000	59	7.132	152.758	1031	117.290
A8K4H1	cDNA FLJ78268, highly similar to Homo sapiens fusion (involved in t(12;16) in malignant liposarcoma), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4	20.57	9	8	10	76	1.000	67	14.086	151.887	525	53.379
Q14019	Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3 - [COTL1_HUMAN]	31.69	2	6	6	71	1.000	71	11.979	151.583	142	15.935
A0A087WUT6	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=4 SV=1 - [A0A087WUT6_HUMAN]	14.26	8	20	20	57	1.000	55	0.000	151.385	1220	138.597
B4DF70	cDNA FLJ60461, highly similar to Peroxiredoxin-2 (EC 1.11.1.15) OS=Homo sapiens PE=2 SV=1 - [B4DF70_HUMAN]	33.88	4	6	7	75	1.000	48	19.096	151.308	183	20.095

B4DXL9	cDNA FLJ53677, highly similar to Drebrin-like protein OS=Homo sapiens PE=2 SV=1 - [B4DXL9_HUMAN]	31.93	3	1	11	55	1.000	5	12.053	151.203	379	42.700
Q2VIN3	RBM1 (Fragment) OS=Homo sapiens PE=4 SV=1 - [Q2VIN3_HUMAN]	34.38	7	1	14	62	1.214	1		151.032	384	41.440
A0A087WUK2	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=4 SV=1 - [A0A087WUK2_HUMAN]	19.28	5	7	8	67	1.009	24	9.111	150.683	363	40.016
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 - [ML12A_HUMAN]	33.92	6	2	7	61	1.000	25	0.000	150.225	171	19.781
A0A087WZH7	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=4 SV=1 - [A0A087WZH7_HUMAN]	38.48	4	7	7	48	1.000	39	0.000	150.069	330	31.577
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	12.29	8	31	31	63	1.000	62	9.729	149.897	2335	273.427
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	13.59	4	7	11	50	1.000	40	0.000	149.600	898	102.289
F8W1I5	Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1 - [F8W1I5_HUMAN]	20	3	1	3	50	1.000	1		149.227	175	19.024
H3BPE1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=1 - [H3BPE1_HUMAN]	5.84	14	2	39	58	0.965	2	33.932	148.008	7555	856.346
Q92835	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Homo sapiens GN=INPP5D PE=1 SV=2 - [SHIP1_HUMAN]	22.37	9	23	25	60	1.000	53	7.461	147.818	1189	133.209
Q9Y281	Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1 - [COF2_HUMAN]	19.28	3	1	4	51	1.887	1		147.782	166	18.725
A0A024RBH7	Thymopoietin, isoform CRA_a OS=Homo sapiens GN=TMPO PE=4 SV=1 - [A0A024RBH7_HUMAN]	36.81	5	2	10	51	0.780	2	5.467	147.452	345	38.714
Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3 - [DC1I2_HUMAN]	20.22	18	13	13	49	1.000	48	0.000	147.231	638	71.412
C9JW96	Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=1 SV=2 - [C9JW96_HUMAN]	34.96	11	9	10	60	1.000	48	5.471	146.948	246	26.875
B0AZQ4	cDNA, FLJ79494, highly similar to Structural maintenance of chromosome 3 OS=Homo sapiens PE=2 SV=1 - [B0AZQ4_HUMAN]	20.62	3	26	26	51	1.000	48	4.513	146.418	1217	141.442
Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 - [SF3A1_HUMAN]	28.12	4	22	22	64	1.000	62	7.369	146.010	793	88.831
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4 - [MACF1_HUMAN]	5.78	21	1	38	57	0.862	1		145.491	7388	837.787
H0Y3P2	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1 - [H0Y3P2_HUMAN]	18.76	17	17	17	50	0.987	50	8.870	144.748	869	98.056
E9PK01	Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1 - [E9PK01_HUMAN]	29.89	27	6	8	65	1.000	46	5.551	144.647	261	28.804
P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - [SYRC_HUMAN]	26.36	5	18	18	53	1.000	51	7.849	144.428	660	75.331
P62917	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]	30.35	7	8	9	55	1.000	54	6.945	144.402	257	28.007
P23193	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2 - [TCEA1_HUMAN]	58.47	10	17	17	58	1.000	50	0.000	144.123	301	33.948
P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24_HUMAN]	47.77	3	10	10	62	0.942	59	14.414	144.123	157	17.768
O60763	General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2 - [USO1_HUMAN]	20.69	2	18	18	50	1.000	49	8.038	143.517	962	107.828
C5IYE7	MHC class I antigen OS=Homo sapiens GN=HLA-Cw PE=3 SV=1 - [C5IYE7_HUMAN]	34.15	458	0	8	50				143.264	366	40.829
Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	55.24	8	14	14	67	1.000	66	11.626	143.003	248	27.728
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	46.39	13	11	12	69	1.000	66	6.922	142.883	194	22.578
B5BTY4	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=2 SV=1 - [B5BTY4_HUMAN]	29.61	12	6	19	56	0.927	16	17.773	142.596	662	73.126
Q16698	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]	36.72	7	11	11	54	1.000	52	9.774	142.183	335	36.045
B3KU28	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=2 SV=1 - [B3KU28_HUMAN]	23.08	20	18	19	55	1.000	51	7.390	142.072	845	95.092
Q8TBW1	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TBW1_HUMAN]	39.57	14	3	19	77	1.000	10	5.785	141.880	374	42.726
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1 - [COX41_HUMAN]	39.64	6	8	8	70	1.000	69	6.890	141.758	169	19.564
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	41.78	4	3	9	59	1.006	14	4.215	141.656	225	24.748
E9PIA8	Palmitoyl-protein thioesterase 1 (Fragment) OS=Homo sapiens GN=PPT1 PE=1 SV=4 - [E9PIA8_HUMAN]	22.44	6	6	6	49	1.000	43	7.923	141.388	205	23.008
E7EQT4	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2 - [E7EQT4_HUMAN]	14.91	5	19	20	56	1.000	47	9.858	140.953	1301	147.275
Q04760	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4 - [LGUL_HUMAN]	39.13	2	10	10	68	0.967	67	9.564	140.805	184	20.764
A0A087WZK9	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=4 SV=1 - [A0A087WZK9_HUMAN]	22.06	12	5	8	49	1.000	39	15.337	140.687	349	39.565
Q8WWM7	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2 - [ATX2L_HUMAN]	17.77	10	17	19	61	1.000	56	6.184	140.673	1075	113.304
P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]	19.8	11	16	16	48	1.000	46	10.130	140.459	798	88.357
Q14157	Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2 - [UBP2L_HUMAN]	17.76	10	12	15	60	1.000	37	0.000	140.158	1087	114.465
B2RDX5	cDNA, FLJ96812, highly similar to Homo sapiens threonyl-tRNA synthetase (TARS), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDX5_HUMAN]	28.27	16	19	20	59	1.000	55	17.773	140.067	711	82.061
Q92896	Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2 - [GSLG1_HUMAN]	17.73	7	23	24	54	1.039	53	9.536	139.758	1179	134.464
Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 - [ERP44_HUMAN]	26.6	1	10	11	64	1.000	59	4.984	139.286	406	46.941
B2ZRD4	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [B2ZRD4_HUMAN]	37	275	0	8	48				139.060	273	31.553
P14598	Neutrophil cytosol factor 1 OS=Homo sapiens GN=NCF1 PE=1 SV=3 - [NCF1_HUMAN]	36.67	11	12	12	53	1.000	49	0.000	138.567	390	44.624
P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 - [S10A4_HUMAN]	25.74	1	4	4	58	1.025	58	15.221	138.515	101	11.721
H0UID5	Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_c OS=Homo sapiens GN=AP2B1 PE=4 SV=1 - [H0UID5_HUMAN]	18.84	22	7	20	54	1.000	18	15.275	138.349	934	104.157
B3KW93	cDNA FLJ42590 fis, clone BRACE3009708, highly similar to Sodium/potassium-transporting ATPase alpha-2chain (EC 3.6.3.9) OS=Homo sapiens PE=2 SV=1 - [B3KW9	13.91	8	1	11	47	1.000	1		138.278	920	101.237
B9EG90	Topoisomerase (DNA) I OS=Homo sapiens GN=TOP1 PE=2 SV=1 - [B9EG90_HUMAN]	26.41	25	20	21	58	1.000	53	12.282	138.250	765	90.643
Q9BTQ7	Similar to ribosomal protein L23 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BTQ7_HUMAN]	50.75	7	6	6	55	1.000	52	10.722	137.876	134	14.141
Q8NI62	Ribosomal protein S2 OS=Homo sapiens GN=OK/KNS-cl.6 PE=2 SV=1 - [Q8NI62_HUMAN]	77.22	3	1	6	52	1.000	1		137.252	79	8.752
B2R5H0	Protein S100 OS=Homo sapiens PE=2 SV=1 - [B2R5H0_HUMAN]	32.38	2	5	5	54	1.028	50	16.290	136.942	105	11.717
Q92974	Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=4 - [ARHG2_HUMAN]	26.77	11	26	26	55	1.000	55	10.241	136.787	986	111.473
A0A024R4E5	High density lipoprotein binding protein (Vigilin), isoform CRA_a OS=Homo sapiens GN=HDLBP PE=4 SV=1 - [A0A024R4E5_HUMAN]	19.95	33	30	30	62	1.000	60	7.269	136.299	1268	141.352
B4DVQ5	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=2 SV=1 - [B4DVQ5_HUMAN]	21.05	21	20	20	61	1.000	59	12.261	136.207	898	103.580
Q9Y5S9	RNA-binding protein 8A OS=Homo sapiens GN=RBM8A PE=1 SV=1 - [RBM8A_HUMAN]	31.61	1	6	6	47	1.000	47	0.000	135.461	174	19.877
P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	30.91	8	16	16	56	1.000	56	10.410	134.838	592	64.575
P27816	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN]	25.35	16	29	29	58	0.994	57	13.211	134.586	1152	120.930
Q9Y3U8	60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3 - [RL36_HUMAN]	34.29	5	4	4	56	1.000	52	0.000	134.353	105	12.246
Q9NX63	MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 - [MIC19_HUMAN]	47.58	5	14	14	45	0.964	45	11.961	134.169	227	26.136
Q01813	ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 - [PFKAP_HUMAN]	22.7	11	14	18	50	1.000	40	6.210	134.137	784	85.542
P62633	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 - [CNBP_HUMAN]	33.33	2	5	5	49	1.000	48	5.746	133.887	177	19.450
E9ASX7	Chaperonin HSP60, mitochondrial OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2020 PE=3 SV=1 - [E9ASX7_LEIMU]	29.51	2	4	14	50	2.556	10	236.330	133.590	566	60.268
Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	3.91	13	1	10	52	0.908	1		133.516	1995	227.732
B4DM97	cDNA FLJ55002, highly similar to Alpha-centractin OS=Homo sapiens PE=2 SV=1 - [B4DM97_HUMAN]	17.66	32	5	7	62	1.000	18	0.000	133.441	334	38.251
G8JLG1	Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2 - [G8JLG1_HUMAN]	19.08	11	25	25	44	1.000	42	7.550	133.111	1211	140.772
P16104	Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2 - [H2AX_HUMAN]	22.38	6	2	5	58	0.949	2	13.371	133.020	143	15.135
Q8TDZ2	Protein-methionine sulfoxide oxidase MICAL1 OS=Homo sapiens GN=MICAL1 PE=1 SV=2 - [MICA1_HUMAN]	12.37	5	17	17	51	0.993	47	13.698	132.742	1067	117.801
E9PHQ0	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 - [E9PHQ0_HUMAN]	17.54	16	24	25	54	1.000	51	11.874	132.606	1260	139.914
Q9UHS8	PRO1975 OS=Homo sapiens PE=2 SV=1 - [Q9UHS8_HUMAN]	31.04	7	2	13	46	1.000	6	11.635	132.463	393	44.119
P42166	Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 - [LAP2A_HUMAN]	17	1	4	9	45	0.714	7	57.172	132.365	694	75.446
A0A087WZZ5	Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=4 SV=1 - [A0A087WZZ5_HUMAN]	25.83	9	23	23	52	1.000	48	14.688	132.051	871	97.525
Q13428	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 - [TCOF_HUMAN]	19.29	10	30	30	55	1.000	54	13.651	132.022	1488	152.015
B7Z5J7	cDNA FLJ58682, highly similar to Vesicle-fusing ATPase (EC 3.6.4.6) OS=Homo sapiens PE=2 SV=1 - [B7Z5J7_HUMAN]	28.69	14	20	21	51	0.968	45	12.067	131.984	739	82.006
Q9Y383	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2 - [LC7L2_HUMAN]	38.01	5	10	16	49	1.000	29	7.468	131.936	392	46.486
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	50.49	3	5	5	57	1.000	51	13.227	131.603	103	11.360
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	41.88	2	6	6	63	1.000	62	9.052	131.526	117	13.284
P09429	High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 - [HMGB1_HUMAN]	31.63	10	6	11	85	0.973	58	12.425	131.507	215	24.878
P61204	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]	35.36	20	3	6	51	1.000	38	4.813	131.496	181	20.588
O43242	26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2 - [PSMD3_HUMAN]	38.39	11	19	19	49	1.000	48	10.474	131.387	534	60.939
B3KTA3	Fascin OS=Homo sapiens PE=2 SV=1 - [B3KTA3_HUMAN]	21.82	5	13	13	52	1.000	50	11.459	131.359	472	52.244
B2R761	cDNA, FLJ93299, highly similar to Homo sapiens sterol carrier protein 2 (SCP2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R761_HUMAN]	21.02	7	15	15	60	1.000	60	6.751	131.217	547	58.984
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	41.52	3	9	9	49	1.000	48	8.811	131.010	224	25.019
Q99879	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3 - [H2B1M_HUMAN]	50.79	6	1	9	58	1.119	1		130.900	126	13.981
Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2 - [AP1B1_HUMAN]	18.86	6	3	20	52	0.798	4	25.749	130.115	949	104.570
Q5JTV8	Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2 - [TOIP1_HUMAN]	23.67	3	2	14	47	0.656	4	38.250	129.639	583	66.208
P30464	HLA class I histocompatibility antigen, B-15 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=2 - [1B15_HUMAN]	23.2	459	0	7	48				129.636	362	40.363
B4DNE4	cDNA FLJ52574, highly similar to Septin-7 OS=Homo sapiens PE=2 SV=1 - [B4DNE4_HUMAN]	31.94	18	13	14	51	1.000	40	10.300	129.118	382	44.616
Q15185	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 - [TEBP_HUMAN]	48.13	4	8	8	49	1.000	48	3.613	129.095	160	18.685
A8K9J7	Histone H2B OS=Homo sapiens PE=2 SV=1 - [A8K9J7_HUMAN]	50.79	21	1	9	58	0.501	1		128.832	126	13.988
B8YBG3	MHC class I antigen OS=Homo sapiens GN=HLA-Cw PE=3 SV=1 - [B8YBG3_HUMAN]	29.51	629	0	8	48				128.581	366	40.934
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13_HUMAN]	39.74	3	8	8	57	0.988	56	10.755	127.926	151	17.212
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 - [HNRPF_HUMAN]	21.69	2	7	8	54	1.000	34	10.616	127.654	415	45.643
P49915	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 - [GUAA_HUMAN]	24.1	4	18	18	45	0.971	41	6.296	127.600	693	76.667
Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]	32.81	18	1	4	57	1.000	1		127.584	128	13.898
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [GNAI2_HUMAN]	36.9	25	6	12	48	1.000	25	3.939	127.364	355	40.425
G3V203	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 - [G3V203_HUMAN]	41.46	3	1	6	45	0.955	1		127.135	164	18.744
A0A087WW66	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=4 SV=1 - [A0A087WW66_HUMAN]	25.92	9	23	23	58	0.992	56	12.172	126.872	953	105.784
Q0QEW2	60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=2 SV=1 - [Q0QEW2_HUMAN]	43.9	8	1	6	45	1.000	1		126.797	164	18.721
Q29RF7	Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1 - [PDS5A_HUMAN]	15.63	3	15	19	43	1.000	31	12.473	126.535	1337	150.734
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 - [NSUN2_HUMAN]	28.55	1	18	18	49	1.000	47	0.000	125.936	767	86.416
A6NLN1	Polypyrimidine tract binding protein 1, isoform CRA_b OS=Homo sapiens GN=PTBP1 PE=1 SV=4 - [A6NLN1_HUMAN]	17.65	14	7	10	49	1.000	26	1.017	125.819	527	56.475
P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	30.1	8	17	17	56	0.985	55	10.398	125.606	412	46.501
O15523	ATP-dependent RNA helicase DDX3Y OS=Homo sapiens GN=DDX3Y PE=1 SV=2 - [DDX3Y_HUMAN]	32.12	8	7	20	49	1.000	11	0.000	125.222	660	73.108
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 - [U520_HUMAN]	12.08	12	24	25	51	1.000	49	18.567	125.056	2136	244.353
B3KMQ6	cDNA FLJ12172 fis, clone MAMMA1000684, highly similar to Opioid growth factor receptor OS=Homo sapiens PE=2 SV=1 - [B3KMQ6_HUMAN]	26	12	14	15	48	1.000	41	12.389	124.936	677	73.324
J3KQ45	Trans-Golgi network integral membrane protein 2 OS=Homo sapiens GN=TGOLN2 PE=1 SV=1 - [J3KQ45_HUMAN]	33.92	3	13	13	45	1.000	45	6.924	124.933	454	47.852
P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	27.39	4	20	25	53	0.942	45	13.026	124.784	847	97.087
P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Homo sapiens GN=PPIF PE=1 SV=1 - [PPIF_HUMAN]	30.92	7	7	10	62	0.981	35	24.423	124.676	207	22.026
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 - [THIO_HUMAN]	20.95	1	2	2	47	1.000	45	6.695	124.582	105	11.730
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_HUMAN]	24.07	8	8	10	49	1.000	27	7.535	123.666	378	39.571
Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2 - [IPYR2_HUMAN]	29.94	12	9	10	47	1.000	45	1.086	123.444	334	37.896
E5RHW4	Erlin-2 (Fragment) OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 - [E5RHW4_HUMAN]	38.17	3	9	12	45	0.971	29	8.314	123.353	338	37.701
Q53HW7	Sulfide dehydrogenase like (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HW7_HUMAN]	27.11	2	1	12	41	1.000	1		122.484	450	49.918
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	26.37	14	12	13	57	1.000	55	10.060	122.174	474	51.262
P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	22.87	4	19	19	55	1.000	51	12.164	122.054	739	83.113
A0A024R889	Spectrin, alpha, non-erythrocytic 1 (Alpha-fodrin), isoform CRA_g OS=Homo sapiens GN=SPTAN1 PE=4 SV=1 - [A0A024R889_HUMAN]	12.4	6	28	28	44	1.000	44	7.268	121.185	2452	282.076
H0Y2Y8	Zyxin (Fragment) OS=Homo sapiens GN=ZYX PE=1 SV=1 - [H0Y2Y8_HUMAN]	22.41	11	9	9	49	1.000	48	11.207	121.136	540	57.606
A2IRN0	Raichu404X OS=Homo sapiens GN=Raichu404X PE=2 SV=1 - [A2IRN0_HUMAN]	8.31	12	2	6	56	1.432	3	57.265	121.081	758	84.962
S4R435	Protein RPS10-NUDT3 (Fragment) OS=Homo sapiens GN=RPS10-NUDT3 PE=3 SV=1 - [S4R435_HUMAN]	20.28	3	3	9	79	0.966	47	11.266	120.977	286	32.576
P62993	Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1 - [GRB2_HUMAN]	42.86	6	10	10	43	1.000	42	6.992	120.890	217	25.190
B3KML1	cDNA FLJ11308 fis, clone PLACE1010074, highly similar to Sorting nexin-2 OS=Homo sapiens PE=2 SV=1 - [B3KML1_HUMAN]	24.86	5	11	13	44	1.000	34	9.981	120.470	519	58.436
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	23.71	2	15	15	49	1.000	47	9.754	120.465	658	73.730
Q8NFC6	Biorientation of chromosomes in cell division protein 1-like 1 OS=Homo sapiens GN=BOD1L1 PE=1 SV=2 - [BD1L1_HUMAN]	7.51	17	19	21	45	1.000	34	0.000	119.571	3051	330.266
B3KS36	cDNA FLJ35376 fis, clone SKMUS2004044, highly similar to Homo sapiens ribosomal protein L3 (RPL3), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [B3	34.18	3	1	15	63	1.174	1		119.523	354	40.120
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	19.9	12	9	10	41	0.889	32	22.875	119.355	623	62.027
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 - [RAB10_HUMAN]	41.5	35	7	11	44	0.920	18	8.849	119.316	200	22.527
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	60.87	1	4	6	36	1.000	19	0.000	119.269	115	11.658
B4E2B5	cDNA FLJ53959, highly similar to Mitochondrial inner membrane protein OS=Homo sapiens PE=2 SV=1 - [B4E2B5_HUMAN]	31.68	1	0	14	43				119.236	404	43.194
Q9Y678	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 - [COPG1_HUMAN]	17.85	4	16	17	47	1.000	43	7.608	119.003	874	97.655
P62316	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 - [SMD2_HUMAN]	50.85	3	7	7	50	1.000	47	7.301	118.893	118	13.518
B2R983	cDNA, FLJ94267, highly similar to Homo sapiens glutathione S-transferase omega 1 (GSTO1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R983_HUMAN]	38.17	4	9	9	50	1.000	50	16.777	118.666	241	27.521
A8K5M4	cDNA FLJ75088, highly similar to Homo sapiens p21 (CDKN1A)-activated kinase 2 (PAK2), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5M4_HUMAN]	32.63	5	9	13	41	1.000	35	11.432	118.205	524	58.007
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 - [XPO1_HUMAN]	13.63	13	15	16	48	1.000	44	12.213	117.923	1071	123.306
C9JQD4	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Homo sapiens GN=PPIH PE=1 SV=1 - [C9JQD4_HUMAN]	42.36	8	6	8	47	1.000	27	6.859	117.744	144	15.790
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	39.42	6	7	7	51	0.996	48	12.092	117.733	137	15.738
Q9NVI7	ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2 - [ATD3A_HUMAN]	19.09	8	4	12	41	0.998	10	16.735	117.468	634	71.325
Q15075	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2 - [EEA1_HUMAN]	15.52	3	24	25	45	1.000	43	5.402	117.422	1411	162.367
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	35.64	7	16	17	44	1.000	43	7.091	117.350	463	51.125
B2RA91	cDNA, FLJ94773, highly similar to Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RA91_I	20.3	6	20	21	41	1.000	39	4.028	117.317	1148	128.847
P49448	Glutamate dehydrogenase 2, mitochondrial OS=Homo sapiens GN=GLUD2 PE=1 SV=2 - [DHE4_HUMAN]	22.58	4	3	14	44	1.087	3	12.458	117.316	558	61.395
Q9NQ39	Putative 40S ribosomal protein S10-like OS=Homo sapiens GN=RPS10P5 PE=5 SV=1 - [RS10L_HUMAN]	30.11	1	3	8	55	1.000	24	10.049	117.284	176	20.108
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 - [BZW1_HUMAN]	24.82	11	11	13	42	1.000	34	7.977	117.028	419	48.013
P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]	51.64	8	10	10	48	2.100	46	21.191	116.836	213	23.263
A0A024R0J9	Heterogeneous nuclear ribonucleoprotein U-like 1, isoform CRA_a OS=Homo sapiens GN=HNRPUL1 PE=4 SV=1 - [A0A024R0J9_HUMAN]	24.21	13	3	16	48	1.000	4	0.000	116.605	756	84.741
B4DV79	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=2 SV=1 - [B4DV79_HUMAN]	20.46	9	14	14	44	1.000	42	4.467	115.662	738	85.081
J3KN66	Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=1 - [J3KN66_HUMAN]	21.87	1	1	13	43	1.000	1		115.575	599	67.781
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	19.62	2	16	16	46	0.981	46	18.062	115.575	795	90.875
Q96AG4	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 - [LRC59_HUMAN]	20.2	1	8	8	53	1.000	53	10.618	115.506	307	34.909
P22102	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 - [PUR2_HUMAN]	15.05	12	12	16	43	1.000	36	12.605	115.388	1010	107.699
Q09028	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3 - [RBBP4_HUMAN]	17.18	6	4	6	45	1.000	21	0.000	115.175	425	47.626
Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	25.25	1	6	7	48	1.000	26	0.000	114.923	305	30.822
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	39.57	3	6	6	41	0.974	40	10.852	114.557	187	21.044
E4W6B6	RPL27/NME2 fusion protein (Fragment) OS=Homo sapiens GN=RPL27 PE=2 SV=1 - [E4W6B6_HUMAN]	57.14	7	7	8	59	1.000	57	9.413	114.508	126	14.248
A6H591	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=2 - [A6H591_HUMAN]	27.47	246	0	6	43				114.186	273	31.719
B4DW58	cDNA FLJ61429, highly similar to Ena/VASP-like protein OS=Homo sapiens PE=2 SV=1 - [B4DW58_HUMAN]	29.92	10	9	9	39	1.000	32	6.395	113.569	381	41.281
A8K897	cDNA FLJ78686, highly similar to Homo sapiens nucleoporin 93kDa (NUP93), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K897_HUMAN]	21.25	13	17	17	40	1.000	39	12.131	113.018	819	93.324
P62195	26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 - [PRS8_HUMAN]	29.56	11	9	11	43	1.000	33	2.855	113.005	406	45.597
E9AZT9	Putative glucose-regulated protein 78 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1200 PE=3 SV=1 - [E9AZT9_LEIMU]	14.89	4	9	11	42	1.000	18	14.143	112.877	658	71.748
E9AYX8	Putative small GTP-binding protein Rab1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0760 PE=3 SV=1 - [E9AYX8_LEIMU]	26	36	1	6	43	1.219	1		112.764	200	22.240
P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 - [SAHH_HUMAN]	37.96	2	13	16	47	1.000	36	22.103	112.583	432	47.685
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	11.75	4	11	11	38	1.000	37	0.091	112.555	1038	119.440
A1Z1D7	MHC class I antigen OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [A1Z1D7_HUMAN]	25.75	361	0	7	41				111.938	365	40.816
A0A087WYB4	Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=4 SV=1 - [A0A087WYB4_HUMAN]	36.45	4	10	10	39	1.000	38	7.401	111.849	310	33.388
B3KY60	cDNA FLJ16777 fis, clone BRHIP2029567, highly similar to Cell division cycle 5-like protein OS=Homo sapiens PE=2 SV=1 - [B3KY60_HUMAN]	15.84	3	14	14	40	1.000	39	0.000	111.741	802	92.220
Q29836	HLA class I histocompatibility antigen, B-67 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 - [1B67_HUMAN]	16.3	323	0	5	41				111.686	362	40.317
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	56.52	3	6	6	52	1.000	46	0.000	111.606	115	12.776
J3QR09	Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [J3QR09_HUMAN]	38.86	7	9	10	45	0.885	36	18.244	111.572	193	23.120
B7Z8Y6	cDNA FLJ58394, highly similar to Platelet endothelial cell adhesion molecule OS=Homo sapiens PE=2 SV=1 - [B7Z8Y6_HUMAN]	13.92	10	11	11	34	1.000	33	14.930	111.316	733	81.728
Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens GN=FKBP5 PE=1 SV=2 - [FKBP5_HUMAN]	21.23	5	5	10	39	1.000	24	0.000	111.106	457	51.180
A2VC08	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [A2VC08_HUMAN]	27.47	348	0	6	41				111.078	273	31.686
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	24.22	3	6	6	48	1.000	48	15.505	110.867	256	27.675
O75534	Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2 - [CSDE1_HUMAN]	27.07	10	21	21	46	1.000	46	6.222	110.814	798	88.829
Q59GB4	Dihydropyrimidinase-like 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GB4_HUMAN]	23.73	19	3	12	43	1.000	19	12.085	110.747	628	68.142
Q01469	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3 - [FABP5_HUMAN]	49.63	2	7	7	44	1.000	39	3.066	110.630	135	15.155
Q59EH7	DnaJ (Hsp40) homolog, subfamily C, member 7 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EH7_HUMAN]	34.99	16	18	18	42	1.000	41	14.401	110.612	483	55.382
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	29.66	11	1	6	48	1.000	17	12.471	110.555	145	17.248
Q9NYF8	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 - [BCLF1_HUMAN]	23.26	12	19	20	43	0.994	40	13.661	110.427	920	106.059
P38606	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 - [VATA_HUMAN]	24.96	4	15	16	43	0.988	40	14.208	110.416	617	68.260
Q13045	Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2 - [FLII_HUMAN]	16.15	12	21	21	45	1.000	43	14.832	110.142	1269	144.660
O75944	Aconitase (Fragment) OS=Homo sapiens GN=ACON PE=2 SV=1 - [O75944_HUMAN]	21	1	2	12	37	1.000	3	0.000	110.004	600	65.306
A0A024R6W0	Aspartate aminotransferase OS=Homo sapiens GN=GOT2 PE=3 SV=1 - [A0A024R6W0_HUMAN]	26.74	4	1	13	38	1.185	2	5.079	109.972	430	47.445
F4ZW65	NF90b OS=Homo sapiens PE=2 SV=1 - [F4ZW65_HUMAN]	23.51	6	1	16	53	1.026	6	3.793	109.918	706	76.424
B7Z468	Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 - [B7Z468_HUMAN]	30.77	40	20	20	55	0.956	52	11.578	109.869	754	80.950
P55795	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 - [HNRH2_HUMAN]	21.38	9	1	9	48	1.451	1		109.772	449	49.232
B7Z4M3	Adenylyl cyclase-associated protein OS=Homo sapiens PE=2 SV=1 - [B7Z4M3_HUMAN]	5.54	8	1	3	54	1.000	2	0.000	109.413	451	49.777
F4ZW66	NF110b OS=Homo sapiens PE=2 SV=1 - [F4ZW66_HUMAN]	19.71	12	3	18	52	1.000	5	0.000	109.324	898	95.718
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [SDHA_HUMAN]	28.01	13	15	15	41	1.000	40	2.573	109.288	664	72.645
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	42.42	1	6	6	40	1.000	40	8.387	109.140	132	14.505

A4D1M6	HCG19809 OS=Homo sapiens GN=LOC392793 PE=3 SV=1 - [A4D1M6_HUMAN]	32	1	1	7	46	0.835	1		109.113	225	24.875
Q9ULZ3	Apoptosis-associated speck-like protein containing a CARD OS=Homo sapiens GN=PYCARD PE=1 SV=2 - [ASC_HUMAN]	33.85	3	6	7	42	1.000	39	0.991	109.071	195	21.613
Q68J68	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [Q68J68_HUMAN]	21.66	309	0	6	39				109.070	337	38.095
Q14847	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2 - [LASP1_HUMAN]	46.74	11	14	14	52	1.000	51	8.159	109.016	261	29.698
A8K8U1	cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8U1_HUMAN]	15.45	7	21	21	42	0.952	41	7.231	108.975	1230	136.231
O19782	HLA-B protein (Fragment) OS=Homo sapiens GN=HLA-B PE=2 SV=1 - [O19782_HUMAN]	21.43	452	0	6	39				108.426	336	38.063
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	31.17	13	7	13	51	1.000	21	5.832	108.412	369	41.305
O43684	Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 - [BUB3_HUMAN]	29.88	4	8	8	42	1.000	42	2.299	107.645	328	37.131
Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	20.94	8	15	15	43	1.000	43	12.770	107.513	597	68.005
Q86UX7	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 - [URP2_HUMAN]	22.19	4	13	13	42	1.000	38	0.646	107.306	667	75.905
E1NZA1	Peroxisome proliferator activated receptor interacting complex protein OS=Homo sapiens GN=PRIC295 PE=2 SV=1 - [E1NZA1_HUMAN]	9.47	4	25	25	39	1.000	38	9.258	107.271	2671	292.558
O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN]	33.54	3	7	7	38	1.000	38	6.038	107.202	161	18.479
B4DP27	cDNA FLJ52153, highly similar to Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DP27_HUMAN]	28.99	5	5	5	43	1.000	43	0.000	107.085	169	19.247
O15143	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 - [ARC1B_HUMAN]	31.45	7	10	10	41	1.000	39	14.230	106.944	372	40.923
Q59G16	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G16_HUMAN]	15.66	6	17	22	42	1.000	30	9.251	106.587	1156	127.298
B1PWD3	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [B1PWD3_HUMAN]	30.4	255	0	6	38				106.537	273	31.477
M0R3D6	60S ribosomal protein L18a (Fragment) OS=Homo sapiens GN=RPL18A PE=1 SV=1 - [M0R3D6_HUMAN]	47.52	12	7	7	41	1.000	39	3.499	106.355	141	16.704
P48634	Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3 - [PRC2A_HUMAN]	11.87	3	17	18	47	1.000	44	0.000	106.112	2157	228.724
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	29.79	4	11	12	41	1.000	38	6.369	106.108	433	48.603
O43776	Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	21.35	10	14	14	49	1.000	49	1.349	106.070	548	62.903
Q9UQ35	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2 - [SRRM2_HUMAN]	10.21	12	22	25	46	1.000	42	19.143	105.875	2752	299.438
B9EIS5	PCM1 protein OS=Homo sapiens GN=PCM1 PE=2 SV=1 - [B9EIS5_HUMAN]	12.05	11	14	24	46	1.021	23	8.220	105.734	2016	227.532
P48444	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	31.12	5	20	20	49	0.951	48	14.168	105.391	511	57.174
P61006	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1 - [RAB8A_HUMAN]	41.06	39	3	9	36	1.000	5	4.487	105.229	207	23.653
B3KUZ8	Aspartate aminotransferase OS=Homo sapiens PE=2 SV=1 - [B3KUZ8_HUMAN]	31	2	1	13	37	0.665	1		104.802	371	41.300
B2DG28	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [B2DG28_HUMAN]	26.37	444	0	6	37				104.779	273	31.569
O15511	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3 - [ARPC5_HUMAN]	71.52	4	10	11	43	1.000	42	9.186	104.244	151	16.310
F8VXL2	Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 - [F8VXL2_HUMAN]	61.7	4	2	2	37	1.000	28	0.000	104.003	47	5.423
P31153	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 - [METK2_HUMAN]	27.85	7	11	12	43	0.999	42	5.356	103.638	395	43.633
M0R0F0	40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 - [M0R0F0_HUMAN]	37	6	8	9	42	0.984	34	11.850	103.621	200	22.377
B3KXZ4	cDNA FLJ46429 fis, clone THYMU3014372, highly similar to DNA replication licensing factor MCM2 OS=Homo sapiens PE=2 SV=1 - [B3KXZ4_HUMAN]	18.69	6	13	13	39	1.000	38	16.245	103.350	808	91.214
B2RBE5	cDNA, FLJ95468, highly similar to Homo sapiens transcriptional coactivator tubedown-100 (TBDN100),transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B2RE	20.9	4	21	22	46	1.000	44	11.821	103.310	866	101.236
Q63HN8	E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3 - [RN213_HUMAN]	6.34	7	31	31	40	1.000	37	10.400	103.270	5207	591.030
B4E1B2	cDNA FLJ53691, highly similar to Serotransferrin OS=Homo sapiens PE=2 SV=1 - [B4E1B2_HUMAN]	25.81	13	14	14	41	1.000	39	5.414	103.020	678	74.783
B4DH52	cDNA FLJ55916, highly similar to General transcription factor II-I OS=Homo sapiens PE=2 SV=1 - [B4DH52_HUMAN]	21.25	11	19	20	42	0.915	37	18.678	103.020	993	111.846
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1 - [AN32A_HUMAN]	26.1	9	6	7	43	1.000	37	11.440	102.776	249	28.568
Q6JBY9	CapZ-interacting protein OS=Homo sapiens GN=RCSD1 PE=1 SV=1 - [CPZIP_HUMAN]	35.82	3	13	13	44	1.000	39	3.598	102.642	416	44.477
B2R659	cDNA, FLJ92803, highly similar to Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R659_HUMAN]	23.51	13	18	19	37	1.057	35	11.788	102.345	736	79.562
B4DM33	cDNA FLJ52068, highly similar to Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens PE=2 SV=1 - [B4DM33_HUMAN]	45.38	3	11	11	33	0.976	32	10.467	102.179	238	26.566
Q08379	Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3 - [GOGA2_HUMAN]	12.28	8	13	13	35	1.000	34	3.130	102.064	1002	113.017
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	37.72	2	8	9	34	1.000	31	5.471	102.041	289	32.639
O76094	Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3 - [SRP72_HUMAN]	21.16	7	11	16	44	1.000	31	8.051	101.970	671	74.560
A8K5K0	cDNA FLJ78309, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=	18.22	3	1	14	41	1.000	1		101.610	856	95.589
D5L9K0	MHC class I antigen OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [D5L9K0_HUMAN]	18.51	552	0	6	38				101.227	362	40.424
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	36.87	4	8	8	44	1.000	42	8.481	100.980	217	24.816
O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	44.17	7	9	9	36	1.000	34	0.439	100.943	206	22.224
C9JFR7	Cytochrome c (Fragment) OS=Homo sapiens GN=CYCS PE=1 SV=1 - [C9JFR7_HUMAN]	47.52	3	6	6	31	1.000	30	7.306	100.657	101	11.326
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [QCR1_HUMAN]	15.63	3	6	7	50	1.677	43	3.260	100.352	480	52.612
O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	18.11	4	11	11	37	1.000	37	4.752	100.349	613	66.859
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	23.99	4	4	6	49	1.000	21	0.000	100.332	271	30.521
H3BQZ7	HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 - [H3BQZ7_HUMAN]	15.42	2	13	13	37	1.000	31	11.145	100.314	746	84.639
A5PLK7	RCC2 protein (Fragment) OS=Homo sapiens GN=RCC2 PE=2 SV=1 - [A5PLK7_HUMAN]	19.69	2	9	9	39	1.000	38	7.057	100.239	457	49.647
A0A024RBE8	Solute carrier family 25 (Mitochondrial carrier phosphate carrier), member 3, isoform CRA_a OS=Homo sapiens GN=SLC25A3 PE=3 SV=1 - [A0A024RBE8_HUMAN]	17.73	9	7	7	45	1.043	42	6.242	99.967	361	39.933
P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4 - [ODO2_	23.18	11	8	9	37	1.022	35	20.035	99.465	453	48.724
Q13148	TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 - [TADBP_HUMAN]	18.12	17	9	9	46	1.000	44	9.812	99.397	414	44.711
B4DDF4	Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=1 - [B4DDF4_HUMAN]	32.21	20	8	10	38	0.960	33	8.219	99.319	298	32.596
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	28.33	17	10	14	28	0.532	14	104.931	99.317	639	65.393
M0R210	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 - [M0R210_HUMAN]	62.79	8	11	11	50	1.000	50	12.741	99.134	129	14.410
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 - [RAD50_HUMAN]	10.21	8	16	16	36	0.941	36	18.458	98.687	1312	153.797
Q2L6I2	ABC50 protein OS=Homo sapiens GN=ABCF1 PE=3 SV=1 - [Q2L6I2_HUMAN]	14	9	9	13	31	1.000	21	2.197	98.375	807	91.623
O43432	Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=2 - [IF4G3_HUMAN]	9.59	8	10	16	37	1.000	16	3.171	98.363	1585	176.542
O94804	Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1 - [STK10_HUMAN]	15.91	2	15	16	40	1.000	38	11.809	98.355	968	112.065
Q9NU22	Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2 - [MDN1_HUMAN]	2.23	5	12	12	46	1.013	46	6.751	98.351	5596	632.420
Q7L576	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1 - [CYFP1_HUMAN]	12.37	23	17	17	40	1.000	38	5.197	98.318	1253	145.089
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]	16.16	4	17	17	43	1.000	41	14.069	97.970	953	107.074
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 - [PSMD2_HUMAN]	20.93	9	17	18	43	1.000	42	11.173	97.959	908	100.136
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	30.32	8	15	16	34	0.988	33	12.571	97.910	587	63.502
E5RJR5	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=1 - [E5RJR5_HUMAN]	30.67	6	7	8	40	1.000	36	8.995	97.902	163	18.708
A8KAK1	cDNA FLJ77398, highly similar to Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1, transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [A8KAK1	10.58	5	14	16	38	1.000	34	6.601	97.549	1531	174.897
O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	14.72	9	18	18	38	1.000	38	12.860	97.078	1304	145.738
J3QL05	Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens GN=SRSF2 PE=1 SV=1 - [J3QL05_HUMAN]	19.23	12	2	2	38	1.000	34	6.627	96.997	130	15.147
F1T0J2	Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=2 SV=1 - [F1T0J2_HUMAN]	9.14	12	27	29	38	1.000	35	6.202	96.763	3184	367.198
A8K521	cDNA FLJ78580, highly similar to Homo sapiens MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (MCM5), mRNA OS=Homo sapiens PE=2 SV=1 -	25.34	10	19	19	39	0.964	38	16.597	96.730	734	82.217
Q5T9A4	ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1 - [ATD3B_HUMAN]	12.5	5	1	9	32	2.180	1		96.610	648	72.527
P84095	Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1 - [RHOG_HUMAN]	49.21	10	6	7	32	1.000	23	1.133	96.490	191	21.295
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3 - [SNAA_HUMAN]	33.56	12	8	9	37	1.000	29	19.196	96.419	295	33.211
A0A087WSV8	DDB1- and CUL4-associated factor 5 OS=Homo sapiens GN=DCAF5 PE=4 SV=1 - [A0A087WSV8_HUMAN]	20.95	14	9	10	42	1.000	40	9.633	96.408	420	50.196
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1 - [PDS5B_HUMAN]	10.3	3	12	16	34	1.000	22	2.921	96.383	1447	164.563
B2R665	cDNA, FLJ92810, highly similar to Homo sapiens protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (PPM1G), mRNA OS=Homo sapiens PE	29.49	6	15	15	37	1.000	35	6.219	96.286	546	59.205
J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDIA PE=1 SV=3 - [J3KTF8_HUMAN]	30.41	7	6	6	41	0.994	41	9.934	96.182	194	21.601
Q9Y5M8	Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 - [SRPRB_HUMAN]	33.58	2	8	8	29	1.000	27	3.579	96.155	271	29.684
Q562M3	Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=3 SV=1 - [Q562M3_HUMAN]	23.3	28	1	2	48	1.000	5	1.742	96.096	103	11.529
A8K644	Splicing factor, arginine/serine-rich 4, isoform CRA_b OS=Homo sapiens GN=SFRS4 PE=2 SV=1 - [A8K644_HUMAN]	14.37	6	4	8	33	1.000	9	0.000	95.759	494	56.675
B4DJB4	cDNA FLJ55931, highly similar to Isocitrate dehydrogenase OS=Homo sapiens PE=2 SV=1 - [B4DJB4_HUMAN]	26.27	12	9	9	40	1.000	39	3.187	95.715	316	34.483
A6NKB8	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=1 - [A6NKB8_HUMAN]	25.04	7	13	13	34	0.982	33	14.143	95.696	611	68.125
A0A024R588	Splicing factor 1, isoform CRA_d OS=Homo sapiens GN=SF1 PE=4 SV=1 - [A0A024R588_HUMAN]	11.31	11	6	6	38	1.000	36	0.000	95.608	548	59.674
E9ASD6	Elongation factor 2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0180 PE=4 SV=1 - [E9ASD6_LEIMU]	24.26	1	15	18	43	1.000	26	10.511	95.589	845	93.997
P35606	Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2 - [COPB2_HUMAN]	16.67	9	16	16	38	0.971	37	9.899	95.524	906	102.422
Q7Z5L9	Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2 - [I2BP2_HUMAN]	22.15	3	8	10	33	1.000	22	3.008	95.436	587	60.987
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	25.06	2	10	13	40	1.000	33	14.409	95.342	411	46.841
Q96C19	EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1 - [EFHD2_HUMAN]	42.92	2	10	11	31	1.001	28	16.241	95.185	240	26.680
B4DZC0	cDNA FLJ51771, highly similar to SWI/SNF-related matrix-associatedactin-dependent regulator of chromatin subfamily A member5 (EC 3.6.1.-) OS=Homo sapiens PE=2	14.87	9	17	17	36	0.998	34	6.306	95.098	995	116.683
A8K964	cDNA FLJ75071, highly similar to Homo sapiens pinin, desmosome associated protein (PNN), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K964_HUMAN]	22.73	6	18	19	36	0.991	34	11.077	95.073	717	81.493
O75368	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1 - [SH3L1_HUMAN]	45.61	3	6	6	37	1.000	36	7.785	94.698	114	12.766
F8W7C6	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=2 - [F8W7C6_HUMAN]	47.24	4	1	7	43	1.000	2	0.000	94.629	163	18.553
Q14978	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2 - [NOLC1_HUMAN]	19.31	7	16	16	42	1.061	42	20.553	94.338	699	73.560
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN]	32.13	9	15	15	37	1.000	36	9.781	94.018	389	44.145
E7EX90	Uncharacterized protein OS=Homo sapiens GN=DCTN1 PE=1 SV=1 - [E7EX90_HUMAN]	15.05	17	17	18	38	1.000	36	3.686	93.941	1256	139.008
Q8IX12	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2 - [CCAR1_HUMAN]	12.17	5	14	16	39	1.000	36	9.683	93.449	1150	132.739
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	46.38	1	3	3	41	1.000	39	3.388	93.414	69	7.836
F5H0C8	Enolase OS=Homo sapiens GN=ENO2 PE=1 SV=1 - [F5H0C8_HUMAN]	11.75	11	1	3	36	1.000	8	0.000	93.403	315	34.741
Q8N959	cDNA FLJ38330 fis, clone FCBBF3025280, highly similar to NDRG1 PROTEIN OS=Homo sapiens PE=2 SV=1 - [Q8N959_HUMAN]	23.53	22	5	5	27	1.000	27	7.785	93.262	323	35.203
P59998	Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 - [ARPC4_HUMAN]	32.14	7	6	6	39	1.000	38	8.947	93.044	168	19.654
B2RDF5	cDNA, FLJ96587, highly similar to Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDF5_HUMAN]	20.63	10	14	14	35	0.982	35	7.727	93.003	640	71.135
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3 - [NDUS1_HUMAN]	20.36	5	14	14	38	1.000	36	0.000	92.980	727	79.417
Q5JR08	Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=3 - [Q5JR08_HUMAN]	38.1	15	1	7	33				92.890	189	21.566
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	37.4	5	5	7	42	0.922	30	10.889	92.717	123	14.543
B4DEA3	cDNA FLJ56531, highly similar to UV excision repair protein RAD23 homolog B OS=Homo sapiens PE=2 SV=1 - [B4DEA3_HUMAN]	24.32	8	7	10	37	1.000	27	7.119	92.551	403	42.283
B2RBA6	cDNA, FLJ95407, highly similar to Homo sapiens MCM7 minichromosome maintenance deficient 7 (S. cerevisiae) (MCM7), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R	20.17	7	15	15	37	0.945	37	13.170	92.210	719	81.229
J3KMY5	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1 - [J3KMY5_HUMAN]	34.46	10	6	6	32	1.043	29	10.015	92.179	148	16.219
Q92930	Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2 - [RAB8B_HUMAN]	43.48	41	3	9	34	0.728	3	11.104	92.086	207	23.569
P41227	N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1 - [NAA10_HUMAN]	39.57	11	9	9	33	1.000	32	1.460	92.083	235	26.442
P18077	60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2 - [RL35A_HUMAN]	44.55	4	6	6	34	0.970	33	11.777	92.068	110	12.530
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	14.39	20	17	17	35	1.000	31	10.915	92.060	1140	126.887
A0A024RAV4	Cold shock domain protein A, isoform CRA_b OS=Homo sapiens GN=CSDA PE=4 SV=1 - [A0A024RAV4_HUMAN]	27.39	8	3	6	27	0.978	5	13.891	91.986	303	31.928
H7C2W9	60S ribosomal protein L31 (Fragment) OS=Homo sapiens GN=RPL31 PE=1 SV=1 - [H7C2W9_HUMAN]	38.89	8	6	6	42	1.000	41	7.432	91.955	108	12.803
A0A087WWS7	Zinc finger protein 14 OS=Homo sapiens GN=ZNF14 PE=4 SV=1 - [A0A087WWS7_HUMAN]	26.42	14	14	14	32	0.965	31	9.265	91.942	579	64.664
A8K5Y7	cDNA FLJ78655, highly similar to Homo sapiens exportin 5 (XPO5), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5Y7_HUMAN]	13.54	8	15	15	39	1.000	38	7.533	91.737	1204	136.221
P30042	ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3 - [ES1_HUMAN]	26.12	5	7	7	33	1.000	33	0.000	91.427	268	28.153
Q15286	Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 - [RAB35_HUMAN]	31.34	36	4	7	32	1.034	8	19.264	91.420	201	23.011
A8K766	cDNA FLJ77343, highly similar to Homo sapiens electron-transfer-flavoprotein, beta polypeptide(ETFB), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K766_HUMAN]	43.53	3	10	10	32	1.000	29	13.623	91.246	255	27.904
B7Z910	cDNA FLJ61711, highly similar to Homo sapiens minor histocompatibility antigen HA-1 (HA-1), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z910_HUMAN]	16.98	13	16	16	36	1.000	35	7.951	90.959	948	104.586
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 - [RAB5C_HUMAN]	38.89	12	4	7	35	1.000	27	2.074	90.769	216	23.468
A8K3Q9	cDNA FLJ76611, highly similar to Homo sapiens ribosomal protein L14 (RPL14), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K3Q9_HUMAN]	44.44	7	11	11	43	1.000	43	8.323	90.516	216	23.440
A0A024R3J7	HCG2032701, isoform CRA_a OS=Homo sapiens GN=hCG_2032701 PE=4 SV=1 - [A0A024R3J7_HUMAN]	10.67	5	8	9	36	1.000	31	6.957	90.463	703	80.376
X1WI28	60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=2 - [X1WI28_HUMAN]	35.32	12	1	8	47	0.850	1		89.762	201	23.057
Q8WVC2	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 - [Q8WVC2_HUMAN]	50.62	3	5	5	42	1.000	42	13.307	89.630	81	8.844
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 - [ODPA_HUMAN]	21.54	16	9	9	37	1.000	35	0.000	89.404	390	43.268
P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A_HUMAN]	32.43	6	5	6	40	1.000	29	0.040	89.376	148	16.551
A6NJA2	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP14 PE=1 SV=2 - [A6NJA2_HUMAN]	22.32	8	13	13	34	1.000	33	3.067	89.371	448	51.054
B4DF00	cDNA FLJ53308, highly similar to 2-oxoglutarate dehydrogenase E1 component, mitochondrial (EC 1.2.4.2) OS=Homo sapiens PE=2 SV=1 - [B4DF00_HUMAN]	13.55	13	12	12	34	1.000	32	6.047	89.229	974	110.456
C9J6B6	Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 - [C9J6B6_HUMAN]	14.53	2	2	14	46	0.992	2	19.093	89.177	757	82.444
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3 - [ODPB_HUMAN]	21.17	4	8	8	36	1.000	36	4.552	89.058	359	39.208
Q16576	Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 - [RBBP7_HUMAN]	18.59	6	4	6	45	0.986	22	32.010	89.042	425	47.790
G3V295	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [G3V295_HUMAN]	41.38	9	9	9	32	1.000	32	9.980	88.972	203	22.827
Q59EC0	Adenosine deaminase, RNA-specific isoform ADAR-a variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EC0_HUMAN]	16.08	6	22	22	42	0.916	41	13.094	88.796	1244	137.747
A8KAQ5	cDNA FLJ77404, highly similar to Homo sapiens small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen) (SNRP70), transcript variant 1, mRNA OS=Homo sapi	33.41	6	12	12	32	1.000	31	5.508	88.718	437	51.465
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 - [PSA5_HUMAN]	33.61	2	4	7	32	1.000	19	0.000	88.595	241	26.394
F8VPD4	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 - [F8VPD4_HUMAN]	11.42	7	19	22	34	1.000	31	18.545	88.517	2162	235.873
B4DPJ2	Annexin OS=Homo sapiens PE=2 SV=1 - [B4DPJ2_HUMAN]	22.87	12	10	10	31	1.000	29	19.848	88.517	411	45.569
O75477	Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 - [ERLN1_HUMAN]	28.03	5	8	11	30	1.018	16	16.914	88.352	346	38.901
Q9UHX1	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1 - [PUF60_HUMAN]	21.11	6	6	13	32	1.004	15	0.569	88.112	559	59.838
E9AYA3	Heat shock protein 70-related protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1240 PE=3 SV=1 - [E9AYA3_LEIMU]	14.66	1	7	9	47	1.000	13	0.000	88.013	641	70.555
A8K984	Structural maintenance of chromosomes protein OS=Homo sapiens PE=2 SV=1 - [A8K984_HUMAN]	12.36	10	19	19	31	0.937	31	9.591	87.979	1197	135.512
O43290	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 - [SNUT1_HUMAN]	22.5	18	14	15	31	1.000	23	17.931	87.685	800	90.200
Q9UHB9	Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2 - [SRP68_HUMAN]	25.36	7	15	15	35	1.000	34	10.067	87.489	627	70.686
B9EG60	Synaptopodin 2 OS=Homo sapiens GN=SYNPO2 PE=2 SV=1 - [B9EG60_HUMAN]	14.51	4	2	20	40	0.943	2	8.716	87.403	1261	136.237
Q9GJG3	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [Q9GJG3_HUMAN]	33.15	554	0	6	35				87.344	181	21.229
D6W5C0	Spectrin, beta, non-erythrocytic 1, isoform CRA_b OS=Homo sapiens GN=SPTBN1 PE=4 SV=1 - [D6W5C0_HUMAN]	11.98	11	25	27	41	1.000	38	3.849	87.273	2278	264.276
H7C3I1	Hsc70-interacting protein (Fragment) OS=Homo sapiens GN=ST13 PE=4 SV=1 - [H7C3I1_HUMAN]	63.01	2	1	7	32	1.000	1		87.253	146	16.319
O75822	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2 - [EIF3J_HUMAN]	37.98	3	10	11	32	1.000	28	8.565	87.203	258	29.045
D3DUP2	WNK lysine deficient protein kinase 1, isoform CRA_d OS=Homo sapiens GN=WNK1 PE=4 SV=1 - [D3DUP2_HUMAN]	8.83	15	18	18	34	0.955	33	6.814	87.002	2107	222.567
B4DL14	ATP synthase subunit gamma OS=Homo sapiens PE=2 SV=1 - [B4DL14_HUMAN]	34	4	9	9	49	1.004	43	7.508	86.988	250	27.495
A0A024RD07	Trinucleotide repeat containing 5, isoform CRA_c OS=Homo sapiens GN=TNRC5 PE=4 SV=1 - [A0A024RD07_HUMAN]	24.46	3	8	8	32	1.000	29	3.034	86.696	278	30.755
P30273	High affinity immunoglobulin epsilon receptor subunit gamma OS=Homo sapiens GN=FCER1G PE=1 SV=1 - [FCERG_HUMAN]	33.72	2	4	4	35	1.000	32	1.045	86.647	86	9.661
Q9UMS6	Synaptopodin-2 OS=Homo sapiens GN=SYNPO2 PE=1 SV=2 - [SYNP2_HUMAN]	16.56	5	1	19	40	1.000	2	0.000	86.604	1093	117.441
B2R932	cDNA, FLJ94187, highly similar to Homo sapiens CD99 antigen (CD99), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R932_HUMAN]	12.97	2	2	2	27	1.000	24	0.000	86.596	185	18.935
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 - [ACADV_HUMAN]	27.79	15	15	15	37	1.000	35	2.724	86.491	655	70.345
P42768	Wiskott-Aldrich syndrome protein OS=Homo sapiens GN=WAS PE=1 SV=4 - [WASP_HUMAN]	21.31	4	11	11	32	1.000	26	6.884	86.376	502	52.880
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1 - [AHSA1_HUMAN]	23.37	7	8	8	31	1.000	30	3.596	86.321	338	38.250
Q8NBJ5	Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1 - [GT251_HUMAN]	19.94	8	14	14	42	1.017	41	6.558	86.217	622	71.590
P26358	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2 - [DNMT1_HUMAN]	12.81	11	18	18	33	1.000	31	10.049	86.188	1616	183.050
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2 - [TFR1_HUMAN]	21.32	6	16	16	37	1.000	36	10.384	86.117	760	84.818
Q5VSQ6	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (Proline 4-hydroxylase), alpha polypeptide I variant (Fragment) OS=Homo sapiens GN=P4HA1 PE=2 SV=1 - [Q5VSQ(	25.47	2	13	13	33	1.000	33	9.359	85.680	534	60.929
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]	23.22	4	11	11	29	1.000	29	11.346	85.669	422	47.434
B7Z2Z1	cDNA FLJ59523, highly similar to Scaffold attachment factor B OS=Homo sapiens PE=2 SV=1 - [B7Z2Z1_HUMAN]	14.92	11	9	15	38	1.000	20	4.285	85.649	811	91.030
Q96C23	Aldose 1-epimerase OS=Homo sapiens GN=GALM PE=1 SV=1 - [GALM_HUMAN]	24.27	6	7	7	29	1.000	29	28.615	85.589	342	37.742
Q53T76	Glycerol-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens GN=GPD2 PE=3 SV=1 - [Q53T76_HUMAN]	17.6	7	13	13	31	1.018	31	9.764	85.521	693	77.204
P0CW22	40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1 - [RS17L_HUMAN]	29.63	9	5	7	37	1.000	29	7.469	85.350	135	15.540
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	35.06	7	6	6	43	1.000	41	4.886	85.269	154	15.926
A0A024R201	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13, isoform CRA_a OS=Homo sapiens GN=PSMD13 PE=4 SV=1 - [A0A024R201_HUMAN]	25	16	10	10	34	1.000	33	12.687	85.201	376	42.891
Q86UY0	Protein BLOC1S5-TXNDC5 OS=Homo sapiens GN=TXNDC5 PE=2 SV=1 - [Q86UY0_HUMAN]	35.28	8	10	12	32	1.000	28	6.831	84.811	360	40.344
P18583	Protein SON OS=Homo sapiens GN=SON PE=1 SV=4 - [SON_HUMAN]	8.9	10	17	18	34	1.000	32	6.889	84.662	2426	263.664
E9AMU3	Putative calmodulin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0910 PE=4 SV=1 - [E9AMU3_LEIMU]	44.3	4	3	8	33	1.000	10	0.000	84.516	149	16.814
A0A024R326	Ribosomal protein L29, isoform CRA_a OS=Homo sapiens GN=RPL29 PE=4 SV=1 - [A0A024R326_HUMAN]	28.03	3	6	6	37	0.994	37	7.014	84.369	157	17.542
E5KLM1	Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens PE=3 SV=1 - [E5KLM1_HUMAN]	20.56	11	1	20	34	0.933	2	24.515	84.137	997	115.839
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	13.93	3	18	18	38	0.970	38	4.720	83.832	1249	138.263
O95782	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 - [AP2A1_HUMAN]	17.09	4	13	19	35	0.945	22	9.459	83.768	977	107.478
Q13185	Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 - [CBX3_HUMAN]	31.69	4	8	8	35	1.000	34	0.000	83.562	183	20.798
O00160	Unconventional myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3 - [MYO1F_HUMAN]	14.57	11	14	18	36	1.004	26	9.478	83.557	1098	124.766
Q8WW12	PEST proteolytic signal-containing nuclear protein OS=Homo sapiens GN=PCNP PE=1 SV=2 - [PCNP_HUMAN]	40.45	2	6	6	30	1.000	30	25.219	83.497	178	18.913
Q8IXJ3	Small nuclear ribonucleoprotein component OS=Homo sapiens GN=SNRP116 PE=2 SV=1 - [Q8IXJ3_HUMAN]	10.82	9	9	10	34	1.000	24	7.282	83.285	850	95.311
P04732	Metallothionein-1E OS=Homo sapiens GN=MT1E PE=1 SV=1 - [MT1E_HUMAN]	67.21	9	1	4	29	1.000	2	0.000	83.233	61	6.009
A0A024R4A5	Trinucleotide repeat containing 15, isoform CRA_a OS=Homo sapiens GN=TNRC15 PE=4 SV=1 - [A0A024R4A5_HUMAN]	11.86	8	15	15	32	1.000	28	18.401	83.213	1298	149.850
Q96T51	RUN and FYVE domain-containing protein 1 OS=Homo sapiens GN=RUFY1 PE=1 SV=2 - [RUFY1_HUMAN]	20.2	12	15	15	29	0.962	29	19.105	83.018	708	79.767
P24844	Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4 - [MYL9_HUMAN]	27.91	5	1	6	40	1.000	5	0.000	83.015	172	19.814
O94826	Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1 - [TOM70_HUMAN]	21.71	4	14	14	34	1.000	34	20.701	82.926	608	67.412
O94776	Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1 - [MTA2_HUMAN]	29.19	5	20	21	36	0.961	33	17.648	82.918	668	74.976
P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	18.69	5	10	10	31	1.049	31	16.513	82.680	567	62.481

B5BU08	U2 small nuclear RNA auxiliary factor 1 isoform a OS=Homo sapiens GN=U2AF1 PE=2 SV=1 - [B5BU08_HUMAN]	24.17	7	6	7	37	1.000	31	0.000	82.636	240	27.855
Q14165	Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1 - [MLEC_HUMAN]	22.26	4	6	6	27	1.000	25	2.186	82.402	292	32.214
E9AZE9	Putative heat shock protein DNAJ OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_2400 PE=3 SV=1 - [E9AZE9_LEIMU]	21.97	1	9	9	28	1.000	27	0.000	82.394	396	43.539
P31689	DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 - [DNJA1_HUMAN]	40.55	5	12	14	34	1.000	28	16.870	82.305	397	44.839
A8KAH7	cDNA FLJ75444, highly similar to Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, alpha (PRKAR2A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8KAH	29.95	6	12	12	29	0.954	29	11.365	82.054	404	45.476
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	17.78	21	18	18	39	1.000	37	9.521	81.994	1097	123.550
I3L0H8	ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 - [I3L0H8_HUMAN]	25.95	21	13	13	29	0.983	28	16.473	81.656	447	50.488
P30085	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3 - [KCY_HUMAN]	22.96	5	5	5	30	1.000	28	7.207	81.503	196	22.208
H3BN98	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 - [H3BN98_HUMAN]	23.63	13	2	6	37	1.000	8	22.364	81.240	237	27.150
E5KLJ7	Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=3 SV=1 - [E5KLJ7_HUMAN]	20.56	14	1	20	33	0.778	1		81.220	997	115.812
Q59GY3	Arginine/serine-rich splicing factor 6 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GY3_HUMAN]	22.58	7	4	8	29	1.336	9	44.974	81.112	279	31.846
E5RIW3	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1 SV=1 - [E5RIW3_HUMAN]	54.76	5	7	7	34	0.972	34	11.243	81.070	84	10.074
B4DZC3	cDNA FLJ55645, highly similar to 5'-3' exoribonuclease 2 (EC 3.1.11.-) OS=Homo sapiens PE=2 SV=1 - [B4DZC3_HUMAN]	11.27	4	11	11	33	0.993	31	7.787	80.906	896	102.351
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1 - [STT3B_HUMAN]	6.9	1	5	6	28	1.000	22	0.000	80.866	826	93.614
D3DRH1	Dedicator of cytokinesis 8, isoform CRA_a OS=Homo sapiens GN=DOCK8 PE=4 SV=1 - [D3DRH1_HUMAN]	9.21	13	19	19	33	0.962	32	13.071	80.864	2031	230.677
B4E2A4	cDNA FLJ53275, highly similar to Homo sapiens spectrin domain with coiled-coils 1 (SPECC1), transcript variant, mRNA OS=Homo sapiens PE=2 SV=1 - [B4E2A4_HUM	21.99	12	17	19	36	1.000	26	3.542	80.831	987	110.226
P40222	Alpha-taxilin OS=Homo sapiens GN=TXLNA PE=1 SV=3 - [TXLNA_HUMAN]	34.25	8	18	19	34	0.990	26	12.127	80.796	546	61.853
P17858	ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [PFKAL_HUMAN]	16.28	8	8	13	29	0.936	18	16.995	80.762	780	84.964
O75937	DnaJ homolog subfamily C member 8 OS=Homo sapiens GN=DNAJC8 PE=1 SV=2 - [DNJC8_HUMAN]	24.9	2	9	9	28	0.943	27	9.721	80.518	253	29.823
B5BUB1	RuvB-like 1 (Fragment) OS=Homo sapiens GN=RUVBL1 PE=2 SV=1 - [B5BUB1_HUMAN]	24.56	8	9	9	25	1.000	25	23.372	80.474	456	50.184
Q13838	Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1 - [DX39B_HUMAN]	25.7	16	7	13	35	0.990	16	26.178	80.358	428	48.960
O75821	Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 - [EIF3G_HUMAN]	36.25	10	12	12	27	1.000	26	3.061	80.349	320	35.589
Q5T123	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 - [Q5T123_HUMAN]	53.41	5	6	6	43	1.000	34	0.876	80.133	88	9.375
B3KNJ4	SUMO-1 activating enzyme subunit 1, isoform CRA_a OS=Homo sapiens GN=SAE1 PE=1 SV=1 - [B3KNJ4_HUMAN]	27.42	10	9	9	27	0.943	27	9.529	79.972	299	33.363
Q9Y3I0	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1 - [RTCB_HUMAN]	25.94	4	11	11	34	0.999	32	6.879	79.555	505	55.175
A8K3A8	cDNA FLJ75085, highly similar to Homo sapiens glutaminyl-tRNA synthetase (QARS), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K3A8_HUMAN]	21.81	15	16	17	37	0.992	35	20.172	79.403	775	87.753
B4DN87	cDNA FLJ52569, highly similar to Collagen-binding protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DN87_HUMAN]	23.17	16	9	9	32	1.000	31	14.387	79.294	397	44.176
Q14008	Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN]	9.06	5	18	18	35	1.000	35	14.712	79.247	2032	225.352
P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 - [SCOT1_HUMAN]	22.12	5	12	12	34	1.000	34	11.304	79.091	520	56.122
O43768	Alpha-endosulfine OS=Homo sapiens GN=ENSA PE=1 SV=1 - [ENSA_HUMAN]	52.89	4	6	7	31	1.000	25	3.416	79.078	121	13.381
Q92608	Dedicator of cytokinesis protein 2 OS=Homo sapiens GN=DOCK2 PE=1 SV=2 - [DOCK2_HUMAN]	10.11	11	20	21	36	1.000	35	17.910	79.075	1830	211.812
B3KW56	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3S6 PE=2 SV=1 - [B3KW56_HUMAN]	22.22	9	10	10	36	1.000	36	9.911	78.848	396	46.415
Q15164	Polyadenylate binding protein II (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q15164_HUMAN]	57.51	2	1	13	29	0.961	1		78.814	193	21.973
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	25.68	27	11	14	26	0.350	20	76.073	78.587	584	58.792
A8K7Q1	cDNA FLJ77770, highly similar to Homo sapiens nucleobindin 1 (NUCB1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K7Q1_HUMAN]	32.97	10	16	17	35	1.000	31	6.462	78.381	461	53.850
E9PBS1	Phosphoribosylaminoimidazole carboxylase (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 - [E9PBS1_HUMAN]	21.07	4	8	9	33	1.000	32	6.110	78.253	413	45.622
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens GN=NUCKS1 PE=1 SV=1 - [NUCKS_HUMAN]	32.92	3	9	9	35	1.000	34	0.152	78.210	243	27.280
I3L3Q7	Complement component 1 Q subcomponent-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=C1QBP PE=1 SV=1 - [I3L3Q7_HUMAN]	25.42	4	4	4	24	1.000	22	0.000	78.082	177	19.994
A8MX94	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=1 - [A8MX94_HUMAN]	44.83	6	6	6	32	1.000	31	8.238	77.859	174	19.468
Q05DH1	Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA7 PE=2 SV=1 - [Q05DH1_HUMAN]	27.31	8	6	6	27	1.000	26	0.000	77.776	238	26.697
A8K9K1	Calcium-transporting ATPase OS=Homo sapiens PE=2 SV=1 - [A8K9K1_HUMAN]	10.12	3	3	10	30	1.000	7	15.776	77.754	998	109.110
A0A060VG62	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1 - [A0A060VG62_HUMAN]	20.55	320	0	4	28				77.650	365	40.793
Q05D04	LRRFIP1 protein (Fragment) OS=Homo sapiens GN=LRRFIP1 PE=2 SV=1 - [Q05D04_HUMAN]	24.32	3	1	13	26	1.197	1		77.639	518	57.163
Q9UPT8	Zinc finger CCCH domain-containing protein 4 OS=Homo sapiens GN=ZC3H4 PE=1 SV=3 - [ZC3H4_HUMAN]	8.98	2	8	9	27	1.000	21	0.000	77.596	1303	140.169
P10606	Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2 - [COX5B_HUMAN]	50.39	3	7	7	36	1.000	35	14.621	77.555	129	13.687
Q5JTZ9	Alanine--tRNA ligase, mitochondrial OS=Homo sapiens GN=AARS2 PE=1 SV=1 - [SYAM_HUMAN]	14.72	1	12	12	26	1.000	26	2.291	77.548	985	107.273
B3KMV5	cDNA FLJ12728 fis, clone NT2RP2000040, highly similar to Protein FAM62A OS=Homo sapiens PE=2 SV=1 - [B3KMV5_HUMAN]	14.4	11	16	17	38	1.000	37	9.352	77.495	1104	122.829
E9AXJ7	ATP synthase subunit beta OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1180 PE=3 SV=1 - [E9AXJ7_LEIMU]	16.03	2	5	6	29	1.002	14	32.483	77.494	499	53.037
P84090	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1 - [ERH_HUMAN]	40.38	2	4	4	31	0.941	29	12.277	77.479	104	12.251
I3L1L3	Myb-binding protein 1A (Fragment) OS=Homo sapiens GN=MYBBP1A PE=1 SV=1 - [I3L1L3_HUMAN]	16.61	7	21	21	42	1.000	38	0.251	77.341	1252	140.154
Q9BRP8	Partner of Y14 and mago OS=Homo sapiens GN=WIBG PE=1 SV=1 - [WIBG_HUMAN]	29.41	1	5	5	25	1.000	21	0.000	77.271	204	22.642
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	29.63	5	14	14	27	1.000	27	6.438	77.033	459	51.772
A0A087WWP4	Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15 PE=4 SV=1 - [A0A087WWP4_HUMAN]	17.79	3	12	13	33	1.000	27	13.883	76.885	933	102.073
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1 - [UBE2N_HUMAN]	25	6	3	4	28	0.975	25	19.269	76.869	152	17.127
Q7Z6I6	Rho GTPase-activating protein 30 OS=Homo sapiens GN=ARHGAP30 PE=1 SV=3 - [RHG30_HUMAN]	11.81	2	14	14	28	1.000	26	0.508	76.506	1101	118.509
Q8NI27	THO complex subunit 2 OS=Homo sapiens GN=THOC2 PE=1 SV=2 - [THOC2_HUMAN]	7.03	9	13	14	29	1.000	28	7.879	76.311	1593	182.659
P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	37.16	7	9	9	29	0.971	29	14.931	76.176	261	28.750
B4DXT2	cDNA FLJ59635, highly similar to Heat shock 70 kDa protein 4L OS=Homo sapiens PE=2 SV=1 - [B4DXT2_HUMAN]	16.85	7	8	11	29	1.000	14	1.995	75.955	813	91.881
P61081	NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1 - [UBC12_HUMAN]	32.24	3	7	7	26	1.000	24	13.100	75.939	183	20.887
H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=1 SV=1 - [H0Y4R1_HUMAN]	22.98	7	9	11	31	1.016	23	6.358	75.715	470	51.035
A0A087WV66	Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=4 SV=1 - [A0A087WV66_HUMAN]	9.65	3	23	23	36	1.000	31	5.841	75.662	3255	358.407
P14927	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=1 SV=2 - [QCR7_HUMAN]	36.04	3	1	5	27	0.979	8	27.149	75.444	111	13.522
Q9Y5B9	FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 - [SP16H_HUMAN]	14.33	2	16	16	32	1.000	29	13.995	75.420	1047	119.838
Q9HAV7	GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2 - [GRPE1_HUMAN]	31.34	2	7	7	35	1.066	35	9.500	75.414	217	24.264
Q7RTQ9	Kinesin light chain 1A OS=Homo sapiens GN=KNS2 PE=2 SV=1 - [Q7RTQ9_HUMAN]	25.84	30	11	16	30	1.000	22	7.269	75.411	538	61.164
P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2 - [ATPD_HUMAN]	13.69	1	2	2	28	1.000	25	0.000	75.308	168	17.479
J3KPM9	Signal transducer and activator of transcription OS=Homo sapiens GN=STAT1 PE=1 SV=1 - [J3KPM9_HUMAN]	14.43	7	10	10	30	0.996	30	6.163	75.240	714	83.308
P20645	Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1 - [MPRD_HUMAN]	22.38	13	5	6	28	1.000	26	15.281	75.187	277	30.973
Q1KLJ5	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [Q1KLJ5_HUMAN]	28.18	274	0	5	30				75.147	181	21.127
E9PBG7	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=1 SV=1 - [E9PBG7_HUMAN]	15.43	17	8	9	27	0.972	22	6.625	75.038	512	57.726
A0A087WUQ6	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=4 SV=1 - [A0A087WUQ6_HUMAN]	28.22	3	5	5	29	1.000	26	11.830	74.931	202	21.924
Q59G46	Thioredoxin-like 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G46_HUMAN]	31.79	7	7	7	27	1.003	26	21.553	74.909	280	31.335
O95232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]	21.3	10	10	10	26	0.982	26	10.068	74.904	432	51.435
H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 - [H0YK49_HUMAN]	30.13	7	5	5	26	0.959	24	16.496	74.857	229	24.145
P51153	Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1 - [RAB13_HUMAN]	30.54	8	4	7	28	1.000	7	1.341	74.842	203	22.760
Q8WYQ7	Galectin OS=Homo sapiens GN=LGALS9 PE=4 SV=1 - [Q8WYQ7_HUMAN]	19.94	17	7	7	27	1.000	24	6.115	74.826	311	34.668
Q9NXV6	CDKN2A-interacting protein OS=Homo sapiens GN=CDKN2AIP PE=1 SV=3 - [CARF_HUMAN]	24.66	5	11	11	24	1.000	20	24.602	74.807	580	61.088
E8NHQ7	ATP synthase subunit alpha OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0500 PE=3 SV=1 - [E8NHQ7_LEIMU]	9.23	2	3	4	22	6.175	6	101.214	74.735	574	62.560
P39748	Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1 - [FEN1_HUMAN]	15.79	7	6	6	26	1.000	26	2.479	74.639	380	42.566
P35269	General transcription factor IIF subunit 1 OS=Homo sapiens GN=GTF2F1 PE=1 SV=2 - [T2FA_HUMAN]	20.7	5	2	11	26	1.000	8	0.000	74.628	517	58.205
A6NL93	Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=1 - [A6NL93_HUMAN]	48.89	10	6	6	24	0.996	24	4.126	74.563	90	9.530
A0A087WYS1	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=4 SV=1 - [A0A087WYS1_HUMAN]	23.03	18	13	13	33	1.000	33	10.367	74.489	508	56.932
O43719	HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1 - [HTSF1_HUMAN]	15.63	4	14	14	29	1.000	29	9.751	74.432	755	85.801
A4FU11	RPS4Y1 protein (Fragment) OS=Homo sapiens GN=RPS4Y1 PE=2 SV=1 - [A4FU11_HUMAN]	27.1	6	3	10	33	0.876	4	21.873	74.426	262	29.276
Q14669	E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1 - [TRIPC_HUMAN]	8.89	6	10	16	27	1.000	15	4.948	74.338	1992	220.296
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4 - [ACPH_HUMAN]	14.75	6	12	12	31	1.000	31	6.702	74.287	732	81.173
J3QRC4	60S ribosomal protein L26 (Fragment) OS=Homo sapiens GN=RPL26 PE=4 SV=1 - [J3QRC4_HUMAN]	32.59	9	1	6	33	1.119	2	30.969	74.132	135	15.740
A8K2Y2	cDNA FLJ78120, highly similar to Homo sapiens eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa (EIF2S3), mRNA OS=Homo sapiens PE=2 SV=1 - [A8I	24.58	7	11	11	31	1.000	30	4.907	73.638	472	51.078
A8K492	cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K492_HUMAN]	10.78	12	9	9	30	1.000	30	0.000	73.594	900	101.080
H0YJH7	Thymopentin (Fragment) OS=Homo sapiens GN=TMPO PE=1 SV=1 - [H0YJH7_HUMAN]	30.38	2	1	6	26	0.853	2	23.841	73.524	237	26.850
O75976	Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2 - [CBPD_HUMAN]	11.01	3	15	15	29	1.000	28	1.144	73.452	1380	152.835
P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	34.93	3	8	12	56	0.981	43	14.399	73.411	209	24.019
P51610	Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [HCFC1_HUMAN]	11.06	6	1	19	29	1.000	1		73.367	2035	208.602
A8KA83	cDNA FLJ78586, highly similar to Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA OS=Homo sapiens PE=2 SV=	36.36	6	6	7	49	1.000	42	16.306	73.201	242	27.300
A0A087WYS0	MICOS complex subunit MIC60 OS=Homo sapiens GN=IMMT PE=4 SV=1 - [A0A087WYS0_HUMAN]	29.03	3	0	11	29				73.066	372	40.476
Q58EY4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 OS=Homo sapiens GN=SMARCC1 PE=2 SV=1 - [Q58EY4_HUMAN]	16.11	13	14	19	33	1.000	21	15.409	72.853	1105	122.834
A6NEM2	HCF N-terminal chain 5 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [A6NEM2_HUMAN]	10.29	5	1	19	29	1.000	1		72.817	2080	213.343
Q9P2R3	Rabankyrin-5 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2 - [ANFY1_HUMAN]	10.27	9	10	11	25	1.000	22	15.568	72.547	1169	128.318
P12036	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4 - [NFH_HUMAN]	2.34	12	1	3	27	1.834	1		72.391	1026	112.411
Q59EM6	Internexin neuronal intermediate filament protein, alpha variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EM6_HUMAN]	5.12	9	1	2	26	1.000	1		72.373	332	37.262
B4DJT7	cDNA FLJ56511, highly similar to Neurofilament triplet M protein OS=Homo sapiens PE=2 SV=1 - [B4DJT7_HUMAN]	2.29	12	1	2	26	1.000	1		72.223	698	78.838
A8K8D9	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens PE=2 SV=1 - [A8K8D9_HUMAN]	23.3	20	14	14	30	1.000	30	8.602	72.176	515	59.277
Q5SSJ5	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1 - [HP1B3_HUMAN]	20.98	6	12	13	31	1.000	30	11.173	72.012	553	61.169
B4E3H3	Phosphoinositide phospholipase C OS=Homo sapiens PE=2 SV=1 - [B4E3H3_HUMAN]	15.19	8	18	19	29	1.000	28	12.102	72.003	1132	132.736
Q16630	Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2 - [CPSF6_HUMAN]	20.15	4	11	11	36	1.000	31	10.781	71.798	551	59.173
I3L2B0	Clustered mitochondria protein homolog (Fragment) OS=Homo sapiens GN=CLUH PE=1 SV=2 - [I3L2B0_HUMAN]	11.65	1	12	12	27	1.000	22	0.000	71.775	1236	138.142
P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	21.11	5	13	13	27	1.000	27	13.419	71.641	611	69.241
H0Y4R4	Torsin-1A-interacting protein 1 (Fragment) OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=1 - [H0Y4R4_HUMAN]	28.72	1	1	9	29	0.918	2	3.155	71.630	296	33.729
Q5T1M5	FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2 - [FKB15_HUMAN]	14.85	6	16	16	25	1.000	23	0.000	71.544	1219	133.547
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 - [F120A_HUMAN]	12.97	1	11	11	24	1.000	23	0.000	71.522	1118	121.811
E9B170	Glyceraldehyde-3-phosphate dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2980 PE=3 SV=1 - [E9B170_LEIMU]	26.59	1	11	11	28	1.000	28	10.338	71.478	361	39.098
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	49.6	3	7	7	35	0.999	34	19.381	71.410	125	13.734
B2R880	cDNA, FLJ93778, highly similar to Homo sapiens CD38 antigen (p45) (CD38), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R880_HUMAN]	32.33	6	11	11	30	1.000	30	6.355	71.406	300	34.291
Q9NZM1	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 - [MYOF_HUMAN]	12.18	3	23	24	30	1.060	29	14.827	71.306	2061	234.561
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]	23.99	7	9	10	32	1.000	29	11.669	71.099	396	44.715
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	34.27	6	6	7	29	0.930	24	13.701	70.630	143	15.798
A0A024R7U6	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=MCM4 PE=3 SV=1 - [A0A024R7U6_HUMAN]	14.95	8	16	16	31	0.974	31	7.688	70.629	863	96.516
P08579	U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens GN=SNRPB2 PE=1 SV=1 - [RU2B_HUMAN]	34.67	3	6	8	30	0.970	17	8.855	70.536	225	25.470
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	31.95	3	6	6	26	1.000	26	9.715	70.525	241	26.472
P49006	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2 - [MRP_HUMAN]	49.23	1	4	4	22	1.000	19	0.000	70.499	195	19.517
Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	23.41	8	7	7	30	1.000	28	4.452	70.392	393	41.893
A4FUT8	JMJD1B protein (Fragment) OS=Homo sapiens GN=JMJD1B PE=2 SV=1 - [A4FUT8_HUMAN]	8.58	4	14	14	23	1.000	23	2.132	70.387	1551	168.950
Q9UBG0	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2 - [MRC2_HUMAN]	7.84	5	12	12	29	1.000	24	5.219	70.374	1479	166.568
Q9NQ29	Putative RNA-binding protein Luc7-like 1 OS=Homo sapiens GN=LUC7L PE=1 SV=1 - [LUC7L_HUMAN]	22.91	9	3	9	25	1.000	5	6.891	70.295	371	43.701
E5KN59	Peptidyl-prolyl cis-trans isomerase D OS=Homo sapiens PE=4 SV=1 - [E5KN59_HUMAN]	17.57	6	6	8	29	0.955	10	18.332	70.257	370	40.738
A0A024RAD5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=3 SV=1 - [A0A024RAD5_HUMAN]	13.16	3	6	6	23	1.000	22	0.000	70.059	456	50.670
P50570	Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 - [DYN2_HUMAN]	16.44	14	15	15	25	1.000	25	8.527	69.973	870	98.003
B4DMH3	Coronin OS=Homo sapiens PE=2 SV=1 - [B4DMH3_HUMAN]	18.08	15	10	12	31	1.000	24	2.622	69.866	437	49.347
P49257	Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2 - [LMAN1_HUMAN]	20	5	11	11	30	1.007	28	8.554	69.785	510	57.513
P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	19.05	10	3	15	37	1.049	5	8.825	69.707	677	76.641
B9EGQ8	SMARCA4 protein OS=Homo sapiens GN=SMARCA4 PE=2 SV=1 - [B9EGQ8_HUMAN]	10.35	14	9	17	27	1.000	13	17.637	69.578	1681	189.330
P12081	Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2 - [SYHC_HUMAN]	23.18	8	7	12	27	1.000	17	10.737	69.564	509	57.374
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	19.97	5	15	15	28	0.992	28	16.650	69.517	796	91.649
Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein OS=Homo sapiens GN=APBB1IP PE=1 SV=1 - [AB1IP_HUMAN]	15.17	17	11	11	33	1.000	32	5.069	69.457	666	73.137
P30084	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 - [ECHM_HUMAN]	37.24	1	9	10	30	1.000	26	6.531	69.434	290	31.367
O60271	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4 - [JIP4_HUMAN]	12.49	22	14	15	30	1.000	27	14.597	69.372	1321	146.115
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	17.34	8	11	11	28	0.949	28	13.643	69.303	640	70.685
Q86VM9	Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=1 SV=2 - [ZCH18_HUMAN]	16.05	9	15	15	29	1.000	28	4.761	69.160	953	106.316
F8W031	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [F8W031_HUMAN]	32.7	10	8	9	23	1.000	20	7.639	69.005	263	29.206
E9B400	Peptidyl-prolyl cis-trans isomerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1630 PE=3 SV=1 - [E9B400_LEIMU]	18.82	3	2	5	28	1.000	8	0.000	68.967	255	28.206
Q09160	HLA class I histocompatibility antigen, A-80 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 - [1A80_HUMAN]	20.82	237	0	5	25				68.906	365	40.766
B7Z4K8	cDNA FLJ52869, highly similar to Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z4K8_HUMAN]	21.12	13	8	10	24	1.000	16	15.164	68.873	393	45.280
B4DWN1	cDNA FLJ52285, highly similar to Vesicular integral-membrane protein VIP36 OS=Homo sapiens PE=2 SV=1 - [B4DWN1_HUMAN]	21.05	7	6	6	31	1.000	31	9.714	68.787	285	32.557
P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	17.12	15	16	16	25	1.000	25	8.294	68.610	882	97.489
B2R802	cDNA, FLJ93681, highly similar to Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R802_HUMAN]	27.66	9	5	7	30	1.011	16	18.131	68.581	282	31.287
P02795	Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1 - [MT2_HUMAN]	67.21	11	1	4	23	4.543	1		68.454	61	6.037
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 - [RANG_HUMAN]	26.87	12	5	6	26	1.000	24	3.119	68.348	201	23.296
E9PKP7	Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=1 SV=1 - [E9PKP7_HUMAN]	21.34	11	17	17	29	1.000	29	21.626	68.347	745	87.380
O75475	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1_HUMAN]	22.45	6	12	13	29	0.865	25	8.396	68.298	530	60.067
B4DH07	cDNA FLJ53321, highly similar to Homo sapiens pitrilysin metallopeptidase 1 (PITRM1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DH07_HUMAN]	12.23	9	12	12	25	1.000	25	13.207	67.944	1030	116.222
F5GZS6	4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=1 - [F5GZS6_HUMAN]	24.04	11	13	13	27	1.000	27	9.701	67.886	599	64.832
Q9NTJ3	Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2 - [SMC4_HUMAN]	13.51	12	16	16	24	0.996	22	15.267	67.803	1288	147.091
P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3 - [RBM25_HUMAN]	14.47	13	13	13	31	1.000	30	16.626	67.675	843	100.124
P09496	Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1 - [CLCA_HUMAN]	24.19	6	8	8	27	1.000	27	7.093	67.414	248	27.060
B4E380	Histone H3 OS=Homo sapiens PE=2 SV=1 - [B4E380_HUMAN]	46.02	12	2	8	41	0.852	6	6.534	67.410	113	12.910
A8K6Q9	cDNA FLJ75882, highly similar to Homo sapiens spastic paraplegia 20, spartin (Troyer syndrome) (SPG20), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6Q9_HUMAN]	17.27	5	12	12	26	1.000	25	9.201	67.210	666	72.787
O94906	Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 - [PRP6_HUMAN]	18.07	1	16	16	25	0.999	24	17.676	67.063	941	106.858
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	23.85	3	6	6	37	0.864	37	12.076	66.915	260	29.228
Q6FH24	VBP1 protein OS=Homo sapiens GN=VBP1 PE=2 SV=1 - [Q6FH24_HUMAN]	45	6	9	9	31	1.000	31	6.695	66.716	160	18.724
A8K8F0	cDNA FLJ76436 OS=Homo sapiens PE=2 SV=1 - [A8K8F0_HUMAN]	29.19	10	9	9	23	0.947	23	8.057	66.494	298	33.194
F5GYN4	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 - [F5GYN4_HUMAN]	33.61	10	7	7	19	1.000	17	0.544	66.417	241	28.033
Q53GT4	Dipeptidylpeptidase III isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GT4_HUMAN]	17.64	12	12	12	28	1.000	28	3.153	66.309	737	82.514
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	17.05	5	9	9	21	1.000	20	7.759	66.309	563	61.294
Q9H3P7	Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 - [GCP60_HUMAN]	16.29	1	6	6	17	1.000	16	0.000	66.253	528	60.556
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 - [HCD2_HUMAN]	50.96	2	11	11	25	1.000	24	8.363	66.240	261	26.906
P84103	Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [SRSF3_HUMAN]	40.24	2	6	7	28	1.000	25	12.732	66.201	164	19.318
Q14657	EKC/KEOPS complex subunit LAGE3 OS=Homo sapiens GN=LAGE3 PE=1 SV=2 - [LAGE3_HUMAN]	27.27	1	2	2	22	1.000	17	0.000	66.125	143	14.795
P04733	Metallothionein-1F OS=Homo sapiens GN=MT1F PE=1 SV=1 - [MT1F_HUMAN]	34.43	6	2	3	26	1.000	12	0.000	66.096	61	6.081
B2RDG0	Proteasome subunit alpha type OS=Homo sapiens PE=2 SV=1 - [B2RDG0_HUMAN]	27.59	13	8	8	26	1.000	26	7.110	66.074	261	29.437
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	38.24	6	2	8	41	0.801	6	16.184	65.992	136	15.394
H7BXI1	Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 - [H7BXI1_HUMAN]	14.25	1	1	12	25	1.000	8	0.000	65.971	884	97.949
B4DNM8	cDNA FLJ53395, highly similar to Prolyl 3-hydroxylase 1 (EC 1.14.11.7) OS=Homo sapiens PE=2 SV=1 - [B4DNM8_HUMAN]	15.81	7	9	9	25	1.049	25	10.433	65.908	601	68.945
B7Z4L7	cDNA FLJ59035, highly similar to RNA-binding region-containing protein 2 OS=Homo sapiens PE=2 SV=1 - [B7Z4L7_HUMAN]	22.55	15	6	6	21	1.000	21	6.568	65.881	337	36.441
A0A024RDE8	PDZ and LIM domain 5, isoform CRA_c OS=Homo sapiens GN=PDLIM5 PE=4 SV=1 - [A0A024RDE8_HUMAN]	23.32	11	12	12	23	1.000	23	21.745	65.859	596	63.935
O95758	Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 PE=1 SV=2 - [PTBP3_HUMAN]	7.79	8	2	5	26	1.107	7	15.225	65.824	552	59.652
Q9HB71	Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2 - [CYBP_HUMAN]	38.6	4	9	10	26	1.000	25	8.934	65.751	228	26.194
P56385	ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2 - [ATP5I_HUMAN]	50.72	2	3	4	26	1.000	23	5.909	65.579	69	7.928
Q9Y3F4	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 - [STRAP_HUMAN]	38.29	3	11	11	25	1.000	24	2.541	65.212	350	38.414
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	27.84	6	9	9	27	1.006	26	8.743	65.178	255	28.415
P61221	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 - [ABCE1_HUMAN]	17.53	4	12	12	23	0.994	23	7.720	65.123	599	67.271
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	23.36	6	7	7	20	1.000	20	0.000	65.036	381	42.617
B4DLN1	Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=1 - [B4DLN1_HUMAN]	11.31	6	3	5	32	1.051	29	14.871	65.010	442	48.069
I3L397	Eukaryotic translation initiation factor 5A-1 (Fragment) OS=Homo sapiens GN=EIF5A PE=1 SV=3 - [I3L397_HUMAN]	30.61	8	5	5	33	0.977	33	11.347	65.001	147	16.108
Q8N1G4	Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1 - [LRC47_HUMAN]	13.04	1	8	8	19	1.000	19	12.847	64.944	583	63.434
A0A024R5A3	Calpain 1, (Mu/I) large subunit, isoform CRA_b OS=Homo sapiens GN=CAPN1 PE=4 SV=1 - [A0A024R5A3_HUMAN]	20.42	16	15	15	26	1.000	26	12.719	64.929	710	81.416
P37108	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 - [SRP14_HUMAN]	32.35	3	6	6	30	0.997	29	11.657	64.925	136	14.561
B4DEW9	cDNA FLJ52478, highly similar to Eukaryotic translation initiation factor 3 subunit 5 OS=Homo sapiens PE=2 SV=1 - [B4DEW9_HUMAN]	34.62	6	7	7	24	1.000	24	4.206	64.817	208	23.152
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 - [GNAI3_HUMAN]	24.86	20	4	9	27	0.835	8	27.068	64.699	354	40.506
I3L3P7	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=1 - [I3L3P7_HUMAN]	45	8	1	5	30	1.146	1		64.660	100	11.470

A8K781	cDNA FLJ75299, highly similar to Xenopus laevis proteasome (prosome, macropain) 26S subunit, ATPase 3, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K781_HUMAN]	30.02	10	11	12	31	1.000	25	17.588	64.559	423	47.292
P05091	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2 - [ALDH2_HUMAN]	17.6	17	7	8	23	1.000	18	0.632	64.299	517	56.346
A0A024R7S3	Clathrin, light polypeptide (Lcb), isoform CRA_c OS=Homo sapiens GN=CLTB PE=4 SV=1 - [A0A024R7S3_HUMAN]	34.12	4	9	9	23	1.000	23	9.840	63.974	211	23.167
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	37.21	28	7	8	25	1.000	19	5.468	63.849	215	23.882
A0A087X178	Protein FAM49B OS=Homo sapiens GN=FAM49B PE=4 SV=1 - [A0A087X178_HUMAN]	33.18	3	1	6	27	1.000	1		63.841	217	24.859
A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1 - [UBA6_HUMAN]	10.74	3	12	12	35	0.961	34	9.780	63.775	1052	117.895
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNPH_HUMAN]	23.53	5	6	6	26	1.000	26	0.270	63.631	289	32.097
P49755	Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2 - [TMEDA_HUMAN]	31.05	5	7	7	31	1.000	27	0.000	63.623	219	24.960
Q08ES8	Cell growth-inhibiting protein 34 OS=Homo sapiens PE=2 SV=1 - [Q08ES8_HUMAN]	25.99	5	6	6	39	1.000	29	4.732	63.562	177	20.082
A8K3Y5	cDNA FLJ78186 OS=Homo sapiens PE=2 SV=1 - [A8K3Y5_HUMAN]	26.12	2	2	11	25	1.055	5	8.623	63.525	379	43.596
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	33.41	4	12	14	32	1.000	28	7.543	63.524	440	49.154
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [SDHB_HUMAN]	19.29	3	9	9	30	1.000	28	0.000	63.286	280	31.609
Q86V81	THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3 - [THOC4_HUMAN]	22.57	2	5	5	23	1.000	21	24.128	63.165	257	26.872
P21281	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 - [VATB2_HUMAN]	21.33	14	11	11	25	1.010	25	4.861	63.038	511	56.465
Q6PKG0	La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 - [LARP1_HUMAN]	16.33	10	17	17	32	0.995	31	3.406	63.013	1096	123.434
P58546	Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2 - [MTPN_HUMAN]	33.9	2	4	4	20	1.000	17	5.617	62.782	118	12.887
B7Z855	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1 - [B7Z855_HUMAN]	17.85	12	17	17	28	1.000	28	13.900	62.650	1003	116.952
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]	16.19	6	9	10	33	1.000	28	5.236	62.510	556	63.071
B2RB52	cDNA, FLJ95314, highly similar to Homo sapiens transducin (beta)-like 2 (TBL2), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B2RB52_HUMAN]	27.29	10	13	13	25	1.000	25	10.160	62.430	447	49.796
B7Z4B2	cDNA FLJ56108, highly similar to Puromycin-sensitive aminopeptidase (EC 3.4.11.-) OS=Homo sapiens PE=2 SV=1 - [B7Z4B2_HUMAN]	13.45	14	11	11	23	1.000	23	14.391	62.411	825	92.807
B4DHX4	cDNA FLJ52902, highly similar to Rab GDP dissociation inhibitor alpha OS=Homo sapiens PE=2 SV=1 - [B4DHX4_HUMAN]	23.98	5	5	8	24	0.943	10	26.903	62.319	417	46.878
K7ES31	Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=1 SV=1 - [K7ES31_HUMAN]	33.58	8	4	4	23	1.000	21	29.204	62.241	137	15.865
C7FDR5	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [C7FDR5_HUMAN]	28.73	343	0	5	26				62.235	181	20.880
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	14.21	1	12	12	24	0.957	24	10.021	62.048	795	87.248
B4DT77	Annexin OS=Homo sapiens PE=2 SV=1 - [B4DT77_HUMAN]	30.36	9	10	10	23	1.000	21	2.962	62.016	336	37.781
A8K6I4	cDNA FLJ76877, highly similar to Homo sapiens superkiller viralicidic activity 2-like 2 (SKIV2L2), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6I4_HUMAN]	10.75	7	12	12	24	1.000	23	7.346	61.994	1042	117.823
Q7Z3U5	Putative uncharacterized protein DKFZp686L0869 OS=Homo sapiens GN=DKFZp686L0869 PE=2 SV=1 - [Q7Z3U5_HUMAN]	10.95	15	12	12	24	1.000	23	3.347	61.809	1242	142.228
A8K5W7	cDNA FLJ75180, highly similar to Homo sapiens mitochondrial isoleucine tRNA synthetase, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5W7_HUMAN]	14.89	2	13	14	23	1.000	21	12.135	61.787	940	105.873
B4E043	KH domain containing, RNA binding, signal transduction associated 1, isoform CRA_b OS=Homo sapiens GN=KHDRBS1 PE=2 SV=1 - [B4E043_HUMAN]	18.73	10	7	9	33	0.973	26	11.620	61.461	347	38.658
A0A087WXI0	Ras-related protein Rab-44 OS=Homo sapiens GN=RAB44 PE=4 SV=1 - [A0A087WXI0_HUMAN]	7.15	3	6	6	21	1.000	18	0.000	61.450	1021	110.782
P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2 - [IF5_HUMAN]	19.26	11	9	9	32	1.000	31	4.476	61.170	431	49.192
P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	38.1	7	3	3	25	1.000	24	0.000	61.081	84	9.455
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1 - [UBR4_HUMAN]	4.71	8	19	19	26	1.000	23	9.201	61.053	5183	573.476
Q0VGA5	SARS protein OS=Homo sapiens GN=SARS PE=2 SV=1 - [Q0VGA5_HUMAN]	12.52	4	6	7	23	1.000	18	17.807	60.717	511	58.370
E5KSX8	Mitochondrial transcription factor A OS=Homo sapiens PE=4 SV=1 - [E5KSX8_HUMAN]	44.31	6	13	13	31	1.070	30	16.768	60.660	246	29.092
P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN]	27.83	7	2	6	22	1.000	14	0.000	60.647	212	23.531
Q8IYB3	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2 - [SRRM1_HUMAN]	10.18	7	2	9	27	1.000	2	0.000	60.634	904	102.274
B0QYK0	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [B0QYK0_HUMAN]	7.28	4	4	4	25	1.000	23	2.832	60.611	618	64.889
P05204	Non-histone chromosomal protein HMG-17 OS=Homo sapiens GN=HMGN2 PE=1 SV=3 - [HMGN2_HUMAN]	44.44	1	5	6	29	0.988	28	9.776	60.559	90	9.387
O14929	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1 - [HAT1_HUMAN]	14.56	3	5	5	17	1.000	17	6.208	60.513	419	49.481
B4DXZ6	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 - [B4DXZ6_HUMAN]	16.28	11	3	10	18	1.007	5	30.984	60.486	608	68.285
Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN]	19.41	3	16	16	25	0.989	25	11.792	60.368	783	87.290
E9PCT1	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=3 - [E9PCT1_HUMAN]	9.02	5	1	8	27	1.000	2	0.000	60.196	820	93.380
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1 - [SGTA_HUMAN]	18.53	3	6	6	24	1.000	21	0.000	60.158	313	34.042
P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 - [UB2L3_HUMAN]	22.08	18	5	6	27	1.000	23	14.966	60.158	154	17.850
Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1 - [HM13_HUMAN]	12.47	2	5	5	23	1.008	23	12.096	60.143	377	41.462
D3DUJ0	AFG3 ATPase family gene 3-like 2 (Yeast), isoform CRA_a (Fragment) OS=Homo sapiens GN=AFG3L2 PE=3 SV=1 - [D3DUJ0_HUMAN]	14.89	6	13	13	24	1.000	23	18.688	60.043	759	84.392
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]	5.39	6	21	21	25	1.000	25	0.000	59.962	4544	504.276
A0A024RDH6	SEC31-like 1 (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=SEC31L1 PE=4 SV=1 - [A0A024RDH6_HUMAN]	9.14	19	10	11	23	1.000	22	7.792	59.958	1181	128.955
Q8TCU6	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein OS=Homo sapiens GN=PREX1 PE=1 SV=3 - [PREX1_HUMAN]	7.17	2	11	11	23	0.952	20	16.448	59.917	1659	186.085
A0A024R7L5	UPF1 regulator of nonsense transcripts homolog (Yeast), isoform CRA_b OS=Homo sapiens GN=UPF1 PE=4 SV=1 - [A0A024R7L5_HUMAN]	10.02	8	11	11	24	1.000	24	12.859	59.848	1118	122.958
Q15056	Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5 - [IF4H_HUMAN]	27.82	7	10	10	30	0.958	29	6.407	59.750	248	27.368
Q53GE7	Tetratricopeptide repeat domain 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GE7_HUMAN]	29.11	4	8	8	23	1.000	23	5.578	59.749	292	33.574
B1AHF3	NADH-cytochrome b5 reductase 3 membrane-bound form (Fragment) OS=Homo sapiens GN=CYB5R3 PE=1 SV=1 - [B1AHF3_HUMAN]	26.53	5	4	4	23	1.000	22	11.829	59.719	147	16.686
Q0PHV3	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [Q0PHV3_HUMAN]	27.07	441	0	5	24				59.583	181	20.894
B2R4A2	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens PE=2 SV=1 - [B2R4A2_HUMAN]	36.04	1	1	5	21	0.865	2	21.693	59.553	111	13.523
A0A024RAJ8	IQ motif containing GTPase activating protein 2, isoform CRA_b OS=Homo sapiens GN=IQGAP2 PE=4 SV=1 - [A0A024RAJ8_HUMAN]	7.94	13	8	14	26	1.000	11	24.080	59.495	1575	180.480
A0A024RDB2	Ras-GTPase activating protein SH3 domain-binding protein 2, isoform CRA_b OS=Homo sapiens GN=G3BP2 PE=4 SV=1 - [A0A024RDB2_HUMAN]	11.58	13	6	6	24	1.000	22	0.000	59.493	449	50.786
Q9NWH9	SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2 - [SLTM_HUMAN]	12.09	12	12	12	20	1.000	19	0.000	59.436	1034	117.079
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 - [PSD12_HUMAN]	22.81	3	10	10	25	1.000	25	5.424	59.245	456	52.871
B2R8W8	cDNA, FLJ94098, highly similar to Homo sapiens RAB3D, member RAS oncogene family (RAB3D), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8W8_HUMAN]	19.18	31	1	5	30	0.963	1		59.239	219	24.252
B4DM03	cDNA FLJ50574, highly similar to ATP-dependent RNA helicase DDX24 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DM03_HUMAN]	16.51	12	9	9	20	1.000	19	0.000	59.227	763	85.457
B4DJI8	cDNA FLJ59702, highly similar to NADPH--cytochrome P450 reductase (EC 1.6.2.4) OS=Homo sapiens PE=2 SV=1 - [B4DJI8_HUMAN]	19.72	3	1	13	33	0.479	1		59.103	573	64.485
P62306	Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1 - [RUXF_HUMAN]	24.42	1	3	3	23	1.000	18	0.000	59.072	86	9.719
H0YDD8	60S acidic ribosomal protein P2 (Fragment) OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [H0YDD8_HUMAN]	59.78	1	1	3	17	1.000	1		59.043	92	9.090
B7Z2C6	cDNA FLJ54515, highly similar to Rho-GTPase-activating protein 4 OS=Homo sapiens PE=2 SV=1 - [B7Z2C6_HUMAN]	14.73	15	13	13	21	1.000	20	13.656	58.967	923	102.219
B2RBP7	cDNA, FLJ95623, highly similar to Homo sapiens differentially expressed in FDCP 6 homolog (mouse) (DEF6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBP7_HUMA	16.16	9	11	11	23	1.000	23	8.338	58.834	631	73.880
O43747	AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=1 SV=5 - [AP1G1_HUMAN]	11.31	14	1	9	22	0.976	1		58.806	822	91.293
A0A087WZ13	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=4 SV=1 - [A0A087WZ13_HUMAN]	9.34	5	5	5	20	1.000	20	2.036	58.784	739	77.795
B4DUF8	cDNA FLJ52165, highly similar to Ubiquitin-conjugating enzyme E2 J1 (EC 6.3.2.19) OS=Homo sapiens PE=2 SV=1 - [B4DUF8_HUMAN]	28.71	2	7	7	17	1.000	17	16.701	58.767	303	33.291
O95336	6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2 - [6PGL_HUMAN]	27.52	4	6	6	24	0.991	24	25.490	58.733	258	27.530
Q00722	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 OS=Homo sapiens GN=PLCB2 PE=1 SV=2 - [PLCB2_HUMAN]	8.78	4	10	10	22	1.000	22	9.797	58.647	1185	133.939
E9PN17	ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=1 - [E9PN17_HUMAN]	31.58	2	2	2	24	1.002	24	20.789	58.586	76	8.447
B4DS79	cDNA FLJ56828, highly similar to Adapter-relatedprotein complex 1 beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DS79_HUMAN]	16.83	4	1	7	19	0.813	2	26.434	58.574	499	53.818
Q53FE8	cDNA FLJ36526 fis, clone TRACH2003347, highly similar to NSFL1 cofactor p47 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FE8_HUMAN]	40	8	12	12	21	1.000	21	2.853	58.504	370	40.547
O00422	Histone deacetylase complex subunit SAP18 OS=Homo sapiens GN=SAP18 PE=1 SV=1 - [SAP18_HUMAN]	37.91	5	8	8	24	1.000	24	10.980	58.380	153	17.550
Q709C8	Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1 - [VP13C_HUMAN]	4.74	4	19	19	26	0.970	26	5.695	58.378	3753	422.124
O00148	ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 - [DX39A_HUMAN]	22.72	11	4	10	23	1.036	6	5.357	58.289	427	49.098
E9ASQ6	Transitional endoplasmic reticulum ATPase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1370 PE=3 SV=1 - [E9ASQ6_LEIMU]	6.75	1	3	7	24	2.467	4	91.638	58.259	785	86.833
Q92804	TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1 - [RBP56_HUMAN]	22.13	7	6	8	26	1.010	15	11.582	58.233	592	61.793
B5BU61	Histone deacetylase OS=Homo sapiens GN=HDAC1 PE=2 SV=1 - [B5BU61_HUMAN]	12.86	7	7	8	31	0.986	28	13.215	58.230	482	55.041
Q5U000	Cathepsin Z OS=Homo sapiens PE=2 SV=1 - [Q5U000_HUMAN]	12.87	2	5	5	23	1.000	23	1.960	58.121	303	33.846
Q86U75	Dihydropyrimidinase-like 2 OS=Homo sapiens PE=2 SV=1 - [Q86U75_HUMAN]	15.67	17	2	8	24	1.000	3	0.000	58.077	619	66.975
B3KM36	cDNA FLJ10153 fis, clone HEMBA1003417, highly similar to BAG family molecular chaperone regulator 2 OS=Homo sapiens PE=2 SV=1 - [B3KM36_HUMAN]	27.96	4	6	6	23	1.013	23	8.627	57.908	211	23.697
P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2 - [UCRI_HUMAN]	25.18	2	8	8	24	1.000	23	11.981	57.797	274	29.649
E9APW3	Enolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1160 PE=3 SV=1 - [E9APW3_LEIMU]	24.24	1	7	7	18	4.547	17	237.728	57.774	429	46.116
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	22.94	9	2	7	21	1.020	6	10.555	57.260	340	37.307
Q5JRA6	Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3 PE=1 SV=1 - [MIA3_HUMAN]	7.39	1	14	14	21	1.000	20	5.853	57.237	1907	213.570
D3DPS3	Arginine/proline rich coiled-coil 1, isoform CRA_b OS=Homo sapiens GN=RPRC1 PE=4 SV=1 - [D3DPS3_HUMAN]	9.88	8	8	8	22	1.000	18	0.000	57.124	840	92.636
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	20.31	6	13	13	20	0.998	20	4.837	56.997	699	78.756
B4DIZ2	cDNA FLJ57995, moderately similar to Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19) OS=Homo sapiens PE=2 SV=1 - [B4DIZ2_HUMAN]	38.85	4	5	5	18	1.000	16	19.172	56.996	139	15.800
Q9HBR0	Putative sodium-coupled neutral amino acid transporter 10 OS=Homo sapiens GN=SLC38A10 PE=1 SV=2 - [S38AA_HUMAN]	12.78	1	11	14	24	1.000	17	19.307	56.972	1119	119.687
G8JLD5	Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 - [G8JLD5_HUMAN]	16.99	12	13	13	22	0.939	22	13.218	56.967	712	79.572
A8K9B9	cDNA FLJ77391, highly similar to Homo sapiens EH-domain containing 4 (EHD4), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9B9_HUMAN]	22	3	10	10	21	1.015	21	6.671	56.856	541	61.117
H7BZT4	Small ubiquitin-related modifier OS=Homo sapiens GN=SUMO2 PE=3 SV=1 - [H7BZT4_HUMAN]	23.16	3	1	2	21	1.000	5	0.000	56.854	95	10.832
E9ARS1	Putative heat shock protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1370 PE=3 SV=1 - [E9ARS1_LEIMU]	14.58	1	12	12	21	1.996	20	136.217	56.587	823	91.896
B4DS96	Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1 - [B4DS96_HUMAN]	17.17	11	1	9	22	1.000	1		56.569	565	63.791
B2R907	cDNA, FLJ94149, highly similar to Homo sapiens CD209 antigen (CD209), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R907_HUMAN]	26.73	15	5	5	23	1.000	23	0.000	56.536	404	45.747
P52888	Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2 - [THOP1_HUMAN]	15.53	10	12	12	23	0.934	22	16.437	56.512	689	78.789
Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2 - [TIM50_HUMAN]	14.45	13	6	6	19	1.000	19	0.381	56.386	353	39.622
D3DWL9	Cleavage and polyadenylation specific factor 1, 160kDa, isoform CRA_a OS=Homo sapiens GN=CPSF1 PE=4 SV=1 - [D3DWL9_HUMAN]	9.74	3	12	12	20	1.000	19	6.284	56.329	1365	151.890
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	23.08	5	11	11	22	0.999	22	4.487	56.326	494	53.767
Q96CP5	PMPCB protein (Fragment) OS=Homo sapiens GN=PMPCB PE=2 SV=2 - [Q96CP5_HUMAN]	21.25	11	9	10	21	1.000	18	16.809	56.321	480	53.475
P46778	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	25.62	4	6	6	29	0.999	29	11.199	56.219	160	18.553
P14550	Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3 - [AK1A1_HUMAN]	25.85	6	8	8	19	1.000	19	14.266	56.170	325	36.550
A8K1J3	cDNA FLJ78534, highly similar to Homo sapiens RAD23 homolog A (S. cerevisiae), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K1J3_HUMAN]	21.82	6	5	8	24	1.000	11	0.000	56.083	362	39.442
Q15428	Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 SV=2 - [SF3A2_HUMAN]	14.44	3	6	6	23	1.000	19	2.281	55.965	464	49.224
Q14151	Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1 - [SAFB2_HUMAN]	6.82	4	2	8	20	0.882	2	1.450	55.891	953	107.408
J3KMX1	Nuclear pore complex protein Nup88 (Fragment) OS=Homo sapiens GN=NUP88 PE=1 SV=1 - [J3KMX1_HUMAN]	11.78	6	8	8	16	1.000	16	12.602	55.884	696	78.830
D3YTB1	60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 - [D3YTB1_HUMAN]	36.84	3	6	6	26	1.000	26	1.783	55.874	133	15.607
Q5QPL9	RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=1 SV=1 - [Q5QPL9_HUMAN]	31.65	10	8	8	21	1.048	20	13.909	55.749	237	24.650
P14324	Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4 - [FPPS_HUMAN]	12.17	6	7	7	21	1.004	21	8.524	55.606	419	48.245
P47813	Eukaryotic translation initiation factor 1A, X-chromosomal OS=Homo sapiens GN=EIF1AX PE=1 SV=2 - [IF1AX_HUMAN]	37.5	4	8	8	23	1.000	23	12.007	55.535	144	16.450
Q16718	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3 - [NDUA5_HUMAN]	27.59	7	4	4	19	1.000	19	8.716	55.531	116	13.450
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 - [DNJB1_HUMAN]	28.24	9	10	11	24	1.000	19	8.974	55.493	340	38.020
E7ET15	U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=1 - [E7ET15_HUMAN]	11.87	10	12	12	23	0.953	23	8.914	55.369	1028	118.175
P20674	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2 - [COX5A_HUMAN]	25.33	4	4	5	25	1.000	21	5.693	55.353	150	16.752
Q9P107	GEM-interacting protein OS=Homo sapiens GN=GMIP PE=1 SV=2 - [GMIP_HUMAN]	13.4	3	10	10	19	1.000	16	4.076	55.311	970	106.617
O60869	Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1 - [EDF1_HUMAN]	53.38	1	12	12	23	1.000	23	19.857	55.101	148	16.359
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 - [PSMD4_HUMAN]	24.67	8	8	8	21	1.000	21	0.000	55.012	377	40.711
Q5F2F8	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP3CB PE=1 SV=1 - [Q5F2F8_HUMAN]	7.46	10	1	3	17	1.000	11	0.000	54.997	496	55.979
B4DWI8	cDNA FLJ57805, highly similar to Homo sapiens paraspeckle component 1 (PSPC1), transcript variant alpha, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DWI8_HUMAN	21.81	4	10	11	26	0.951	25	17.069	54.842	463	52.546
Q9H3K6	BolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1 - [BOLA2_HUMAN]	37.21	4	3	3	19	1.000	19	4.866	54.835	86	10.110
Q3ZCW5	SUCLG2 protein (Fragment) OS=Homo sapiens GN=SUCLG2 PE=2 SV=1 - [Q3ZCW5_HUMAN]	22.38	6	9	9	20	0.990	18	13.595	54.731	362	38.743
Q13347	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1 - [EIF3I_HUMAN]	29.85	4	9	9	22	1.000	22	2.726	54.657	325	36.479
Q9UBS4	DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1 - [DJB11_HUMAN]	21.23	3	7	7	18	1.000	18	15.545	54.615	358	40.489
Q8TBT6	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TBT6_HUMAN]	16.83	2	5	5	22	1.018	22	18.178	54.597	315	34.468
Q9H4A6	Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 - [GOLP3_HUMAN]	20.13	7	4	5	20	1.000	13	0.000	54.566	298	33.790
B4DM78	cDNA FLJ58199, highly similar to Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DM78_HUMAN]	16.11	2	1	8	16	1.000	3	0.000	54.497	565	62.995
F5H669	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) OS=Homo sapiens GN=CPSF7 PE=1 SV=1 - [F5H669_HUMAN]	22.46	15	7	7	20	0.995	20	1.163	54.398	374	41.241
O14828	Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 PE=1 SV=3 - [SCAM3_HUMAN]	24.5	2	7	7	19	1.000	17	8.916	54.311	347	38.262
P18085	ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 - [ARF4_HUMAN]	27.22	15	3	5	23	1.000	13	8.674	54.299	180	20.498
Q9H444	Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1 - [CHM4B_HUMAN]	28.57	3	7	7	17	1.000	17	4.298	54.204	224	24.935
A0A024R8V0	Septin 9, isoform CRA_a OS=Homo sapiens GN=SEPT9 PE=3 SV=1 - [A0A024R8V0_HUMAN]	17.25	23	8	8	21	1.000	21	9.249	54.157	568	63.594
Q53FH8	Sorting nexin 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FH8_HUMAN]	20.79	10	8	9	20	0.970	18	12.287	54.151	404	46.786
O96008	Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1 - [TOM40_HUMAN]	18.28	3	4	4	21	1.000	20	5.203	54.017	361	37.869
O95817	BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 - [BAG3_HUMAN]	16.7	3	6	6	18	1.000	15	2.404	53.902	575	61.557
B4DP97	cDNA FLJ52934, highly similar to Tyrosine-protein phosphatase non-receptortype substrate 1 OS=Homo sapiens PE=2 SV=1 - [B4DP97_HUMAN]	13.64	15	4	5	17	1.000	12	0.000	53.896	484	52.871
X5CMH5	TAP2 OS=Homo sapiens GN=TAP2 PE=3 SV=1 - [X5CMH5_HUMAN]	10.38	12	8	8	19	1.000	18	8.197	53.874	703	77.646
Q54A51	Basigin (Ok blood group), isoform CRA_a OS=Homo sapiens GN=hEMMPRIN PE=2 SV=1 - [Q54A51_HUMAN]	26.02	9	7	7	23	1.000	23	7.505	53.845	269	29.203
G3V1C3	Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=1 SV=1 - [G3V1C3_HUMAN]	22.94	6	13	13	24	1.000	23	3.587	53.682	510	57.525
Q9BPW0	Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP5C PE=2 SV=2 - [Q9BPW0_HUMAN]	21.07	11	11	11	20	0.955	20	7.390	53.681	484	55.061
Q9NX58	Cell growth-regulating nucleolar protein OS=Homo sapiens GN=LYAR PE=1 SV=2 - [LYAR_HUMAN]	28.76	2	1	10	20	2.243	1		53.668	379	43.588
Q99447	Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens GN=PCYT2 PE=1 SV=1 - [PCY2_HUMAN]	21.08	9	10	10	20	0.968	19	17.408	53.660	389	43.808
B3KQ25	Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 - [B3KQ25_HUMAN]	32.12	12	7	7	20	1.000	20	20.393	53.555	193	22.441
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	26.42	7	2	5	23	0.918	11	7.341	53.388	106	12.433
P20339	Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2 - [RAB5A_HUMAN]	38.6	7	4	7	18	1.000	11	7.334	53.313	215	23.644
Q5STZ8	ATP-binding cassette sub-family F member 1 (Fragment) OS=Homo sapiens GN=ABCF1 PE=1 SV=4 - [Q5STZ8_HUMAN]	12.35	3	2	6	16	1.000	7	0.000	53.301	340	38.353
Q96FJ2	Dynein light chain 2, cytoplasmic OS=Homo sapiens GN=DYNLL2 PE=1 SV=1 - [DYL2_HUMAN]	32.58	2	2	2	19	1.000	15	0.000	53.259	89	10.343
Q6FI81	Anamorsin OS=Homo sapiens GN=CIAPIN1 PE=1 SV=2 - [CPIN1_HUMAN]	29.81	9	9	9	23	0.972	23	11.705	53.143	312	33.561
Q9Y277	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 - [VDAC3_HUMAN]	23.67	6	6	7	22	0.979	18	11.357	53.091	283	30.639
Q9UI12	V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1 - [VATH_HUMAN]	18.84	11	8	8	17	0.997	17	1.370	53.005	483	55.847
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	41.86	6	4	4	28	0.974	28	9.453	52.988	86	10.105
A8K7D9	Importin subunit alpha OS=Homo sapiens PE=2 SV=1 - [A8K7D9_HUMAN]	17.2	6	7	7	16	0.975	16	6.670	52.974	529	57.798
E9PFN5	Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=1 - [E9PFN5_HUMAN]	26.32	5	4	4	22	1.000	20	0.000	52.973	190	21.693
F6IQB2	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1 - [F6IQB2_HUMAN]	15.47	248	0	4	21				52.956	349	39.099
A8K686	cDNA FLJ77316, highly similar to Homo sapiens interferon, gamma-inducible protein 30 (IFI30), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K686_HUMAN]	13.2	3	3	3	24	1.113	21	18.255	52.887	250	28.005
Q15155	Nodal modulator 1 OS=Homo sapiens GN=NOMO1 PE=1 SV=5 - [NOMO1_HUMAN]	11.87	11	14	14	22	1.000	22	16.720	52.777	1222	134.239
Q9UBB4	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1 - [ATX10_HUMAN]	25.68	6	11	11	18	1.000	17	10.271	52.751	475	53.455
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1 - [LETM1_HUMAN]	17.32	2	11	11	24	1.000	23	13.778	52.728	739	83.302
O43823	A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1 - [AKAP8_HUMAN]	10.12	5	5	5	17	1.000	15	0.000	52.626	692	76.061
Q53GG0	Epithelial protein lost in neoplasm beta variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GG0_HUMAN]	17.65	8	14	14	22	1.000	21	8.434	52.594	759	85.201
Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2 - [AIMP1_HUMAN]	19.87	3	7	7	24	1.000	24	5.508	52.507	312	34.331
Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	24.86	5	9	9	23	0.925	23	14.731	52.459	370	40.397
C9J0D1	Histone H2A OS=Homo sapiens GN=H2AFV PE=3 SV=1 - [C9J0D1_HUMAN]	21.31	5	1	3	24	0.940	2	8.643	52.419	122	13.155
P60981	Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 - [DEST_HUMAN]	34.55	3	6	7	21	1.000	14	5.930	52.391	165	18.493
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1 - [PSMD6_HUMAN]	18.77	5	9	9	19	1.000	19	18.281	52.325	389	45.502
Q96C01	Protein FAM136A OS=Homo sapiens GN=FAM136A PE=1 SV=1 - [F136A_HUMAN]	47.1	5	7	7	19	1.000	19	15.709	52.158	138	15.631
Q9Y262	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 - [EIF3L_HUMAN]	21.45	12	11	11	22	1.000	22	12.398	52.080	564	66.684
P23368	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1 - [MAOM_HUMAN]	13.7	6	8	8	20	1.000	20	9.107	52.044	584	65.402
Q53F35	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53F35_HUMAN]	12.4	17	4	5	24	1.000	16	18.564	51.976	250	28.655
E9ARM6	Putative rab7 GTP binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0890 PE=3 SV=1 - [E9ARM6_LEIMU]	8.52	4	1	2	17	2.369	1		51.685	223	24.117
E9AZ81	Glycosomal phosphoenolpyruvate carboxykinase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1805 PE=3 SV=1 - [E9AZ81_LEIMU	24.19	3	12	12	22	1.000	22	0.000	51.551	525	58.371
Q96G03	Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4 - [PGM2_HUMAN]	14.54	8	10	10	21	1.014	20	12.753	51.488	612	68.240
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	47.22	3	5	5	13	1.000	13	10.380	51.284	108	12.580
B2RBL3	cDNA, FLJ95575, highly similar to Homo sapiens endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBL3_HUMAN]	22.2	5	9	9	19	1.158	19	10.564	51.220	482	49.892
B4E324	cDNA FLJ60397, highly similar to Lysosomal protective protein (EC 3.4.16.5) OS=Homo sapiens PE=2 SV=1 - [B4E324_HUMAN]	11.04	11	5	6	22	1.000	18	11.730	51.212	480	54.235
G5EA31	Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=1 - [G5EA31_HUMAN]	7.2	4	7	7	19	1.000	18	7.484	51.205	1042	111.914
B2R6K4	cDNA, FLJ92996, highly similar to Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2I	19.12	16	3	6	19	0.952	8	9.304	51.186	340	37.277
C9JZI7	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=1 SV=1 - [C9JZI7_HUMAN]	18.35	17	5	6	23	1.000	16	11.214	51.169	278	31.820
Q5QNZ2	ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=1 - [Q5QNZ2_HUMAN]	33.33	5	8	8	19	1.000	18	7.298	51.096	195	22.261
P84085	ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 - [ARF5_HUMAN]	33.33	14	3	6	19	1.023	6	7.454	51.069	180	20.517
Q7Z4Y4	GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens GN=AK3 PE=2 SV=1 - [Q7Z4Y4_HUMAN]	35.68	4	8	8	19	1.000	18	6.656	51.007	227	25.605
Q12797	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3 - [ASPH_HUMAN]	11.35	11	7	7	24	1.000	23	7.430	50.982	758	85.809
Q16666	Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16 PE=1 SV=3 - [IF16_HUMAN]	12.99	5	8	8	20	1.000	20	5.329	50.968	785	88.199
B4E245	cDNA FLJ61538, highly similar to Switch-associated protein 70 OS=Homo sapiens PE=2 SV=1 - [B4E245_HUMAN]	17.05	5	11	11	19	1.000	18	13.946	50.935	516	61.268
Q96I24	Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2 - [FUBP3_HUMAN]	16.78	1	7	10	23	1.017	12	9.109	50.895	572	61.602
A0A024R4X1	Protein kinase C and casein kinase substrate in neurons 2, isoform CRA_a OS=Homo sapiens GN=PACSIN2 PE=4 SV=1 - [A0A024R4X1_HUMAN]	14.02	9	7	7	21	1.000	21	7.949	50.894	435	49.990
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 - [PP1A_HUMAN]	23.03	11	2	7	17	1.130	5	28.103	50.782	330	37.488

P55854	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2 - [SUMO3_HUMAN]	20.39	4	1	2	19	0.882	3	1.360	50.774	103	11.630
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1 - [KAP0_HUMAN]	21.78	23	9	9	17	0.978	16	10.919	50.763	381	42.955
H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment) OS=Homo sapiens GN=GSPT1 PE=1 SV=1 - [H3BR35_HUMAN]	22.11	8	12	12	23	1.000	23	12.749	50.651	475	52.909
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]	9.77	6	15	15	30	1.000	30	10.975	50.545	1474	163.188
Q13617	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2 - [CUL2_HUMAN]	10.07	4	7	7	22	1.000	20	10.364	50.478	745	86.927
S4R456	40S ribosomal protein S15 (Fragment) OS=Homo sapiens GN=RPS15 PE=1 SV=1 - [S4R456_HUMAN]	29.41	7	3	3	43	1.000	43	21.532	50.393	68	8.021
P52948	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 - [NUP98_HUMAN]	7.76	10	14	14	20	0.959	20	11.475	50.386	1817	197.457
O75400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 - [PR40A_HUMAN]	9.3	6	2	9	17	0.895	4	6.008	50.263	957	108.737
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 - [PSDE_HUMAN]	16.13	5	7	7	19	1.000	18	18.917	50.172	310	34.555
B2RAH7	cDNA, FLJ94921, highly similar to Homo sapiens prolyl endopeptidase (PREP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAH7_HUMAN]	14.79	3	10	10	22	1.000	22	9.600	50.157	710	80.682
Q13283	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 - [G3BP1_HUMAN]	25.32	11	8	8	23	1.000	22	1.086	50.107	466	52.132
B4DTU7	10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens PE=2 SV=1 - [B4DTU7_HUMAN]	13.76	14	11	11	19	1.000	19	9.609	50.084	923	101.651
Q96JH7	Deubiquitinating protein VCIP135 OS=Homo sapiens GN=VCPIP1 PE=1 SV=2 - [VCIP1_HUMAN]	12.85	2	13	13	20	1.000	19	0.000	50.042	1222	134.236
D6REQ6	Ribonuclease T2 OS=Homo sapiens GN=RNASET2 PE=1 SV=1 - [D6REQ6_HUMAN]	23.39	9	5	5	20	1.000	20	8.434	50.040	218	25.293
B3KQF0	cDNA FLJ90354 fis, clone NT2RP2003390, highly similar to Translocation protein SEC63 homolog OS=Homo sapiens PE=2 SV=1 - [B3KQF0_HUMAN]	10.39	5	7	7	15	1.000	15	2.721	50.006	760	87.944
O14776	Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=2 - [TCRG1_HUMAN]	10.75	4	12	13	25	1.000	21	0.000	49.935	1098	123.823
Q13217	DnaJ homolog subfamily C member 3 OS=Homo sapiens GN=DNAJC3 PE=1 SV=1 - [DNJC3_HUMAN]	18.06	7	10	11	21	1.069	18	26.971	49.772	504	57.544
K7EMH1	60S ribosomal protein L22 (Fragment) OS=Homo sapiens GN=RPL22 PE=1 SV=1 - [K7EMH1_HUMAN]	33.71	8	3	3	19	1.000	18	14.687	49.701	89	10.416
P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	21.39	4	6	7	22	1.000	11	22.351	49.660	346	36.903
B2R6A3	cDNA, FLJ92860, highly similar to Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1 (SLC9A3R1), mRNA OS=Homo sapiens PE	23.46	5	7	7	17	1.000	14	2.341	49.559	358	38.875
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1 - [NDUS3_HUMAN]	32.58	6	9	9	30	0.993	30	3.774	49.440	264	30.223
P05771	Protein kinase C beta type OS=Homo sapiens GN=PRKCB PE=1 SV=4 - [KPCB_HUMAN]	9.99	13	5	8	20	0.983	10	13.638	49.420	671	76.819
Q9UPN1	Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CC PE=3 SV=1 - [Q9UPN1_HUMAN]	22.11	12	1	6	16	0.889	4	17.865	49.392	294	33.752
D9HTE9	Plasma membrane citrate carrier OS=Homo sapiens GN=SLC25A1 PE=2 SV=1 - [D9HTE9_HUMAN]	22.64	4	8	8	23	1.000	23	5.890	49.357	318	35.030
E9PFH4	Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=1 - [E9PFH4_HUMAN]	14.47	6	10	10	19	1.000	19	4.116	49.338	857	96.607
B4DKY1	cDNA FLJ59563, highly similar to Cysteinyl-tRNA synthetase (EC 6.1.1.16) OS=Homo sapiens PE=2 SV=1 - [B4DKY1_HUMAN]	17.05	11	13	13	20	0.987	20	12.688	49.232	739	84.225
E7EQV9	Ribosomal protein L15 (Fragment) OS=Homo sapiens GN=RPL15 PE=1 SV=1 - [E7EQV9_HUMAN]	38.51	9	7	7	25	1.000	24	13.754	49.169	174	20.497
Q9NR12	PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1 - [PDLI7_HUMAN]	23.41	5	10	11	23	0.919	19	12.559	49.015	457	49.813
F8VRH0	Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=1 SV=2 - [F8VRH0_HUMAN]	11.61	2	0	4	18				49.002	310	32.015
E7EV93	Pericentriolar material 1 protein (Fragment) OS=Homo sapiens GN=PCM1 PE=1 SV=1 - [E7EV93_HUMAN]	11.35	3	1	10	20	1.058	2	8.970	48.975	749	84.016
B4DT82	cDNA FLJ50662, highly similar to Solute carrier family 2, facilitated glucosetransporter member 5 OS=Homo sapiens PE=2 SV=1 - [B4DT82_HUMAN]	12.44	8	8	8	23	1.009	22	14.237	48.936	386	42.262
O60884	DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1 - [DNJA2_HUMAN]	19.66	5	10	10	23	0.939	23	12.688	48.763	412	45.717
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	20.8	5	9	9	19	1.000	19	15.006	48.755	423	46.290
A8K5T7	cDNA FLJ75365, highly similar to Homo sapiens SUGT1B (SUGT1) mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5T7_HUMAN]	28.77	4	3	11	21	0.843	7	19.324	48.642	365	41.026
Q9Y3R5	Protein dopey-2 OS=Homo sapiens GN=DOPEY2 PE=1 SV=5 - [DOP2_HUMAN]	3.22	1	8	8	17	1.000	17	0.000	48.620	2298	258.068
P17096	High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3 - [HMGA1_HUMAN]	38.32	7	4	4	23	1.009	23	9.670	48.581	107	11.669
E9AMU9	Elongation factor-1 gamma OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0970 PE=4 SV=1 - [E9AMU9_LEIMU]	12.38	2	5	6	20	1.000	15	0.000	48.558	404	46.172
Q5VTR2	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2 - [BRE1A_HUMAN]	13.03	6	10	13	19	1.000	15	18.307	48.538	975	113.592
S4R418	Bridging integrator 2 (Fragment) OS=Homo sapiens GN=BIN2 PE=1 SV=2 - [S4R418_HUMAN]	20.15	9	8	9	20	1.000	17	0.000	48.517	536	58.988
Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 - [RBM14_HUMAN]	20.48	6	12	12	22	0.969	22	14.257	48.435	669	69.449
D6RGI3	Septin 11, isoform CRA_b OS=Homo sapiens GN=SEPT11 PE=1 SV=1 - [D6RGI3_HUMAN]	15.29	10	2	6	21	0.944	6	8.582	48.273	425	48.975
B2R4D5	Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens PE=2 SV=1 - [B2R4D5_HUMAN]	17.42	4	4	4	32	1.000	31	13.033	48.221	178	20.507
E9PL01	Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=1 - [E9PL01_HUMAN]	33.76	7	5	5	20	1.000	18	6.290	48.201	157	17.017
Q9NVP1	ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DDX18_HUMAN]	9.1	3	8	8	18	1.000	18	6.927	48.055	670	75.359
B4DJK9	Perilipin OS=Homo sapiens PE=2 SV=1 - [B4DJK9_HUMAN]	26.41	6	11	11	17	1.014	17	5.654	47.997	409	45.107
B2R4V4	cDNA, FLJ92232, highly similar to Homo sapiens barrier to autointegration factor 1 (BANF1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R4V4_HUMAN]	24.72	6	4	4	20	1.000	19	5.659	47.961	89	10.010
O00483	Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 - [NDUA4_HUMAN]	40.74	1	4	4	22	0.905	22	14.927	47.899	81	9.364
Q14258	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 - [TRI25_HUMAN]	11.9	10	6	7	15	0.980	14	10.979	47.880	630	70.928
P08567	Pleckstrin OS=Homo sapiens GN=PLEK PE=1 SV=3 - [PLEK_HUMAN]	11.43	2	4	4	15	1.000	13	6.904	47.747	350	40.099
Q9BY44	Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=1 SV=3 - [EIF2A_HUMAN]	18.97	5	10	10	22	0.983	22	10.118	47.731	585	64.949
O43488	Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3 - [ARK72_HUMAN]	21.17	5	7	8	22	1.000	17	15.668	47.724	359	39.564
O43615	Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2 - [TIM44_HUMAN]	27.21	8	13	13	20	0.983	20	16.669	47.703	452	51.323
B3KX23	cDNA FLJ44516 fis, clone UTERU3002600, highly similar to Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (DDX42), transcript variant 2, mRNA OS=Homo	19.29	7	12	13	20	0.975	18	4.029	47.642	674	73.236
Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205_HUMAN]	7.01	6	13	13	18	0.952	18	13.961	47.608	2012	227.776
P04181	Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 - [OAT_HUMAN]	17.54	2	6	7	19	1.000	18	15.808	47.593	439	48.504
Q08378	Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2 - [GOGA3_HUMAN]	10.21	1	14	14	18	0.991	17	14.506	47.583	1498	167.252
Q7Z4V5	Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2 PE=1 SV=1 - [HDGR2_HUMAN]	13.41	10	9	10	20	1.005	18	15.672	47.462	671	74.272
Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 - [ANKH1_HUMAN]	5.66	17	8	12	20	1.000	11	11.945	47.437	2542	269.291
V9HW35	Epididymis secretory protein Li 55 OS=Homo sapiens GN=HEL-S-55 PE=2 SV=1 - [V9HW35_HUMAN]	29.63	2	4	4	19	1.000	19	6.540	47.279	162	17.020
Q96C86	m7GpppX diphosphatase OS=Homo sapiens GN=DCPS PE=1 SV=2 - [DCPS_HUMAN]	18.99	2	5	5	18	1.000	17	5.569	47.264	337	38.585
B2RDR4	cDNA, FLJ96732, highly similar to Homo sapiens testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDR4_	25.65	9	10	10	16	0.964	16	14.714	47.244	421	47.934
P09661	U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 - [RU2A_HUMAN]	18.82	7	6	6	18	0.993	17	10.305	47.137	255	28.398
G3V256	Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 - [G3V256_HUMAN]	15.21	14	9	9	18	1.000	17	10.498	47.133	605	68.307
Q9NW64	Pre-mRNA-splicing factor RBM22 OS=Homo sapiens GN=RBM22 PE=1 SV=1 - [RBM22_HUMAN]	17.62	3	10	10	19	1.000	19	8.554	47.130	420	46.865
B2RE11	cDNA, FLJ96865 OS=Homo sapiens PE=2 SV=1 - [B2RE11_HUMAN]	41.48	5	8	8	23	1.000	21	21.580	47.114	176	18.418
Q8TAT6	Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3 - [NPL4_HUMAN]	15.3	6	9	9	17	0.998	16	10.372	47.096	608	68.077
E9PB90	Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=1 - [E9PB90_HUMAN]	9.56	8	7	8	17	1.048	15	7.028	47.020	889	98.909
P25774	Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3 - [CATS_HUMAN]	15.71	3	5	5	19	1.046	19	11.242	46.914	331	37.471
E9PKG1	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 - [E9PKG1_HUMAN]	16.62	12	6	6	17	1.000	14	12.344	46.792	325	37.685
B2RB23	cDNA, FLJ95265, highly similar to Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (ACAA2), nuclear gene encoding i	28.97	7	10	10	19	1.021	17	7.281	46.748	397	41.983
H0Y9V9	60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [H0Y9V9_HUMAN]	22.22	8	4	5	23	1.000	21	6.277	46.693	189	21.556
P29218	Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1 PE=1 SV=1 - [IMPA1_HUMAN]	26.71	9	7	7	16	0.993	16	13.821	46.671	277	30.169
A6H8X9	Centrosomal protein 170kDa OS=Homo sapiens GN=CEP170 PE=2 SV=1 - [A6H8X9_HUMAN]	8.49	15	11	11	18	0.897	17	19.457	46.493	1460	161.340
Q9Y263	Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2 - [PLAP_HUMAN]	12.33	4	9	10	18	1.080	17	28.940	46.488	795	87.101
Q9H2G2	STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 - [SLK_HUMAN]	11.42	2	13	15	22	0.905	17	39.721	46.364	1235	142.607
Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	23.19	5	6	6	16	1.000	15	8.607	46.343	276	30.589
Q5UIP0	Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN]	4.13	4	10	10	16	0.996	16	14.747	46.336	2472	274.294
P55145	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3 - [MANF_HUMAN]	28.02	2	6	6	18	1.000	17	19.135	46.229	182	20.687
H0YK42	Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=1 - [H0YK42_HUMAN]	16.12	5	4	5	16	0.998	10	21.254	46.148	304	35.571
A0A075B793	GRIP1-associated protein 1 OS=Homo sapiens GN=GRIPAP1 PE=1 SV=2 - [A0A075B793_HUMAN]	11.85	8	9	9	15	1.000	15	10.769	46.120	810	92.697
B4DFV1	Protein kinase C OS=Homo sapiens PE=2 SV=1 - [B4DFV1_HUMAN]	19.4	11	12	13	19	1.000	17	17.529	46.096	603	69.112
P80217	Interferon-induced 35 kDa protein OS=Homo sapiens GN=IFI35 PE=1 SV=5 - [IN35_HUMAN]	19.23	1	6	6	20	1.001	19	7.358	46.014	286	31.527
Q9UII2	ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1 - [ATIF1_HUMAN]	30.19	2	4	4	20	1.000	19	3.779	45.965	106	12.241
B4DH29	DNA-directed RNA polymerase OS=Homo sapiens PE=2 SV=1 - [B4DH29_HUMAN]	9.55	7	10	10	19	1.000	19	7.303	45.925	1099	125.139
Q8TEM1	Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3 - [PO210_HUMAN]	7.37	1	14	14	23	1.000	23	18.080	45.905	1887	204.983
Q9UHL4	Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3 - [DPP2_HUMAN]	17.07	8	7	7	17	1.023	16	5.233	45.858	492	54.307
P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	18.27	5	9	15	20	1.000	11	2.026	45.831	843	96.635
A0A024RAR8	Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator, isoform CRA_a OS=Homo sapiens GN=ARTS-1 PE=4 SV=1 - [A0A024RAR8_HUMAN]	9.14	8	9	9	18	1.013	16	21.762	45.775	941	107.136
Q13243	Serine/arginine-rich splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=1 SV=1 - [SRSF5_HUMAN]	15.44	7	3	4	17	1.014	14	10.574	45.768	272	31.245
B4DP99	cDNA FLJ51496, highly similar to Tyrosine-protein kinase CSK (EC 2.7.10.2) OS=Homo sapiens PE=2 SV=1 - [B4DP99_HUMAN]	21.05	8	8	8	17	1.000	17	7.843	45.763	399	44.708
Q9H6Z4	Ran-binding protein 3 OS=Homo sapiens GN=RANBP3 PE=1 SV=1 - [RANB3_HUMAN]	21.87	14	10	10	17	1.000	16	2.659	45.757	567	60.173
A8K586	AP-3 complex subunit beta OS=Homo sapiens PE=2 SV=1 - [A8K586_HUMAN]	11.52	8	15	15	20	1.027	20	17.028	45.689	1094	121.214
A0A024R3R5	Lamin B receptor, isoform CRA_a OS=Homo sapiens GN=LBR PE=4 SV=1 - [A0A024R3R5_HUMAN]	15.93	5	14	14	28	0.993	28	9.247	45.594	615	70.685
P52306	Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3 - [GDS1_HUMAN]	17.96	9	8	9	16	1.036	12	14.100	45.568	607	66.275
R4GN98	Protein S100 (Fragment) OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [R4GN98_HUMAN]	25.88	2	1	3	21	0.226	11	15.880	45.539	85	9.675
B4E106	cDNA FLJ53399, highly similar to Monocarboxylate transporter 1 OS=Homo sapiens PE=2 SV=1 - [B4E106_HUMAN]	11.25	6	6	6	17	1.000	17	4.236	45.471	480	51.845
P36543	V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1 - [VATE1_HUMAN]	32.74	3	8	8	17	1.000	17	12.992	45.416	226	26.129
E9AN39	Isocitrate dehydrogenase [NADP] OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0290 PE=3 SV=1 - [E9AN39_LEIMU]	24.6	1	8	11	20	1.060	10	15.022	45.385	435	48.372
O75348	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 - [VATG1_HUMAN]	21.19	1	3	3	20	1.000	20	1.613	45.344	118	13.749
E9ATH3	Adenosylhomocysteinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3910 PE=3 SV=1 - [E9ATH3_LEIMU]	19.45	1	6	8	17	3.407	9	325.884	45.333	437	47.841
D6R9Z7	Cytochrome c oxidase subunit 7C, mitochondrial OS=Homo sapiens GN=COX7C PE=1 SV=1 - [D6R9Z7_HUMAN]	32.14	3	2	2	19	1.014	18	6.264	45.309	56	6.378
C9JFE4	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=2 - [C9JFE4_HUMAN]	16.56	9	7	7	16	1.000	15	16.310	45.206	471	53.338
P06730	Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2 - [IF4E_HUMAN]	30.41	7	6	6	18	1.000	18	3.413	45.157	217	25.082
K7EP07	Tubulin-folding cofactor B (Fragment) OS=Homo sapiens GN=TBCB PE=1 SV=3 - [K7EP07_HUMAN]	38.24	6	6	6	15	1.000	14	13.280	45.156	170	19.296
Q8WY22	BRI3-binding protein OS=Homo sapiens GN=BRI3BP PE=1 SV=1 - [BRI3B_HUMAN]	9.16	1	1	2	14	1.000	11	1.897	45.149	251	27.818
B7Z2K7	cDNA FLJ53289, highly similar to Ribosomal protein S6 kinase alpha-1 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B7Z2K7_HUMAN]	15.82	23	5	10	16	1.000	9	29.565	45.135	594	67.337
Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]	16.62	4	11	11	24	1.000	23	6.721	45.060	740	82.380
Q9BR63	FARSB protein (Fragment) OS=Homo sapiens GN=FARSB PE=2 SV=2 - [Q9BR63_HUMAN]	15.56	6	10	10	19	1.011	17	12.378	45.049	585	65.659
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	24.4	1	13	13	21	0.951	21	14.562	45.039	418	47.337
Q96HI4	Glycylpeptide N-tetradecanoyltransferase (Fragment) OS=Homo sapiens GN=NMT1 PE=2 SV=2 - [Q96HI4_HUMAN]	18.42	6	9	9	19	1.000	18	12.046	45.023	494	56.568
B3KSZ1	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1 - [B3KSZ1_HUMAN]	24.42	8	5	6	21	0.931	13	18.703	44.972	217	24.077
O60234	Glia maturation factor gamma OS=Homo sapiens GN=GMFG PE=1 SV=1 - [GMFG_HUMAN]	22.54	7	1	3	16	0.998	6	1.499	44.915	142	16.790
A8QI98	DIS3 OS=Homo sapiens PE=2 SV=1 - [A8QI98_HUMAN]	6.89	6	8	8	15	1.000	15	0.703	44.909	958	108.989
A0A087WVM4	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=4 SV=1 - [A0A087WVM4_HUMAN]	10.08	9	8	9	19	1.000	17	3.387	44.878	913	99.249
B3KVV1	cDNA FLJ41563 fis, clone CTONG1000341, highly similar to THROMBOMODULIN OS=Homo sapiens PE=2 SV=1 - [B3KVV1_HUMAN]	8.8	2	4	4	12	1.000	12	3.954	44.822	557	58.633
Q9Y5A9	YTH domain-containing family protein 2 OS=Homo sapiens GN=YTHDF2 PE=1 SV=2 - [YTHD2_HUMAN]	11.92	4	6	8	16	0.975	9	7.988	44.774	579	62.296
P14854	Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2 - [CX6B1_HUMAN]	40.7	2	4	4	21	1.000	21	0.000	44.647	86	10.186
B7Z2X0	cDNA FLJ60543, highly similar to Active breakpoint cluster region-related protein OS=Homo sapiens PE=2 SV=1 - [B7Z2X0_HUMAN]	10.53	12	10	10	19	1.000	19	10.472	44.601	769	88.019
Q14571	Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2 - [ITPR2_HUMAN]	2.3	2	3	8	20	1.188	4	28.788	44.598	2701	307.867
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 - [UBP5_HUMAN]	14.92	2	10	10	22	1.000	22	10.208	44.547	858	95.725
B4E0K9	Alpha-mannosidase OS=Homo sapiens PE=2 SV=1 - [B4E0K9_HUMAN]	13.26	9	12	12	18	1.000	17	12.846	44.542	950	107.398
H3BU16	Hematological and neurological-expressed 1-like protein (Fragment) OS=Homo sapiens GN=HN1L PE=1 SV=1 - [H3BU16_HUMAN]	43.71	8	6	7	17	0.913	16	13.557	44.511	167	17.593
F5H5P4	Proto-oncogene vav OS=Homo sapiens GN=VAV1 PE=1 SV=2 - [F5H5P4_HUMAN]	14.58	4	13	13	19	0.963	19	11.290	44.484	789	91.672
P52298	Nuclear cap-binding protein subunit 2 OS=Homo sapiens GN=NCBP2 PE=1 SV=1 - [NCBP2_HUMAN]	30.13	7	6	6	17	1.000	15	1.441	44.451	156	17.990
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]	16.94	8	9	9	21	1.000	21	9.427	44.449	484	54.854
P13693	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 - [TCTP_HUMAN]	37.21	12	7	7	19	1.000	18	6.111	44.311	172	19.583
Q5HYL6	Putative uncharacterized protein DKFZp686E1899 OS=Homo sapiens GN=DKFZp686E1899 PE=2 SV=1 - [Q5HYL6_HUMAN]	21.02	4	6	8	17	1.000	13	3.457	44.158	352	39.530
P18031	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 - [PTN1_HUMAN]	17.7	2	7	7	15	1.000	15	8.436	44.128	435	49.935
B5BU32	Thymidine kinase OS=Homo sapiens GN=TK1 PE=2 SV=1 - [B5BU32_HUMAN]	21.37	7	5	5	16	1.000	15	12.837	44.102	234	25.380
P61927	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 - [RL37_HUMAN]	42.27	4	7	7	24	0.963	24	9.294	44.077	97	11.071
A0A024R8Q1	Glucosidase, alpha acid (Pompe disease, glycogen storage disease type II), isoform CRA_a OS=Homo sapiens GN=GAA PE=3 SV=1 - [A0A024R8Q1_HUMAN]	8.51	5	3	7	16	1.027	4	13.021	44.071	952	105.271
P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 - [PP2AA_HUMAN]	30.42	13	1	8	17	0.884	2	6.738	44.048	309	35.571
B4DKU9	Coronin OS=Homo sapiens PE=2 SV=1 - [B4DKU9_HUMAN]	7.62	12	7	7	15	0.996	15	16.013	44.041	906	98.386
O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	9.61	2	7	7	14	0.978	14	10.367	44.026	791	88.836
Q7Z518	NADH dehydrogenase OS=Homo sapiens PE=2 SV=1 - [Q7Z518_HUMAN]	23.16	16	10	10	19	1.000	17	6.026	43.976	354	40.651
J7I296	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [J7I296_HUMAN]	18.78	214	0	4	19				43.919	181	20.825
A0MZ66	Shootin-1 OS=Homo sapiens GN=KIAA1598 PE=1 SV=4 - [SHOT1_HUMAN]	16.01	3	11	12	19	1.000	16	12.626	43.909	631	71.596
H3BP71	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=2 - [H3BP71_HUMAN]	9.99	15	8	11	16	0.876	13	10.754	43.906	961	108.982
P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]	20.8	8	11	11	26	1.000	25	10.807	43.731	375	42.648
B7Z6F7	cDNA FLJ61705, highly similar to Symplekin OS=Homo sapiens PE=2 SV=1 - [B7Z6F7_HUMAN]	8.87	5	12	12	20	1.000	20	13.392	43.702	1274	141.043
A6H8Y5	Nibrin OS=Homo sapiens GN=NBN PE=2 SV=1 - [A6H8Y5_HUMAN]	7.82	10	5	6	19	1.000	13	0.000	43.679	754	84.921
Q14XT3	Cytochrome oxidase subunit II (Fragment) OS=Homo sapiens PE=4 SV=1 - [Q14XT3_HUMAN]	19.67	288	2	3	20	1.030	5	4.338	43.663	122	13.729
G5E9L0	ADP-ribosylation factor GTPase-activating protein 2 OS=Homo sapiens GN=ARFGAP2 PE=1 SV=2 - [G5E9L0_HUMAN]	17.24	18	9	9	16	0.920	16	15.794	43.638	493	53.444
O60493	Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1 SV=3 - [SNX3_HUMAN]	27.16	1	4	5	17	0.942	15	8.925	43.563	162	18.751
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 - [HPRT_HUMAN]	17.43	2	3	3	15	1.000	15	10.459	43.506	218	24.564
Q7Z7H5	Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens GN=TMED4 PE=1 SV=1 - [TMED4_HUMAN]	20.7	3	4	6	19	1.025	11	3.685	43.506	227	25.926
A8K4W7	cDNA FLJ76284, highly similar to Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4W7_HUMA	23.42	6	6	7	17	0.966	16	7.919	43.389	333	35.026
A8K607	cDNA FLJ76855, highly similar to Homo sapiens exportin 7 (XPO7), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K607_HUMAN]	7.27	6	8	8	16	1.000	15	5.879	43.282	1087	123.847
D3JTA7	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [D3JTA7_HUMAN]	14.92	187	0	3	18				43.240	181	21.079
M0QZR4	Rho guanine nucleotide exchange factor 1 OS=Homo sapiens GN=ARHGEF1 PE=1 SV=1 - [M0QZR4_HUMAN]	12.6	10	12	12	18	0.927	18	21.393	43.227	968	108.257
Q9UHV9	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1 - [PFD2_HUMAN]	44.16	1	7	7	15	0.831	14	17.440	43.217	154	16.638
H3BQB1	Adenine phosphoribosyltransferase (Fragment) OS=Homo sapiens GN=APRT PE=1 SV=1 - [H3BQB1_HUMAN]	20.37	5	4	4	19	1.000	19	9.609	43.122	162	17.550
Q9GZU8	Protein FAM192A OS=Homo sapiens GN=FAM192A PE=1 SV=1 - [F192A_HUMAN]	28.74	22	7	8	18	1.000	16	0.000	43.103	254	28.895
E9PG73	Peptidyl-prolyl cis-trans isomerase G OS=Homo sapiens GN=PPIG PE=1 SV=1 - [E9PG73_HUMAN]	9.34	8	10	10	18	1.000	15	4.113	43.072	739	87.036
P61020	Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1 - [RAB5B_HUMAN]	26.05	6	2	5	16	1.000	9	0.000	42.877	215	23.692
A0A087X1K9	Acyl-protein thioesterase 1 OS=Homo sapiens GN=LYPLA1 PE=4 SV=1 - [A0A087X1K9_HUMAN]	27.71	7	5	5	16	0.974	16	17.017	42.801	166	17.969
U3KQE2	Calpain small subunit 1 (Fragment) OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 - [U3KQE2_HUMAN]	23.6	8	3	3	22	1.000	17	0.541	42.793	161	18.434
Q10713	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens GN=PMPCA PE=1 SV=2 - [MPPA_HUMAN]	19.43	3	9	10	17	0.928	16	11.859	42.760	525	58.216
B3KTD5	cDNA FLJ38083 fis, clone CTONG2016408, highly similar to UBX domain-containing protein 2 OS=Homo sapiens PE=2 SV=1 - [B3KTD5_HUMAN]	16.42	3	5	5	14	1.000	14	5.793	42.738	274	31.258
A8K3F6	cDNA FLJ77654, highly similar to Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K	15.29	7	1	5	16	1.017	2	11.507	42.732	340	37.557
H0YDD4	Acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Homo sapiens GN=DLAT PE=1 SV=1 - [H0YDD4_HUMAN]	16.91	9	8	8	19	1.000	19	11.406	42.700	479	51.169
P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	33.67	1	3	3	15	1.000	14	5.518	42.689	98	11.133
Q9NR31	GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 - [SAR1A_HUMAN]	21.21	9	3	5	16	1.072	10	20.228	42.678	198	22.353
B2RE46	cDNA, FLJ96923, highly similar to Homo sapiens ribophorin II (RPN2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RE46_HUMAN]	7.45	6	4	4	14	1.030	14	8.023	42.606	631	69.291
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5 - [PP6R1_HUMAN]	4.54	3	3	3	17	1.000	15	0.000	42.570	881	96.664
Q9GZT9	Egl nine homolog 1 OS=Homo sapiens GN=EGLN1 PE=1 SV=1 - [EGLN1_HUMAN]	16.9	8	1	6	14	1.214	2	28.618	42.544	426	45.992
A0A087X0K1	Calcium-binding protein 39 OS=Homo sapiens GN=CAB39 PE=4 SV=1 - [A0A087X0K1_HUMAN]	16.52	4	7	7	15	0.913	15	13.495	42.535	339	39.428
P22059	Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1 - [OSBP1_HUMAN]	10.04	2	8	8	16	1.000	15	15.973	42.496	807	89.365
R4RYZ7	Hypoxia-inducible factor prolyl hydroxylase 2 OS=Homo sapiens GN=EGLN1 PE=4 SV=1 - [R4RYZ7_HUMAN]	16.9	9	1	6	13	0.969	1		42.495	426	45.976
Q14677	Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 PE=1 SV=1 - [EPN4_HUMAN]	14.24	2	9	9	16	0.965	16	17.640	42.404	625	68.216
Q9BTC0	Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5 - [DIDO1_HUMAN]	6.96	9	14	14	22	1.000	19	1.287	42.389	2240	243.723
E9B6L3	6-phosphogluconate dehydrogenase, decarboxylating OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3340 PE=3 SV=1 - [E9B6L3_LEIMU]	14.2	1	8	8	17	1.051	15	43.314	42.386	479	52.135
A5YKK6	CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2 - [CNOT1_HUMAN]	5.22	11	12	12	19	1.000	18	11.879	42.352	2376	266.768
X5M224	MHC class I antigen OS=Homo sapiens GN=HLA-C PE=3 SV=1 - [X5M224_HUMAN]	10.66	73	1	2	10	1.000	5	9.768	42.304	366	41.002
E9AMI1	Stress-induced protein sti1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_1110 PE=4 SV=1 - [E9AMI1_LEIMU]	17.61	1	8	8	14	1.506	13	66.782	42.266	545	62.056
B4DDH8	cDNA FLJ55184, highly similar to Homo sapiens leukocyte receptor cluster (LRC) member 4 (LENG4), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DDH8_HUMAN]	13.44	6	5	5	16	1.000	16	7.385	42.235	454	50.530
Q9BVG4	Protein PBDC1 OS=Homo sapiens GN=PBDC1 PE=1 SV=1 - [PBDC1_HUMAN]	24.89	3	6	6	13	1.000	13	14.552	42.231	233	26.041
B4DLT2	cDNA FLJ56637, highly similar to Nuclear pore complex protein Nup155 OS=Homo sapiens PE=2 SV=1 - [B4DLT2_HUMAN]	8.87	4	10	10	16	1.000	16	0.000	42.168	1353	151.137
A0A024R5L7	Phosphatidylinositol binding clathrin assembly protein, isoform CRA_c OS=Homo sapiens GN=PICALM PE=4 SV=1 - [A0A024R5L7_HUMAN]	5.08	13	3	3	14	0.936	14	9.907	42.110	610	66.351
Q12834	Cell division cycle protein 20 homolog OS=Homo sapiens GN=CDC20 PE=1 SV=2 - [CDC20_HUMAN]	10.22	4	5	5	14	1.000	13	5.094	42.092	499	54.689
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1 - [ADAS_HUMAN]	12.92	7	7	7	15	0.882	14	27.644	42.021	658	72.866
E7ETK0	40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1 - [E7ETK0_HUMAN]	35.11	3	5	5	21	1.000	21	14.493	41.965	131	15.187
A0A087WV29	N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=4 SV=1 - [A0A087WV29_HUMAN]	9.47	3	4	7	16	1.004	7	14.516	41.938	834	93.475
E9PJ81	UBX domain-containing protein 1 (Fragment) OS=Homo sapiens GN=UBXN1 PE=1 SV=1 - [E9PJ81_HUMAN]	38.28	10	9	9	17	1.000	14	10.768	41.791	290	32.592
P17252	Protein kinase C alpha type OS=Homo sapiens GN=PRKCA PE=1 SV=4 - [KPCA_HUMAN]	11.46	11	5	8	19	1.037	9	13.997	41.765	672	76.700
Q15717	ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2 - [ELAV1_HUMAN]	24.85	3	7	7	16	0.960	16	6.587	41.727	326	36.069
B2R4V2	cDNA, FLJ92227, highly similar to Homo sapiens ribosomal protein L36a-like (RPL36AL), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R4V2_HUMAN]	26.42	3	2	5	19	1.000	7	10.239	41.667	106	12.519
A0A024R7P3	ATPase type 13A1, isoform CRA_f OS=Homo sapiens GN=ATP13A1 PE=3 SV=1 - [A0A024R7P3_HUMAN]	9.39	7	9	9	17	1.000	17	6.785	41.613	1086	121.032
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 - [PP1B_HUMAN]	17.74	10	2	6	14	1.422	3	47.818	41.577	327	37.163

A0A024R1T5	2',3'-cyclic nucleotide 3' phosphodiesterase, isoform CRA_a OS=Homo sapiens GN=CNP PE=4 SV=1 - [A0A024R1T5_HUMAN]	26.93	18	11	12	20	1.027	19	24.877	41.477	401	45.070
Q96JJ7	Protein disulfide-isomerase TMX3 OS=Homo sapiens GN=TMX3 PE=1 SV=2 - [TMX3_HUMAN]	14.32	4	5	6	15	1.000	13	11.886	41.477	454	51.839
B2R7U4	cDNA, FLJ93605, highly similar to Homo sapiens heme oxygenase (decycling) 1 (HMOX1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7U4_HUMAN]	20.83	6	5	5	17	1.038	17	11.363	41.411	288	32.782
B4DDB5	cDNA FLJ54284, highly similar to Transcription initiation factor IIF alpha subunit (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DDB5_HUMAN]	22.65	1	1	10	18				41.307	415	46.352
P55735	Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3 - [SEC13_HUMAN]	20.5	7	5	5	14	0.992	14	10.182	41.287	322	35.518
J7FP01	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [J7FP01_HUMAN]	15.47	245	0	3	17				41.282	181	21.065
P11766	Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 - [ADHX_HUMAN]	26.74	6	10	10	25	1.000	25	6.087	41.255	374	39.698
Q06124	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 - [PTN11_HUMAN]	14.07	7	8	9	19	1.000	17	0.000	41.191	597	68.393
P51531	Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2 PE=1 SV=2 - [SMCA2_HUMAN]	6.67	13	3	11	16	1.000	3	22.585	41.125	1590	181.166
Q9HAB8	Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS PE=1 SV=2 - [PPCS_HUMAN]	19.94	2	6	6	14	0.942	14	24.587	41.108	311	33.984
Q9UEH5	24-kDa subunit of complex I (Fragment) OS=Homo sapiens GN=NDUFV2 PE=4 SV=1 - [Q9UEH5_HUMAN]	27.71	7	6	6	16	1.000	14	8.881	41.041	231	25.414
A0A087WXU3	Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=4 SV=1 - [A0A087WXU3_HUMAN]	12.81	2	1	12	18	0.909	1		41.011	921	102.308
Q15435	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1 - [PP1R7_HUMAN]	20	7	8	8	15	0.999	14	7.226	40.937	360	41.539
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	22.86	13	1	2	19	0.910	13	10.056	40.873	70	8.213
E5RHG8	Transcription elongation factor B polypeptide 1 (Fragment) OS=Homo sapiens GN=TCEB1 PE=1 SV=1 - [E5RHG8_HUMAN]	59.55	3	4	4	12	1.000	11	8.949	40.861	89	9.954
Q96T88	E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1 - [UHRF1_HUMAN]	12.99	5	7	8	13	1.000	9	6.673	40.807	793	89.757
A2RRC9	IQ motif containing GTPase activating protein 3 OS=Homo sapiens GN=IQGAP3 PE=2 SV=1 - [A2RRC9_HUMAN]	4.05	5	4	8	18	1.000	4	0.000	40.778	1631	184.404
B3KRM2	Serine/threonine-protein phosphatase OS=Homo sapiens PE=2 SV=1 - [B3KRM2_HUMAN]	30.42	15	1	8	16				40.770	309	35.536
P62837	Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 - [UB2D2_HUMAN]	12.24	5	2	2	16	1.000	16	2.252	40.767	147	16.724
B4DRV2	cDNA FLJ53646, highly similar to Succinyl-CoA ligase (ADP-forming) beta-chain, mitochondrial (EC 6.2.1.5) OS=Homo sapiens PE=2 SV=1 - [B4DRV2_HUMAN]	14.32	11	6	6	15	1.000	15	14.199	40.731	405	43.847
P36871	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 - [PGM1_HUMAN]	19.04	5	9	9	12	0.965	12	18.686	40.706	562	61.411
B3KVX6	cDNA FLJ41699 fis, clone HCHON2004776, highly similar to Homo sapiens cytoskeleton-associated protein 4 (CKAP4), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KVX	14.59	10	6	8	14	1.022	10	6.821	40.700	521	58.116
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1 PE=1 SV=1 - [PPIL1_HUMAN]	40.36	1	6	6	18	1.000	18	3.131	40.690	166	18.225
J3QR29	Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=1 SV=2 - [J3QR29_HUMAN]	9.49	28	8	8	17	1.000	17	14.552	40.687	748	87.056
G3V4F7	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1 - [G3V4F7_HUMAN]	21.14	3	10	10	16	0.962	15	6.669	40.667	440	48.638
Q9H2J4	Phosducin-like protein 3 OS=Homo sapiens GN=PDCL3 PE=1 SV=1 - [PDCL3_HUMAN]	15.06	4	4	4	11	1.000	11	4.132	40.622	239	27.597
A0A087WUW6	NF-kappa-B essential modulator OS=Homo sapiens GN=IKBKG PE=4 SV=1 - [A0A087WUW6_HUMAN]	19.9	11	8	8	15	1.000	15	23.431	40.619	412	47.355
F4NC03	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [F4NC03_HUMAN]	7.72	64	0	2	15				40.583	337	38.286
P07305	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3 - [H10_HUMAN]	17.01	1	4	4	14	1.350	14	10.538	40.529	194	20.850
B5MCX3	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [B5MCX3_HUMAN]	23.68	12	7	7	16	0.952	16	14.454	40.514	321	36.917
P46063	ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3 - [RECQ1_HUMAN]	14.48	7	11	11	19	1.000	18	6.926	40.503	649	73.410
A0A087WYK8	Nardilysin OS=Homo sapiens GN=NRD1 PE=4 SV=1 - [A0A087WYK8_HUMAN]	6.71	10	7	7	13	1.000	13	19.910	40.443	1148	131.059
A6NDG6	Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 - [PGP_HUMAN]	14.64	2	5	5	15	0.940	15	15.672	40.435	321	33.985
Q09472	Histone acetyltransferase p300 OS=Homo sapiens GN=EP300 PE=1 SV=2 - [EP300_HUMAN]	3.52	3	6	7	14	1.000	9	0.000	40.342	2414	263.990
E9AQX4	Putative prohibitin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1610 PE=4 SV=1 - [E9AQX4_LEIMU]	9.33	1	2	3	15	1.000	3	0.000	40.328	268	30.252
B4E302	cDNA FLJ56209, highly similar to Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E302_HUMAN]	16.67	17	10	10	18	1.000	17	9.185	40.301	792	86.111
P41226	Ubiquitin-like modifier-activating enzyme 7 OS=Homo sapiens GN=UBA7 PE=1 SV=2 - [UBA7_HUMAN]	11.36	1	10	10	16	1.000	15	0.000	40.280	1012	111.624
B4DWC4	cDNA FLJ61180, highly similar to Chloride intracellular channel protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DWC4_HUMAN]	15.92	4	3	3	12	1.004	12	6.019	40.250	245	27.800
P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	16.41	6	6	6	15	1.000	15	0.000	40.232	323	36.353
B2R9T9	cDNA, FLJ94551 OS=Homo sapiens PE=2 SV=1 - [B2R9T9_HUMAN]	15.23	5	4	4	14	1.000	13	16.707	40.232	243	26.178
A8K940	cDNA FLJ77630, highly similar to Homo sapiens BPY2 interacting protein 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K940_HUMAN]	7.74	2	6	6	15	1.000	11	16.268	40.228	1059	112.158
J3QSV6	Ribosomal L1 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=RSL1D1 PE=1 SV=1 - [J3QSV6_HUMAN]	13.26	8	6	6	15	0.970	15	4.502	40.223	430	48.179
P78318	Immunoglobulin-binding protein 1 OS=Homo sapiens GN=IGBP1 PE=1 SV=1 - [IGBP1_HUMAN]	13.86	1	3	3	14	1.000	14	0.000	40.200	339	39.198
Q6XQN6	Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT PE=1 SV=2 - [PNCB_HUMAN]	12.27	7	7	7	15	0.982	14	2.696	40.108	538	57.542
Q6MZT3	Putative uncharacterized protein DKFZp686C1054 OS=Homo sapiens GN=DKFZp686C1054 PE=2 SV=1 - [Q6MZT3_HUMAN]	15.26	5	8	8	15	1.000	14	10.711	40.103	439	48.460
Q9NRX4	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1 - [PHP14_HUMAN]	28.8	2	4	4	23	1.000	19	3.465	40.079	125	13.824
Q92556	Engulfment and cell motility protein 1 OS=Homo sapiens GN=ELMO1 PE=1 SV=2 - [ELMO1_HUMAN]	13.2	7	8	10	16	0.938	12	13.800	40.008	727	83.776
A4QN19	SEC16A protein (Fragment) OS=Homo sapiens GN=SEC16A PE=2 SV=1 - [A4QN19_HUMAN]	8.4	12	12	12	18	1.000	17	17.241	39.882	1727	186.378
Q96SB3	Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2 - [NEB2_HUMAN]	8.83	3	1	7	16	0.919	4	20.869	39.880	815	89.138
A0A087X079	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=4 SV=1 - [A0A087X079_HUMAN]	15.86	42	5	6	15	1.000	12	10.302	39.829	473	51.880
G3V0I5	NADH dehydrogenase (Ubiquinone) flavoprotein 1, 51kDa, isoform CRA_c OS=Homo sapiens GN=NDUFV1 PE=1 SV=1 - [G3V0I5_HUMAN]	15.1	13	7	7	11	1.119	11	13.909	39.774	457	50.022
O94874	E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2 - [UFL1_HUMAN]	12.22	4	10	10	15	0.867	12	17.398	39.741	794	89.540
O00151	PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4 - [PDLI1_HUMAN]	21.58	1	6	6	13	0.882	13	5.009	39.738	329	36.049
B8ZZU8	Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 - [B8ZZU8_HUMAN]	31.86	3	5	5	17	1.000	17	12.246	39.722	113	12.519
Q3ZTT7	SH3 domain binding protein 1 OS=Homo sapiens GN=SH3BP1 PE=2 SV=1 - [Q3ZTT7_HUMAN]	14.87	5	8	8	15	0.911	12	13.904	39.687	632	67.916
P0DJD0	RANBP2-like and GRIP domain-containing protein 1 OS=Homo sapiens GN=RGPD1 PE=2 SV=1 - [RGPD1_HUMAN]	5.21	7	1	10	17	1.000	1		39.675	1748	196.539
H0Y5H6	Ubiquitin-associated protein 2-like (Fragment) OS=Homo sapiens GN=UBAP2L PE=1 SV=1 - [H0Y5H6_HUMAN]	12.79	2	1	4	15	1.000	1		39.545	383	40.195
Q8IZ83	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2 - [A16A1_HUMAN]	10.47	5	8	8	15	1.000	15	10.655	39.515	802	85.074
P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=4 - [DUT_HUMAN]	29.76	7	7	7	14	0.982	14	30.246	39.509	252	26.547
Q7Z417	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1 - [NUFP2_HUMAN]	17.12	5	9	10	17	0.975	14	8.464	39.366	695	76.075
B7Z7P8	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=1 - [B7Z7P8_HUMAN]	17.26	5	7	7	16	1.005	16	10.945	39.301	423	47.446
P08240	Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2 - [SRPR_HUMAN]	13.95	5	9	9	19	0.991	19	14.644	39.268	638	69.767
B2R8A2	cDNA, FLJ93804, highly similar to Homo sapiens gp25L2 protein (HSGP25L2G), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8A2_HUMAN]	22.43	3	5	7	20	1.000	10	0.000	39.135	214	25.062
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	23.25	5	8	9	18	1.000	16	11.300	39.078	314	34.272
B3KPZ2	cDNA FLJ32487 fis, clone SKNSH1000002, highly similar to Prostaglandin E synthase 2 (EC 5.3.99.3) OS=Homo sapiens PE=2 SV=1 - [B3KPZ2_HUMAN]	13.26	5	6	6	14	0.982	14	11.668	39.073	377	41.943
O15400	Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4 - [STX7_HUMAN]	19.16	3	4	5	10	1.000	9	28.664	39.041	261	29.797
Q9NR45	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN]	16.71	5	6	6	15	0.969	15	11.823	38.974	359	40.281
O43665	Regulator of G-protein signaling 10 OS=Homo sapiens GN=RGS10 PE=1 SV=2 - [RGS10_HUMAN]	16.76	1	3	3	11	1.000	9	4.164	38.732	173	20.223
B3KM89	cDNA FLJ10528 fis, clone NT2RP2000943, highly similar to Protein transport protein Sec24D OS=Homo sapiens PE=2 SV=1 - [B3KM89_HUMAN]	9.93	8	9	9	16	1.000	16	11.069	38.675	906	100.183
B4DPY2	cDNA FLJ59286, highly similar to Pre-mRNA-processing factor 40 homolog A (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DPY2_HUMAN]	11.27	3	1	8	14	1.206	1		38.621	816	92.839
F8VQX7	Oxysterol-binding protein (Fragment) OS=Homo sapiens GN=OSBPL8 PE=1 SV=1 - [F8VQX7_HUMAN]	7.07	11	5	5	13	1.000	13	10.679	38.612	721	81.606
B2RAQ8	cDNA, FLJ95058, highly similar to Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A),nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapien	12.94	4	9	9	14	0.919	13	20.833	38.604	773	88.283
Q13422	DNA-binding protein Ikaros OS=Homo sapiens GN=IKZF1 PE=1 SV=1 - [IKZF1_HUMAN]	25.24	15	9	10	17	1.000	16	0.000	38.600	519	57.491
O60216	Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2 - [RAD21_HUMAN]	13.31	3	6	6	14	1.000	13	0.000	38.532	631	71.645
B4DDP8	cDNA FLJ55953, highly similar to ADP-dependent glucokinase (EC 2.7.1.147) OS=Homo sapiens PE=2 SV=1 - [B4DDP8_HUMAN]	11.78	6	3	4	12	1.000	10	10.453	38.524	416	45.627
R9WWI7	SEC62 splice variant OS=Homo sapiens PE=2 SV=1 - [R9WWI7_HUMAN]	40.91	8	8	8	16	1.000	16	16.554	38.514	220	25.802
D6RG15	Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=1 SV=1 - [D6RG15_HUMAN]	27.17	6	5	6	14	1.000	12	7.512	38.419	254	28.865
Q9UMS4	Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1 - [PRP19_HUMAN]	9.33	4	5	5	15	0.958	15	14.064	38.369	504	55.146
P84074	Neuron-specific calcium-binding protein hippocalcin OS=Homo sapiens GN=HPCA PE=1 SV=2 - [HPCA_HUMAN]	17.1	10	4	4	19	1.000	18	6.716	38.327	193	22.413
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	14.58	1	3	3	13	1.000	13	0.000	38.187	336	35.306
P50579	Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 - [MAP2_HUMAN]	14.44	10	4	4	16	1.000	13	0.000	38.146	478	52.858
Q15052	Rho guanine nucleotide exchange factor 6 OS=Homo sapiens GN=ARHGEF6 PE=1 SV=2 - [ARHG6_HUMAN]	14.43	4	10	11	16	1.000	13	20.255	38.038	776	87.443
E9AQA0	Glutamate dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_1010 PE=4 SV=1 - [E9AQA0_LEIMU]	11.9	1	12	12	17	1.000	17	0.494	38.027	1017	114.580
B7Z592	cDNA FLJ61635, highly similar to Homo sapiens likely ortholog of mouse immediate early response, erythropoietin 4 (LEREPO4), mRNA OS=Homo sapiens PE=2 SV=1 -	13.27	5	6	6	14	0.989	13	11.210	38.018	392	44.863
O95218	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2 PE=1 SV=2 - [ZRAB2_HUMAN]	24.85	1	9	9	15	1.000	14	31.524	37.926	330	37.382
A0A024R7W5	YTH domain family, member 3, isoform CRA_a OS=Homo sapiens GN=YTHDF3 PE=4 SV=1 - [A0A024R7W5_HUMAN]	16.48	9	4	8	16	0.859	6	13.853	37.866	534	58.275
C9K0U8	Single-stranded DNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=SSBP1 PE=1 SV=1 - [C9K0U8_HUMAN]	25.62	5	3	3	17	1.073	17	10.406	37.732	121	14.122
Q5U0B3	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 8 OS=Homo sapiens PE=2 SV=1 - [Q5U0B3_HUMAN]	27.24	8	10	10	17	0.962	17	12.176	37.533	257	29.903
A0A024RBT2	HCG1782202, isoform CRA_c OS=Homo sapiens GN=hCG_1782202 PE=4 SV=1 - [A0A024RBT2_HUMAN]	28.31	11	5	6	14	1.000	11	2.420	37.521	166	18.907
Q9UDY4	DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1 - [DNJB4_HUMAN]	15.13	4	1	4	12	1.000	2	0.000	37.470	337	37.783
M0R0Q7	DNA ligase OS=Homo sapiens GN=LIG1 PE=1 SV=1 - [M0R0Q7_HUMAN]	11.5	10	9	9	15	1.000	14	0.920	37.469	800	88.333
Q14161	ARF GTPase-activating protein GIT2 OS=Homo sapiens GN=GIT2 PE=1 SV=2 - [GIT2_HUMAN]	10.28	12	7	9	13	0.975	10	6.067	37.458	759	84.490
Q01650	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2 - [LAT1_HUMAN]	6.31	2	3	3	12	1.000	11	5.959	37.412	507	54.974
Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1 - [RBGPR_HUMAN]	8.97	3	11	12	17	0.979	15	8.588	37.369	1393	155.886
H3BQQ2	Zinc finger protein 598 OS=Homo sapiens GN=ZNF598 PE=1 SV=1 - [H3BQQ2_HUMAN]	8.6	2	7	8	14	1.000	13	37.070	37.357	849	93.230
B4DEK2	cDNA FLJ59182, highly similar to Splicing factor, arginine/serine-rich 7 OS=Homo sapiens PE=2 SV=1 - [B4DEK2_HUMAN]	45.45	6	7	8	18	1.000	15	17.135	37.356	165	18.803
E9AWB4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1020 PE=4 SV=1 - [E9AWB4_LEIMU]	47.86	1	6	6	14	1.000	13	0.000	37.340	117	12.499
A8K885	cDNA FLJ77179, highly similar to Homo sapiens sorting nexin 6 (SNX6) mRNA OS=Homo sapiens PE=2 SV=1 - [A8K885_HUMAN]	15.76	8	5	6	14	0.959	12	17.651	37.326	406	46.619
Q92576	PHD finger protein 3 OS=Homo sapiens GN=PHF3 PE=1 SV=3 - [PHF3_HUMAN]	4.56	9	9	9	15	1.000	15	0.000	37.305	2039	229.339
A0A087X0M4	Kanadaptin OS=Homo sapiens GN=SLC4A1AP PE=4 SV=1 - [A0A087X0M4_HUMAN]	8.36	4	6	6	13	1.000	13	0.000	37.303	742	82.839
O95671	N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3 - [ASML_HUMAN]	7.57	4	4	4	11	1.000	11	0.000	37.281	621	68.813
I3L0Y5	ATP synthase F(0) complex subunit C1, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5G1 PE=3 SV=1 - [I3L0Y5_HUMAN]	7.14	8	1	1	18	1.087	18	10.823	37.271	98	10.032
Q96HE7	ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 - [ERO1A_HUMAN]	16.67	6	5	6	14	1.000	12	0.000	37.198	468	54.358
A8K132	cDNA FLJ75476, highly similar to Homo sapiens glutaminase (GLS), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K132_HUMAN]	8.52	5	2	5	11	1.158	6	9.863	37.194	669	73.462
Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 - [ADRM1_HUMAN]	14.99	5	6	6	20	1.000	17	10.898	37.104	407	42.127
E9B376	Nucleoside diphosphate kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2950 PE=3 SV=1 - [E9B376_LEIMU]	38.41	1	4	5	16	1.000	13	0.000	37.073	151	16.663
A0A024R529	Dihydroxyacetone kinase 2 homolog (Yeast), isoform CRA_a OS=Homo sapiens GN=DAK PE=4 SV=1 - [A0A024R529_HUMAN]	5.39	7	2	2	15	1.000	12	0.000	37.064	575	58.940
Q8WU79	Stromal membrane-associated protein 2 OS=Homo sapiens GN=SMAP2 PE=1 SV=1 - [SMAP2_HUMAN]	17.48	4	9	9	21	1.000	21	6.463	37.043	429	46.755
K4DI93	Cullin 4B, isoform CRA_e OS=Homo sapiens GN=CUL4B PE=1 SV=1 - [K4DI93_HUMAN]	8.67	3	3	7	14	1.000	5	0.000	37.000	900	102.691
E9PID8	Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 - [E9PID8_HUMAN]	12.79	5	3	4	14	1.000	8	0.468	36.888	438	46.636
E5KND7	Elongation factor G, mitochondrial OS=Homo sapiens GN=GFM1 PE=3 SV=1 - [E5KND7_HUMAN]	9.59	5	7	7	14	1.000	14	10.460	36.846	751	83.432
Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCHL5 PE=1 SV=3 - [UCHL5_HUMAN]	21.58	12	7	7	13	1.000	13	14.168	36.835	329	37.583
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	16.42	3	4	4	14	1.000	14	1.634	36.816	201	22.822
B4DXB0	cDNA FLJ51133, highly similar to Ribonucleoside-diphosphate reductase large subunit (EC 1.17.4.1) OS=Homo sapiens PE=2 SV=1 - [B4DXB0_HUMAN]	14.74	10	9	9	14	0.955	14	14.750	36.806	570	64.724
B7Z475	cDNA FLJ55712, highly similar to F-box-like/WD repeat protein TBL1XR1 OS=Homo sapiens PE=2 SV=1 - [B7Z475_HUMAN]	17.82	6	5	5	11	1.000	11	8.508	36.781	376	40.731
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	15.91	2	4	4	14	1.000	13	23.055	36.654	264	29.185
Q8N766	ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1 - [EMC1_HUMAN]	5.74	2	6	6	14	1.032	14	7.056	36.631	993	111.689
B7Z5V6	cDNA FLJ57046, highly similar to Lysosomal alpha-glucosidase (EC 3.2.1.20) OS=Homo sapiens PE=2 SV=1 - [B7Z5V6_HUMAN]	8.07	3	1	5	13	1.000	1		36.628	644	71.749
B4DKX4	cDNA FLJ58014, highly similar to Homo sapiens programmed cell death 4, transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DKX4_HUMAN]	12.09	4	6	6	13	1.000	13	17.512	36.607	455	50.197
A0A024RCT1	TAP binding protein (Tapasin), isoform CRA_c OS=Homo sapiens GN=TAPBP PE=4 SV=1 - [A0A024RCT1_HUMAN]	9.6	6	4	4	15	1.012	14	5.591	36.559	448	47.541
Q01826	DNA-binding protein SATB1 OS=Homo sapiens GN=SATB1 PE=1 SV=1 - [SATB1_HUMAN]	9.44	10	5	7	14	1.000	10	3.031	36.474	763	85.903
U3NG26	Truncated Bruton agammaglobulinemia tyrosine kinase OS=Homo sapiens GN=BTK PE=2 SV=1 - [U3NG26_HUMAN]	18.49	47	9	10	16	1.000	15	9.606	36.473	568	65.470
P61619	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2 - [S61A1_HUMAN]	13.45	18	7	7	16	0.996	16	5.043	36.434	476	52.231
Q9BRA2	Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 - [TXD17_HUMAN]	18.7	4	2	2	13	1.000	12	1.146	36.417	123	13.932
P62854	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	50.43	5	5	5	17	0.959	17	15.616	36.339	115	13.007
Q9BR76	Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 - [COR1B_HUMAN]	16.36	7	8	10	20	0.947	15	9.424	36.325	489	54.200
Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 - [ILKAP_HUMAN]	17.86	6	7	8	18	1.000	17	10.711	36.308	392	42.880
Q9NV96	Cell cycle control protein 50A OS=Homo sapiens GN=TMEM30A PE=1 SV=1 - [CC50A_HUMAN]	15.51	4	5	5	13	1.000	13	0.000	36.306	361	40.658
D3DTX6	Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=4 SV=1 - [D3DTX6_HUMAN]	9.55	3	2	8	15	0.897	3	16.213	36.296	817	89.280
B2R858	cDNA, FLJ93750, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 (DDX6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R858_HUMAN]	15.89	3	6	6	15	0.917	15	12.931	36.263	472	53.183
Q53S54	Putative uncharacterized protein CUL3 (Fragment) OS=Homo sapiens GN=CUL3 PE=3 SV=1 - [Q53S54_HUMAN]	10.99	8	8	8	14	0.901	13	8.330	36.237	746	86.411
O96019	Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1 - [ACL6A_HUMAN]	18.18	7	7	7	13	1.041	13	13.527	36.232	429	47.430
Q09161	Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 - [NCBP1_HUMAN]	8.86	5	6	7	13	0.959	12	20.187	36.231	790	91.781
B4DJB1	cDNA FLJ53049, highly similar to AP-2 complex subunit mu-1 OS=Homo sapiens PE=2 SV=1 - [B4DJB1_HUMAN]	16.53	15	6	6	14	0.945	14	11.037	36.192	375	42.674
A8K103	cDNA FLJ75454, highly similar to Homo sapiens arrestin, beta 1 (ARRB1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K103_HUMAN]	15.07	10	5	6	12	1.000	11	4.869	36.149	418	47.035
Q9UNE7	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2 - [CHIP_HUMAN]	23.76	4	8	8	15	1.000	15	20.226	35.987	303	34.834
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 - [PLOD3_HUMAN]	12.87	9	9	9	15	1.000	15	5.800	35.971	738	84.731
B7Z5Z9	cDNA FLJ51066, highly similar to Ras-related protein Rab-6A OS=Homo sapiens PE=2 SV=1 - [B7Z5Z9_HUMAN]	30.56	34	2	5	15	1.050	5	5.790	35.931	144	16.608
B2R7G6	cDNA, FLJ93437, highly similar to Homo sapiens histidyl-tRNA synthetase-like (HARSL), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7G6_HUMAN]	17.79	7	4	9	14	0.966	4	17.618	35.886	506	56.853
Q71SV8	Crn-related protein kim1 OS=Homo sapiens PE=2 SV=1 - [Q71SV8_HUMAN]	11.38	3	8	8	13	1.000	11	20.736	35.869	852	99.643
Q7Z478	ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2 - [DHX29_HUMAN]	5.41	2	8	9	12	1.000	11	6.457	35.850	1369	155.139
P98175	RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3 - [RBM10_HUMAN]	11.4	3	9	11	16	0.899	11	19.384	35.762	930	103.469
B3KRW2	cDNA FLJ34977 fis, clone NTONG2005822, highly similar to Homo sapiens RAB11 family interacting protein 1 (class I) (RAB11FIP1), transcript variant 1, mRNA OS=Hon	14.94	4	6	6	14	1.000	14	3.649	35.752	415	45.358
P24928	DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 - [RPB1_HUMAN]	6.85	5	12	12	16	1.000	14	0.000	35.708	1970	217.039
Q86U42	Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1 PE=1 SV=3 - [PABP2_HUMAN]	11.44	4	4	4	14	1.000	14	7.348	35.696	306	32.729
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2 - [ITAM_HUMAN]	8.42	5	8	9	13	1.103	12	8.125	35.665	1152	127.099
A7E2D8	Calcium-transporting ATPase OS=Homo sapiens GN=ATP2B4 PE=2 SV=1 - [A7E2D8_HUMAN]	8.93	17	4	9	13	1.000	5	18.167	35.564	1164	128.749
B4DU15	cDNA FLJ54549, highly similar to Pumilio homolog 1 OS=Homo sapiens PE=2 SV=1 - [B4DU15_HUMAN]	8.14	12	4	7	13	1.000	9	0.000	35.562	1044	111.605
Q7RTV0	PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1 - [PHF5A_HUMAN]	40	1	5	5	12	1.000	11	5.853	35.481	110	12.397
Q5RLJ0	CLE OS=Homo sapiens PE=2 SV=1 - [Q5RLJ0_HUMAN]	20.49	4	6	6	16	1.044	15	13.718	35.479	244	27.952
Q53F19	Uncharacterized protein C17orf85 OS=Homo sapiens GN=C17orf85 PE=1 SV=2 - [CQ085_HUMAN]	8.06	3	4	5	15	1.000	9	25.945	35.469	620	70.549
Q07DU7	Peroxidoxin 1 OS=Leishmania aethiopica GN=Pxn1 PE=4 SV=1 - [Q07DU7_9TRYP]	33.16	3	2	6	16	2.651	5	189.472	35.464	190	21.278
O75152	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3 - [ZC11A_HUMAN]	11.48	11	9	9	14	1.000	14	5.180	35.461	810	89.076
Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	16.46	5	5	5	12	1.108	12	13.498	35.456	322	35.596
Q07812	Apoptosis regulator BAX OS=Homo sapiens GN=BAX PE=1 SV=1 - [BAX_HUMAN]	29.17	5	4	4	16	1.000	16	25.898	35.434	192	21.171
B7Z7M6	cDNA FLJ53680, highly similar to Kinesin-like protein KIF2C OS=Homo sapiens PE=2 SV=1 - [B7Z7M6_HUMAN]	12.42	9	6	7	12	1.000	9	26.218	35.405	612	68.775
E9AY41	Putative 10 kDa heat shock protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0620 PE=3 SV=1 - [E9AY41_LEIMU]	42	1	3	3	16	5.691	15	116.258	35.368	100	10.695
Q9H773	dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1 - [DCTP1_HUMAN]	31.76	2	5	5	13	1.000	13	10.972	35.361	170	18.669
Q9BUH6	Uncharacterized protein C9orf142 OS=Homo sapiens GN=C9orf142 PE=1 SV=2 - [CI142_HUMAN]	29.41	1	5	5	12	0.873	8	20.315	35.360	204	21.626
P20290	Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1 - [BTF3_HUMAN]	28.16	3	4	6	19	1.000	13	0.000	35.345	206	22.154
Q13586	Stromal interaction molecule 1 OS=Homo sapiens GN=STIM1 PE=1 SV=3 - [STIM1_HUMAN]	10.8	13	7	7	11	1.000	9	1.631	35.340	685	77.375
O94973	AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2 - [AP2A2_HUMAN]	8.31	11	3	9	16	0.986	4	9.537	35.207	939	103.895
R9WQY1	Fragile X mental retardation 1 OS=Homo sapiens GN=FMR1 PE=2 SV=1 - [R9WQY1_HUMAN]	9.72	11	1	5	11	0.790	4	47.076	35.204	566	63.942
Q9Y6A5	Transforming acidic coiled-coil-containing protein 3 OS=Homo sapiens GN=TACC3 PE=1 SV=1 - [TACC3_HUMAN]	9.43	5	8	8	13	1.000	12	1.213	35.195	838	90.304
Q7L5N7	Lysophosphatidylcholine acyltransferase 2 OS=Homo sapiens GN=LPCAT2 PE=1 SV=1 - [PCAT2_HUMAN]	10.48	3	6	6	13	1.003	13	8.195	35.184	544	60.169
Q6NX51	Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=2 SV=1 - [Q6NX51_HUMAN]	10.68	9	8	8	11	0.954	10	21.597	35.167	974	110.429
A0A087X1R5	IK cytokine, down-regulator of HLA II, isoform CRA_a OS=Homo sapiens GN=IK PE=4 SV=1 - [A0A087X1R5_HUMAN]	15.98	12	8	8	18	1.000	17	0.000	35.147	557	65.614
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN]	6.77	3	6	6	15	1.000	15	0.000	35.134	812	89.247
Q9C0J8	pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2 - [WDR33_HUMAN]	10.7	3	12	12	16	1.010	16	13.301	35.113	1336	145.799
Q8ND24	RING finger protein 214 OS=Homo sapiens GN=RNF214 PE=1 SV=2 - [RN214_HUMAN]	9.1	4	5	6	12	1.000	6	3.842	35.111	703	77.619
Q6P1J9	Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1 - [CDC73_HUMAN]	18.27	2	10	10	15	0.912	15	13.713	35.095	531	60.539
P01009	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3 - [A1AT_HUMAN]	14.11	15	6	6	16	0.946	16	15.191	35.024	418	46.707
B3KMD4	A kinase (PRKA) anchor protein 8-like, isoform CRA_d OS=Homo sapiens GN=AKAP8L PE=2 SV=1 - [B3KMD4_HUMAN]	7.77	7	4	4	16	1.000	15	0.000	34.972	386	42.734
P67870	Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=1 - [CSK2B_HUMAN]	19.53	10	4	4	18	1.000	16	2.997	34.961	215	24.926
Q96F88	Processing of 1, ribonuclease P/MRP subunit (S. cerevisiae) OS=Homo sapiens GN=POP1 PE=2 SV=1 - [Q96F88_HUMAN]	9.67	3	9	9	14	1.000	14	5.325	34.958	1024	114.608
Q03169	Tumor necrosis factor alpha-induced protein 2 OS=Homo sapiens GN=TNFAIP2 PE=1 SV=2 - [TNAP2_HUMAN]	9.33	8	6	6	11	1.000	10	0.000	34.930	654	72.616
Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 - [RHG01_HUMAN]	14.58	5	6	6	18	0.992	17	35.006	34.876	439	50.404
O14497	AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3 - [ARI1A_HUMAN]	5.08	9	10	10	14	1.000	14	0.000	34.826	2285	241.892
E9B665	Putative 60S ribosomal protein L5 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1880 PE=3 SV=1 - [E9B665_LEIMU]	17.7	1	6	6	13	1.000	11	0.000	34.825	305	34.008
Q53GF0	Cytidine 5'-monophosphate N-acetylneuraminic acid synthetase variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GF0_HUMAN]	14.98	4	6	6	13	1.000	13	2.109	34.774	434	48.299
O14737	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3 - [PDCD5_HUMAN]	28	6	5	5	13	1.000	13	10.822	34.747	125	14.276
P35658	Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 - [NU214_HUMAN]	6.65	10	10	10	16	0.994	12	19.110	34.743	2090	213.488
Q9UNS2	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3 - [CSN3_HUMAN]	15.37	6	6	6	11	1.000	11	22.150	34.733	423	47.842
P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	19.13	11	7	7	14	1.005	14	15.451	34.669	392	42.246
P27986	Phosphatidylinositol 3-kinase regulatory subunit alpha OS=Homo sapiens GN=PIK3R1 PE=1 SV=2 - [P85A_HUMAN]	11.6	15	7	9	13	1.000	11	17.152	34.634	724	83.547
O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3 - [OGT1_HUMAN]	7.46	6	7	7	12	0.997	12	14.881	34.603	1046	116.850
Q9P2X0	Dolichol-phosphate mannosyltransferase subunit 3 OS=Homo sapiens GN=DPM3 PE=1 SV=2 - [DPM3_HUMAN]	23.91	5	2	2	11	1.000	9	10.772	34.573	92	10.087
V5YQL4	Adenosylhomocysteinase OS=Homo sapiens GN=FGFR2-AHCYL1 PE=2 SV=1 - [V5YQL4_HUMAN]	6.67	48	3	8	16	1.000	6	6.416	34.560	1169	130.813
H3BPJ9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=1 - [H3BPJ9_HUMAN]	27.33	3	4	4	10	1.052	10	16.922	34.558	161	19.246

A0A024R0Y2	HCG30204, isoform CRA_a OS=Homo sapiens GN=hCG_30204 PE=4 SV=1 - [A0A024R0Y2_HUMAN]	4.63	14	10	10	15	1.000	15	8.288	34.542	2268	257.075
B4DXI8	cDNA FLJ51373, highly similar to 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens PE=2 SV=1 - [B4DXI8_HUMAN]	17	5	6	6	15	0.980	15	19.606	34.530	247	28.280
B3LEU8	TMEM214 protein (Fragment) OS=Homo sapiens GN=TMEM214 PE=2 SV=1 - [B3LEU8_HUMAN]	9.51	10	6	6	15	1.000	15	0.000	34.517	673	75.391
Q9NWB6	Arginine and glutamate-rich protein 1 OS=Homo sapiens GN=ARGLU1 PE=1 SV=1 - [ARGL1_HUMAN]	21.98	8	7	8	14	0.971	13	18.041	34.426	273	33.197
B4DG62	cDNA FLJ56506, highly similar to Hexokinase-1 (EC 2.7.1.1) OS=Homo sapiens PE=2 SV=1 - [B4DG62_HUMAN]	10.93	10	8	10	14	1.017	11	2.930	34.420	915	102.246
Q9NVS2	28S ribosomal protein S18a, mitochondrial OS=Homo sapiens GN=MRPS18A PE=1 SV=1 - [RT18A_HUMAN]	29.59	2	7	7	14	1.000	14	12.837	34.370	196	22.170
Q9H3N1	Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1 - [TMX1_HUMAN]	24.29	4	7	7	13	0.967	13	15.526	34.331	280	31.771
B4DQT8	cDNA FLJ61158, highly similar to ADP-ribosylation factor-like protein 8B OS=Homo sapiens PE=2 SV=1 - [B4DQT8_HUMAN]	15.82	5	3	3	13	1.069	13	13.935	34.318	177	20.585
B4DT46	cDNA FLJ57889, highly similar to Cytochrome b-245 light chain OS=Homo sapiens PE=2 SV=1 - [B4DT46_HUMAN]	19.08	2	2	2	23	1.000	23	16.411	34.305	131	14.011
E9B549	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2580 PE=4 SV=1 - [E9B549_LEIMU]	20	1	4	4	12	1.000	11	0.000	34.260	205	22.558
B4E1E2	cDNA FLJ61530, highly similar to Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens PE=2 SV=1 - [B4E1E2_HUMAN]	12.25	7	8	8	12	1.000	12	24.409	34.235	661	74.808
E9B6I9	Putative ATP-dependent RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3100 PE=3 SV=1 - [E9B6I9_LEIMU]	9.07	1	7	7	11	1.000	10	0.000	34.192	926	100.816
A0A024RCB5	Chitinase domain containing 1, isoform CRA_a OS=Homo sapiens GN=CHID1 PE=3 SV=1 - [A0A024RCB5_HUMAN]	12.69	10	5	5	12	1.000	12	2.107	34.178	386	44.090
Q8WYA6	Beta-catenin-like protein 1 OS=Homo sapiens GN=CTNNBL1 PE=1 SV=1 - [CTBL1_HUMAN]	9.41	2	6	6	14	0.920	14	13.256	34.129	563	65.132
Q9H9A5	CCR4-NOT transcription complex subunit 10 OS=Homo sapiens GN=CNOT10 PE=1 SV=1 - [CNO10_HUMAN]	9.14	6	6	6	10	1.000	9	0.000	34.108	744	82.258
D9ZGF8	Rho-associated protein kinase OS=Homo sapiens GN=ROCK1 PE=3 SV=1 - [D9ZGF8_HUMAN]	6.43	2	9	9	13	1.000	13	2.066	34.101	1354	158.145
D6W646	HCG22253, isoform CRA_a OS=Homo sapiens GN=hCG_22253 PE=4 SV=1 - [D6W646_HUMAN]	9.36	5	7	8	14	1.000	10	8.931	34.079	1015	114.008
B4E0R0	cDNA FLJ54220, highly similar to Long-chain-fatty-acid--CoA ligase 1 (EC 6.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B4E0R0_HUMAN]	13.7	12	8	8	14	1.012	14	10.195	34.079	664	74.206
G5E9G6	E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1 - [G5E9G6_HUMAN]	19.3	7	1	6	11	1.000	2	0.000	34.031	430	45.295
H0YEM1	Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Homo sapiens GN=PUF60 PE=1 SV=1 - [H0YEM1_HUMAN]	27.38	6	1	8	18	1.000	1		33.945	336	35.809
P25098	Beta-adrenergic receptor kinase 1 OS=Homo sapiens GN=ADRBK1 PE=1 SV=2 - [ARBK1_HUMAN]	12.77	6	10	10	15	1.000	15	17.444	33.943	689	79.522
Q9BQA9	Uncharacterized protein C17orf62 OS=Homo sapiens GN=C17orf62 PE=1 SV=1 - [CQ062_HUMAN]	16.04	8	3	3	12	0.946	10	7.526	33.842	187	20.761
Q6UXH1	Cysteine-rich with EGF-like domain protein 2 OS=Homo sapiens GN=CRELD2 PE=1 SV=1 - [CREL2_HUMAN]	13.88	3	5	5	11	1.000	11	11.873	33.801	353	38.166
Q567R0	UQCRH protein OS=Homo sapiens GN=UQCRH PE=2 SV=1 - [Q567R0_HUMAN]	28.24	2	3	3	14	1.007	12	13.682	33.785	85	9.947
A0A024QZ63	HCG27198, isoform CRA_c OS=Homo sapiens GN=hCG_27198 PE=4 SV=1 - [A0A024QZ63_HUMAN]	5.3	9	10	11	15	1.000	14	3.830	33.770	2039	231.097
Q8N4Q1	Mitochondrial intermembrane space import and assembly protein 40 OS=Homo sapiens GN=CHCHD4 PE=1 SV=1 - [MIA40_HUMAN]	28.87	2	4	4	14	1.000	13	0.000	33.667	142	15.986
O14617	AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=1 SV=1 - [AP3D1_HUMAN]	8.5	7	10	10	14	1.031	14	15.336	33.629	1153	130.076
A0A024RBC7	Calcium-transporting ATPase OS=Homo sapiens GN=ATP2B1 PE=3 SV=1 - [A0A024RBC7_HUMAN]	7.95	16	6	11	14	1.000	7	6.467	33.611	1220	134.600
B7Z6C9	cDNA FLJ61658, highly similar to Transmembrane 9 superfamily protein member 1 OS=Homo sapiens PE=2 SV=1 - [B7Z6C9_HUMAN]	7.85	11	6	6	12	0.999	12	5.887	33.576	815	92.427
C9JKQ2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 (Fragment) OS=Homo sapiens GN=NDUFB3 PE=1 SV=1 - [C9JKQ2_HUMAN]	16.92	2	1	1	12	1.000	12	0.000	33.547	65	7.581
Q9Y2S6	Translation machinery-associated protein 7 OS=Homo sapiens GN=TMA7 PE=1 SV=1 - [TMA7_HUMAN]	43.75	14	3	4	24	0.972	18	11.191	33.511	64	7.062
Q7KZ85	Transcription elongation factor SPT6 OS=Homo sapiens GN=SUPT6H PE=1 SV=2 - [SPT6H_HUMAN]	6.78	1	10	10	15	1.000	15	14.840	33.500	1726	198.949
Q9H0L4	Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 - [CSTFT_HUMAN]	11.53	1	5	6	12	1.000	8	0.000	33.433	616	64.396
Q9BRZ2	E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens GN=TRIM56 PE=1 SV=3 - [TRI56_HUMAN]	9.4	2	6	6	11	1.000	8	0.000	33.432	755	81.437
E9AST6	Putative universal minicircle sequence binding protein (UMSBP) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1640 PE=4 SV=1 - [E9AST6_	19.13	1	5	5	13	1.000	10	0.000	33.300	298	30.828
Q96RS6	NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 - [NUDC1_HUMAN]	7.55	1	5	5	12	0.998	12	24.441	33.255	583	66.713
O15031	Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3 - [PLXB2_HUMAN]	6.04	9	10	10	14	1.000	13	14.757	33.254	1838	204.997
B3KY11	cDNA FLJ46571 fis, clone THYMU3041428, highly similar to Probable ATP-dependent RNA helicase DDX23 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KY11_HUM	13	7	11	11	14	1.000	12	5.412	33.187	800	93.177
B4E3A8	cDNA FLJ53963, highly similar to Leukocyte elastase inhibitor OS=Homo sapiens PE=2 SV=1 - [B4E3A8_HUMAN]	21.11	2	8	8	14	1.029	14	18.885	33.170	341	38.661
F5GXJ9	CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=1 - [F5GXJ9_HUMAN]	14.1	5	8	8	12	0.984	12	14.076	33.159	532	59.491
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]	13.21	5	2	4	10	1.000	7	5.023	33.149	318	34.812
Q12965	Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2 - [MYO1E_HUMAN]	5.05	5	2	6	11	1.176	2	23.528	33.135	1108	126.982
A8K6F0	cDNA FLJ75449, highly similar to Homo sapiens aquarius homolog (mouse) (AQR), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6F0_HUMAN]	4.58	4	7	7	13	0.996	11	2.914	33.122	1485	171.187
B2R7M3	cDNA, FLJ93510, highly similar to Homo sapiens JTV1 gene (JTV1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7M3_HUMAN]	21.25	4	7	7	14	1.000	13	15.218	33.120	320	35.425
Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1 - [SLIRP_HUMAN]	50.46	9	6	6	15	1.031	15	22.016	33.111	109	12.341
F8VVL1	Density-regulated protein OS=Homo sapiens GN=DENR PE=1 SV=1 - [F8VVL1_HUMAN]	30	4	5	5	10	1.000	8	10.298	33.078	160	17.759
Q8NFH9	MLL/SEPTIN6 fusion protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8NFH9_HUMAN]	11.63	34	2	7	19	0.930	3	32.009	33.067	559	63.104
Q7L0Y3	Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2 - [MRRP1_HUMAN]	17.87	2	7	7	12	1.048	12	15.178	33.065	403	47.317
P17174	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3 - [AATC_HUMAN]	17.92	3	7	7	12	0.988	12	24.272	33.025	413	46.219
B8ZZT4	Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1 - [B8ZZT4_HUMAN]	27.27	3	3	3	12	0.430	12	9.292	33.017	99	11.185
B4DGM3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=1 SV=1 - [B4DGM3_HUMAN]	11.2	7	3	4	12	0.917	5	12.886	33.014	393	44.743
B4DRY5	cDNA FLJ54538, highly similar to Transportin-2 OS=Homo sapiens PE=2 SV=1 - [B4DRY5_HUMAN]	7.61	10	2	6	14	1.000	5	0.000	32.999	880	99.601
H0YH87	Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=1 - [H0YH87_HUMAN]	6	13	3	6	13	1.006	7	29.478	32.996	916	98.055
Q13129	Zinc finger protein Rlf OS=Homo sapiens GN=RLF PE=1 SV=2 - [RLF_HUMAN]	5.59	2	9	9	14	1.000	13	0.000	32.963	1914	217.813
A0A024RBS6	tRNA pseudouridine synthase OS=Homo sapiens GN=PUS1 PE=3 SV=1 - [A0A024RBS6_HUMAN]	20.12	10	7	7	16	1.000	16	8.745	32.956	338	37.807
Q86TU7	Histone-lysine N-methyltransferase setd3 OS=Homo sapiens GN=SETD3 PE=1 SV=1 - [SETD3_HUMAN]	7.74	3	5	5	12	1.000	12	5.776	32.940	594	67.215
B4DYZ7	cDNA FLJ54316, highly similar to DNA polymerase subunit delta 3 OS=Homo sapiens PE=2 SV=1 - [B4DYZ7_HUMAN]	15.24	11	7	7	12	1.000	12	2.943	32.927	466	51.310
B4DZV0	cDNA FLJ50318, highly similar to Lymphoid-restricted membrane protein OS=Homo sapiens PE=2 SV=1 - [B4DZV0_HUMAN]	11.43	6	4	4	11	1.000	9	0.736	32.925	446	50.380
Q8N3D4	EH domain-binding protein 1-like protein 1 OS=Homo sapiens GN=EHBP1L1 PE=1 SV=2 - [EH1L1_HUMAN]	6.11	3	7	7	13	1.000	12	0.000	32.899	1523	161.756
Q14166	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2 - [TTL12_HUMAN]	10.4	2	7	7	13	0.990	13	28.356	32.890	644	74.356
B7Z361	Reticulon OS=Homo sapiens PE=2 SV=1 - [B7Z361_HUMAN]	12.2	15	2	3	16	0.984	8	3.046	32.853	205	22.913
E9B278	Putative ADP-ribosylation factor OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2790 PE=3 SV=1 - [E9B278_LEIMU]	22.47	12	2	4	14	1.304	4	40.885	32.802	178	20.116
Q96ST3	Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2 - [SIN3A_HUMAN]	3.38	2	5	5	14	1.000	14	12.654	32.739	1273	145.085
B2RCZ7	Ethylmalonic encephalopathy 1, isoform CRA_a OS=Homo sapiens GN=ETHE1 PE=2 SV=1 - [B2RCZ7_HUMAN]	27.31	4	5	5	12	1.020	12	7.892	32.736	227	24.940
Q92879	CUGBP Elav-like family member 1 OS=Homo sapiens GN=CELF1 PE=1 SV=2 - [CELF1_HUMAN]	10.08	10	2	5	16	0.920	2	12.463	32.725	486	52.030
O15427	Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1 - [MOT4_HUMAN]	8.82	5	4	4	13	1.002	12	5.118	32.715	465	49.437
Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3 - [DC1L1_HUMAN]	23.71	5	9	9	17	1.000	14	5.740	32.713	523	56.544
E9PD43	Negative elongation factor E (Fragment) OS=Homo sapiens GN=NELFE PE=1 SV=1 - [E9PD43_HUMAN]	25	6	5	5	11	1.000	9	0.000	32.683	260	30.046
H7C4T5	Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=1 SV=1 - [H7C4T5_HUMAN]	16.72	16	6	6	18	0.997	17	2.942	32.677	329	35.797
O75381	Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=1 SV=1 - [PEX14_HUMAN]	13.26	3	6	6	11	1.000	11	22.732	32.674	377	41.212
B4DEQ0	cDNA FLJ59482, highly similar to Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (EC 1.5.5.1) OS=Homo sapiens PE=2 SV=1 - [B4DEQ0_HUMA	13.31	5	7	7	11	1.026	11	17.459	32.647	556	61.346
Q5FWY2	GNAS complex locus OS=Homo sapiens GN=GNAS PE=2 SV=2 - [Q5FWY2_HUMAN]	10.53	19	2	3	10	0.969	4	4.691	32.647	380	44.222
H3BRD2	Sulfhydryl oxidase (Fragment) OS=Homo sapiens GN=GFER PE=1 SV=1 - [H3BRD2_HUMAN]	26.62	7	2	2	10	1.000	6	0.000	32.645	139	15.786
P20962	Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2 - [PTMS_HUMAN]	23.53	5	4	4	15	1.013	15	6.513	32.606	102	11.523
B7WPG3	Uncharacterized protein OS=Homo sapiens GN=HNRPLL PE=1 SV=1 - [B7WPG3_HUMAN]	13.98	8	5	6	13	0.937	9	16.115	32.534	508	56.415
A4UJ43	Brain type mu-glutathione S-transferase OS=Homo sapiens GN=GSTM3 PE=2 SV=1 - [A4UJ43_HUMAN]	19.05	4	5	6	12	0.950	11	17.483	32.498	210	24.802
A0A024QZH6	Serine arginine-rich pre-mRNA splicing factor SR-A1, isoform CRA_a OS=Homo sapiens GN=SR-A1 PE=4 SV=1 - [A0A024QZH6_HUMAN]	6.17	9	6	7	12	1.000	11	17.581	32.494	1312	139.182
A8K9U6	cDNA FLJ76121, highly similar to Homo sapiens zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9U6_HU	6.76	4	6	6	12	1.000	12	9.838	32.483	902	101.392
P21283	V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4 - [VATC1_HUMAN]	14.92	3	7	7	14	0.999	14	12.930	32.476	382	43.914
Q9H098	Protein FAM107B OS=Homo sapiens GN=FAM107B PE=1 SV=1 - [F107B_HUMAN]	38.93	9	4	5	13	1.000	11	5.074	32.464	131	15.548
B4DY09	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=2 SV=1 - [B4DY09_HUMAN]	18.47	5	5	5	13	1.000	13	13.745	32.413	352	38.886
O14545	TRAF-type zinc finger domain-containing protein 1 OS=Homo sapiens GN=TRAFD1 PE=1 SV=1 - [TRAD1_HUMAN]	11	5	6	6	11	1.000	11	0.000	32.404	582	64.800
P02656	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1 - [APOC3_HUMAN]	16.16	2	1	1	7	1.000	7	7.482	32.365	99	10.845
Q6ZR21	cDNA FLJ46716 fis, clone TRACH3018108, highly similar to 51 kDa FK506-binding protein OS=Homo sapiens PE=2 SV=1 - [Q6ZR21_HUMAN]	14.04	1	2	7	14	0.990	3	1.436	32.361	456	50.933
Q14966	Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 PE=1 SV=2 - [ZN638_HUMAN]	6.27	10	12	12	16	1.000	15	12.145	32.360	1978	220.488
P40306	Proteasome subunit beta type-10 OS=Homo sapiens GN=PSMB10 PE=1 SV=1 - [PSB10_HUMAN]	11.36	3	4	4	12	0.941	12	9.076	32.328	273	28.918
Q9H2G0	CTCL tumor antigen se37-2 OS=Homo sapiens GN=UBE3A PE=2 SV=1 - [Q9H2G0_HUMAN]	9.86	5	7	7	11	1.000	11	0.000	32.320	852	97.905
B4DMV9	cDNA FLJ53363, highly similar to EH-domain-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DMV9_HUMAN]	18.95	12	9	9	13	1.099	13	14.017	32.318	475	53.735
B2RAW0	cDNA, FLJ95154, highly similar to Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA OS=Homo sapiens PE=2 SV=1 -	6.75	5	5	5	14	1.000	14	2.146	32.311	770	82.419
Q12769	Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3 - [NU160_HUMAN]	5.29	4	7	7	12	0.982	12	32.888	32.289	1436	162.017
Q9Y4E8	Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 PE=1 SV=3 - [UBP15_HUMAN]	6.01	9	6	7	13	1.019	10	7.930	32.265	981	112.348
B3KSI7	cDNA FLJ36374 fis, clone THYMU2008185, highly similar to Xaa-Pro aminopeptidase 1 (EC 3.4.11.9) OS=Homo sapiens PE=2 SV=1 - [B3KSI7_HUMAN]	11.96	5	3	7	12	0.992	7	6.318	32.170	552	62.109
J3KMX2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens GN=SMARCD2 PE=1 SV=1 - [J3KMX2_HUMAN]	15.13	5	6	6	12	1.000	12	0.241	32.144	456	52.205
Q13242	Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 - [SRSF9_HUMAN]	26.24	5	6	6	10	1.018	10	8.205	32.125	221	25.526
E9B5P1	Pyruvate kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0030 PE=3 SV=1 - [E9B5P1_LEIMU]	11.04	2	5	5	11	1.427	11	56.538	32.120	498	53.986
J3QSD7	Cyclin-dependent kinase 12 (Fragment) OS=Homo sapiens GN=CDK12 PE=1 SV=1 - [J3QSD7_HUMAN]	5.5	50	5	7	14	1.000	10	0.000	32.114	1201	133.577
A8K9U0	cDNA FLJ78260, highly similar to Homo sapiens RNA binding motif protein 4, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9U0_HUMAN]	23.9	9	6	6	11	1.000	10	3.633	32.093	364	40.259
O75116	Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4 - [ROCK2_HUMAN]	6.2	5	10	10	13	1.000	13	4.526	32.006	1388	160.799
O15187	T-cluster binding protein OS=Homo sapiens GN=TIAL1 PE=2 SV=1 - [O15187_HUMAN]	24.15	14	4	7	15	1.000	10	20.866	32.005	265	29.631
H0YM23	Ankyrin repeat domain-containing protein 17 (Fragment) OS=Homo sapiens GN=ANKRD17 PE=1 SV=1 - [H0YM23_HUMAN]	3.38	6	3	7	13	1.000	1		31.958	2487	263.202
Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1 SV=2 - [PDXD1_HUMAN]	8.12	9	6	6	12	1.000	11	8.323	31.948	788	86.652
B3KVN0	cDNA FLJ16785 fis, clone NT2RI2015342, highly similar to Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens PE=2 SV=1 - [B3KVN0_H	8.65	7	4	4	14	1.000	14	0.000	31.873	416	45.839
B4DLA3	cDNA FLJ58509, highly similar to Cullin-1 OS=Homo sapiens PE=2 SV=1 - [B4DLA3_HUMAN]	9.82	5	8	8	12	0.997	12	10.157	31.797	703	81.464
Q16512	Serine/threonine-protein kinase N1 OS=Homo sapiens GN=PKN1 PE=1 SV=2 - [PKN1_HUMAN]	12	8	9	10	15	1.000	14	15.691	31.760	942	103.868
Q15050	Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 - [RRS1_HUMAN]	10.41	1	6	6	13	1.090	13	17.719	31.741	365	41.168
M0R2S2	Spermatogenesis-associated protein 22 OS=Homo sapiens GN=SPATA22 PE=4 SV=1 - [M0R2S2_HUMAN]	13.2	8	5	5	12	0.922	12	12.004	31.724	447	49.826
Q13442	28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1 - [HAP28_HUMAN]	44.75	2	10	10	16	0.987	16	9.466	31.711	181	20.618
A8K6G9	cDNA FLJ76871, highly similar to Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6G9_HUMAN]	8.64	10	9	11	13	1.000	10	0.000	31.681	1227	140.387
A0A087X020	Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=4 SV=1 - [A0A087X020_HUMAN]	17.6	2	6	6	12	0.969	12	16.471	31.607	250	28.846
Q15654	Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3 - [TRIP6_HUMAN]	15.97	6	5	5	10	0.799	9	34.230	31.577	476	50.255
Q9UJY4	ADP-ribosylation factor-binding protein GGA2 OS=Homo sapiens GN=GGA2 PE=1 SV=3 - [GGA2_HUMAN]	10.93	3	5	5	10	1.000	10	6.828	31.519	613	67.108
C9JP16	Cartilage-associated protein OS=Homo sapiens GN=CRTAP PE=1 SV=1 - [C9JP16_HUMAN]	18.16	9	7	7	16	1.000	13	10.928	31.491	358	41.406
P13747	HLA class I histocompatibility antigen, alpha chain E OS=Homo sapiens GN=HLA-E PE=1 SV=3 - [HLAE_HUMAN]	6.7	21	1	2	9	0.745	2	45.796	31.321	358	40.132
A0A024R755	Calumenin, isoform CRA_a OS=Homo sapiens GN=CALU PE=4 SV=1 - [A0A024R755_HUMAN]	20	6	6	6	15	1.000	15	9.312	31.314	315	37.111
B4DY32	Asparagine synthetase OS=Homo sapiens PE=2 SV=1 - [B4DY32_HUMAN]	15.27	4	9	9	14	1.000	14	24.782	31.271	478	54.827
Q13131	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 - [AAPK1_HUMAN]	11.63	6	6	6	10	0.944	10	12.574	31.213	559	63.969
O15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Homo sapiens GN=INPPL1 PE=1 SV=2 - [SHIP2_HUMAN]	6.04	5	5	7	14	1.000	7	6.761	31.201	1258	138.513
A8K520	cDNA FLJ78340, highly similar to Homo sapiens proline synthetase co-transcribed homolog (PROSC), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K520_HUMAN]	25.09	8	7	7	13	1.000	13	6.639	31.144	275	30.267
E9PM92	Small acidic protein (Fragment) OS=Homo sapiens GN=C11orf58 PE=1 SV=1 - [E9PM92_HUMAN]	39.1	4	5	5	13	1.110	11	21.766	31.131	156	17.496
Q9UKJ3	G patch domain-containing protein 8 OS=Homo sapiens GN=GPATCH8 PE=1 SV=2 - [GPTC8_HUMAN]	6.92	1	9	9	12	1.000	12	0.190	31.116	1502	164.098
Q6DD88	Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1 - [ATLA3_HUMAN]	16.08	4	7	7	13	1.060	13	8.701	31.087	541	60.503
Q14694	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 - [UBP10_HUMAN]	7.89	6	5	5	11	0.978	11	3.266	31.075	798	87.080
V9GYD9	CUGBP Elav-like family member 2 OS=Homo sapiens GN=CELF2 PE=1 SV=1 - [V9GYD9_HUMAN]	6.82	18	1	4	16	0.560	2	77.199	31.074	440	46.592
B7Z6B3	cDNA FLJ53094, highly similar to Receptor expression-enhancing protein 5 OS=Homo sapiens PE=2 SV=1 - [B7Z6B3_HUMAN]	18.59	8	4	4	11	0.988	11	12.601	31.025	156	17.746
Q15293	Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1 - [RCN1_HUMAN]	17.22	2	5	5	12	1.000	11	3.291	30.954	331	38.866
Q9H0B6	Kinesin light chain 2 OS=Homo sapiens GN=KLC2 PE=1 SV=1 - [KLC2_HUMAN]	13.83	8	3	8	11	1.000	3	16.014	30.917	622	68.892
B2R673	cDNA, FLJ92818, highly similar to Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R673_HUMAN]	9.58	5	5	5	11	1.053	11	25.053	30.899	501	54.013
E7ER77	Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=1 SV=1 - [E7ER77_HUMAN]	9.87	4	8	8	12	1.071	12	22.951	30.881	841	93.100
Q8IWB7	WD repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=WDFY1 PE=1 SV=1 - [WDFY1_HUMAN]	14.15	3	6	6	11	0.993	11	27.831	30.875	410	46.293
A0A024R725	Inosine-5'-monophosphate dehydrogenase OS=Homo sapiens GN=IMPDH1 PE=3 SV=1 - [A0A024R725_HUMAN]	13.42	11	4	6	14	0.762	6	35.181	30.873	380	40.958
A8K0J3	cDNA FLJ76732, highly similar to Homo sapiens TAO kinase 3 (TAOK3), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K0J3_HUMAN]	9.58	6	7	9	12	1.000	10	0.000	30.841	898	105.265
Q9NY27	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens GN=PPP4R2 PE=1 SV=3 - [PP4R2_HUMAN]	12.95	5	6	6	12	0.997	12	31.713	30.814	417	46.869
Q96CS3	FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2 - [FAF2_HUMAN]	12.13	3	5	5	11	1.000	10	0.620	30.757	445	52.591
E9B4I1	Malate dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0140 PE=3 SV=1 - [E9B4I1_LEIMU]	18.04	2	5	5	12	1.000	11	0.000	30.683	316	33.717
O75592	E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2 PE=1 SV=3 - [MYCB2_HUMAN]	2.39	4	10	10	15	1.000	15	7.157	30.664	4640	509.759
B4E0W3	cDNA FLJ60386, moderately similar to Signal-induced proliferation-associated protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E0W3_HUMAN]	10.64	3	9	9	13	1.077	12	13.681	30.656	940	101.745
B7ZL14	FNBP1 protein OS=Homo sapiens GN=FNBP1 PE=1 SV=1 - [B7ZL14_HUMAN]	17.6	6	10	10	11	1.047	10	25.864	30.651	551	64.031
P84101	Small EDRK-rich factor 2 OS=Homo sapiens GN=SERF2 PE=1 SV=1 - [SERF2_HUMAN]	42.37	6	4	4	11	1.006	11	8.269	30.580	59	6.896
Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2 - [PGAM5_HUMAN]	17.65	7	6	6	10	1.040	8	12.060	30.484	289	31.985
B1AJQ6	Syntaxin-12 (Fragment) OS=Homo sapiens GN=STX12 PE=1 SV=2 - [B1AJQ6_HUMAN]	26.98	4	5	5	11	1.000	11	21.823	30.475	215	24.561
A8K7W3	cDNA FLJ75780, highly similar to Homo sapiens SGT1, suppressor of G2 allele of SKP1 (SUGT1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K7W3_HUMAN]	26.73	1	1	9	15	1.285	1		30.428	333	37.810
M0QXM4	Amino acid transporter OS=Homo sapiens GN=SLC1A5 PE=1 SV=1 - [M0QXM4_HUMAN]	8.49	6	3	3	12	1.000	12	2.195	30.419	365	39.418
Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Homo sapiens GN=PPP1R10 PE=1 SV=1 - [PP1RA_HUMAN]	6.49	2	6	6	12	1.000	11	8.243	30.370	940	98.996
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1 - [FKBP3_HUMAN]	28.13	3	8	8	15	0.945	14	8.426	30.364	224	25.161
A0A024R862	GTPase activating protein and VPS9 domains 1, isoform CRA_b OS=Homo sapiens GN=GAPVD1 PE=4 SV=1 - [A0A024R862_HUMAN]	4.52	12	2	7	11	1.018	2	8.502	30.348	1460	162.796
Q59HA5	Cyclin G-associated kinase variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59HA5_HUMAN]	8.86	9	8	8	12	1.000	11	13.452	30.312	1196	130.708
P02671	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2 - [FIBA_HUMAN]	7.97	6	7	7	14	1.000	13	0.000	30.308	866	94.914
O75907	Diacylglycerol O-acyltransferase 1 OS=Homo sapiens GN=DGAT1 PE=1 SV=2 - [DGAT1_HUMAN]	4.3	1	1	1	9	1.000	8	0.000	30.243	488	55.242
Q07DU4	Peroxidoxin 2 OS=Leishmania aethiopica GN=Pxn2 PE=4 SV=1 - [Q07DU4_9TRYP]	29.65	1	1	5	14	1.434	3	31.645	30.243	199	22.127
O14684	Prostaglandin E synthase OS=Homo sapiens GN=PTGES PE=1 SV=2 - [PTGES_HUMAN]	17.11	2	4	4	12	1.064	12	18.426	30.234	152	17.091
E9B078	Putative 40S ribosomal protein S17 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2555 PE=3 SV=1 - [E9B078_LEIMU]	19.58	4	3	5	13	1.000	5	0.000	30.146	143	16.398
Q4G0J3	La-related protein 7 OS=Homo sapiens GN=LARP7 PE=1 SV=1 - [LARP7_HUMAN]	10.14	10	4	5	13	1.000	11	0.000	30.139	582	66.857
Q9Y282	Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Homo sapiens GN=ERGIC3 PE=1 SV=1 - [ERGI3_HUMAN]	15.93	12	7	7	16	0.995	16	11.223	30.138	383	43.194
H7C3G9	N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=2 - [H7C3G9_HUMAN]	17.06	8	6	6	12	1.044	12	23.821	30.064	340	36.865
A0A087WXK9	Thyroid receptor-interacting protein 11 OS=Homo sapiens GN=TRIP11 PE=4 SV=1 - [A0A087WXK9_HUMAN]	5.11	6	9	10	11	0.988	10	4.184	29.997	1978	227.283
P98179	Putative RNA-binding protein 3 OS=Homo sapiens GN=RBM3 PE=1 SV=1 - [RBM3_HUMAN]	26.11	1	5	5	15	0.941	14	9.046	29.987	157	17.160
B3KSZ4	cDNA FLJ37346 fis, clone BRAMY2021310, highly similar to Transcriptional repressor p66 beta OS=Homo sapiens PE=2 SV=1 - [B3KSZ4_HUMAN]	13.15	2	4	5	12	1.000	6	0.000	29.942	593	65.218
Q53TD0	Putative uncharacterized protein SP100 (Fragment) OS=Homo sapiens GN=SP100 PE=4 SV=1 - [Q53TD0_HUMAN]	7.59	5	4	9	33	0.995	6	9.184	29.937	843	96.489
C9J0K6	Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [C9J0K6_HUMAN]	21.94	3	3	3	12	1.041	12	20.036	29.934	155	17.594
A1L179	KIF5C protein (Fragment) OS=Homo sapiens GN=KIF5C PE=2 SV=1 - [A1L179_HUMAN]	10.31	17	1	9	17	1.077	1		29.931	863	99.038
Q96T58	Msx2-interacting protein OS=Homo sapiens GN=SPEN PE=1 SV=1 - [MINT_HUMAN]	0.66	1	1	3	24	1.275	1		29.914	3664	402.004
Q96C36	Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 - [P5CR2_HUMAN]	24.69	11	6	7	12	0.990	8	8.845	29.876	320	33.616
Q9NZZ3	Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1 - [CHMP5_HUMAN]	26.03	1	5	5	13	0.945	13	8.365	29.848	219	24.555
E9B3B4	Dihydrolipoyl dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3310 PE=4 SV=1 - [E9B3B4_LEIMU]	14.92	1	7	7	11	1.093	11	36.027	29.750	476	50.456
Q15554	Telomeric repeat-binding factor 2 OS=Homo sapiens GN=TERF2 PE=1 SV=3 - [TERF2_HUMAN]	14.02	5	7	7	11	1.000	10	0.000	29.750	542	59.557
Q12789	General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 - [TF3C1_HUMAN]	3.75	4	6	6	10	1.000	10	1.438	29.717	2109	238.725
Q3MHD2	Protein LSM12 homolog OS=Homo sapiens GN=LSM12 PE=1 SV=2 - [LSM12_HUMAN]	14.36	3	3	3	11	1.000	11	0.409	29.714	195	21.687
Q7L294	SAPS3 protein (Fragment) OS=Homo sapiens GN=SAPS3 PE=2 SV=1 - [Q7L294_HUMAN]	24.11	11	6	6	12	1.000	11	0.000	29.662	336	36.211
H3BV55	Phosphomannomutase OS=Homo sapiens GN=PMM2 PE=1 SV=1 - [H3BV55_HUMAN]	30.14	15	6	6	11	1.071	10	33.800	29.658	219	25.240
B4E290	cDNA FLJ50039, highly similar to Homo sapiens solute carrier family 25, member 24, transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B4E290_HUMAN]	16.77	4	8	8	12	1.099	12	14.106	29.647	477	53.262
Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1 OS=Homo sapiens GN=MAD1L1 PE=1 SV=2 - [MD1L1_HUMAN]	10.31	11	8	9	12	1.000	11	7.944	29.587	718	83.016
B1AUU8	Epidermal growth factor receptor substrate 15 OS=Homo sapiens GN=EPS15 PE=1 SV=1 - [B1AUU8_HUMAN]	9.32	6	8	8	12	0.934	11	16.618	29.581	762	83.603
B3KTL8	cDNA FLJ38476 fis, clone FEBRA2022504, highly similar to YTH domain protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KTL8_HUMAN]	8.59	3	1	5	12	1.129	2	18.101	29.566	559	60.835
H7BYV1	Interferon-induced transmembrane protein 2 (Fragment) OS=Homo sapiens GN=IFITM2 PE=4 SV=1 - [H7BYV1_HUMAN]	21.62	11	1	1	12	1.000	11	0.000	29.558	74	8.191
Q02127	Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Homo sapiens GN=DHODH PE=1 SV=3 - [PYRD_HUMAN]	13.16	4	5	5	13	1.000	13	4.424	29.550	395	42.841
O75934	Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 - [SPF27_HUMAN]	24.44	2	7	7	10	0.986	10	25.003	29.504	225	26.115
B3KY04	cDNA FLJ46506 fis, clone THYMU3030752, highly similar to BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens PE=2 SV=1 - [B3KY04_HUMAN]	20.92	2	6	6	12	1.000	10	35.771	29.497	325	35.709
P27694	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2 - [RFA1_HUMAN]	10.06	3	2	8	11	0.920	3	25.095	29.494	616	68.095
Q96KC8	DnaJ homolog subfamily C member 1 OS=Homo sapiens GN=DNAJC1 PE=1 SV=1 - [DNJC1_HUMAN]	15.88	5	7	7	11	0.953	10	12.849	29.488	554	63.843
B4DKZ2	cDNA FLJ56653, highly similar to Ribosomal protein S6 kinase alpha-3 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DKZ2_HUMAN]	10.28	31	3	8	11	0.996	4	6.616	29.459	710	80.545
Q15404	Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 PE=1 SV=3 - [RSU1_HUMAN]	24.19	3	8	8	19	1.000	19	22.972	29.436	277	31.521
B7SBB1	Aryl hydrocarbon receptor interacting protein OS=Homo sapiens GN=AIP PE=4 SV=1 - [B7SBB1_HUMAN]	28.88	27	8	8	11	0.954	11	7.037	29.421	329	37.477
M0QYG8	Glia maturation factor gamma OS=Homo sapiens GN=GMFG PE=1 SV=1 - [M0QYG8_HUMAN]	33.33	3	1	3	11	0.955	1		29.391	93	10.982
Q68E01	Integrator complex subunit 3 OS=Homo sapiens GN=INTS3 PE=1 SV=1 - [INT3_HUMAN]	9.88	1	7	7	10	0.897	10	12.955	29.385	1043	117.994
P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	9.93	4	4	4	11	1.000	11	5.440	29.363	423	48.424
O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	29.23	2	3	4	10	1.000	8	0.000	29.354	195	21.658
P10155	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2 - [RO60_HUMAN]	8.55	5	6	6	12	0.942	12	14.896	29.354	538	60.631
P23219	Prostaglandin G/H synthase 1 OS=Homo sapiens GN=PTGS1 PE=1 SV=2 - [PGH1_HUMAN]	11.35	3	6	6	13	1.071	12	10.154	29.332	599	68.642
B2RBV7	cDNA, FLJ95721, highly similar to Homo sapiens cullin 4A (CUL4A), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBV7_HUMAN]	9.26	4	2	6	11	0.839	4	37.989	29.324	659	76.756

J3KRI4	Cytoplasmic dynein 1 light intermediate chain 2 (Fragment) OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1 - [J3KRI4_HUMAN]	33.53	3	5	5	11	1.000	11	0.000	29.288	167	17.767
Q96JZ5	SM-11044 binding protein, isoform CRA_b OS=Homo sapiens GN=SMBP PE=2 SV=1 - [Q96JZ5_HUMAN]	3.85	7	2	2	9	1.000	9	33.175	29.271	545	62.899
A0A087X1B7	Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=4 SV=1 - [A0A087X1B7_HUMAN]	30.26	3	2	2	10	1.000	10	0.000	29.269	76	8.515
B2RD51	cDNA, FLJ96455, highly similar to Homo sapiens Down syndrome critical region gene 2 (DSCR2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RD51_HUMAN]	13.19	3	3	3	8	1.000	8	0.000	29.256	288	32.861
Q9NXH9	tRNA (guanine(26)-N(2))-dimethyltransferase OS=Homo sapiens GN=TRMT1 PE=1 SV=1 - [TRM1_HUMAN]	9.26	12	5	5	10	1.000	9	0.000	29.237	659	72.188
B7Z6W5	Cystathionine beta-synthase OS=Homo sapiens PE=2 SV=1 - [B7Z6W5_HUMAN]	10.15	9	5	5	10	0.976	10	22.819	29.219	463	51.069
P28340	DNA polymerase delta catalytic subunit OS=Homo sapiens GN=POLD1 PE=1 SV=2 - [DPOD1_HUMAN]	7.14	10	7	8	11	0.901	8	15.602	29.219	1107	123.553
B2R8G6	cDNA, FLJ93891, Homo sapiens FK506 binding protein 8, 38kDa (FKBP8), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8G6_HUMAN]	17.98	7	6	6	12	0.970	12	15.081	29.173	356	38.471
B4DF48	cDNA FLJ61221, highly similar to Protein FAM21C OS=Homo sapiens PE=2 SV=1 - [B4DF48_HUMAN]	7.04	19	6	6	12	1.000	11	7.453	29.156	1023	111.726
P27707	Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 - [DCK_HUMAN]	18.08	5	4	4	10	1.000	10	0.000	29.150	260	30.499
B4E1L0	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=2 SV=1 - [B4E1L0_HUMAN]	10.8	5	5	6	12	0.826	10	16.405	29.134	435	47.909
Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial OS=Homo sapiens GN=CHCHD2 PE=1 SV=1 - [CHCH2_HUMAN]	15.23	2	2	2	9	1.000	8	30.514	29.099	151	15.503
A4LAA3	Alpha thalassemia/mental retardation syndrome X-linked OS=Homo sapiens GN=ATRX PE=4 SV=1 - [A4LAA3_HUMAN]	3.33	6	7	8	13	1.000	8	13.756	29.091	2492	282.412
P33897	ATP-binding cassette sub-family D member 1 OS=Homo sapiens GN=ABCD1 PE=1 SV=2 - [ABCD1_HUMAN]	8.99	5	5	5	13	1.000	13	26.810	29.042	745	82.885
Q9Y285	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	8.27	4	4	4	11	1.000	11	29.686	29.030	508	57.528
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 - [GLRX3_HUMAN]	21.79	1	8	8	13	1.000	12	16.154	29.009	335	37.408
B4DLF8	cDNA FLJ60295, highly similar to Retinoblastoma-binding protein 5 OS=Homo sapiens PE=2 SV=1 - [B4DLF8_HUMAN]	9.51	3	4	4	11	1.000	11	0.000	28.997	410	44.805
B4DIQ0	cDNA FLJ51692, highly similar to mRNA capping enzyme OS=Homo sapiens PE=2 SV=1 - [B4DIQ0_HUMAN]	7.92	6	4	4	10	1.000	9	0.000	28.978	568	65.178
A0A024RBR1	Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein), isoform CRA_b OS=Homo sapiens GN=RSN PE=4 SV=1 - [A0A024RBR1_HUMAN]	4.77	16	7	8	12	1.000	10	13.904	28.942	1427	160.891
Q96HY6	DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1 PE=1 SV=2 - [DDRGK_HUMAN]	17.52	4	3	6	11	0.905	5	11.818	28.846	314	35.589
Q9BZU1	PNAS-20 OS=Homo sapiens PE=2 SV=1 - [Q9BZU1_HUMAN]	25.32	1	1	2	12	2.165	1		28.819	79	9.019
Q9P016	Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1 - [THYN1_HUMAN]	23.56	1	7	7	11	0.926	11	20.663	28.798	225	25.681
Q9H078	Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1 - [CLPB_HUMAN]	6.65	9	5	5	12	1.029	11	9.523	28.797	707	78.680
E3W994	CLIP-associating protein 2 OS=Homo sapiens GN=CLASP2 PE=1 SV=2 - [E3W994_HUMAN]	8.56	21	9	9	11	1.000	11	11.177	28.795	1273	138.778
O95466	Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3 - [FMNL_HUMAN]	8.45	4	6	10	15	1.000	8	8.406	28.759	1100	121.777
J3QLC9	Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=1 SV=1 - [J3QLC9_HUMAN]	15.07	16	5	5	11	1.000	10	2.048	28.728	365	40.753
Q92541	RNA polymerase-associated protein RTF1 homolog OS=Homo sapiens GN=RTF1 PE=1 SV=4 - [RTF1_HUMAN]	11.69	3	10	10	11	1.000	11	9.270	28.708	710	80.265
B4E0K4	cDNA FLJ58659, highly similar to Homo sapiens pre-B-cell leukemia transcription factor interacting protein 1 (PBXIP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4E0K4_	11.28	5	6	6	12	1.000	10	20.795	28.686	576	64.579
O43148	mRNA cap guanine-N7 methyltransferase OS=Homo sapiens GN=RNMT PE=1 SV=1 - [MCES_HUMAN]	9.24	8	5	5	10	1.008	10	17.769	28.685	476	54.809
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2 - [LIS1_HUMAN]	20.49	5	6	7	13	1.000	9	0.000	28.641	410	46.608
O95292	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3 - [VAPB_HUMAN]	17.7	7	3	4	11	0.985	3	22.291	28.623	243	27.211
Q53G19	Mitochondrial ribosomal protein L11 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G19_HUMAN]	38.54	4	7	7	12	1.014	12	26.951	28.622	192	20.642
P60983	Glia maturation factor beta OS=Homo sapiens GN=GMFB PE=1 SV=2 - [GMFB_HUMAN]	25.35	4	2	3	11	1.000	5	29.507	28.537	142	16.702
Q96GA7	Serine dehydratase-like OS=Homo sapiens GN=SDSL PE=1 SV=1 - [SDSL_HUMAN]	16.11	4	5	5	9	1.000	9	9.537	28.535	329	34.652
O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2 - [IDH3B_HUMAN]	11.95	7	5	5	13	1.000	13	19.704	28.529	385	42.157
T1WFC1	Golgi-associated PDZ and coiled-coil motif containing protein transcript variant 4 OS=Homo sapiens GN=GOPC PE=2 SV=1 - [T1WFC1_HUMAN]	17.34	3	6	6	10	0.980	10	15.128	28.516	398	43.835
Q9NVH1	DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2 - [DJC11_HUMAN]	6.26	4	4	4	10	1.021	10	15.011	28.514	559	63.239
H3BPF6	Prefoldin subunit 5 (Fragment) OS=Homo sapiens GN=PFDN5 PE=1 SV=1 - [H3BPF6_HUMAN]	26.97	3	4	4	11	1.000	11	7.924	28.495	152	17.146
Q66K91	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPB PE=2 SV=1 - [Q66K91_HUMAN]	22.08	13	5	5	14	1.000	13	16.261	28.408	231	23.640
B2RAL6	cDNA, FLJ94991, highly similar to Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL), mRNA (	7.52	4	9	9	13	1.000	12	8.848	28.376	1170	128.787
A0A024R6M2	KIAA2010, isoform CRA_a OS=Homo sapiens GN=KIAA2010 PE=4 SV=1 - [A0A024R6M2_HUMAN]	8.41	9	4	7	11	0.971	6	5.957	28.363	820	93.837
H3BN55	Ras-related protein Rab-27A (Fragment) OS=Homo sapiens GN=RAB27A PE=1 SV=1 - [H3BN55_HUMAN]	22.7	7	4	4	12	1.000	10	1.585	28.353	185	20.966
Q15843	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1 - [NEDD8_HUMAN]	39.51	5	3	4	13	1.038	11	13.862	28.285	81	9.066
Q9Y452	Leucocyte antigen B (Fragment) OS=Homo sapiens GN=HLA-B PE=4 SV=1 - [Q9Y452_HUMAN]	24.72	229	0	3	11				28.241	89	10.603
F8W785	Golgi integral membrane protein 4 OS=Homo sapiens GN=GOLIM4 PE=1 SV=1 - [F8W785_HUMAN]	10.48	2	6	6	13	1.000	11	2.375	28.237	668	78.713
C9J3L8	Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=1 - [C9J3L8_HUMAN]	7.17	6	2	2	12	1.000	12	3.052	28.225	265	29.555
A8K379	cDNA FLJ75641, highly similar to Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K379_H	17.58	48	5	9	15	1.011	7	1.554	28.162	512	58.582
H0YHG0	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [H0YHG0_HUMAN]	13.38	9	7	7	14	0.821	14	15.712	28.155	523	59.148
Q2TAY7	WD40 repeat-containing protein SMU1 OS=Homo sapiens GN=SMU1 PE=1 SV=2 - [SMU1_HUMAN]	9.75	1	5	5	11	1.078	11	11.202	28.149	513	57.507
A0A087X1H5	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ACAP2 PE=4 SV=1 - [A0A087X1H5_HUMAN]	6.95	5	5	5	11	1.066	11	9.451	28.141	777	87.965
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4 - [F1142_HUMAN]	17.23	12	7	7	11	1.000	11	3.135	28.116	505	55.434
A0A024RAJ5	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein, isoform CRA_a OS=Homo sapiens GN=COL4A3BP PE=4 SV=1 - [A0A024RAJ5_HUMAN]	8.86	2	6	6	10	1.000	10	0.000	28.092	598	67.964
Q9NSK0	Kinesin light chain 4 OS=Homo sapiens GN=KLC4 PE=1 SV=3 - [KLC4_HUMAN]	10.34	8	2	6	10	1.000	4	0.000	28.066	619	68.598
Q13907	Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens GN=IDI1 PE=1 SV=2 - [IDI1_HUMAN]	13.66	3	5	5	9	0.963	9	13.573	28.053	227	26.302
Q4LE74	MYO9B variant protein (Fragment) OS=Homo sapiens GN=MYO9B variant protein PE=2 SV=1 - [Q4LE74_HUMAN]	5.13	7	9	9	12	1.000	12	9.228	28.041	2028	229.571
G5E9W7	28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=1 SV=1 - [G5E9W7_HUMAN]	17.87	8	6	6	10	1.000	10	8.986	28.038	319	36.783
B4E206	cDNA FLJ55441, highly similar to Nuclear pore complex protein Nup133 OS=Homo sapiens PE=2 SV=1 - [B4E206_HUMAN]	6.23	5	8	8	11	1.000	11	18.273	28.033	1140	127.322
Q5TBB1	Ribonuclease H2 subunit B OS=Homo sapiens GN=RNASEH2B PE=1 SV=1 - [RNH2B_HUMAN]	15.71	4	6	6	14	0.992	14	12.558	28.006	312	35.116
P39880	Homeobox protein cut-like 1 OS=Homo sapiens GN=CUX1 PE=1 SV=3 - [CUX1_HUMAN]	7.44	2	4	9	12	1.000	3	8.500	28.006	1505	164.087
P42696	RNA-binding protein 34 OS=Homo sapiens GN=RBM34 PE=1 SV=2 - [RBM34_HUMAN]	9.53	4	4	4	10	1.000	9	6.493	27.999	430	48.535
Q8TF01	Arginine/serine-rich protein PNISR OS=Homo sapiens GN=PNISR PE=1 SV=2 - [PNISR_HUMAN]	5.22	3	5	5	11	1.000	11	12.471	27.997	805	92.521
Q96JB5	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=1 SV=2 - [CK5P3_HUMAN]	15.22	12	8	8	13	1.000	13	13.334	27.975	506	56.885
P28288	ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1 - [ABCD3_HUMAN]	7.59	3	5	5	12	1.011	12	9.024	27.955	659	75.428
P17612	cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2 - [KAPCA_HUMAN]	19.09	19	7	7	11	1.000	11	8.194	27.955	351	40.564
Q8NFQ8	Torsin-1A-interacting protein 2 OS=Homo sapiens GN=TOR1AIP2 PE=1 SV=1 - [TOIP2_HUMAN]	15.11	1	6	7	12	1.000	9	0.000	27.952	470	51.232
Q6IBT1	Proteasome subunit beta type OS=Homo sapiens GN=PSMB7 PE=2 SV=1 - [Q6IBT1_HUMAN]	14.44	5	4	4	12	1.017	12	20.196	27.948	277	29.918
P38432	Coilin OS=Homo sapiens GN=COIL PE=1 SV=1 - [COIL_HUMAN]	5.56	1	4	4	8	1.000	7	0.000	27.944	576	62.570
B3KRY3	cDNA FLJ35079 fis, clone PLACE6005283, highly similar to Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens PE=2 SV=1 - [B3KRY3_HUMAN]	7.09	3	3	3	10	1.035	10	10.604	27.936	395	42.558
P41223	Protein BUD31 homolog OS=Homo sapiens GN=BUD31 PE=1 SV=2 - [BUD31_HUMAN]	31.94	3	6	6	15	1.006	14	13.429	27.907	144	16.989
E7EST9	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP19 PE=1 SV=1 - [E7EST9_HUMAN]	6.28	8	7	7	10	1.130	8	14.198	27.902	1321	145.472
Q96DI9	POLDIP3 protein (Fragment) OS=Homo sapiens GN=POLDIP3 PE=2 SV=2 - [Q96DI9_HUMAN]	17.03	11	7	7	11	0.999	11	15.935	27.898	417	45.630
Q9BVJ8	HEXA protein (Fragment) OS=Homo sapiens GN=HEXA PE=2 SV=2 - [Q9BVJ8_HUMAN]	13.94	15	6	7	14	0.925	11	9.353	27.882	409	47.064
Q9UN37	Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1 - [VPS4A_HUMAN]	13.96	7	5	7	14	0.993	8	6.414	27.859	437	48.867
Q6P2E9	Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1 - [EDC4_HUMAN]	5.21	2	7	7	11	1.000	11	8.067	27.841	1401	151.567
Q86YP4	Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A PE=1 SV=1 - [P66A_HUMAN]	7.9	12	4	5	10	0.948	4	41.478	27.830	633	68.021
Q9UIG0	Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2 - [BAZ1B_HUMAN]	4.45	1	7	8	10	0.866	9	21.568	27.712	1483	170.796
Q9Y3B3	Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens GN=TMED7 PE=1 SV=2 - [TMED7_HUMAN]	12.95	4	3	3	12	1.049	12	24.446	27.673	224	25.156
Q59EF6	Calpain 2, large [catalytic] subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EF6_HUMAN]	11.25	7	8	8	12	0.940	12	11.678	27.624	729	83.056
Q9HCG8	Pre-mRNA-splicing factor CWC22 homolog OS=Homo sapiens GN=CWC22 PE=1 SV=3 - [CWC22_HUMAN]	7.05	2	6	6	12	1.000	12	0.000	27.617	908	105.402
Q8NBJ4	Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 PE=1 SV=1 - [GOLM1_HUMAN]	21.95	4	7	7	11	1.011	10	3.087	27.581	401	45.306
O14981	TATA-binding protein-associated factor 172 OS=Homo sapiens GN=BTAF1 PE=1 SV=2 - [BTAF1_HUMAN]	2.97	4	5	5	11	1.000	11	0.000	27.561	1849	206.756
Q99598	Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1 - [TSNAX_HUMAN]	14.14	6	5	5	10	0.869	10	24.923	27.544	290	33.092
B4DV28	cDNA FLJ54170, highly similar to Cytosolic nonspecific dipeptidase OS=Homo sapiens PE=2 SV=1 - [B4DV28_HUMAN]	16.41	22	7	7	14	1.002	14	1.484	27.529	463	51.469
A0A024RCR6	HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens GN=BAT3 PE=4 SV=1 - [A0A024RCR6_HUMAN]	8.7	15	6	6	10	1.000	10	14.113	27.521	1126	118.629
Q9UG63	ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2 - [ABCF2_HUMAN]	13.16	3	8	8	11	1.033	11	16.373	27.515	623	71.245
P55160	Nck-associated protein 1-like OS=Homo sapiens GN=NCKAP1L PE=1 SV=3 - [NCKPL_HUMAN]	5.94	6	7	7	10	1.000	10	9.761	27.495	1127	128.071
A8KAE0	cDNA FLJ78476, highly similar to Homo sapiens WD repeat and HMG-box DNA binding protein 1 (WDHD1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 -	4.25	7	5	5	9	0.878	9	21.454	27.484	1129	125.936
B7Z7P4	cDNA FLJ53627, highly similar to Antigen peptide transporter 1 OS=Homo sapiens PE=2 SV=1 - [B7Z7P4_HUMAN]	7.86	6	4	4	11	1.023	11	9.187	27.454	547	59.902
Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1 - [ACAD9_HUMAN]	12.4	7	8	8	11	0.887	11	19.838	27.451	621	68.717
B4DT94	cDNA FLJ53652, highly similar to Mitochondrial 28S ribosomal protein S27 OS=Homo sapiens PE=2 SV=1 - [B4DT94_HUMAN]	15.36	8	5	5	10	0.947	5	13.997	27.449	358	41.312
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	14.83	5	7	7	11	1.150	11	20.805	27.420	418	45.366
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2 - [IF2B2_HUMAN]	7.85	3	5	5	9	0.962	9	26.761	27.361	599	66.081
Q86TY5	Galectin OS=Homo sapiens PE=2 SV=1 - [Q86TY5_HUMAN]	42.98	6	6	6	10	1.167	10	19.097	27.350	121	13.888
P46734	Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 - [MP2K3_HUMAN]	8.93	13	3	3	9	0.998	9	7.471	27.345	347	39.293
A0A087X0W7	Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=4 SV=1 - [A0A087X0W7_HUMAN]	14.25	9	6	6	11	0.974	11	16.612	27.341	421	46.263
B2R6S9	cDNA, FLJ93097, highly similar to Homo sapiens low density lipoprotein receptor-related protein associated protein 1 (LRPAP1), mRNA OS=Homo sapiens PE=2 SV=1 -	19.89	4	8	8	13	1.062	13	15.420	27.326	357	41.455
A8K8N5	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1 - [A8K8N5_HUMAN]	9.3	7	11	11	15	1.000	15	7.635	27.315	1118	127.414
B2R776	cDNA, FLJ93315, highly similar to Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 2 (KCNAB2), transcript variant 2, mRNA OS=	15.58	20	6	6	12	0.899	12	18.046	27.310	353	39.263
E9B396	Putative ribosomal protein L3 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3130 PE=3 SV=1 - [E9B396_LEIMU]	12.89	2	3	6	10	1.000	4	7.838	27.224	419	47.558
F8W8I6	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=1 SV=1 - [F8W8I6_HUMAN]	13.25	9	1	6	12	1.001	4	0.109	27.218	385	42.808
F8VWH9	ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=1 SV=1 - [F8VWH9_HUMAN]	19.12	9	6	6	10	1.000	9	7.377	27.209	340	37.086
Q9H3Z4	DnaJ homolog subfamily C member 5 OS=Homo sapiens GN=DNAJC5 PE=1 SV=1 - [DNJC5_HUMAN]	19.19	2	4	4	11	1.000	11	13.993	27.177	198	22.134
B4DWG1	cDNA FLJ55643, highly similar to SEC23-interacting protein OS=Homo sapiens PE=2 SV=1 - [B4DWG1_HUMAN]	8.24	4	7	7	13	1.000	12	8.899	27.163	789	89.650
C9J050	Choline-phosphate cytidylyltransferase A (Fragment) OS=Homo sapiens GN=PCYT1A PE=1 SV=1 - [C9J050_HUMAN]	25.6	14	8	8	13	1.033	13	16.489	27.160	293	33.690
B5BU25	U2 small nuclear RNA auxiliary factor 2 isoform b OS=Homo sapiens GN=U2AF2 PE=2 SV=1 - [B5BU25_HUMAN]	16.14	3	8	8	12	1.000	12	9.516	27.153	471	53.103
Q9BW27	Nuclear pore complex protein Nup85 OS=Homo sapiens GN=NUP85 PE=1 SV=1 - [NUP85_HUMAN]	10.21	13	5	5	9	0.941	9	20.455	27.152	656	74.971
B7ZL34	PUM2 protein OS=Homo sapiens GN=PUM2 PE=2 SV=1 - [B7ZL34_HUMAN]	6.19	5	3	6	11	1.000	7	8.295	27.150	985	105.937
D3DWB6	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP9X PE=3 SV=1 - [D3DWB6_HUMAN]	4.58	7	9	9	12	1.000	9	0.000	27.100	2379	271.081
Q9Y6W5	Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3 - [WASF2_HUMAN]	10.44	5	6	6	12	0.957	12	22.685	27.089	498	54.250
Q5T8P6	RNA-binding protein 26 OS=Homo sapiens GN=RBM26 PE=1 SV=3 - [RBM26_HUMAN]	9.33	6	8	9	11	1.076	10	18.941	27.067	1007	113.527
Q0VDF9	Heat shock 70 kDa protein 14 OS=Homo sapiens GN=HSPA14 PE=1 SV=1 - [HSP7E_HUMAN]	7.27	3	4	4	10	0.988	10	11.484	27.041	509	54.760
Q00534	Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1 - [CDK6_HUMAN]	25.46	45	6	7	12	0.876	10	13.862	26.992	326	36.915
E9ALU6	Putative ATP-dependent Clp protease subunit, heat shock protein 100 (HSP100) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1270 PE=	9.25	1	7	9	12	1.000	9	3.792	26.930	865	96.755
Q14108	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCRB2_HUMAN]	10.67	2	5	5	13	1.126	11	17.753	26.926	478	54.255
M0R3F4	BRISC and BRCA1-A complex member 1 (Fragment) OS=Homo sapiens GN=BABAM1 PE=1 SV=1 - [M0R3F4_HUMAN]	28.73	12	4	4	10	1.000	9	1.424	26.910	181	19.624
Q7Z612	Acidic ribosomal phosphoprotein P1 OS=Homo sapiens PE=2 SV=1 - [Q7Z612_HUMAN]	5.31	5	1	1	16	1.004	8	5.020	26.900	113	11.392
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 - [OXSR1_HUMAN]	9.3	4	3	4	8	1.000	7	5.872	26.889	527	57.986
Q9BZE9	Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 - [ASPC1_HUMAN]	12.84	5	5	5	12	1.000	11	10.586	26.877	553	60.146
P52594	Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens GN=AGFG1 PE=1 SV=2 - [AGFG1_HUMAN]	10.85	5	6	6	14	1.000	13	20.395	26.860	562	58.224
P52294	Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3 - [IMA5_HUMAN]	13.57	10	4	7	11	0.965	6	25.634	26.807	538	60.184
S4R3Q6	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens GN=VPS26A PE=1 SV=1 - [S4R3Q6_HUMAN]	24.34	5	5	5	13	0.989	12	18.916	26.799	226	26.181
A0A075B7B5	SLIT-ROBO Rho GTPase-activating protein 2 OS=Homo sapiens GN=SRGAP2 PE=1 SV=1 - [A0A075B7B5_HUMAN]	5.07	15	2	4	9	1.253	4	20.725	26.773	789	90.852
B3KWP7	cDNA FLJ43538 fis, clone PLACE7008431, highly similar to Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, gamma (PIP5K2C), mRNA OS=Homo sapi	7.95	5	3	3	13	1.000	12	0.000	26.757	352	40.177
F8WCU9	AT-rich interactive domain-containing protein 2 OS=Homo sapiens GN=ARID2 PE=1 SV=1 - [F8WCU9_HUMAN]	2.99	9	4	4	10	1.000	10	0.000	26.708	1639	175.042
B3KNT3	Steroid receptor RNA activator 1, isoform CRA_a OS=Homo sapiens GN=SRA1 PE=2 SV=1 - [B3KNT3_HUMAN]	26.16	2	4	4	12	1.000	10	15.265	26.687	237	25.827
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSB6_HUMAN]	16.74	3	4	4	10	1.000	10	19.092	26.683	239	25.341
P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]	17.98	2	4	5	10	1.000	7	0.901	26.676	267	30.759
Q9BPX3	Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1 - [CND3_HUMAN]	5.91	3	6	6	11	0.961	10	13.282	26.660	1015	114.262
Q8TD55	Pleckstrin homology domain-containing family O member 2 OS=Homo sapiens GN=PLEKHO2 PE=2 SV=1 - [PKHO2_HUMAN]	10.61	3	6	6	10	1.074	10	16.385	26.657	490	53.317
B4DTZ7	cDNA FLJ57146, highly similar to Homo sapiens LMBR1 domain containing 2 (LMBRD2), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DTZ7_HUMAN]	6.28	2	4	4	13	1.017	12	14.045	26.647	589	69.290
Q14696	LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2 - [MESD_HUMAN]	18.38	2	5	5	15	1.000	15	7.350	26.586	234	26.060
E9AVH9	Proteasome subunit alpha type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1830 PE=3 SV=1 - [E9AVH9_LEIMU]	10.66	1	1	3	10	6.905	1		26.578	244	26.840
E9AKP0	Peptidyl-prolyl cis-trans isomerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0120 PE=3 SV=1 - [E9AKP0_LEIMU]	11.76	4	1	3	12	2.660	2	53.908	26.570	187	20.421
P50135	Histamine N-methyltransferase OS=Homo sapiens GN=HNMT PE=1 SV=1 - [HNMT_HUMAN]	17.47	3	4	4	10	1.000	8	1.626	26.555	292	33.274
A8K7W1	cDNA FLJ75779, highly similar to Homo sapiens docking protein 2, 56kDa (DOK2), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K7W1_HUMAN]	17.23	5	6	6	9	1.000	9	6.067	26.550	412	45.379
Q53FD7	Nucleoporin 54kDa variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FD7_HUMAN]	12.62	5	6	7	10	1.007	9	4.743	26.530	507	55.343
Q53F37	SAR1a gene homolog 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53F37_HUMAN]	21.21	9	2	4	11	0.853	5	4.499	26.515	198	22.396
V9HWJ5	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=HEL-S-90n PE=2 SV=1 - [V9HWJ5_HUMAN]	16.84	5	5	5	18	0.972	18	11.949	26.507	297	30.796
Q9BXW7	Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 - [CECR5_HUMAN]	12.53	3	4	4	9	1.000	9	9.618	26.503	423	46.292
P30519	Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2 - [HMOX2_HUMAN]	14.56	12	5	5	10	0.871	10	25.162	26.468	316	36.010
A0A087WUD1	Zinc finger protein 787 OS=Homo sapiens GN=ZNF787 PE=4 SV=1 - [A0A087WUD1_HUMAN]	13.35	2	4	4	7	1.000	5	0.000	26.458	382	40.403
J3KT51	Hematological and neurological-expressed 1 protein OS=Homo sapiens GN=HN1 PE=1 SV=1 - [J3KT51_HUMAN]	21.15	4	3	3	9	1.033	9	20.885	26.446	104	11.005
E9ATT5	40S ribosomal protein SA OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5010 PE=3 SV=1 - [E9ATT5_LEIMU]	13.01	3	3	4	11	1.000	7	0.000	26.441	246	27.552
Q9H1B7	Interferon regulatory factor 2-binding protein-like OS=Homo sapiens GN=IRF2BPL PE=1 SV=1 - [I2BPL_HUMAN]	4.02	1	1	3	11	0.725	1		26.425	796	82.607
Q8N995	cDNA FLJ38173 fis, clone FCBBF1000053, highly similar to HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC OS=Homo sapiens PE=2 SV=1 - [Q8N9!	10.41	4	5	5	10	0.973	9	11.088	26.377	509	56.203
J3KS15	Peptidyl-tRNA hydrolase ICT1, mitochondrial (Fragment) OS=Homo sapiens GN=ICT1 PE=1 SV=1 - [J3KS15_HUMAN]	20.83	2	4	4	9	1.000	9	6.337	26.350	192	21.891
A0A087WZP8	Caspase-4 OS=Homo sapiens GN=CASP4 PE=4 SV=1 - [A0A087WZP8_HUMAN]	11.82	8	3	3	8	1.000	6	0.000	26.308	330	37.885
O15173	Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1 - [PGRC2_HUMAN]	13	2	2	3	7	1.012	4	10.048	26.302	223	23.804
Q5QNY5	Peroxisomal biogenesis factor 19 (Fragment) OS=Homo sapiens GN=PEX19 PE=1 SV=1 - [Q5QNY5_HUMAN]	38.72	7	4	7	9	1.000	5	12.690	26.298	235	26.120
Q96QR8	Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3 - [PURB_HUMAN]	14.42	1	4	4	8	1.000	8	0.808	26.290	312	33.220
A0A024QZW7	Nucleoporin 153kDa, isoform CRA_a OS=Homo sapiens GN=NUP153 PE=4 SV=1 - [A0A024QZW7_HUMAN]	5.22	2	7	7	9	1.000	9	3.627	26.278	1475	153.873
A8K8N7	Phosphoribosylformylglycinamidine synthase (FGAR amidotransferase), isoform CRA_b OS=Homo sapiens GN=PFAS PE=2 SV=1 - [A8K8N7_HUMAN]	6.43	8	10	10	14	0.969	14	15.577	26.278	1338	144.633
Q96SI9	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1 - [STRBP_HUMAN]	3.57	3	2	3	10	0.913	5	2.415	26.259	672	73.606
B8XPJ7	Soluble catechol-O-methyltransferase OS=Homo sapiens GN=COMT PE=2 SV=1 - [B8XPJ7_HUMAN]	21.72	9	4	5	11	0.960	10	13.602	26.239	221	24.463
Q92544	Transmembrane 9 superfamily member 4 OS=Homo sapiens GN=TM9SF4 PE=1 SV=2 - [TM9S4_HUMAN]	10.59	5	7	7	11	1.000	11	1.320	26.166	642	74.470
B2R9L6	cDNA, FLJ94450, highly similar to Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R9L6_HUMAN]	12.9	46	4	5	9	1.000	6	0.000	26.158	372	42.720
Q8WXX5	DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1 - [DNJC9_HUMAN]	29.62	2	7	7	11	1.000	11	10.694	26.128	260	29.891
A8K566	cDNA FLJ78246, highly similar to Homo sapiens splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K566_HUMAN]	15.97	6	7	7	12	0.986	11	2.108	26.080	501	58.754
Q96K76	Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens GN=USP47 PE=1 SV=3 - [UBP47_HUMAN]	3.27	3	3	4	9	1.035	7	5.115	26.066	1375	157.212
Q06787	Fragile X mental retardation protein 1 OS=Homo sapiens GN=FMR1 PE=1 SV=1 - [FMR1_HUMAN]	7.44	11	1	5	10	0.799	2	34.278	26.056	632	71.131
A8K4G7	cDNA FLJ78528, highly similar to Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4G7_HUMAN]	18.47	9	8	10	13	0.997	8	2.931	26.053	444	49.242
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1 - [2ABA_HUMAN]	14.54	8	7	7	11	1.000	10	16.785	26.034	447	51.659
Q8N7H5	RNA polymerase II-associated factor 1 homolog OS=Homo sapiens GN=PAF1 PE=1 SV=2 - [PAF1_HUMAN]	12.81	3	6	6	11	0.947	10	9.280	26.032	531	59.939
Q9NVM6	DnaJ homolog subfamily C member 17 OS=Homo sapiens GN=DNAJC17 PE=1 SV=1 - [DJC17_HUMAN]	8.88	2	3	3	7	1.000	6	0.000	26.019	304	34.666
Q9UKY7	Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 SV=1 - [CDV3_HUMAN]	32.95	8	4	4	9	1.000	9	12.802	25.990	258	27.318
E5RIU6	Cyclin-dependent kinase 1 (Fragment) OS=Homo sapiens GN=CDK1 PE=1 SV=2 - [E5RIU6_HUMAN]	24.87	64	3	5	11	0.917	6	17.596	25.979	189	21.724
B4DRB3	cDNA FLJ52431, highly similar to Retinoblastoma-associated protein OS=Homo sapiens PE=2 SV=1 - [B4DRB3_HUMAN]	8.21	6	6	6	8	0.982	8	17.049	25.979	816	93.791
A0A087WWS1	THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=4 SV=1 - [A0A087WWS1_HUMAN]	8.07	6	6	6	9	1.000	9	8.258	25.974	657	75.605
B4DLP1	cDNA FLJ52560 OS=Homo sapiens PE=2 SV=1 - [B4DLP1_HUMAN]	14.93	14	5	5	9	0.918	9	12.706	25.935	355	38.774
B4DLS8	cDNA FLJ55983, highly similar to U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens PE=2 SV=1 - [B4DLS8_HUMAN]	7.17	5	5	5	9	0.985	9	21.347	25.891	669	75.802
E9ANF6	Putative seryl-tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0100 PE=3 SV=1 - [E9ANF6_LEIMU]	10.97	1	4	5	9	1.523	5	68.965	25.878	474	52.873
Q4TZM4	Hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1 - [Q4TZM4_HUMAN]	31.68	63	3	3	11	1.017	11	16.832	25.861	101	11.016
D3DS96	Bromodomain adjacent to zinc finger domain, 1A, isoform CRA_c OS=Homo sapiens GN=BAZ1A PE=4 SV=1 - [D3DS96_HUMAN]	7.33	6	10	10	12	0.998	12	27.241	25.856	1555	178.463
P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 - [ALDR_HUMAN]	17.41	6	5	5	12	1.000	12	3.418	25.833	316	35.830
P61326	Protein mago nashi homolog OS=Homo sapiens GN=MAGOH PE=1 SV=1 - [MGN_HUMAN]	32.88	6	5	6	14	1.000	13	7.531	25.833	146	17.153
Q9BWM7	Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=2 - [SFXN3_HUMAN]	9.54	3	3	3	8	1.176	8	15.186	25.811	325	35.956
A8K8K1	cDNA FLJ76936, highly similar to Homo sapiens RNA terminal phosphate cyclase domain 1 (RTCD1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8K1_HUMAN]	10.11	3	5	5	10	0.981	9	16.147	25.783	366	39.295
Q2NL82	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 - [TSR1_HUMAN]	11.44	2	8	8	9	1.000	8	8.034	25.783	804	91.752
B2R7V4	cDNA, FLJ93619, highly similar to Homo sapiens PRP4 pre-mRNA processing factor 4 homolog (yeast) (PRPF4), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7V4_HUM	10.73	2	1	5	8	0.930	2	10.760	25.776	522	58.412
Q5T1M7	60 kDa U4/U6 snRNP-specific spliceosomal protein OS=Homo sapiens GN=PRPF4 PE=2 SV=1 - [Q5T1M7_HUMAN]	10.56	3	1	5	8	0.970	2	4.493	25.759	521	58.284
O00505	Importin subunit alpha-4 OS=Homo sapiens GN=KPNA3 PE=1 SV=2 - [IMA4_HUMAN]	6.33	3	1	3	10	0.843	5	25.757	25.739	521	57.775
P56381	ATP synthase subunit epsilon, mitochondrial OS=Homo sapiens GN=ATP5E PE=1 SV=2 - [ATP5E_HUMAN]	43.14	1	3	3	11	0.983	10	9.089	25.718	51	5.776
Q5JPE4	Putative uncharacterized protein DKFZp667O202 OS=Homo sapiens GN=DKFZp667O202 PE=4 SV=1 - [Q5JPE4_HUMAN]	28.18	4	6	6	11	1.000	11	6.902	25.679	181	20.380
B4E1D4	cDNA FLJ54399, highly similar to Golgin subfamily A member 5 OS=Homo sapiens PE=2 SV=1 - [B4E1D4_HUMAN]	12.97	4	7	7	10	1.000	10	8.497	25.660	640	73.086
Q5VSN0	SH3 domain-containing kinase-binding protein 1 OS=Homo sapiens GN=SH3KBP1 PE=1 SV=1 - [Q5VSN0_HUMAN]	10.49	6	3	4	9	1.000	7	0.000	25.638	553	61.395
B4DDG7	cDNA FLJ57898, highly similar to Adaptor-relatedprotein complex 1 mu-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DDG7_HUMAN]	14.53	13	5	5	11	1.000	11	6.049	25.630	351	40.229
Q9NZL9	Methionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B PE=1 SV=1 - [MAT2B_HUMAN]	19.46	5	7	7	11	0.957	11	16.775	25.609	334	37.528
P35251	Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4 - [RFC1_HUMAN]	4.7	3	4	5	8	1.046	7	10.221	25.568	1148	128.175
B2R9I9	cDNA, FLJ94417, highly similar to Homo sapiens WD repeat domain 57 (U5 snRNP specific) (WDR57), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R9I9_HUMAN]	7.84	2	3	3	7	0.881	7	8.279	25.549	357	39.242

Q9NSY1	BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=2 - [BMP2K_HUMAN]	4.91	3	3	4	10	0.968	7	10.108	25.463	1161	129.091
G3XAH6	Poly(A) polymerase alpha OS=Homo sapiens GN=PAPOLA PE=1 SV=1 - [G3XAH6_HUMAN]	5.25	20	4	4	9	1.000	8	1.514	25.456	724	80.576
I3L4R8	Replication protein A 70 kDa DNA-binding subunit (Fragment) OS=Homo sapiens GN=RPA1 PE=1 SV=1 - [I3L4R8_HUMAN]	16.93	1	1	7	10	1.221	2	30.238	25.450	313	35.207
E9B6A1	Kinetoplastid membrane protein-11 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2220 PE=4 SV=1 - [E9B6A1_LEIMU]	41.3	3	5	5	12	1.794	12	104.180	25.398	92	11.201
Q9P287	BRCA2 and CDKN1A-interacting protein OS=Homo sapiens GN=BCCIP PE=1 SV=1 - [BCCIP_HUMAN]	17.2	3	6	6	12	0.922	12	11.133	25.374	314	35.957
P13612	Integrin alpha-4 OS=Homo sapiens GN=ITGA4 PE=1 SV=3 - [ITA4_HUMAN]	7.07	9	7	7	11	0.958	10	14.643	25.367	1032	114.827
Q0P607	Splicing factor, arginine/serine-rich 15 OS=Homo sapiens GN=SFRS15 PE=2 SV=1 - [Q0P607_HUMAN]	4.1	2	4	4	10	0.715	7	27.136	25.360	1146	125.662
Q5VT94	Growth hormone-inducible transmembrane protein OS=Homo sapiens GN=GHITM PE=1 SV=1 - [Q5VT94_HUMAN]	6.46	9	2	2	11	0.993	10	1.563	25.353	325	35.259
H3BPK3	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment) OS=Homo sapiens GN=HAGH PE=1 SV=1 - [H3BPK3_HUMAN]	15.9	6	3	3	12	0.988	12	4.453	25.341	239	26.398
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2 - [BIEA_HUMAN]	18.24	1	5	5	8	0.996	8	1.179	25.331	296	33.407
F8W9S7	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=1 - [F8W9S7_HUMAN]	3.75	10	1	6	10				25.315	1412	157.365
Q6NUM7	AGPAT5 protein (Fragment) OS=Homo sapiens GN=AGPAT5 PE=2 SV=1 - [Q6NUM7_HUMAN]	10.67	3	4	4	10	1.000	10	13.796	25.307	356	41.138
B4DH39	cDNA FLJ57028, highly similar to Long-chain-fatty-acid--CoA ligase 4 (EC 6.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B4DH39_HUMAN]	10.77	9	5	6	14	1.000	13	12.731	25.305	650	72.097
Q13895	Bystin OS=Homo sapiens GN=BYSL PE=1 SV=3 - [BYST_HUMAN]	20.37	2	6	6	9	1.000	9	0.000	25.299	437	49.570
O00629	Importin subunit alpha-3 OS=Homo sapiens GN=KPNA4 PE=1 SV=1 - [IMA3_HUMAN]	9.02	3	2	4	9	1.000	4	0.000	25.295	521	57.851
B4DWS6	cDNA FLJ61181, highly similar to Homo sapiens hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DWS6_HUMAN]	17.11	5	5	5	11	1.000	11	11.877	25.287	304	33.507
P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	3.72	6	5	5	11	1.000	11	0.000	25.283	967	109.471
A0A087WZY4	Metaxin 1, isoform CRA_b OS=Homo sapiens GN=MTX1 PE=4 SV=1 - [A0A087WZY4_HUMAN]	8.15	3	4	4	8	0.966	8	24.839	25.263	466	51.431
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 - [GRHPR_HUMAN]	21.95	4	6	6	11	0.962	11	14.770	25.258	328	35.646
G3V599	cTAGE family member 5 OS=Homo sapiens GN=CTAGE5 PE=4 SV=1 - [G3V599_HUMAN]	6.5	18	7	8	10	0.978	8	19.915	25.241	1339	151.626
Q53F20	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53F20_HUMAN]	28.95	13	5	6	17	1.000	13	11.514	25.122	266	30.416
H0Y3C5	Tyrosine-protein kinase HCK OS=Homo sapiens GN=HCK PE=1 SV=1 - [H0Y3C5_HUMAN]	12.95	51	5	9	15	1.000	7	7.996	25.110	525	59.473
E9PCJ7	Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 - [E9PCJ7_HUMAN]	9.72	9	4	4	10	1.012	10	9.266	25.070	360	41.129
B4DRW6	Alpha-1,4 glucan phosphorylase OS=Homo sapiens PE=2 SV=1 - [B4DRW6_HUMAN]	9.13	4	1	7	10	1.000	1		25.052	832	95.843
B4DIU6	cDNA FLJ59542, highly similar to Sad1/unc-84-like protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DIU6_HUMAN]	9.77	17	7	7	11	1.000	11	0.000	25.045	706	79.035
Q13057	Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4 - [COASY_HUMAN]	8.16	5	5	5	9	1.000	9	12.386	24.996	564	62.290
Q92667	A-kinase anchor protein 1, mitochondrial OS=Homo sapiens GN=AKAP1 PE=1 SV=1 - [AKAP1_HUMAN]	8.19	5	6	6	9	1.000	8	17.416	24.986	903	97.281
Q149P0	GBF1 protein OS=Homo sapiens GN=GBF1 PE=2 SV=1 - [Q149P0_HUMAN]	3.29	7	5	6	12	1.000	9	0.000	24.985	1855	205.885
H0YHC3	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 - [H0YHC3_HUMAN]	30.3	20	4	5	11	1.000	6	0.217	24.961	198	23.403
E9ANK8	Putative aminopeptidase (Metallo-peptidase, clan mf, family m17) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0630 PE=4 SV=1 - [E9ANK8	7.29	2	4	4	10	3.023	10	366.401	24.954	535	56.895
E9ASP6	Fructose-bisphosphate aldolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1260 PE=3 SV=1 - [E9ASP6_LEIMU]	13.75	1	6	6	9	3.746	9	83.736	24.946	371	40.808
Q05BX6	RABEP1 protein (Fragment) OS=Homo sapiens GN=RABEP1 PE=2 SV=1 - [Q05BX6_HUMAN]	9.64	4	8	8	13	1.000	13	9.237	24.927	716	82.327
E9B6R4	Putative T-complex protein 1, eta subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3860 PE=3 SV=1 - [E9B6R4_LEIMU]	7.89	2	3	4	10	1.000	5	0.000	24.920	570	61.692
A8K6X9	cDNA FLJ76427, highly similar to Homo sapiens SH2 domain binding protein 1 (tetratricopeptide repeat containing) (SH2BP1), mRNA OS=Homo sapiens PE=2 SV=1 - [A	5.97	3	7	7	10	1.000	9	0.000	24.878	1173	133.448
Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2 - [APMAP_HUMAN]	11.3	2	5	5	8	1.089	8	12.215	24.869	416	46.451
B4DQR2	cDNA FLJ57562, highly similar to Cleavage and polyadenylation specificityfactor 73 kDa subunit OS=Homo sapiens PE=2 SV=1 - [B4DQR2_HUMAN]	11.82	6	4	4	6	1.173	6	26.465	24.841	406	45.899
B5MCF9	Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 - [B5MCF9_HUMAN]	13.13	5	5	5	8	0.892	5	14.984	24.841	571	66.036
E9AXJ1	Aldehyde dehydrogenase, mitochondrial OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1120 PE=3 SV=1 - [E9AXJ1_LEIMU]	11.22	1	5	5	7	4.052	7	56.226	24.833	499	54.225
E9AT73	Succinyl-CoA ligase subunit beta OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2950 PE=3 SV=1 - [E9AT73_LEIMU]	15.25	1	6	6	9	1.538	9	70.915	24.828	413	44.070
Q9ULT8	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3 - [HECD1_HUMAN]	3.95	11	8	8	11	1.000	10	3.185	24.804	2610	289.203
B4DVB5	cDNA FLJ56724, highly similar to Polycomb complex protein RING1 OS=Homo sapiens PE=2 SV=1 - [B4DVB5_HUMAN]	16.67	4	3	3	6	0.988	5	1.729	24.776	282	29.721
E5RJT0	Eukaryotic translation initiation factor 3 subunit H (Fragment) OS=Homo sapiens GN=EIF3H PE=1 SV=1 - [E5RJT0_HUMAN]	14.75	1	1	4	10				24.692	244	28.357
P53582	Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=2 - [MAP11_HUMAN]	7.51	5	2	2	7	1.000	7	0.181	24.680	386	43.187
B7ZKM0	SART3 protein OS=Homo sapiens GN=SART3 PE=1 SV=1 - [B7ZKM0_HUMAN]	6.9	22	5	6	10	0.891	7	4.784	24.656	927	105.517
Q9UES0	SNARE protein Ykt6 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9UES0_HUMAN]	16.75	4	4	4	11	0.909	11	50.437	24.652	191	21.593
B2RA56	Nicalin OS=Homo sapiens PE=2 SV=1 - [B2RA56_HUMAN]	12.86	4	5	5	9	1.000	9	1.143	24.651	552	61.720
Q5IRN4	Myocyte enhancer factor 2D/deleted in azoospermia associated protein 1 fusion protein OS=Homo sapiens GN=MEF2D/DAZAP1 fusion PE=2 SV=1 - [Q5IRN4_HUMAN]	10.34	21	2	4	7	0.944	2	8.540	24.634	474	50.382
P09914	Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 - [IFIT1_HUMAN]	9.21	3	4	4	7	1.372	7	49.557	24.582	478	55.325
E9ATM0	Proteasome regulatory ATPase subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4360 PE=3 SV=1 - [E9ATM0_LEIMU]	10.51	2	2	4	11	1.000	2	0.000	24.577	409	45.544
G3V169	Caspase OS=Homo sapiens GN=CASP1 PE=1 SV=1 - [G3V169_HUMAN]	18.8	9	6	8	11	0.915	8	6.717	24.576	367	40.917
F8VU51	YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=1 - [F8VU51_HUMAN]	3.96	14	1	6	9	1.000	3	0.000	24.526	1440	160.641
Q8N5K1	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 - [CISD2_HUMAN]	40	3	5	5	10	1.045	10	7.874	24.512	135	15.268
E9ARI8	Aconitate hydratase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0510 PE=3 SV=1 - [E9ARI8_LEIMU]	7.14	1	7	7	10	2.117	10	159.355	24.468	896	97.410
B4DZZ8	cDNA FLJ52943, highly similar to Zinc transporter SLC39A7 OS=Homo sapiens PE=2 SV=1 - [B4DZZ8_HUMAN]	8.82	5	6	6	12	1.000	12	2.250	24.444	374	39.574
D3DSU3	Kinesin family member 13B, isoform CRA_a OS=Homo sapiens GN=KIF13B PE=3 SV=1 - [D3DSU3_HUMAN]	5.7	4	5	7	11	1.000	5	7.056	24.429	1562	174.692
O75323	Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1 - [NIPS2_HUMAN]	19.58	5	5	7	9	0.969	7	15.971	24.393	286	33.721
Q6I7N8	Lymphoid specific helicase variant9 OS=Homo sapiens GN=HELLS PE=2 SV=1 - [Q6I7N8_HUMAN]	6.55	6	4	4	8	1.000	8	1.131	24.378	809	93.903
Q53H82	Beta-lactamase-like protein 2 OS=Homo sapiens GN=LACTB2 PE=1 SV=2 - [LACB2_HUMAN]	17.01	1	5	5	13	1.000	13	5.188	24.350	288	32.785
H3BPC4	SUMO-conjugating enzyme UBC9 (Fragment) OS=Homo sapiens GN=UBE2I PE=1 SV=2 - [H3BPC4_HUMAN]	52.86	6	3	3	10	1.000	10	4.160	24.338	70	7.994
A0A024RDY9	Rho guanine nucleotide exchange factor (GEF) 7, isoform CRA_b OS=Homo sapiens GN=ARHGEF7 PE=4 SV=1 - [A0A024RDY9_HUMAN]	9.44	12	5	6	10	0.986	8	9.471	24.315	646	73.094
K7EK33	DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=4 SV=2 - [K7EK33_HUMAN]	10.84	6	1	3	7	1.146	2	20.475	24.302	406	43.228
P55008	Allograft inflammatory factor 1 OS=Homo sapiens GN=AIF1 PE=1 SV=1 - [AIF1_HUMAN]	25.85	8	4	5	11	1.155	9	3.074	24.261	147	16.693
E9ANC6	Putative rab1 small GTP-binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_1160 PE=3 SV=1 - [E9ANC6_LEIMU]	15.28	28	2	3	9	1.000	2	0.000	24.258	216	24.561
E9AZR7	Putative ribosomal protein S20 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1010 PE=3 SV=1 - [E9AZR7_LEIMU]	16.38	1	2	3	7	1.000	6	0.000	24.242	116	13.003
Q96DB5	Regulator of microtubule dynamics protein 1 OS=Homo sapiens GN=RMDN1 PE=1 SV=1 - [RMD1_HUMAN]	15.61	11	4	5	8	1.000	7	3.569	24.198	314	35.785
Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 PE=1 SV=2 - [PLCB3_HUMAN]	5.19	1	6	6	10	0.991	10	1.339	24.161	1234	138.713
A0A087WT27	Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=4 SV=1 - [A0A087WT27_HUMAN]	11.11	7	5	5	10	0.948	10	8.974	24.153	441	49.064
B1AK13	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (Hydroxymethylglutaricaciduria), isoform CRA_b OS=Homo sapiens GN=HMGCL PE=2 SV=1 - [B1AK13_HUMAN]	14.33	8	5	5	11	1.050	10	7.302	24.133	300	31.714
F5H4Z7	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 - [F5H4Z7_HUMAN]	20.81	8	3	3	9	1.000	9	0.000	24.117	173	18.784
Q99543	DnaJ homolog subfamily C member 2 OS=Homo sapiens GN=DNAJC2 PE=1 SV=4 - [DNJC2_HUMAN]	14.98	7	10	10	11	1.000	11	8.019	24.116	621	71.952
Q9Y5J9	Mitochondrial import inner membrane translocase subunit Tim8 B OS=Homo sapiens GN=TIMM8B PE=1 SV=1 - [TIM8B_HUMAN]	31.33	3	3	3	8	1.001	8	18.862	24.103	83	9.338
Q13769	THO complex subunit 5 homolog OS=Homo sapiens GN=THOC5 PE=1 SV=2 - [THOC5_HUMAN]	8.35	9	6	6	10	0.925	9	11.631	24.073	683	78.458
Q8NCW5	NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP PE=1 SV=2 - [NNRE_HUMAN]	18.75	6	6	6	12	1.000	11	2.291	23.989	288	31.654
B2RDV7	tRNA-dihydrouridine(47) synthase [NAD(P)(+)] OS=Homo sapiens PE=2 SV=1 - [B2RDV7_HUMAN]	12.62	9	5	5	9	1.000	5	0.000	23.982	650	72.574
Q99698	Lysosomal-trafficking regulator OS=Homo sapiens GN=LYST PE=1 SV=3 - [LYST_HUMAN]	1.47	2	3	3	8	1.000	7	0.000	23.978	3801	428.866
O43670	BUB3-interacting and GLEBS motif-containing protein ZNF207 OS=Homo sapiens GN=ZNF207 PE=1 SV=1 - [ZN207_HUMAN]	9.41	12	5	5	10	1.000	10	16.666	23.956	478	50.717
E9ALH7	Putative 60S ribosomal protein L13 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2460 PE=4 SV=1 - [E9ALH7_LEIMU]	25	1	6	6	10	1.000	10	21.693	23.953	220	24.729
Q15648	Mediator of RNA polymerase II transcription subunit 1 OS=Homo sapiens GN=MED1 PE=1 SV=4 - [MED1_HUMAN]	2.47	5	4	4	8	1.150	8	23.835	23.910	1581	168.373
E9ANP0	40S ribosomal protein S5 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0960 PE=4 SV=1 - [E9ANP0_LEIMU]	12.63	1	1	2	9	1.205	1		23.900	190	21.273
B2RDD7	Protein arginine N-methyltransferase 5 OS=Homo sapiens PE=2 SV=1 - [B2RDD7_HUMAN]	9.89	13	6	6	9	0.993	9	14.741	23.894	637	72.664
G3V5E1	Cyclin-K OS=Homo sapiens GN=CCNK PE=1 SV=1 - [G3V5E1_HUMAN]	8.2	3	3	3	10	1.000	10	4.930	23.887	378	43.377
A8K6A5	cDNA FLJ77742, highly similar to Homo sapiens integrin, alpha 5 (fibronectin receptor, alpha polypeptide), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6A5_HUMAN]	5.15	5	5	5	9	0.982	9	17.490	23.879	1049	114.412
C9JUK7	Leukosialin (Fragment) OS=Homo sapiens GN=SPN PE=1 SV=1 - [C9JUK7_HUMAN]	5.35	2	2	2	9	1.000	9	9.870	23.802	355	35.940
Q9Y608	Leucine-rich repeat flightless-interacting protein 2 OS=Homo sapiens GN=LRRFIP2 PE=1 SV=1 - [LRRF2_HUMAN]	6.1	3	3	5	8	0.854	4	17.744	23.801	721	82.121
O96005	Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1 - [CLPT1_HUMAN]	5.53	3	4	4	10	1.000	10	5.821	23.796	669	76.048
Q4G0F5	Vacuolar protein sorting-associated protein 26B OS=Homo sapiens GN=VPS26B PE=1 SV=2 - [VP26B_HUMAN]	18.15	1	5	5	10	1.000	10	0.000	23.770	336	39.130
E9ASA6	Peptidylprolyl isomerase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1530 PE=4 SV=1 - [E9ASA6_LEIMU]	9.26	1	4	4	9	1.268	9	36.295	23.764	432	47.746
H0YIQ2	YLP motif-containing protein 1 (Fragment) OS=Homo sapiens GN=YLPM1 PE=1 SV=1 - [H0YIQ2_HUMAN]	5.83	15	5	10	12	1.000	5	0.000	23.763	1595	180.174
A0A024R7C4	Uncharacterized protein OS=Homo sapiens GN=FLJ12949 PE=4 SV=1 - [A0A024R7C4_HUMAN]	7.67	8	5	5	12	1.000	10	7.958	23.762	574	67.382
Q8IWJ2	GRIP and coiled-coil domain-containing protein 2 OS=Homo sapiens GN=GCC2 PE=1 SV=4 - [GCC2_HUMAN]	3.5	21	6	7	11	1.000	7	0.000	23.731	1684	195.789
Q9NTJ5	Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=1 SV=2 - [SAC1_HUMAN]	12.44	8	8	8	15	1.000	15	13.991	23.722	587	66.924
B3KU96	cDNA FLJ39433 fis, clone PROST2004142, highly similar to GDP-L-fucose synthetase (EC 1.1.1.271) OS=Homo sapiens PE=2 SV=1 - [B3KU96_HUMAN]	29.81	7	4	4	8	0.924	8	16.820	23.720	161	17.685
Q9C0C9	E2/E3 hybrid ubiquitin-protein ligase UBE2O OS=Homo sapiens GN=UBE2O PE=1 SV=3 - [UBE2O_HUMAN]	4.72	3	5	5	9	1.000	9	0.000	23.713	1292	141.205
F8W7U8	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=1 - [F8W7U8_HUMAN]	2.83	4	3	3	8	0.872	8	20.437	23.711	707	80.472
A8K168	Malic enzyme OS=Homo sapiens PE=2 SV=1 - [A8K168_HUMAN]	7.87	4	5	5	9	0.993	9	3.286	23.678	572	64.095
Q14160	Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4 - [SCRIB_HUMAN]	6.87	4	8	8	11	0.965	10	11.311	23.645	1630	174.778
P01834	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 - [IGKC_HUMAN]	49.06	26	3	3	6	0.968	5	4.805	23.614	106	11.602
P16152	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]	11.91	5	3	3	8	1.000	7	29.300	23.581	277	30.356
Q96RE7	Nucleus accumbens-associated protein 1 OS=Homo sapiens GN=NACC1 PE=1 SV=1 - [NACC1_HUMAN]	11.57	3	5	5	9	1.000	7	0.000	23.574	527	57.222
Q9UBU9	Nuclear RNA export factor 1 OS=Homo sapiens GN=NXF1 PE=1 SV=1 - [NXF1_HUMAN]	9.53	10	6	6	9	0.979	9	3.114	23.571	619	70.139
C9JZG2	Trifunctional purine biosynthetic protein adenosine-3 (Fragment) OS=Homo sapiens GN=GART PE=1 SV=1 - [C9JZG2_HUMAN]	38.24	2	1	5	9	1.137	2	19.253	23.551	136	14.451
H0YI98	Dynactin subunit 2 (Fragment) OS=Homo sapiens GN=DCTN2 PE=1 SV=1 - [H0YI98_HUMAN]	22.76	10	6	6	9	1.000	9	2.185	23.530	268	29.308
E9B478	Putative heat shock protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2390 PE=3 SV=1 - [E9B478_LEIMU]	8.83	1	4	6	9	1.000	7	0.000	23.530	634	72.067
O75530	Polycomb protein EED OS=Homo sapiens GN=EED PE=1 SV=2 - [EED_HUMAN]	5.44	4	2	2	10	1.000	7	0.000	23.524	441	50.166
Q9UI10	Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 - [EI2BD_HUMAN]	12.81	7	1	5	9	0.775	2	39.250	23.506	523	57.521
E9AST5	Putative poly-zinc finger protein 2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1635 PE=4 SV=1 - [E9AST5_LEIMU]	23.7	1	3	3	8	1.792	8	101.434	23.505	135	14.568
O75911	Short-chain dehydrogenase/reductase 3 OS=Homo sapiens GN=DHRS3 PE=1 SV=2 - [DHRS3_HUMAN]	12.25	5	4	4	8	1.079	8	40.646	23.483	302	33.527
Q969H8	UPF0556 protein C19orf10 OS=Homo sapiens GN=C19orf10 PE=1 SV=1 - [CS010_HUMAN]	18.5	3	5	5	12	0.996	12	3.951	23.482	173	18.783
P13984	General transcription factor IIF subunit 2 OS=Homo sapiens GN=GTF2F2 PE=1 SV=2 - [T2FB_HUMAN]	14.06	1	4	4	10	0.910	10	14.091	23.473	249	28.363
P20336	Ras-related protein Rab-3A OS=Homo sapiens GN=RAB3A PE=1 SV=1 - [RAB3A_HUMAN]	15.45	33	1	4	11	1.000	1		23.434	220	24.968
Q8IXB1	DnaJ homolog subfamily C member 10 OS=Homo sapiens GN=DNAJC10 PE=1 SV=2 - [DJC10_HUMAN]	8.83	10	6	6	9	1.046	9	21.604	23.425	793	91.021
B4DP22	cDNA FLJ55993, highly similar to Retinoid-inducible serine carboxypeptidase (EC 3.4.16.-) OS=Homo sapiens PE=2 SV=1 - [B4DP22_HUMAN]	14.18	4	6	6	11	1.038	11	6.268	23.399	402	45.103
O60784	Target of Myb protein 1 OS=Homo sapiens GN=TOM1 PE=1 SV=2 - [TOM1_HUMAN]	11.79	11	5	5	8	1.014	8	7.818	23.398	492	53.785
E9APT0	Putative calpain-like cysteine peptidase (Putative cysteine peptidase, clan ca, family c2) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0850	32.17	1	4	4	9	1.000	9	246.223	23.388	115	12.941
B3KM48	cDNA FLJ10286 fis, clone HEMBB1001384, highly similar to COP9 signalosome complex subunit 4 OS=Homo sapiens PE=2 SV=1 - [B3KM48_HUMAN]	15.76	6	6	6	11	0.979	11	29.797	23.363	406	46.226
E9B3B0	T-complex protein 1 subunit alpha OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3270 PE=3 SV=1 - [E9B3B0_LEIMU]	8.79	1	4	4	8	1.000	7	0.000	23.345	546	59.153
Q6NYC8	Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1 - [PPR18_HUMAN]	12.23	2	5	5	13	1.000	10	0.000	23.319	613	67.902
A0A024R2H0	TBC1 domain family, member 5, isoform CRA_a OS=Homo sapiens GN=TBC1D5 PE=4 SV=1 - [A0A024R2H0_HUMAN]	4.4	4	3	3	8	1.000	7	0.000	23.288	795	89.003
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1 OS=Homo sapiens GN=CHAMP1 PE=1 SV=2 - [CHAP1_HUMAN]	7.14	2	6	6	10	0.807	10	35.158	23.265	812	89.043
P56545	C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 - [CTBP2_HUMAN]	10.34	13	1	6	10				23.252	445	48.914
Q9ULU4	Protein kinase C-binding protein 1 OS=Homo sapiens GN=ZMYND8 PE=1 SV=2 - [PKCB1_HUMAN]	6.41	6	6	6	11	1.000	10	0.000	23.221	1186	131.610
Q9Y399	28S ribosomal protein S2, mitochondrial OS=Homo sapiens GN=MRPS2 PE=1 SV=1 - [RT02_HUMAN]	11.82	3	4	4	9	1.000	9	5.961	23.194	296	33.228
P19474	E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1 - [RO52_HUMAN]	14.53	2	7	7	11	1.000	11	12.379	23.186	475	54.135
O60885	Bromodomain-containing protein 4 OS=Homo sapiens GN=BRD4 PE=1 SV=2 - [BRD4_HUMAN]	4.63	8	5	6	9	1.027	8	11.269	23.186	1362	152.124
U3PXP0	Alpha globin chain (Fragment) OS=Homo sapiens GN=HBA2 PE=3 SV=1 - [U3PXP0_HUMAN]	47.06	11	2	2	12	1.151	12	29.440	23.167	51	5.699
A0A087WYR0	Signal recognition particle 19 kDa protein OS=Homo sapiens GN=SRP19 PE=4 SV=1 - [A0A087WYR0_HUMAN]	24.17	3	2	2	7	1.000	7	1.441	23.152	120	13.645
B2R860	cDNA, FLJ93752, highly similar to Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R860_HUMAN]	13.21	7	2	4	7	0.988	4	9.056	23.138	318	34.648
Q15813	Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 - [TBCE_HUMAN]	9.68	2	5	5	8	0.982	8	8.838	23.131	527	59.309
E9PRR7	Protein FRG1 (Fragment) OS=Homo sapiens GN=FRG1 PE=1 SV=1 - [E9PRR7_HUMAN]	30.17	8	3	3	8	1.000	7	21.189	23.106	116	12.508
A0A087X142	Septin-8 OS=Homo sapiens GN=SEPT8 PE=4 SV=1 - [A0A087X142_HUMAN]	5.4	7	1	3	12	0.834	1		23.103	426	49.325
B1ANM7	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=1 - [B1ANM7_HUMAN]	7.55	5	4	4	9	0.973	9	9.474	23.094	490	55.963
A0A024R5K3	NADH dehydrogenase (Ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase), isoform CRA_b OS=Homo sapiens GN=NDUFS8 PE=4 SV=1 - [A0A024R5K	26.16	9	4	4	9	0.977	8	3.447	23.059	172	19.201
M0QWZ7	Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 PE=1 SV=1 - [M0QWZ7_HUMAN]	12.74	10	5	5	9	1.000	8	0.000	23.054	518	58.146
H0Y3T6	45 kDa calcium-binding protein (Fragment) OS=Homo sapiens GN=SDF4 PE=1 SV=1 - [H0Y3T6_HUMAN]	16.05	4	3	4	9	1.001	8	7.442	23.041	243	28.094
B1APM4	Sterol O-acyltransferase 1 (Fragment) OS=Homo sapiens GN=SOAT1 PE=1 SV=1 - [B1APM4_HUMAN]	8.85	3	4	4	12	1.000	11	0.000	23.041	260	29.874
P80294	Metallothionein-1H OS=Homo sapiens GN=MT1H PE=1 SV=1 - [MT1H_HUMAN]	45.9	4	1	2	9	1.000	1		23.031	61	6.034
B3KRW4	cDNA FLJ34980 fis, clone OCBBF2000522, highly similar to Rab GTPase-binding effector protein 2 OS=Homo sapiens PE=2 SV=1 - [B3KRW4_HUMAN]	6.85	7	5	5	9	0.911	7	13.954	23.027	569	63.488
E9ALH4	Vacuolar protein sorting-associated protein 4 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2500 PE=3 SV=1 - [E9ALH4_LEIMU]	6.74	4	1	2	8	1.000	2	0.000	23.026	445	49.959
E9AJG4	Complete genome, chromosome 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_01_0770 PE=3 SV=1 - [E9AJG4_LEIMU]	11.18	1	4	5	8	1.246	6	33.495	22.993	456	51.054
Q96CP2	FLYWCH family member 2 OS=Homo sapiens GN=FLYWCH2 PE=1 SV=1 - [FWCH2_HUMAN]	22.14	3	2	2	8	1.000	8	0.000	22.992	140	14.555
E9AW21	Putative endoribonuclease L-PSP (Pb5) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0200 PE=4 SV=1 - [E9AW21_LEIMU]	22.09	1	3	3	10	1.409	10	73.162	22.980	163	16.779
Q5JNW7	Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=1 - [Q5JNW7_HUMAN]	28.17	5	6	6	8	0.925	8	10.992	22.975	252	27.832
B0AZS5	cDNA, FLJ79515, highly similar to Kinesin-like protein KIF2 OS=Homo sapiens PE=2 SV=1 - [B0AZS5_HUMAN]	11.52	5	4	4	8	1.000	8	8.247	22.918	660	74.982
C9J1X0	Uncharacterized protein OS=Homo sapiens GN=WDR91 PE=1 SV=1 - [C9J1X0_HUMAN]	8.15	3	5	5	8	1.000	8	35.937	22.905	712	79.190
O43617	Trafficking protein particle complex subunit 3 OS=Homo sapiens GN=TRAPPC3 PE=1 SV=1 - [TPPC3_HUMAN]	20.56	4	4	4	8	0.944	8	18.694	22.904	180	20.261
E9APE7	40S ribosomal protein S4 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1230 PE=3 SV=1 - [E9APE7_LEIMU]	18.68	2	5	5	9	1.514	9	31.022	22.881	273	30.635
C9JG97	Angio-associated migratory cell protein OS=Homo sapiens GN=AAMP PE=1 SV=1 - [C9JG97_HUMAN]	10.84	6	4	4	7	1.045	7	6.592	22.873	415	44.665
K7ERP4	Glutathione peroxidase (Fragment) OS=Homo sapiens GN=GPX4 PE=1 SV=1 - [K7ERP4_HUMAN]	27.1	10	4	4	8	0.978	8	9.446	22.858	155	17.618
H7C0E5	Zinc finger protein ZPR1 (Fragment) OS=Homo sapiens GN=ZPR1 PE=1 SV=1 - [H7C0E5_HUMAN]	17.1	5	5	6	6	0.992	6	9.532	22.823	386	42.626
B2RCM6	cDNA, FLJ96161 OS=Homo sapiens PE=2 SV=1 - [B2RCM6_HUMAN]	12.25	3	2	2	8	0.930	5	10.806	22.801	253	28.177
B3KUJ0	cDNA FLJ39996 fis, clone STOMA2002166, highly similar to Splicing factor 3B subunit 4 OS=Homo sapiens PE=2 SV=1 - [B3KUJ0_HUMAN]	5.9	4	3	3	7	1.000	7	8.328	22.795	424	44.455
E2QRB9	Glycosyl-phosphatidylinositol-anchored molecule-like protein OS=Homo sapiens GN=GML PE=3 SV=2 - [E2QRB9_HUMAN]	8.04	12	4	4	11	0.959	11	16.389	22.791	460	50.691
P20338	Ras-related protein Rab-4A OS=Homo sapiens GN=RAB4A PE=1 SV=3 - [RAB4A_HUMAN]	13.76	33	2	3	8	1.349	2	3.739	22.758	218	24.374
Q92665	28S ribosomal protein S31, mitochondrial OS=Homo sapiens GN=MRPS31 PE=1 SV=3 - [RT31_HUMAN]	6.84	1	1	4	8	1.000	8	1.404	22.729	395	45.290
B4DUP5	cDNA FLJ60165, highly similar to Translation initiation factor eIF-2B subunit delta OS=Homo sapiens PE=2 SV=1 - [B4DUP5_HUMAN]	21.15	6	1	5	9	0.700	2	56.698	22.728	312	34.775
Q658K0	Putative uncharacterized protein DKFZp564P2364 OS=Homo sapiens GN=DKFZp564P2364 PE=2 SV=1 - [Q658K0_HUMAN]	7.98	5	6	6	9	1.000	9	0.000	22.714	940	107.572
Q96BY6	Dedicator of cytokinesis protein 10 OS=Homo sapiens GN=DOCK10 PE=1 SV=3 - [DOC10_HUMAN]	4.16	23	7	9	10	1.000	8	10.495	22.701	2186	249.373
B4DPT1	cDNA FLJ51524, highly similar to Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens PE=2 SV=1 - [B4DPT1_HUMAN]	18.61	4	6	6	9	1.000	9	16.752	22.632	489	55.231
B7Z425	Syntaxin 4A (Placental), isoform CRA_a OS=Homo sapiens GN=STX4A PE=2 SV=1 - [B7Z425_HUMAN]	21	6	4	4	9	1.000	8	0.000	22.625	219	25.246
Q9UKK9	ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1 - [NUDT5_HUMAN]	25.11	6	5	5	9	0.999	9	6.435	22.609	219	24.312
B2RD19	cDNA, FLJ96419, highly similar to Homo sapiens fructosamine-3-kinase-related protein (FN3KRP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RD19_HUMAN]	13.79	3	6	6	9	0.885	9	13.771	22.596	309	34.330
Q05CW7	NAT10 protein (Fragment) OS=Homo sapiens GN=NAT10 PE=2 SV=1 - [Q05CW7_HUMAN]	8.3	2	1	4	10	1.000	1		22.587	554	62.345
D5L9D9	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1 - [D5L9D9_HUMAN]	11.05	57	0	2	9				22.559	181	20.888
Q86VS8	Protein Hook homolog 3 OS=Homo sapiens GN=HOOK3 PE=1 SV=2 - [HOOK3_HUMAN]	9.19	3	5	5	8	0.985	8	2.177	22.550	718	83.074
B3KM58	cDNA FLJ10358 fis, clone NT2RM2001238, highly similar to Glutaminase kidney isoform, mitochondrial (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KM58_HUMAN]	13.21	6	1	4	7	1.174	2	19.671	22.547	371	41.109
Q9GZY6	Linker for activation of T-cells family member 2 OS=Homo sapiens GN=LAT2 PE=1 SV=1 - [NTAL_HUMAN]	10.7	5	2	2	6	1.000	6	0.000	22.533	243	26.534
Q6IPN0	Reticulon OS=Homo sapiens GN=RTN4 PE=2 SV=1 - [Q6IPN0_HUMAN]	10.2	9	3	3	12	0.888	12	17.503	22.508	343	36.895
E7EVX8	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=1 - [E7EVX8_HUMAN]	9.74	8	5	5	9	1.000	8	22.402	22.486	493	54.732
P25490	Transcriptional repressor protein YY1 OS=Homo sapiens GN=YY1 PE=1 SV=2 - [TYY1_HUMAN]	14.49	3	6	6	8	0.959	8	13.237	22.462	414	44.685
Q8NHJ6	Leukocyte immunoglobulin-like receptor subfamily B member 4 OS=Homo sapiens GN=LILRB4 PE=1 SV=3 - [LIRB4_HUMAN]	15.85	17	5	5	9	1.000	8	0.000	22.457	448	49.325
B7Z6Y2	cDNA FLJ54942, highly similar to Homo sapiens bridging integrator 1 (BIN1), transcript variant 10, mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z6Y2_HUMAN]	17.92	18	6	7	11	1.061	9	16.698	22.425	385	43.139
B3KUJ5	Histone deacetylase OS=Homo sapiens PE=2 SV=1 - [B3KUJ5_HUMAN]	7.42	12	3	4	12	0.999	9	5.557	22.372	458	51.939
F2Z2U4	Transformation/transcription domain-associated protein OS=Homo sapiens GN=TRRAP PE=1 SV=3 - [F2Z2U4_HUMAN]	1.38	4	5	6	9	0.931	8	10.571	22.360	3848	435.858
E7ET76	Gamma-glutamyltranspeptidase 1 (Fragment) OS=Homo sapiens GN=GGT1 PE=4 SV=1 - [E7ET76_HUMAN]	7.99	18	4	4	10	1.000	10	12.915	22.334	463	50.029
P49773	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2 - [HINT1_HUMAN]	18.25	6	4	4	8	0.962	8	10.959	22.331	126	13.793
P78356	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta OS=Homo sapiens GN=PIP4K2B PE=1 SV=1 - [PI42B_HUMAN]	9.13	5	1	3	8	0.969	4	3.885	22.307	416	47.348
B2RAH5	Protein phosphatase 1 regulatory subunit 12 OS=Homo sapiens PE=2 SV=1 - [B2RAH5_HUMAN]	5.83	9	5	5	8	1.000	8	32.123	22.302	1030	115.259
Q96BS4	FBL protein (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=2 - [Q96BS4_HUMAN]	22.31	13	5	5	10	1.000	9	7.408	22.292	260	28.432
B4DGN8	cDNA FLJ53377, highly similar to Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 (EC 1.14.11.4) OS=Homo sapiens PE=2 SV=1 - [B4DGN8_HUMAN]	7.54	7	5	6	11	1.032	8	5.487	22.265	690	79.349
B4DS67	cDNA FLJ59967 OS=Homo sapiens PE=2 SV=1 - [B4DS67_HUMAN]	5.36	3	1	1	7	1.030	6	4.835	22.243	224	24.057
Q9UKX7	Nuclear pore complex protein Nup50 OS=Homo sapiens GN=NUP50 PE=1 SV=2 - [NUP50_HUMAN]	8.97	2	5	5	11	1.000	11	0.000	22.241	468	50.113
B3KSU9	cDNA FLJ37014 fis, clone BRACE2010203, highly similar to Zinc phosphodiesterase ELAC protein 2 (EC 3.1.26.11) OS=Homo sapiens PE=2 SV=1 - [B3KSU9_HUMAN]	7.34	8	4	4	12	1.000	12	7.509	22.241	586	65.332
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3 - [2AAB_HUMAN]	4.33	6	1	4	10	0.847	1		22.212	601	66.171
Q96EE3	Nucleoporin SEH1 OS=Homo sapiens GN=SEH1L PE=1 SV=3 - [SEH1_HUMAN]	13.33	5	4	4	8	1.000	8	3.458	22.205	360	39.623
B7Z591	Transmembrane and coiled-coil domains 1, isoform CRA_a OS=Homo sapiens GN=TMCO1 PE=2 SV=1 - [B7Z591_HUMAN]	17.61	6	3	3	8	1.011	8	37.771	22.188	176	19.884
Q9NRX5	Serine incorporator 1 OS=Homo sapiens GN=SERINC1 PE=1 SV=1 - [SERC1_HUMAN]	4.86	1	2	2	7	0.981	7	13.261	22.176	453	50.461
A8K0A4	cDNA FLJ77631, highly similar to Homo sapiens HLA-B associated transcript 5 (BAT5), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K0A4_HUMAN]	7.71	3	4	4	8	1.120	7	10.349	22.142	558	63.219
E9B6R2	Proteasome subunit beta type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3840 PE=3 SV=1 - [E9B6R2_LEIMU]	7.48	1	2	2	9	1.000	8	0.000	22.128	254	27.531
B7ZKN7	BLM protein OS=Homo sapiens GN=BLM PE=2 SV=1 - [B7ZKN7_HUMAN]	2.02	7	2	2	11	0.934	5	10.080	22.121	1042	116.989

O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 SV=3 - [NDUA7_HUMAN]	55.75	5	6	6	9	1.000	9	3.178	22.119	113	12.544
X5D7T7	C-terminal binding protein 1 isoform D OS=Homo sapiens GN=CTBP1 PE=2 SV=1 - [X5D7T7_HUMAN]	13.07	13	1	5	9	1.000	1		22.064	329	36.024
M0QXN5	Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=1 - [M0QXN5_HUMAN]	7.17	2	3	3	7	1.183	7	20.286	22.049	446	45.588
B7Z2L0	B-cell receptor-associated protein 29 OS=Homo sapiens GN=BCAP29 PE=1 SV=1 - [B7Z2L0_HUMAN]	21.09	9	4	4	8	0.923	8	7.432	22.016	147	17.363
B3KNC3	cDNA FLJ14222 fis, clone NT2RP3003992, highly similar to Nucleolar complex protein 2 homolog OS=Homo sapiens PE=2 SV=1 - [B3KNC3_HUMAN]	6.81	4	5	5	10	0.956	10	12.503	21.986	749	84.864
E9ANA1	Putative small GTP-binding protein Rab11 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0910 PE=3 SV=1 - [E9ANA1_LEIMU]	10.58	27	1	2	8	1.000	1		21.967	208	23.344
K7EJX0	Mothers against decapentaplegic homolog 2 (Fragment) OS=Homo sapiens GN=SMAD2 PE=1 SV=1 - [K7EJX0_HUMAN]	28.11	18	6	6	7	1.000	7	0.000	21.906	217	24.478
O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2 - [CLPX_HUMAN]	11.06	4	7	7	9	1.010	8	14.061	21.904	633	69.181
Q9NPL8	Complex I assembly factor TIMMDC1, mitochondrial OS=Homo sapiens GN=TIMMDC1 PE=1 SV=2 - [TIDC1_HUMAN]	13.68	4	3	3	6	0.995	6	13.812	21.902	285	32.158
B4E0Q4	Suppressor of Ty 5 homolog (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=SUPT5H PE=2 SV=1 - [B4E0Q4_HUMAN]	7.08	4	7	7	8	1.000	8	11.396	21.899	946	104.318
B4DK32	cDNA FLJ61095, highly similar to Ubiquitin conjugation factor E4 A (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DK32_HUMAN]	3.25	3	3	3	6	1.000	5	5.606	21.892	1045	119.732
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3 - [TOM22_HUMAN]	26.06	2	2	2	7	1.000	7	0.000	21.887	142	15.512
B9A018	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=1 SV=1 - [B9A018_HUMAN]	8.02	7	5	5	8	1.000	8	0.000	21.866	536	62.005
Q96CT7	Coiled-coil domain-containing protein 124 OS=Homo sapiens GN=CCDC124 PE=1 SV=1 - [CC124_HUMAN]	24.66	2	6	6	8	0.990	8	5.315	21.852	223	25.820
H0YD64	Solute carrier family 43 member 3 (Fragment) OS=Homo sapiens GN=SLC43A3 PE=1 SV=1 - [H0YD64_HUMAN]	14.6	6	2	2	10	1.031	10	29.554	21.840	137	15.773
Q14289	Protein-tyrosine kinase 2-beta OS=Homo sapiens GN=PTK2B PE=1 SV=2 - [FAK2_HUMAN]	5.55	5	7	7	9	1.000	9	7.173	21.837	1009	115.800
B4DWZ7	cDNA FLJ56802, highly similar to LanC-like protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DWZ7_HUMAN]	5.79	3	2	2	6	1.089	6	12.675	21.833	432	48.853
O15371	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 - [EIF3D_HUMAN]	8.76	6	5	5	8	0.949	8	7.688	21.817	548	63.932
E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=1 - [E9PEM5_HUMAN]	2.68	5	5	5	7	1.000	6	31.732	21.788	2575	286.793
P17900	Ganglioside GM2 activator OS=Homo sapiens GN=GM2A PE=1 SV=4 - [SAP3_HUMAN]	18.65	5	4	4	8	0.997	8	8.716	21.759	193	20.825
K0J5S8	TRK-fused gene protein isoform 4 OS=Homo sapiens GN=TFG PE=2 SV=1 - [K0J5S8_HUMAN]	20.36	10	5	5	9	1.000	9	11.945	21.750	280	30.902
B3KM95	Phosphatidate cytidylyltransferase OS=Homo sapiens PE=2 SV=1 - [B3KM95_HUMAN]	11.24	3	4	4	8	1.000	7	0.000	21.718	445	51.326
H0Y8B3	Adenosylhomocysteinase (Fragment) OS=Homo sapiens GN=AHCYL2 PE=3 SV=1 - [H0Y8B3_HUMAN]	13.51	4	1	5	9	0.825	1		21.697	518	58.077
B3KRB7	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta, isoform CRA_a OS=Homo sapiens GN=IKBKB PE=2 SV=1 - [B3KRB7_HUMAN]	9.19	4	4	4	9	1.121	8	24.577	21.692	533	60.781
P43358	Melanoma-associated antigen 4 OS=Homo sapiens GN=MAGEA4 PE=1 SV=2 - [MAGA4_HUMAN]	18.3	13	4	5	9	0.984	8	8.357	21.686	317	34.877
V9H019	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=2 SV=1 - [V9H019_HUMAN]	9.51	23	7	7	8	0.943	8	29.715	21.683	810	90.798
Q6UW46	VGPW2523 OS=Homo sapiens GN=UNQ2523 PE=2 SV=1 - [Q6UW46_HUMAN]	11.11	1	2	4	9	1.000	5	0.000	21.670	315	35.942
Q8TD16	Protein bicaudal D homolog 2 OS=Homo sapiens GN=BICD2 PE=1 SV=1 - [BICD2_HUMAN]	6.8	1	6	6	8	1.000	8	20.880	21.666	824	93.476
Q52LJ0	Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 - [FA98B_HUMAN]	12.42	3	3	4	9	0.971	5	4.321	21.644	330	37.167
F8W9X7	Coiled-coil domain-containing protein 93 OS=Homo sapiens GN=CCDC93 PE=1 SV=1 - [F8W9X7_HUMAN]	6.83	2	4	4	8	1.000	7	15.525	21.634	630	72.996
B4DRA5	cDNA FLJ61346, highly similar to Protein transport protein Sec23B OS=Homo sapiens PE=2 SV=1 - [B4DRA5_HUMAN]	7.95	10	5	6	10	1.000	9	4.981	21.630	742	83.756
B1PL87	Bid (Fragment) OS=Homo sapiens PE=2 SV=1 - [B1PL87_HUMAN]	17.65	3	2	2	7	0.961	6	10.463	21.619	136	15.326
B4DQF1	cDNA FLJ55810, highly similar to Golgi reassembly-stacking protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DQF1_HUMAN]	14.19	4	3	3	10	0.910	8	14.029	21.614	310	31.774
K7EPV0	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial OS=Homo sapiens GN=COA3 PE=1 SV=1 - [K7EPV0_HUMAN]	39.44	2	4	4	8	1.042	8	14.743	21.602	71	7.801
B2R7W0	cDNA, FLJ93628, Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2),nuclear gene encodi	16.28	7	6	6	11	1.143	9	9.626	21.585	344	37.297
H0YNG3	Signal peptidase complex catalytic subunit SEC11A OS=Homo sapiens GN=SEC11A PE=1 SV=1 - [H0YNG3_HUMAN]	19.63	8	4	4	12	1.000	12	0.000	21.530	163	18.639
B2RB99	cDNA, FLJ95387 OS=Homo sapiens PE=2 SV=1 - [B2RB99_HUMAN]	14.38	5	4	4	9	1.000	9	12.352	21.528	306	33.777
B4DL66	cDNA FLJ56297, highly similar to Rattus norvegicus ubiquitin-conjugating enzyme E2Z (putative) (Ube2z), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DL66_HUMAN]	14.63	8	4	4	9	1.000	9	7.641	21.522	287	32.871
B4DLR8	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [B4DLR8_HUMAN]	14.85	7	4	4	9	1.039	9	15.367	21.517	202	22.779
Q9HC35	Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4 PE=1 SV=3 - [EMAL4_HUMAN]	11.21	14	9	9	11	1.000	11	1.395	21.500	981	108.848
Q9P253	Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens GN=VPS18 PE=1 SV=2 - [VPS18_HUMAN]	4.32	3	4	4	10	1.000	10	1.469	21.498	973	110.116
Q08209	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens GN=PPP3CA PE=1 SV=1 - [PP2BA_HUMAN]	9.98	11	3	5	8	1.088	3	15.733	21.450	521	58.650
Q13287	N-myc-interactor OS=Homo sapiens GN=NMI PE=1 SV=2 - [NMI_HUMAN]	22.15	6	7	7	10	0.926	10	17.001	21.405	307	35.035
Q9UQS5	NADH-ubiquinone oxidoreductase B22 subunit (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9UQS5_HUMAN]	28.43	6	2	2	9	1.000	9	6.265	21.387	102	12.293
E7ESK6	Syndecan OS=Homo sapiens GN=SDC2 PE=1 SV=1 - [E7ESK6_HUMAN]	20.61	8	4	4	9	1.000	9	0.000	21.367	165	18.377
Q96DP0	cDNA FLJ31479 fis, clone NT2NE2001634, moderately similar to NADH-UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT (EC 1.6.5.3) OS=Homo sapiens PE=2 SV=1	13.82	1	5	5	10	1.000	10	2.837	21.365	456	49.215
E9B4X7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1520 PE=4 SV=1 - [E9B4X7_LEIMU]	36.36	1	5	5	10	1.917	10	118.496	21.347	132	14.315
B2R8V7	cDNA, FLJ94082, highly similar to Homo sapiens interferon consensus sequence binding protein 1(ICSBP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8V7_HUMAN]	12.44	8	5	5	8	0.945	8	14.598	21.328	426	48.353
E7EQ69	N-alpha-acetyltransferase 50 OS=Homo sapiens GN=NAA50 PE=1 SV=1 - [E7EQ69_HUMAN]	31.55	8	5	5	10	1.000	10	8.995	21.286	168	19.299
Q9NW13	RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3 - [RBM28_HUMAN]	14.23	5	8	9	10	1.000	8	0.000	21.278	759	85.685
A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2 - [SMHD1_HUMAN]	3.14	2	6	6	8	1.000	8	0.330	21.259	2005	226.231
B3KMK0	cDNA FLJ11217 fis, clone PLACE1008044, highly similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 OS=Homo sapiens PE=2 SV=1 - [B3KMK0_HUMAN]	5.56	2	3	3	7	1.000	7	11.286	21.247	593	69.162
H0YAL7	Eukaryotic translation elongation factor 1 epsilon-1 (Fragment) OS=Homo sapiens GN=EEF1E1 PE=4 SV=1 - [H0YAL7_HUMAN]	19.85	5	3	3	8	1.000	8	1.534	21.213	136	15.329
Q9H3S7	Tyrosine-protein phosphatase non-receptor type 23 OS=Homo sapiens GN=PTPN23 PE=1 SV=1 - [PTN23_HUMAN]	4.03	6	6	6	8	1.000	8	0.000	21.192	1636	178.861
F8VPF7	Voltage-gated hydrogen channel 1 (Fragment) OS=Homo sapiens GN=HVCN1 PE=4 SV=2 - [F8VPF7_HUMAN]	7.01	3	1	1	7	1.000	7	0.000	21.185	214	24.817
A1L0T0	Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 - [ILVBL_HUMAN]	4.59	5	3	3	9	1.000	9	0.000	21.183	632	67.825
B3KVY9	cDNA FLJ41755 fis, clone HSYRA2009102, highly similar to Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Homo sapiens PE=2 SV=1 - [B3KVY9_HUMAN]	9.95	3	4	4	7	1.000	7	6.451	21.169	412	45.042
D3DP46	Signal peptidase complex subunit 3 homolog (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=SPCS3 PE=4 SV=1 - [D3DP46_HUMAN]	11.67	2	2	2	10	1.000	10	0.819	21.146	180	20.300
E9ATU4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5100 PE=4 SV=1 - [E9ATU4_LEIMU]	3.66	1	3	3	7	1.000	6	0.000	21.139	984	105.819
B2RBY7	cDNA, FLJ95770 OS=Homo sapiens PE=2 SV=1 - [B2RBY7_HUMAN]	10	3	3	3	8	1.000	8	10.367	21.139	380	41.589
B4DRU9	cDNA FLJ57179, highly similar to Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DRU9_HU	3.74	3	3	3	8	1.000	8	19.988	21.123	668	75.527
O43181	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Homo sapiens GN=NDUFS4 PE=1 SV=1 - [NDUS4_HUMAN]	11.43	2	2	2	8	1.000	7	0.000	21.093	175	20.095
Q27J81	Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 - [INF2_HUMAN]	3.76	1	4	4	7	1.000	5	26.168	21.064	1249	135.540
Q05DB2	PREB protein OS=Homo sapiens GN=PREB PE=2 SV=1 - [Q05DB2_HUMAN]	17.1	5	5	5	8	0.972	8	24.118	21.028	345	37.808
Q9NTZ6	RNA-binding protein 12 OS=Homo sapiens GN=RBM12 PE=1 SV=1 - [RBM12_HUMAN]	9.12	7	8	8	9	1.000	9	6.324	21.016	932	97.333
Q5BKZ1	DBIRD complex subunit ZNF326 OS=Homo sapiens GN=ZNF326 PE=1 SV=2 - [ZN326_HUMAN]	6.19	1	4	4	8	1.000	7	0.000	21.016	582	65.613
Q8WW22	DnaJ homolog subfamily A member 4 OS=Homo sapiens GN=DNAJA4 PE=1 SV=1 - [DNJA4_HUMAN]	14.36	10	4	6	7	1.274	5	30.265	21.016	397	44.769
P63218	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3 - [GBG5_HUMAN]	33.82	1	3	3	9	0.956	9	6.742	21.008	68	7.314
C9JLU1	DNA-directed RNA polymerases I, II, and III subunit RPABC3 (Fragment) OS=Homo sapiens GN=POLR2H PE=1 SV=3 - [C9JLU1_HUMAN]	19.46	2	2	2	6	1.000	6	8.283	20.986	149	16.985
O75340	Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1 - [PDCD6_HUMAN]	20.42	5	6	6	12	1.000	12	17.354	20.958	191	21.855
Q8NF37	Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 - [PCAT1_HUMAN]	3.75	2	2	2	7	1.000	6	0.000	20.910	534	59.113
A0PJ79	MRPL1 protein (Fragment) OS=Homo sapiens GN=MRPL1 PE=2 SV=1 - [A0PJ79_HUMAN]	15.89	4	5	5	9	0.970	8	21.629	20.901	302	34.424
Q6NZY4	Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2 - [ZCHC8_HUMAN]	7.5	6	5	5	8	1.000	7	6.465	20.885	707	78.529
E9AP69	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0450 PE=4 SV=1 - [E9AP69_LEIMU]	28.93	1	4	4	8	3.021	8	351.536	20.875	121	13.315
B4DKE6	cDNA FLJ60629, highly similar to Replication factor C subunit 3 OS=Homo sapiens PE=2 SV=1 - [B4DKE6_HUMAN]	12.13	5	3	3	6	1.000	6	3.862	20.826	305	34.810
A0A024R394	Cysteine and histidine-rich domain (CHORD)-containing 1, isoform CRA_c OS=Homo sapiens GN=CHORDC1 PE=4 SV=1 - [A0A024R394_HUMAN]	18.07	8	6	6	9	1.000	9	0.000	20.796	332	37.510
P55081	Microfibrillar-associated protein 1 OS=Homo sapiens GN=MFAP1 PE=1 SV=2 - [MFAP1_HUMAN]	11.39	1	5	6	13	1.000	8	0.000	20.774	439	51.927
C9JW69	Regulator of chromosome condensation (Fragment) OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [C9JW69_HUMAN]	13.44	6	4	4	9	0.995	9	3.923	20.738	372	39.559
B4DTT0	cDNA FLJ51090, highly similar to N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) OS=Homo sapiens PE=2 SV=1 - [B4DTT0_HUMAN]	5.97	9	3	3	7	1.000	7	1.408	20.736	469	53.386
P82094	TATA element modulatory factor OS=Homo sapiens GN=TMF1 PE=1 SV=2 - [TMF1_HUMAN]	7.5	4	9	9	10	0.915	10	34.263	20.728	1093	122.767
P82675	28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5 PE=1 SV=2 - [RT05_HUMAN]	10.47	2	5	5	8	1.000	8	4.126	20.726	430	47.976
B4DUF1	cDNA FLJ59760, highly similar to 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) OS=Homo sapiens PE=2 SV=1 - [B4DUF1_HUMAN]	7.72	5	5	5	7	1.000	7	2.700	20.722	661	75.798
C9JA28	Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=1 SV=1 - [C9JA28_HUMAN]	16.09	3	4	4	10	0.983	10	7.636	20.716	174	20.149
A0A087WUK0	AP2-associated protein kinase 1 OS=Homo sapiens GN=AAK1 PE=4 SV=1 - [A0A087WUK0_HUMAN]	6.21	6	4	5	9	1.000	7	0.000	20.708	789	85.706
Q9NRA2	Sialin OS=Homo sapiens GN=SLC17A5 PE=1 SV=2 - [S17A5_HUMAN]	8.69	4	5	5	11	1.121	9	10.540	20.692	495	54.604
P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	27.01	3	3	3	6	0.944	6	20.062	20.668	137	14.485
P55327	Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=1 SV=2 - [TPD52_HUMAN]	14.73	6	3	3	7	1.000	7	1.731	20.652	224	24.312
B7Z1C5	Glutathione synthetase OS=Homo sapiens PE=2 SV=1 - [B7Z1C5_HUMAN]	11.85	3	6	6	8	0.998	8	16.098	20.594	405	44.810
Q9H936	Mitochondrial glutamate carrier 1 OS=Homo sapiens GN=SLC25A22 PE=1 SV=1 - [GHC1_HUMAN]	7.12	5	2	2	7	1.000	7	0.000	20.588	323	34.448
P14735	Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4 - [IDE_HUMAN]	6.38	6	6	6	8	1.043	8	26.048	20.571	1019	117.893
E9AM47	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0320 PE=4 SV=1 - [E9AM47_LEIMU]	10.32	1	4	4	8	1.000	8	0.000	20.569	349	36.530
Q4TT76	OTTHUMP00000041238 (Fragment) OS=Homo sapiens GN=LA04NC01-25A3.2-001 PE=4 SV=1 - [Q4TT76_HUMAN]	9.35	8	3	3	7	1.000	5	0.000	20.562	417	45.921
Q6DKJ4	Nucleoredoxin OS=Homo sapiens GN=NXN PE=1 SV=2 - [NXN_HUMAN]	9.89	3	4	4	6	0.978	5	3.356	20.559	435	48.362
P55769	NHP2-like protein 1 OS=Homo sapiens GN=NHP2L1 PE=1 SV=3 - [NH2L1_HUMAN]	15.63	3	2	2	6	1.000	6	5.997	20.533	128	14.165
C9JRJ5	LIM domain-containing protein 1 OS=Homo sapiens GN=LIMD1 PE=1 SV=1 - [C9JRJ5_HUMAN]	4.68	2	3	3	6	1.000	6	0.000	20.528	620	65.493
A8K923	cDNA FLJ78690, highly similar to Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K923_HUMAN]	6.54	10	6	6	8	1.000	7	2.747	20.516	933	105.155
O75663	TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 - [TIPRL_HUMAN]	14.34	1	4	4	9	1.000	9	14.192	20.500	272	31.424
C9JEL3	Eukaryotic translation initiation factor 4E type 2 (Fragment) OS=Homo sapiens GN=EIF4E2 PE=1 SV=1 - [C9JEL3_HUMAN]	23.94	8	4	4	8	1.000	6	0.000	20.484	213	24.587
P01034	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1 - [CYTC_HUMAN]	28.77	1	3	3	7	1.000	6	9.725	20.483	146	15.789
Q92793	CREB-binding protein OS=Homo sapiens GN=CREBBP PE=1 SV=3 - [CBP_HUMAN]	1.6	4	3	4	7	1.000	4	0.000	20.455	2442	265.182
O15269	Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1 - [SPTC1_HUMAN]	11.63	4	6	6	10	0.966	10	23.732	20.447	473	52.710
B2RNR6	Zinc finger RNA binding protein OS=Homo sapiens GN=ZFR PE=2 SV=1 - [B2RNR6_HUMAN]	8.85	6	7	7	9	1.000	9	6.645	20.394	1074	116.941
O00186	Syntaxin-binding protein 3 OS=Homo sapiens GN=STXBP3 PE=1 SV=2 - [STXB3_HUMAN]	10.14	1	6	6	7	1.023	7	23.788	20.377	592	67.721
H0YNE0	Mortality factor 4-like protein 1 (Fragment) OS=Homo sapiens GN=MORF4L1 PE=1 SV=1 - [H0YNE0_HUMAN]	11.27	11	2	2	6	1.000	5	51.392	20.376	213	24.517
Q9H6T3	RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 PE=1 SV=2 - [RPAP3_HUMAN]	9.02	1	6	6	7	1.079	6	19.389	20.310	665	75.672
Q14344	Guanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2 - [GNA13_HUMAN]	10.34	14	3	4	9	0.502	3	67.204	20.292	377	44.022
P61513	60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2 - [RL37A_HUMAN]	35.87	8	3	3	11	1.000	11	0.000	20.279	92	10.268
Q59G98	TIA1 protein variant (Fragment) OS=Homo sapiens PE=4 SV=1 - [Q59G98_HUMAN]	10.99	8	1	6	9	1.000	1		20.268	464	51.297
Q14692	Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1 - [BMS1_HUMAN]	3.35	1	4	4	7	1.000	7	0.000	20.264	1282	145.716
P51571	Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1 - [SSRD_HUMAN]	13.29	2	2	2	9	1.000	9	17.198	20.260	173	18.987
E9AQB1	60S acidic ribosomal protein P2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_1203 PE=3 SV=1 - [E9AQB1_LEIMU]	50.45	1	3	3	9	1.000	9	0.000	20.233	111	10.993
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	14.95	5	4	4	8	0.806	6	29.246	20.233	194	21.621
B2R577	Protein S100 OS=Homo sapiens PE=2 SV=1 - [B2R577_HUMAN]	24.44	1	1	3	11	0.585	1		20.222	90	10.101
P06280	Alpha-galactosidase A OS=Homo sapiens GN=GLA PE=1 SV=1 - [AGAL_HUMAN]	12.35	4	5	5	9	1.000	9	11.652	20.202	429	48.735
G3V5V3	Nuclear export mediator factor NEMF (Fragment) OS=Homo sapiens GN=NEMF PE=1 SV=3 - [G3V5V3_HUMAN]	4.1	3	5	5	10	0.920	9	18.807	20.179	999	113.949
Q86U86	Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1 - [PB1_HUMAN]	4.14	6	6	6	8	1.000	8	0.000	20.171	1689	192.825
B3KN05	cDNA FLJ13129 fis, clone NT2RP3002969, highly similar to Long-chain-fatty-acid--CoA ligase 3 (EC 6.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B3KN05_HUMAN]	9.59	9	5	6	10	1.022	9	16.160	20.143	709	79.172
B2RE74	cDNA, FLJ94876, highly similar to Homo sapiens fructose-1,6-bisphosphatase 1 (FBP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RE74_HUMAN]	17.16	6	6	6	9	0.918	9	21.169	20.082	338	36.764
Q5JRI1	Serine/arginine-rich-splicing factor 10 OS=Homo sapiens GN=SRSF10 PE=1 SV=1 - [Q5JRI1_HUMAN]	24.42	6	5	5	10	1.219	10	10.845	20.082	172	20.900
A1L3A9	TBC1 domain family, member 9B (With GRAM domain) OS=Homo sapiens GN=TBC1D9B PE=2 SV=1 - [A1L3A9_HUMAN]	2.6	8	2	2	7	1.000	5	22.543	20.078	1232	138.453
O43314	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2 OS=Homo sapiens GN=PPIP5K2 PE=1 SV=3 - [VIP2_HUMAN]	5.87	10	6	6	8	1.000	7	41.546	20.058	1243	140.318
Q9BTY7	Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1 - [HGH1_HUMAN]	12.31	5	5	5	8	0.990	8	5.906	20.041	390	42.103
H0YC07	Oxidation resistance protein 1 (Fragment) OS=Homo sapiens GN=OXR1 PE=1 SV=1 - [H0YC07_HUMAN]	11	3	5	5	8	1.000	6	0.000	20.021	518	58.481
Q7Z422	SUZ domain-containing protein 1 OS=Homo sapiens GN=SZRD1 PE=1 SV=1 - [SZRD1_HUMAN]	18.42	4	3	3	7	0.782	7	20.318	20.008	152	16.987
Q9Y5Q9	General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1 - [TF3C3_HUMAN]	5.53	2	5	5	8	1.000	8	7.803	19.998	886	101.208
P42025	Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1 - [ACTY_HUMAN]	5.05	1	2	3	8	0.911	5	13.882	19.971	376	42.267
B7ZKR9	DNA-directed RNA polymerase OS=Homo sapiens GN=POLR1A PE=2 SV=1 - [B7ZKR9_HUMAN]	4.3	10	5	6	7	1.000	6	0.000	19.968	1720	194.662
Q86YS6	Ras-related protein Rab-43 OS=Homo sapiens GN=RAB43 PE=1 SV=1 - [RAB43_HUMAN]	10.38	27	1	2	7	1.000	1		19.959	212	23.325
Q9Y295	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1 - [DRG1_HUMAN]	12.81	2	4	4	8	1.004	8	7.975	19.947	367	40.517
E9PFR3	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D PE=1 SV=1 - [E9PFR3_HUMAN]	7.74	9	4	5	7	0.987	6	12.272	19.877	594	69.073
Q9NT62	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1 - [ATG3_HUMAN]	11.15	3	4	4	7	0.886	7	9.602	19.838	314	35.841
Q96AT1	Uncharacterized protein KIAA1143 OS=Homo sapiens GN=KIAA1143 PE=1 SV=2 - [K1143_HUMAN]	21.43	1	4	4	9	0.983	8	6.183	19.822	154	17.455
E8NHJ1	Putative uncharacterized protein LmxM_08_1040_1 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_08_1040_1 PE=3 SV=1 - [E8NHJ	6.76	22	3	4	8	1.190	3	26.266	19.818	503	54.171
Q9H1H9	Kinesin-like protein KIF13A OS=Homo sapiens GN=KIF13A PE=1 SV=2 - [KI13A_HUMAN]	1.61	2	1	3	7	1.906	1		19.818	1805	202.183
Q9BTE3	Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 - [MCMBP_HUMAN]	6.85	1	4	4	7	1.000	7	0.000	19.793	642	72.934
O43819	Protein SCO2 homolog, mitochondrial OS=Homo sapiens GN=SCO2 PE=1 SV=3 - [SCO2_HUMAN]	19.92	2	4	4	6	1.027	5	6.444	19.787	266	29.791
B4E123	Tyrosine-protein kinase OS=Homo sapiens PE=2 SV=1 - [B4E123_HUMAN]	6.21	7	5	6	8	1.000	7	7.652	19.785	934	104.707
A8KA50	cDNA FLJ78617 (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8KA50_HUMAN]	6.63	5	6	6	8	1.000	7	17.473	19.766	1267	137.349
E7EPA1	Phosphoribosyl pyrophosphate synthase-associated protein 2 (Fragment) OS=Homo sapiens GN=PRPSAP2 PE=1 SV=1 - [E7EPA1_HUMAN]	11.19	16	3	3	11	1.041	10	16.188	19.753	268	29.623
B4DII5	Importin subunit alpha OS=Homo sapiens PE=2 SV=1 - [B4DII5_HUMAN]	10.69	6	4	6	8	1.066	5	11.201	19.743	533	59.603
Q13418	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 - [ILK_HUMAN]	13.72	1	7	7	11	1.000	11	3.878	19.743	452	51.386
Q1JUQ5	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=FKBP12-Exip2 PE=1 SV=1 - [Q1JUQ5_HUMAN]	15.22	4	1	1	6	1.000	6	0.000	19.738	92	10.112
F5GYQ2	Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 - [F5GYQ2_HUMAN]	24.69	3	2	2	6	1.000	6	7.539	19.650	81	9.250
Q5HYL4	Putative uncharacterized protein DKFZp686E1893 OS=Homo sapiens GN=DKFZp686E1893 PE=2 SV=1 - [Q5HYL4_HUMAN]	4.87	2	3	3	8	1.000	8	0.000	19.625	636	69.371
B4DES6	cDNA FLJ52441, highly similar to Zinc finger protein 512 OS=Homo sapiens PE=2 SV=1 - [B4DES6_HUMAN]	8.66	6	4	5	9	1.000	6	0.000	19.617	462	53.087
O60832	H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3 - [DKC1_HUMAN]	12.26	6	6	6	7	0.973	6	8.839	19.617	514	57.638
A5PKX5	Alpha-mannosidase OS=Homo sapiens GN=MAN2A1 PE=2 SV=1 - [A5PKX5_HUMAN]	2.45	2	4	4	7	1.000	7	38.938	19.609	1143	130.954
Q8N1G2	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 OS=Homo sapiens GN=CMTR1 PE=1 SV=1 - [CMTR1_HUMAN]	7.07	3	5	6	9	0.987	8	9.212	19.594	835	95.260
B3KMR5	cDNA FLJ12434 fis, clone NT2RM1000037, highly similar to Homo sapiens KIAA0690 protein OS=Homo sapiens PE=2 SV=1 - [B3KMR5_HUMAN]	5.24	4	6	6	8	1.000	8	18.984	19.550	1297	143.581
P20138	Myeloid cell surface antigen CD33 OS=Homo sapiens GN=CD33 PE=1 SV=2 - [CD33_HUMAN]	8.24	1	3	3	7	0.873	7	39.409	19.515	364	39.800
Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2 - [BIG1_HUMAN]	2.54	21	3	5	9	1.000	6	9.290	19.504	1849	208.635
O75131	Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 - [CPNE3_HUMAN]	6.89	8	4	4	6	0.970	6	13.558	19.492	537	60.092
Q92625	Ankyrin repeat and SAM domain-containing protein 1A OS=Homo sapiens GN=ANKS1A PE=1 SV=4 - [ANS1A_HUMAN]	3.09	15	3	3	8	1.000	8	3.366	19.486	1134	123.032
Q5J8M4	Migration-inducing gene 14 OS=Homo sapiens PE=2 SV=1 - [Q5J8M4_HUMAN]	9.38	5	4	4	9	0.924	9	10.495	19.473	352	39.453
B3KP14	cDNA FLJ30937 fis, clone FEBRA2007247, highly similar to G-rich sequence factor 1 OS=Homo sapiens PE=2 SV=1 - [B3KP14_HUMAN]	13.59	11	5	5	8	1.162	7	13.670	19.463	412	46.666
B7Z410	cDNA FLJ50791, highly similar to Nitrilase homolog 1 (EC 3.5.-.-) OS=Homo sapiens PE=2 SV=1 - [B7Z410_HUMAN]	11.54	3	3	3	6	0.942	6	15.710	19.458	312	34.243
Q99808	Equilibrative nucleoside transporter 1 OS=Homo sapiens GN=SLC29A1 PE=1 SV=3 - [S29A1_HUMAN]	10.53	3	3	3	7	1.000	7	20.371	19.415	456	50.186
Q12996	Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1 - [CSTF3_HUMAN]	7.39	5	5	5	9	1.035	9	30.530	19.394	717	82.869
Q8WWI5	Choline transporter-like protein 1 OS=Homo sapiens GN=SLC44A1 PE=1 SV=1 - [CTL1_HUMAN]	4.41	3	3	3	8	1.088	7	6.283	19.385	657	73.253
Q15417	Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 - [CNN3_HUMAN]	13.07	7	1	4	7	1.000	1		19.366	329	36.391
B7Z421	cDNA FLJ51227, highly similar to Homo sapiens KIN, antigenic determinant of recA protein homolog, mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z421_HUMAN]	7.99	2	3	3	7	1.000	6	0.000	19.366	288	32.746
B2RTX8	WAPAL protein OS=Homo sapiens GN=WAPAL PE=2 SV=1 - [B2RTX8_HUMAN]	4.9	4	6	6	8	0.945	8	8.632	19.361	1184	132.143
Q8N1H4	cDNA FLJ40872 fis, clone TUTER2000283, highly similar to Homo sapiens transformer-2-beta (SFRS10) gene OS=Homo sapiens PE=2 SV=1 - [Q8N1H4_HUMAN]	24.6	7	5	6	9	1.027	8	4.249	19.349	252	29.183
G5E9C0	SP110 nuclear body protein, isoform CRA_b OS=Homo sapiens GN=SP110 PE=1 SV=1 - [G5E9C0_HUMAN]	5.3	6	3	3	6	1.153	4	18.478	19.328	547	61.701
A0A024R1M8	Apolipoprotein L, 2, isoform CRA_a OS=Homo sapiens GN=APOL2 PE=4 SV=1 - [A0A024R1M8_HUMAN]	12.17	4	3	4	7	1.000	6	4.783	19.289	337	37.055
B2RCJ6	cDNA, FLJ96114, highly similar to Homo sapiens bromodomain and WD repeat domain containing 2 (BRWD2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RCJ6_HUMA	3.35	7	4	4	10	0.995	10	22.461	19.274	1224	136.690
Q29926	HLA-A protein (Fragment) OS=Homo sapiens GN=HLA-A PE=2 SV=1 - [Q29926_HUMAN]	62.5	56	1	3	6	1.013	1		19.273	56	6.014
O60739	Eukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2 - [EIF1B_HUMAN]	26.55	4	2	2	6	1.000	5	0.000	19.247	113	12.816
Q9H115	Beta-soluble NSF attachment protein OS=Homo sapiens GN=NAPB PE=1 SV=2 - [SNAB_HUMAN]	6.71	4	1	2	9	1.000	2	0.000	19.241	298	33.535
F5GYV5	ADP-ribosylation factor-like protein 6-interacting protein 4 (Fragment) OS=Homo sapiens GN=ARL6IP4 PE=1 SV=1 - [F5GYV5_HUMAN]	12.8	7	2	2	5	1.000	5	0.000	19.229	211	23.673
P48426	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2 - [PI42A_HUMAN]	11.33	6	2	4	7	0.944	3	1.344	19.200	406	46.195
A6NIT2	Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform OS=Homo sapiens GN=PHKA1 PE=1 SV=1 - [A6NIT2_HUMAN]	1.35	4	2	2	9	0.908	5	20.797	19.190	1181	132.549
Q15007	Pre-mRNA-splicing regulator WTAP OS=Homo sapiens GN=WTAP PE=1 SV=2 - [FL2D_HUMAN]	12.12	4	3	3	8	1.000	6	3.688	19.164	396	44.217
B4DU69	cDNA FLJ56583, highly similar to Argininosuccinate lyase (EC 4.3.2.1) OS=Homo sapiens PE=2 SV=1 - [B4DU69_HUMAN]	19.82	4	4	4	7	1.000	7	7.525	19.164	217	24.550
Q14690	Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 - [RRP5_HUMAN]	4.49	3	8	8	10	1.000	10	15.722	19.161	1871	208.570
Q2TU78	Proliferation-inducing protein 45 OS=Homo sapiens GN=PIG45 PE=2 SV=1 - [Q2TU78_HUMAN]	24.12	14	2	3	6	0.913	4	9.763	19.149	199	20.627
Q5U0B9	Stem cell growth factor; lymphocyte secreted C-type lectin OS=Homo sapiens GN=CLEC11A PE=2 SV=1 - [Q5U0B9_HUMAN]	16.72	5	5	5	7	1.013	7	20.539	19.147	323	35.573
G5E9Z2	Cisplatin resistance related protein CRR9p, isoform CRA_c OS=Homo sapiens GN=CLPTM1L PE=1 SV=1 - [G5E9Z2_HUMAN]	11.11	3	4	4	7	0.884	6	12.268	19.146	369	43.252
B7Z3K0	cDNA FLJ51645, highly similar to Serine/threonine-protein kinase P>AK 1 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B7Z3K0_HUMAN]	18.68	13	3	7	10	1.000	3	16.907	19.141	455	50.832
B4DXL4	cDNA FLJ59781, highly similar to Nucleolar complex protein 3 homolog OS=Homo sapiens PE=2 SV=1 - [B4DXL4_HUMAN]	5.79	3	3	3	6	0.903	6	14.490	19.139	501	57.398
Q15018	BRISC complex subunit Abro1 OS=Homo sapiens GN=FAM175B PE=1 SV=2 - [F175B_HUMAN]	12.29	1	5	5	7	1.000	7	7.857	19.132	415	46.872
Q5C9Z4	Nucleolar MIF4G domain-containing protein 1 OS=Homo sapiens GN=NOM1 PE=1 SV=1 - [NOM1_HUMAN]	5.93	1	4	4	8	1.000	7	0.000	19.117	860	96.198
A0A024R014	RAN binding protein 9, isoform CRA_b OS=Homo sapiens GN=RANBP9 PE=4 SV=1 - [A0A024R014_HUMAN]	8.08	3	3	3	6	1.000	5	0.000	19.101	569	59.509
E9B1S0	Putative vacuolar-type proton translocating pyrophosphatase 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1220 PE=3 SV=1 - [E9B1S0_L	9.1	1	6	6	11	1.000	11	0.000	19.076	802	83.668
C9J6B1	Ras-related protein Ral-B (Fragment) OS=Homo sapiens GN=RALB PE=1 SV=1 - [C9J6B1_HUMAN]	11.38	7	1	2	7	0.986	4	15.888	19.073	167	18.718
A0A024R258	Ubiquilin 1, isoform CRA_d OS=Homo sapiens GN=UBQLN1 PE=4 SV=1 - [A0A024R258_HUMAN]	8.38	5	1	3	7	1.000	5	43.673	19.060	561	59.183
O43914	TYRO protein tyrosine kinase-binding protein OS=Homo sapiens GN=TYROBP PE=1 SV=1 - [TYOBP_HUMAN]	20.35	3	2	2	5	1.004	5	14.314	19.054	113	12.171
Q92947	Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1 - [GCDH_HUMAN]	8.22	16	5	5	8	0.867	8	8.009	19.042	438	48.096
F5GYT8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=2 - [F5GYT8_HUMAN]	6.78	9	3	3	7	1.000	5	0.000	19.037	575	63.966

P49840	Glycogen synthase kinase-3 alpha OS=Homo sapiens GN=GSK3A PE=1 SV=2 - [GSK3A_HUMAN]	10.35	6	2	3	5	0.703	4	51.485	19.035	483	50.949
P60468	Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2 - [SC61B_HUMAN]	30.21	3	4	4	9	1.000	9	9.338	19.030	96	9.968
O00161	Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=1 SV=1 - [SNP23_HUMAN]	26.54	12	5	5	6	1.000	6	14.907	19.022	211	23.340
Q8N183	Mimitin, mitochondrial OS=Homo sapiens GN=NDUFAF2 PE=1 SV=1 - [MIMIT_HUMAN]	23.08	3	3	3	8	1.000	7	0.000	19.018	169	19.844
A0A024RCU9	SFRS protein kinase 1, isoform CRA_e OS=Homo sapiens GN=SRPK1 PE=4 SV=1 - [A0A024RCU9_HUMAN]	13.87	14	5	7	8	1.000	3	29.277	19.002	548	61.924
A0A024R478	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis), isoform CRA_a OS=Homo sapiens GN=COPS7B PE=4 SV=1 - [A0A024R478_HUMAN]	24.84	8	3	3	6	1.000	6	4.974	18.956	157	18.145
Q5T200	Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1 - [ZC3HD_HUMAN]	4.2	7	8	8	10	1.000	8	29.652	18.928	1668	196.519
B4DU91	cDNA FLJ55368, highly similar to Epsin-1 OS=Homo sapiens PE=2 SV=1 - [B4DU91_HUMAN]	8.4	9	4	4	7	1.000	7	1.030	18.905	536	55.798
E9PI38	Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 - [E9PI38_HUMAN]	30.81	19	6	6	8	0.137	8	28.351	18.901	185	20.826
Q71UH4	DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B PE=3 SV=1 - [Q71UH4_HUMAN]	2.38	8	3	5	8	1.108	4	19.529	18.897	1598	180.501
Q9NQX3	Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1 - [GEPH_HUMAN]	8.42	9	6	6	7	1.000	7	28.732	18.888	736	79.698
B4DVZ9	cDNA FLJ61177, highly similar to Phosphatidylinositol-4-phosphate 5-kinasetype-1 gamma (EC 2.7.1.68) OS=Homo sapiens PE=2 SV=1 - [B4DVZ9_HUMAN]	6.41	3	4	4	7	1.000	7	0.000	18.882	640	70.142
B4DFY5	Mitogen-activated protein kinase kinase 1, isoform CRA_d OS=Homo sapiens GN=MAP2K1 PE=2 SV=1 - [B4DFY5_HUMAN]	12.94	6	3	5	9	1.000	4	7.523	18.847	371	41.352
Q99961	Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 - [SH3G1_HUMAN]	15.76	16	7	7	9	0.854	9	14.092	18.847	368	41.464
E9AQ29	Ribonucleoprotein p18, mitochondrial,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0275 PE=4 SV=1 - [E9AQ29_LEIMU]	10.16	1	2	2	10	1.000	10	0.000	18.846	187	21.230
Q14554	Protein disulfide-isomerase A5 OS=Homo sapiens GN=PDIA5 PE=1 SV=1 - [PDIA5_HUMAN]	4.43	2	3	3	8	1.000	7	0.000	18.831	519	59.556
Q96G25	Mediator of RNA polymerase II transcription subunit 8 OS=Homo sapiens GN=MED8 PE=1 SV=2 - [MED8_HUMAN]	14.55	1	4	4	8	0.961	8	16.121	18.821	268	29.062
A9QQ22	Actin nucleation promoting factor (Fragment) OS=Homo sapiens GN=WASH PE=4 SV=1 - [A9QQ22_HUMAN]	11.46	25	4	4	7	1.039	6	13.192	18.801	410	43.796
H3BV22	Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP4C PE=1 SV=1 - [H3BV22_HUMAN]	15.27	18	1	3	6	0.864	3	64.183	18.798	203	23.130
Q9UKK3	Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3 - [PARP4_HUMAN]	3.07	3	5	5	7	1.000	7	9.545	18.791	1724	192.472
Q86VR2	Protein FAM134C OS=Homo sapiens GN=FAM134C PE=1 SV=1 - [F134C_HUMAN]	5.15	7	2	2	7	1.000	7	0.000	18.772	466	51.364
Q9Y4X5	E3 ubiquitin-protein ligase ARIH1 OS=Homo sapiens GN=ARIH1 PE=1 SV=2 - [ARI1_HUMAN]	7.72	5	4	4	8	0.942	8	26.675	18.770	557	64.076
Q9NPF4	Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens GN=OSGEP PE=1 SV=1 - [OSGEP_HUMAN]	10.15	6	3	3	7	1.000	5	1.114	18.768	335	36.403
Q9BTV4	Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1 - [TMM43_HUMAN]	11	3	5	5	7	1.056	7	6.953	18.708	400	44.847
Q96GX3	KIAA0118 protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96GX3_HUMAN]	9.71	2	2	2	7	0.786	7	116.925	18.702	175	19.336
F8VXB1	Coatomer subunit zeta-1 (Fragment) OS=Homo sapiens GN=COPZ1 PE=1 SV=1 - [F8VXB1_HUMAN]	22.83	9	2	2	7	1.000	7	5.376	18.682	92	10.621
O43402	ER membrane protein complex subunit 8 OS=Homo sapiens GN=EMC8 PE=1 SV=1 - [EMC8_HUMAN]	9.52	1	3	3	6	0.943	6	11.996	18.666	210	23.758
Q96MW5	Conserved oligomeric Golgi complex subunit 8 OS=Homo sapiens GN=COG8 PE=1 SV=2 - [COG8_HUMAN]	6.21	6	4	4	7	0.949	6	13.298	18.663	612	68.380
Q96EL3	39S ribosomal protein L53, mitochondrial OS=Homo sapiens GN=MRPL53 PE=1 SV=1 - [RM53_HUMAN]	40.18	1	3	3	8	1.000	8	67.893	18.653	112	12.099
A8K8B7	cDNA FLJ76723 OS=Homo sapiens PE=2 SV=1 - [A8K8B7_HUMAN]	6.87	8	4	4	6	0.850	6	11.608	18.625	553	60.586
A0A024RD56	Tight junction associated protein 1 (Peripheral), isoform CRA_a OS=Homo sapiens GN=TJAP1 PE=4 SV=1 - [A0A024RD56_HUMAN]	5.3	6	3	3	5	0.979	5	18.254	18.594	547	60.684
Q96RT1	Protein LAP2 OS=Homo sapiens GN=ERBB2IP PE=1 SV=2 - [LAP2_HUMAN]	3.97	3	5	5	7	1.086	7	22.127	18.577	1412	158.200
V9HWG4	Epididymis luminal protein 37 OS=Homo sapiens GN=HEL37 PE=2 SV=1 - [V9HWG4_HUMAN]	3.43	5	7	7	9	1.000	9	0.000	18.575	2098	236.958
Q9BQB6	Vitamin K epoxide reductase complex subunit 1 OS=Homo sapiens GN=VKORC1 PE=1 SV=1 - [VKOR1_HUMAN]	12.27	5	2	2	7	1.021	7	3.669	18.568	163	18.223
H3BRV9	Nuclear transport factor 2 (Fragment) OS=Homo sapiens GN=NUTF2 PE=1 SV=1 - [H3BRV9_HUMAN]	13.08	3	1	2	8	0.795	3	5.090	18.551	107	12.151
P01859	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 - [IGHG2_HUMAN]	13.5	8	3	4	8	1.000	5	0.000	18.539	326	35.878
P48059	LIM and senescent cell antigen-like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 PE=1 SV=4 - [LIMS1_HUMAN]	16	12	5	5	8	1.005	8	10.670	18.526	325	37.226
Q9HD42	Charged multivesicular body protein 1a OS=Homo sapiens GN=CHMP1A PE=1 SV=1 - [CHM1A_HUMAN]	19.39	5	5	5	9	1.000	9	8.474	18.518	196	21.689
O14879	Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 - [IFIT3_HUMAN]	9.18	2	3	3	6	1.000	6	7.142	18.500	490	55.950
K7EMM8	Putative oxidoreductase GLYR1 (Fragment) OS=Homo sapiens GN=GLYR1 PE=1 SV=2 - [K7EMM8_HUMAN]	10.88	6	5	5	8	0.907	8	13.006	18.476	524	57.289
E9ALK3	Putative GTP-binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2200 PE=3 SV=1 - [E9ALK3_LEIMU]	3.62	1	2	3	7	1.000	6	0.000	18.471	691	76.850
Q5VW32	BRO1 domain-containing protein BROX OS=Homo sapiens GN=BROX PE=1 SV=1 - [BROX_HUMAN]	4.87	5	2	2	8	1.000	8	11.850	18.462	411	46.447
A0A024R3B4	Uncharacterized protein OS=Homo sapiens GN=HSPC148 PE=4 SV=1 - [A0A024R3B4_HUMAN]	31.25	3	3	3	7	0.992	7	1.219	18.454	96	11.059
O15212	Prefoldin subunit 6 OS=Homo sapiens GN=PFDN6 PE=1 SV=1 - [PFD6_HUMAN]	25.58	3	5	5	8	0.896	8	21.303	18.448	129	14.574
B3KPC7	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens PE=2 SV=1 - [B3KPC7_HUMAN]	18.3	2	2	3	6	0.835	5	27.153	18.420	153	16.961
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	4.17	5	7	7	7	1.000	7	0.000	18.415	1845	204.160
P07108	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2 - [ACBP_HUMAN]	47.13	9	3	4	13	1.000	11	2.358	18.403	87	10.038
Q9BQD2	Signal transducer and activator of transcription OS=Homo sapiens PE=2 SV=1 - [Q9BQD2_HUMAN]	5.01	13	4	5	7	1.000	6	14.030	18.402	679	76.078
B4DYZ9	cDNA FLJ53462, highly similar to Transcription intermediary factor 1-alpha OS=Homo sapiens PE=2 SV=1 - [B4DYZ9_HUMAN]	7.39	5	6	7	9	1.000	7	0.000	18.393	961	107.636
B2RBP3	cDNA, FLJ95615, highly similar to Homo sapiens ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)(UBE1C), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBP3_H	11.88	5	5	5	7	1.066	7	9.516	18.385	463	51.789
P42356	Phosphatidylinositol 4-kinase alpha OS=Homo sapiens GN=PI4KA PE=1 SV=3 - [PI4KA_HUMAN]	1.76	13	3	3	6	1.031	5	53.575	18.379	2044	231.170
B7Z788	cDNA FLJ59090, highly similar to Vacuolar ATP synthase subunit d (EC 3.6.3.14) OS=Homo sapiens PE=2 SV=1 - [B7Z788_HUMAN]	9.49	8	3	3	7	1.083	7	3.362	18.361	274	31.630
A0A024QZL1	Proteoglycan 1, secretory granule, isoform CRA_a OS=Homo sapiens GN=PRG1 PE=4 SV=1 - [A0A024QZL1_HUMAN]	24.68	2	4	4	6	0.949	6	22.519	18.351	158	17.613
Q5JXX2	Mortality factor 4-like protein 2 (Fragment) OS=Homo sapiens GN=MORF4L2 PE=1 SV=1 - [Q5JXX2_HUMAN]	16.95	9	3	3	6	1.000	5	10.374	18.350	177	19.819
S4R369	39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=1 - [S4R369_HUMAN]	12.42	5	5	5	7	1.000	7	0.000	18.347	483	54.918
E9AK51	Putative ubiquitin-conjugating enzyme e2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0680 PE=3 SV=1 - [E9AK51_LEIMU]	20.95	1	2	3	10	1.000	7	0.000	18.344	148	17.039
M0QZK8	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1 - [M0QZK8_HUMAN]	29.13	5	3	3	6	0.894	6	6.080	18.343	103	11.571
Q13948	Protein CASP OS=Homo sapiens GN=CUX1 PE=1 SV=2 - [CASP_HUMAN]	7.96	4	1	6	7	1.046	1		18.291	678	77.408
C9JLV4	Apoptotic protease-activating factor 1 OS=Homo sapiens GN=APAF1 PE=4 SV=1 - [C9JLV4_HUMAN]	3.1	4	3	4	9	0.931	3	10.667	18.270	1163	132.379
A0A024R094	Poly(A) binding protein interacting protein 1, isoform CRA_a OS=Homo sapiens GN=PAIP1 PE=4 SV=1 - [A0A024R094_HUMAN]	8.82	5	3	3	7	1.000	7	0.000	18.245	306	34.992
Q9NRY4	Rho GTPase-activating protein 35 OS=Homo sapiens GN=ARHGAP35 PE=1 SV=3 - [RHG35_HUMAN]	4.27	4	5	6	8	0.986	6	2.093	18.187	1499	170.407
O43818	U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens GN=RRP9 PE=1 SV=1 - [U3IP2_HUMAN]	8.42	1	3	4	7	0.992	4	56.158	18.145	475	51.809
Q9NYK5	39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3 - [RM39_HUMAN]	12.43	2	5	5	9	1.000	9	14.789	18.131	338	38.687
Q6UX04	Peptidyl-prolyl cis-trans isomerase CWC27 homolog OS=Homo sapiens GN=CWC27 PE=1 SV=1 - [CWC27_HUMAN]	12.29	2	6	6	8	0.869	7	14.994	18.118	472	53.814
P53701	Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 - [CCHL_HUMAN]	13.06	2	3	3	7	0.977	6	18.359	18.093	268	30.582
Q96A33	Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1 - [CCD47_HUMAN]	7.25	3	5	5	9	1.036	9	37.692	18.074	483	55.838
E7ES08	High mobility group protein B3 (Fragment) OS=Homo sapiens GN=HMGB3 PE=1 SV=1 - [E7ES08_HUMAN]	18.09	6	3	5	21	0.975	8	9.946	18.041	188	21.431
A0A024R1T4	Trinucleotide repeat containing 6B, isoform CRA_b OS=Homo sapiens GN=TNRC6B PE=4 SV=1 - [A0A024R1T4_HUMAN]	3.34	6	4	4	9	1.000	7	0.000	18.039	1527	162.068
B4E2T4	cDNA FLJ54121, highly similar to Cysteine and glycine-rich protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E2T4_HUMAN]	25	12	3	3	6	0.899	6	16.590	18.038	140	14.961
C9J8D4	Mannosyl-oligosaccharide glucosidase (Fragment) OS=Homo sapiens GN=MOGS PE=1 SV=3 - [C9J8D4_HUMAN]	9.35	6	5	5	8	0.952	8	19.190	18.032	492	54.129
B7ZKK7	EIF2AK2 protein OS=Homo sapiens GN=EIF2AK2 PE=2 SV=1 - [B7ZKK7_HUMAN]	9.52	7	5	5	9	0.904	8	7.654	18.021	546	61.472
E9ARS2	Putative pyruvate dehydrogenase E1 component alpha subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1380 PE=4 SV=1 - [E9ARS2_I	7.94	1	4	4	7	1.769	7	102.256	18.020	378	42.700
E9AUA1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6650 PE=4 SV=1 - [E9AUA1_	4.52	1	3	3	6	1.000	6	0.000	18.005	553	60.776
Q8NC56	LEM domain-containing protein 2 OS=Homo sapiens GN=LEMD2 PE=1 SV=1 - [LEMD2_HUMAN]	7.95	4	5	5	8	1.010	8	25.096	17.983	503	56.940
B4DG42	cDNA FLJ53753, highly similar to Myeloid-associated differentiation marker OS=Homo sapiens PE=2 SV=1 - [B4DG42_HUMAN]	10.18	6	2	2	6	0.940	3	9.228	17.969	285	31.204
A0A024RAC0	Leucine zipper protein 1, isoform CRA_a OS=Homo sapiens GN=LUZP1 PE=4 SV=1 - [A0A024RAC0_HUMAN]	5.3	4	4	5	7	1.025	6	9.813	17.969	1076	120.231
Q96HY7	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial OS=Homo sapiens GN=DHTKD1 PE=1 SV=2 - [DHTK1_HUMAN]	7.62	3	5	5	7	1.000	7	0.000	17.963	919	103.011
B3KNS8	cDNA FLJ30322 fis, clone BRACE2006703, highly similar to Surfeit locus protein 6 OS=Homo sapiens PE=2 SV=1 - [B3KNS8_HUMAN]	19.39	2	6	6	8	1.000	7	30.296	17.886	361	41.484
A8K2L4	cDNA FLJ76079, highly similar to Homo sapiens lymphocyte-specific protein 1 (LSP1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2L4_HUMAN]	21.53	4	1	4	5	1.000	1		17.885	339	37.225
P51398	28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3 PE=1 SV=1 - [RT29_HUMAN]	6.53	11	3	3	7	0.929	7	17.782	17.877	398	45.538
Q9NX14	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial OS=Homo sapiens GN=NDUFB11 PE=1 SV=1 - [NDUBB_HUMAN]	7.19	2	1	1	6	0.937	6	10.818	17.834	153	17.306
P82970	High mobility group nucleosome-binding domain-containing protein 5 OS=Homo sapiens GN=HMGN5 PE=1 SV=1 - [HMGN5_HUMAN]	20.21	7	4	4	5	0.972	4	6.876	17.834	282	31.506
O95861	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1 - [BPNT1_HUMAN]	17.53	6	5	5	8	1.095	8	15.087	17.804	308	33.371
S4R329	ER membrane protein complex subunit 4 OS=Homo sapiens GN=EMC4 PE=1 SV=1 - [S4R329_HUMAN]	38.89	6	2	2	7	1.000	6	0.000	17.800	72	7.799
F8VV56	CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=1 - [F8VV56_HUMAN]	16.55	6	3	3	10	1.212	10	6.765	17.776	145	16.010
B4DHN0	Mitogen-activated protein kinase OS=Homo sapiens PE=2 SV=1 - [B4DHN0_HUMAN]	19.83	5	6	7	9	0.985	7	8.689	17.776	348	40.395
E9B4Q3	Elongation factor 1-beta OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0820 PE=3 SV=1 - [E9B4Q3_LEIMU]	18.03	2	4	4	7	1.000	7	0.000	17.746	244	26.061
A8K3S0	cDNA FLJ76127, highly similar to Homo sapiens replication factor C (activator 1) 5, 36.5kDa (RFC5), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K3S	7.65	7	3	3	6	0.949	6	13.501	17.742	340	38.442
B4DKA9	cDNA FLJ61306, weakly similar to Serine/threonine-protein phosphatase 4 regulatory subunit 3 OS=Homo sapiens PE=2 SV=1 - [B4DKA9_HUMAN]	4.71	5	1	4	6	1.072	1		17.738	849	97.361
B7ZC39	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=1 SV=1 - [B7ZC39_HUMAN]	7.22	5	2	3	6	1.000	3	0.000	17.717	374	41.642
Q9BQA1	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1 - [MEP50_HUMAN]	11.99	3	3	3	6	1.000	6	2.228	17.650	342	36.701
Q5VTL8	Pre-mRNA-splicing factor 38B OS=Homo sapiens GN=PRPF38B PE=1 SV=1 - [PR38B_HUMAN]	6.59	1	5	5	8	0.999	7	37.754	17.650	546	64.429
Q12824	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 PE=1 SV=2 - [SNF5_HUMAN]	14.29	9	4	4	6	0.809	5	25.246	17.645	385	44.113
Q96SQ9	Cytochrome P450 2S1 OS=Homo sapiens GN=CYP2S1 PE=2 SV=2 - [CP2S1_HUMAN]	10.12	5	4	4	6	1.000	6	12.666	17.640	504	55.781
A0A087WWE6	Disks large-associated protein 4 (Fragment) OS=Homo sapiens GN=DLGAP4 PE=4 SV=1 - [A0A087WWE6_HUMAN]	34.78	4	2	2	5	1.000	5	0.000	17.633	46	4.931
Q9Y512	Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3 - [SAM50_HUMAN]	5.97	1	3	3	7	0.981	7	12.730	17.631	469	51.943
Q9NSI2	Protein FAM207A OS=Homo sapiens GN=FAM207A PE=1 SV=2 - [F207A_HUMAN]	13.91	2	2	2	6	1.000	5	0.000	17.618	230	25.441
P62330	ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 - [ARF6_HUMAN]	12	11	1	2	8	1.362	2	41.078	17.606	175	20.069
Q969S3	Zinc finger protein 622 OS=Homo sapiens GN=ZNF622 PE=1 SV=1 - [ZN622_HUMAN]	9.85	1	5	5	6	1.093	6	23.023	17.585	477	54.237
Q96F86	Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1 - [EDC3_HUMAN]	5.71	2	3	3	6	0.951	6	17.796	17.580	508	56.042
B4E1T1	cDNA FLJ54081, highly similar to Keratin, type II cytoskeletal 5 OS=Homo sapiens PE=2 SV=1 - [B4E1T1_HUMAN]	9.55	35	3	6	11	0.243	4	24.050	17.574	555	58.814
Q96SP2	cDNA FLJ14726 fis, clone NT2RP3001727, highly similar to Rattus norvegicus implantation-associated protein (IAG2) mRNA OS=Homo sapiens PE=2 SV=1 - [Q96SP2_	11.93	8	3	3	9	1.000	9	4.626	17.572	218	24.362
Q8N2K0	Monoacylglycerol lipase ABHD12 OS=Homo sapiens GN=ABHD12 PE=1 SV=2 - [ABD12_HUMAN]	11.81	6	4	4	6	0.870	6	19.276	17.571	398	45.068
E9AKA4	Actin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_1230 PE=3 SV=1 - [E9AKA4_LEIMU]	5.83	2	2	2	6	6.504	6	84.746	17.567	360	40.457
B2RBF2	cDNA, FLJ95480, highly similar to Homo sapiens RAS guanyl releasing protein 2 (calcium and DAG-regulated) (RASGRP2), transcript variant 2, mRNA OS=Homo sapier	5.91	10	5	5	8	0.893	8	6.912	17.542	609	69.231
Q5H909	Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2 - [Q5H909_HUMAN]	11.39	6	4	4	7	0.984	6	6.406	17.539	588	63.100
Q9Y5A7	NEDD8 ultimate buster 1 OS=Homo sapiens GN=NUB1 PE=1 SV=2 - [NUB1_HUMAN]	5.04	9	3	3	6	0.954	5	7.026	17.539	615	70.494
B2R5I8	cDNA, FLJ92490, highly similar to Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5I8_HUMAN]	13.78	2	3	3	5	1.024	5	10.667	17.537	225	24.941
Q9H3U1	Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1 - [UN45A_HUMAN]	5.51	1	6	6	7	0.975	7	10.063	17.525	944	103.011
P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3 - [ODB2_HUM	11.62	3	6	6	10	1.000	10	0.124	17.514	482	53.453
Q5TEJ8	Protein THEMIS2 OS=Homo sapiens GN=THEMIS2 PE=2 SV=1 - [THMS2_HUMAN]	7.78	3	3	3	6	1.000	6	0.000	17.505	643	72.003
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Homo sapiens GN=NDUFB7 PE=1 SV=4 - [NDUB7_HUMAN]	32.12	1	4	4	12	1.182	10	25.173	17.486	137	16.391
J3QRU8	ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 - [J3QRU8_HUMAN]	6.05	10	2	5	7	0.745	3	8.912	17.481	694	76.759
Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2 - [NSDHL_HUMAN]	8.85	2	3	3	7	1.000	7	6.339	17.478	373	41.874
Q2M389	WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2 - [WASH7_HUMAN]	4.86	11	6	6	7	1.002	6	5.078	17.477	1173	136.316
E8NHK1	WGS CADB00000000 data, contig 48 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_16_1460a_1 PE=4 SV=1 - [E8NHK1_LEIMU]	76.08	4	3	3	7	1.000	7	0.000	17.466	694	76.142
J3KSY7	Protein CASC3 (Fragment) OS=Homo sapiens GN=CASC3 PE=1 SV=1 - [J3KSY7_HUMAN]	13.9	5	3	3	5	1.000	5	7.807	17.465	223	25.746
O15270	Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1 - [SPTC2_HUMAN]	5.52	2	3	3	6	1.000	6	0.000	17.424	562	62.884
P33241	Lymphocyte-specific protein 1 OS=Homo sapiens GN=LSP1 PE=1 SV=1 - [LSP1_HUMAN]	21.53	11	1	4	5	1.208	1		17.421	339	37.169
O43760	Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1 - [SNG2_HUMAN]	15.18	5	4	4	10	1.000	10	1.809	17.419	224	24.794
E9PNL8	Diacylglycerol kinase OS=Homo sapiens GN=DGKZ PE=3 SV=1 - [E9PNL8_HUMAN]	6.79	7	4	4	7	0.873	7	7.686	17.404	707	78.878
Q5VUA4	Zinc finger protein 318 OS=Homo sapiens GN=ZNF318 PE=1 SV=2 - [ZN318_HUMAN]	2.02	11	4	6	8	1.000	5	0.000	17.375	2279	250.958
B4DZF1	cDNA FLJ56541, highly similar to Ubiquilin-2 OS=Homo sapiens PE=2 SV=1 - [B4DZF1_HUMAN]	14.65	3	2	4	9	1.000	6	0.000	17.364	512	54.965
H3BPW3	Ubiquinone biosynthesis protein COQ9, mitochondrial (Fragment) OS=Homo sapiens GN=COQ9 PE=1 SV=1 - [H3BPW3_HUMAN]	26.47	10	2	2	4	1.000	3	0.000	17.362	102	11.415
Q9NVE7	Pantothenate kinase 4 OS=Homo sapiens GN=PANK4 PE=1 SV=1 - [PANK4_HUMAN]	3.88	117	2	3	5	0.967	3	110.973	17.361	773	85.937
Q9UNZ5	Leydig cell tumor 10 kDa protein homolog OS=Homo sapiens GN=C19orf53 PE=1 SV=1 - [L10K_HUMAN]	25.25	3	4	4	6	0.846	6	13.893	17.357	99	10.570
Q9UK41	Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1 - [VPS28_HUMAN]	21.27	4	4	4	6	1.073	5	38.356	17.354	221	25.409
P49711	Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN]	11.42	2	8	8	9	1.000	9	12.972	17.320	727	82.732
P09669	Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2 - [COX6C_HUMAN]	28	1	3	3	9	1.000	9	27.167	17.306	75	8.776
P19484	Transcription factor EB OS=Homo sapiens GN=TFEB PE=1 SV=3 - [TFEB_HUMAN]	5.04	20	1	3	9	1.000	6	0.000	17.296	476	52.832
E9AWJ4	Putative 60S ribosomal protein L17 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0040 PE=3 SV=1 - [E9AWJ4_LEIMU]	16.87	1	3	3	6	1.131	6	18.460	17.275	166	19.071
Q5HY54	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 - [Q5HY54_HUMAN]	2.65	14	3	8	9	1.000	3	0.000	17.273	2607	276.378
Q59FR0	Basic FGF-repressed Zic binding protein isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FR0_HUMAN]	7.98	11	2	2	6	1.009	6	4.075	17.269	213	24.577
E7ETT4	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=1 - [E7ETT4_HUMAN]	13.69	19	5	5	6	1.000	5	13.072	17.265	482	52.390
P01876	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2 - [IGHA1_HUMAN]	16.15	21	5	5	7	1.000	5	0.000	17.247	353	37.631
Q99996	A-kinase anchor protein 9 OS=Homo sapiens GN=AKAP9 PE=1 SV=3 - [AKAP9_HUMAN]	2.56	15	7	10	11	1.000	7	0.000	17.228	3911	453.387
E9ASC5	Stress-inducible protein STI1 homolog OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0070 PE=4 SV=1 - [E9ASC5_LEIMU]	9.41	1	2	2	6	1.553	6	72.106	17.204	255	28.959
A8KAP0	cDNA FLJ75279, highly similar to Homo sapiens elongation factor RNA polymerase II (ELL), mRNA OS=Homo sapiens PE=2 SV=1 - [A8KAP0_HUMAN]	7.25	7	4	4	7	1.196	6	27.049	17.199	621	68.322
B7ZKJ7	UAP1L1 protein (Fragment) OS=Homo sapiens GN=UAP1L1 PE=2 SV=1 - [B7ZKJ7_HUMAN]	13.67	4	5	5	7	0.991	7	9.799	17.198	373	42.090
Q9BZQ8	Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1 - [NIBAN_HUMAN]	6.25	3	4	5	7	1.000	6	2.678	17.163	928	103.070
B2R7P6	cDNA, FLJ93543, highly similar to Homo sapiens phosphotidylinositol transfer protein, beta (PITPNB),mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7P6_HUMAN]	14.39	5	4	4	7	1.088	6	16.330	17.131	271	31.448
Q9NUF9	Nucleoside diphosphate kinase (Fragment) OS=Homo sapiens GN=c371H6.2 PE=3 SV=1 - [Q9NUF9_HUMAN]	28.1	7	3	4	8	1.000	5	7.099	17.126	153	17.285
Q13573	SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=1 SV=1 - [SNW1_HUMAN]	16.79	12	7	7	12	0.878	12	23.475	17.125	536	61.456
B4DLF2	cDNA FLJ57526 OS=Homo sapiens PE=2 SV=1 - [B4DLF2_HUMAN]	4.25	5	5	5	6	0.979	6	25.091	17.119	1011	117.009
P29084	Transcription initiation factor IIE subunit beta OS=Homo sapiens GN=GTF2E2 PE=1 SV=1 - [T2EB_HUMAN]	13.4	4	4	4	7	1.000	7	0.000	17.100	291	33.023
E9AUD1	Protein disulfide-isomerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6940 PE=3 SV=1 - [E9AUD1_LEIMU]	15.01	1	8	8	10	1.074	10	14.771	17.097	473	52.155
E7EMC7	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 - [E7EMC7_HUMAN]	8.99	8	1	2	5	1.000	4	0.000	17.065	378	40.987
Q6GTX8	Leukocyte-associated immunoglobulin-like receptor 1 OS=Homo sapiens GN=LAIR1 PE=1 SV=1 - [LAIR1_HUMAN]	14.98	9	3	3	7	0.864	7	18.052	17.065	287	31.393
B4E216	cDNA FLJ57339, highly similar to Complement C3 OS=Homo sapiens PE=2 SV=1 - [B4E216_HUMAN]	3.46	3	4	4	7	1.000	7	0.000	17.062	1098	122.515
Q9P032	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 OS=Homo sapiens GN=NDUFAF4 PE=1 SV=1 - [NDUF4_HUMAN]	18.86	1	4	4	8	1.034	8	7.284	17.056	175	20.254
Q6IEH8	Transcriptional regulator OS=Homo sapiens GN=NIPBL PE=2 SV=1 - [Q6IEH8_HUMAN]	3.21	6	10	10	12	1.000	11	2.777	17.043	2804	315.869
E9ARX1	Putative ADP,ATP carrier protein 1, mitochondrial OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0200 PE=3 SV=1 - [E9ARX1_LEIMU]	7.57	2	3	3	7	2.995	7	156.470	17.039	317	35.121
Q92917	G patch domain and KOW motifs-containing protein OS=Homo sapiens GN=GPKOW PE=1 SV=2 - [GPKOW_HUMAN]	6.72	1	3	3	6	1.000	5	12.833	17.024	476	52.197
Q9UI09	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Homo sapiens GN=NDUFA12 PE=1 SV=1 - [NDUAC_HUMAN]	24.14	6	3	3	6	1.000	5	0.000	17.020	145	17.104
E9AYS6	Kinetoplast-associated protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0240 PE=4 SV=1 - [E9AYS6_LEIMU]	81.72	1	1	1	5	1.299	5	40.263	17.018	1346	145.584
Q7Z6E9	E3 ubiquitin-protein ligase RBBP6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1 - [RBBP6_HUMAN]	3.4	12	7	8	10	0.967	8	4.929	16.981	1792	201.442
F8W689	DNA-binding protein RFX5 (Fragment) OS=Homo sapiens GN=RFX5 PE=1 SV=1 - [F8W689_HUMAN]	10.91	9	5	5	7	0.809	6	22.413	16.979	596	63.074
E9ANI1	Putative 14-3-3 protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0350 PE=4 SV=1 - [E9ANI1_LEIMU]	10.67	1	3	3	6	11.778	6	78.718	16.974	253	29.128
A0A087WY55	Chromosome 6 open reading frame 55, isoform CRA_b OS=Homo sapiens GN=VTA1 PE=4 SV=1 - [A0A087WY55_HUMAN]	23.57	4	7	7	9	1.000	8	1.183	16.968	280	31.082
B4E2P4	cDNA FLJ58474, highly similar to Xaa-Pro aminopeptidase 1 (EC 3.4.11.9) OS=Homo sapiens PE=2 SV=1 - [B4E2P4_HUMAN]	13.64	3	1	5	6	1.000	1		16.937	440	49.564
A0A024R6D1	NIMA (Never in mitosis gene a)-related kinase 9, isoform CRA_a OS=Homo sapiens GN=NEK9 PE=4 SV=1 - [A0A024R6D1_HUMAN]	5.11	5	5	5	8	1.000	8	10.808	16.936	979	107.081
O15226	NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF PE=1 SV=2 - [NKRF_HUMAN]	6.23	5	5	5	7	0.928	7	25.202	16.929	690	77.624
O75427	Leucine-rich repeat and calponin homology domain-containing protein 4 OS=Homo sapiens GN=LRCH4 PE=1 SV=2 - [LRCH4_HUMAN]	10.54	5	5	5	9	1.000	9	0.000	16.915	683	73.405
P52790	Hexokinase-3 OS=Homo sapiens GN=HK3 PE=1 SV=2 - [HXK3_HUMAN]	7.69	3	6	6	6	1.000	6	0.000	16.910	923	98.962
O60231	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 OS=Homo sapiens GN=DHX16 PE=1 SV=2 - [DHX16_HUMAN]	4.23	3	3	3	7	1.000	5	0.000	16.909	1041	119.189
Q9UK61	Protein FAM208A OS=Homo sapiens GN=FAM208A PE=1 SV=3 - [F208A_HUMAN]	2.22	3	4	4	8	1.000	8	15.792	16.895	1670	188.914
E9B0H1	Putative aspartyl-tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_0460 PE=3 SV=1 - [E9B0H1_LEIMU]	3.45	2	1	2	7	1.000	1		16.874	550	62.325
B4DSL6	cDNA FLJ57190, highly similar to Actin-binding protein anillin OS=Homo sapiens PE=2 SV=1 - [B4DSL6_HUMAN]	5.79	6	6	6	8	1.000	8	6.978	16.870	1001	110.779
Q9HCN4	GPN-loop GTPase 1 OS=Homo sapiens GN=GPN1 PE=1 SV=1 - [GPN1_HUMAN]	8.56	1	3	3	6	1.046	6	10.395	16.861	374	41.714
Q6P163	APOC2 protein OS=Homo sapiens GN=APOC2 PE=2 SV=1 - [Q6P163_HUMAN]	25	3	2	2	6	1.007	6	3.016	16.857	72	8.141
F1T0L5	ATP-dependent RNA helicase DDX51 OS=Homo sapiens GN=DDX51 PE=2 SV=1 - [F1T0L5_HUMAN]	10.06	2	4	4	6	1.000	5	0.000	16.852	666	72.441
P42126	Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1 - [ECI1_HUMAN]	10.6	3	3	3	6	0.967	6	4.853	16.829	302	32.795
P52701	DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2 - [MSH6_HUMAN]	4.19	5	6	6	8	0.914	8	13.756	16.829	1360	152.689
Q01780	Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 - [EXOSX_HUMAN]	5.2	4	5	5	7	0.826	6	29.804	16.799	885	100.768
B7Z792	cDNA FLJ53932, highly similar to NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial (EC 1.6.5.3) OS=Homo sapiens PE=2 SV=1 - [B7Z792_HUMAN]	3.45	4	2	2	8	0.952	8	15.915	16.798	406	46.367
Q8IXI1	Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2 - [MIRO2_HUMAN]	8.74	5	3	4	7	0.956	6	6.704	16.782	618	68.075
K4EN11	GAPDH (Fragment) OS=Homo sapiens PE=4 SV=1 - [K4EN11_HUMAN]	51.85	1	1	1	5	1.000	5	0.000	16.760	27	2.830
Q8TDW0	Volume-regulated anion channel subunit LRRC8C OS=Homo sapiens GN=LRRC8C PE=1 SV=2 - [LRC8C_HUMAN]	4.36	4	3	3	7	1.000	7	13.014	16.757	803	92.390
E9APX4	Putative ubiquitin/ribosomal protein S27a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1270 PE=4 SV=1 - [E9APX4_LEIMU]	20.39	2	3	3	6	1.000	6	0.000	16.755	152	16.959
Q5JSL3	Dedicator of cytokinesis protein 11 OS=Homo sapiens GN=DOCK11 PE=1 SV=2 - [DOC11_HUMAN]	1.83	16	3	4	6	1.000	3	37.277	16.753	2073	237.519
Q9UI26	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1 - [IPO11_HUMAN]	6.46	8	7	7	9	1.000	9	8.261	16.727	975	112.463
E9API2	Ubiquitin-conjugating enzyme-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1580 PE=4 SV=1 - [E9API2_LEIMU]	15.22	1	2	2	5	1.000	5	0.000	16.724	138	16.023
E9B573	Regulatory subunit of protein kinase a-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2820 PE=4 SV=1 - [E9B573_LEIMU]	9.29	1	5	5	6	1.000	6	0.000	16.722	646	71.691
B3KRM8	Translin, isoform CRA_b OS=Homo sapiens GN=TSN PE=2 SV=1 - [B3KRM8_HUMAN]	17.68	6	4	4	7	1.101	7	20.420	16.722	181	20.938
Q05209	Tyrosine-protein phosphatase non-receptor type 12 OS=Homo sapiens GN=PTPN12 PE=1 SV=3 - [PTN12_HUMAN]	6.28	5	4	4	7	1.000	7	26.535	16.703	780	88.051
E9B705	Putative peptidyl-prolyl cis-trans isomerase (Cyclophilin-40) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4770 PE=4 SV=1 - [E9B705_LEIN	11.3	1	4	4	7	1.370	7	49.309	16.688	354	38.492
H3BV04	Secretory carrier-associated membrane protein 2 (Fragment) OS=Homo sapiens GN=SCAMP2 PE=1 SV=1 - [H3BV04_HUMAN]	10.31	8	3	3	6	1.054	4	9.399	16.663	194	21.970
B4DLL8	cDNA FLJ59335, highly similar to Transmembrane glycoprotein NMB OS=Homo sapiens PE=2 SV=1 - [B4DLL8_HUMAN]	4.18	10	2	2	7	1.358	7	2.474	16.657	455	50.547
B7Z8F4	cDNA FLJ56523, highly similar to ATP-dependent RNA helicase DHX8 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B7Z8F4_HUMAN]	3.13	9	2	4	7	0.647	2	33.729	16.636	1181	133.873

B7Z5N7	cDNA FLJ58612, highly similar to Sec1 family domain-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B7Z5N7_HUMAN]	12.47	6	6	6	10	0.937	10	17.994	16.636	457	51.511
Q8NB90	Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3 - [SPAT5_HUMAN]	5.82	2	4	5	7	1.000	5	0.000	16.635	893	97.843
Q9H2U1	ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=1 SV=2 - [DHX36_HUMAN]	4.46	3	3	3	4	1.000	4	0.000	16.632	1008	114.688
E9AS96	Cysteine peptidase A (CBA) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1420 PE=3 SV=1 - [E9AS96_LEIMU]	5.65	11	2	3	7	1.091	2	12.980	16.622	354	38.721
A0A024R0F6	Tripartite motif-containing 33, isoform CRA_a OS=Homo sapiens GN=TRIM33 PE=4 SV=1 - [A0A024R0F6_HUMAN]	3.64	7	3	4	8	1.000	5	31.309	16.600	1127	122.444
B4DS69	Arfaptin-1 OS=Homo sapiens GN=ARFIP1 PE=1 SV=1 - [B4DS69_HUMAN]	14.51	5	2	3	8	1.000	6	0.000	16.584	193	22.041
D6RF48	Syntaxin-18 OS=Homo sapiens GN=STX18 PE=1 SV=1 - [D6RF48_HUMAN]	20.13	5	7	7	9	0.989	8	18.746	16.568	308	35.399
H0Y8N0	Transmembrane protein 33 (Fragment) OS=Homo sapiens GN=TMEM33 PE=1 SV=1 - [H0Y8N0_HUMAN]	12.26	4	2	2	6	1.090	6	25.178	16.548	155	17.905
Q9Y5Z4	Heme-binding protein 2 OS=Homo sapiens GN=HEBP2 PE=1 SV=1 - [HEBP2_HUMAN]	18.05	3	3	3	5	0.884	5	11.422	16.528	205	22.861
Q86U79	Adenosine kinase OS=Homo sapiens PE=2 SV=1 - [Q86U79_HUMAN]	15.94	2	4	4	7	0.880	5	7.862	16.491	345	38.713
D3DP13	Fibrinogen beta chain, isoform CRA_e OS=Homo sapiens GN=FGB PE=4 SV=1 - [D3DP13_HUMAN]	17.15	4	5	5	7	1.000	4	8.843	16.490	344	39.711
B4DM79	cDNA FLJ53848, highly similar to Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens PE=2 SV=1 - [B4DM79_HUMAN]	5.34	6	3	3	6	1.042	6	6.910	16.474	543	60.666
B4DDF8	cDNA FLJ51786, highly similar to Retinal dehydrogenase 1 (EC 1.2.1.36) OS=Homo sapiens PE=2 SV=1 - [B4DDF8_HUMAN]	7.11	14	1	3	8	1.000	2	0.000	16.470	422	45.968
Q7L9L4	MOB kinase activator 1B OS=Homo sapiens GN=MOB1B PE=1 SV=3 - [MOB1B_HUMAN]	13.89	5	3	3	7	1.000	6	4.839	16.460	216	25.075
P49841	Glycogen synthase kinase-3 beta OS=Homo sapiens GN=GSK3B PE=1 SV=2 - [GSK3B_HUMAN]	7.14	4	1	2	4	1.000	3	0.000	16.446	420	46.715
E9ANS8	Proteasome subunit beta type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0030 PE=3 SV=1 - [E9ANS8_LEIMU]	7.77	1	2	2	5	1.553	5	72.811	16.432	283	30.482
A8K4K1	cDNA FLJ78216, highly similar to Homo sapiens lysosomal neuraminidase, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4K1_HUMAN]	7.23	6	4	4	7	0.918	7	12.805	16.416	415	45.310
A0A024R6Q8	Bromodomain containing 7, isoform CRA_b OS=Homo sapiens GN=BRD7 PE=4 SV=1 - [A0A024R6Q8_HUMAN]	3.15	3	2	2	6	1.000	6	0.000	16.404	508	57.428
A0A087WXZ6	High affinity immunoglobulin gamma Fc receptor IB (Fragment) OS=Homo sapiens GN=FCGR1B PE=4 SV=1 - [A0A087WXZ6_HUMAN]	8.8	4	3	3	5	1.060	5	8.669	16.403	250	28.947
E9AK58	Complete genome, chromosome 4 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0750 PE=4 SV=1 - [E9AK58_LEIMU]	13.15	1	2	4	15	2.879	2	344.125	16.378	213	24.541
J3QLI9	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [J3QLI9_HUMAN]	17.33	3	2	2	5	1.000	5	19.221	16.353	75	8.388
Q92618	Zinc finger protein 516 OS=Homo sapiens GN=ZNF516 PE=1 SV=1 - [ZN516_HUMAN]	3.87	3	4	4	6	1.000	5	0.000	16.342	1163	124.211
B2R6N0	cDNA, FLJ93029, highly similar to Homo sapiens COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis) (COPS2), mRNA OS=Homo sapiens PE=2 SV='	9.26	7	5	5	11	1.001	10	3.643	16.332	443	51.583
G3V2S6	V-type proton ATPase subunit D OS=Homo sapiens GN=ATP6V1D PE=1 SV=1 - [G3V2S6_HUMAN]	23.44	13	4	4	6	0.922	6	6.504	16.323	192	21.908
Q9H0Q0	Protein FAM49A OS=Homo sapiens GN=FAM49A PE=1 SV=1 - [FA49A_HUMAN]	7.12	4	1	2	8	0.918	1		16.320	323	37.289
A2IXV5	MIR-10 OS=Homo sapiens GN=MIR cl-10 PE=2 SV=1 - [A2IXV5_HUMAN]	2.18	2	1	1	5	1.000	5	0.000	16.315	597	64.964
Q6UX53	Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=2 SV=2 - [MET7B_HUMAN]	13.93	2	3	3	7	1.000	7	0.000	16.306	244	27.756
P37268	Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 - [FDFT_HUMAN]	11.99	7	5	5	8	0.983	8	12.846	16.301	417	48.084
Q5GJ64	Hypothetical rhabdomyosarcoma antigen MU-RMS-40.5 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q5GJ64_HUMAN]	8.74	18	6	6	8	1.000	7	0.000	16.299	755	84.417
Q9BVS4	Serine/threonine-protein kinase RIO2 OS=Homo sapiens GN=RIOK2 PE=1 SV=2 - [RIOK2_HUMAN]	9.06	3	4	4	5	0.904	4	14.980	16.298	552	63.243
O00635	Tripartite motif-containing protein 38 OS=Homo sapiens GN=TRIM38 PE=1 SV=1 - [TRI38_HUMAN]	4.73	3	2	2	5	1.000	5	0.000	16.278	465	53.381
P62312	U6 snRNA-associated Sm-like protein LSm6 OS=Homo sapiens GN=LSM6 PE=1 SV=1 - [LSM6_HUMAN]	33.75	1	3	3	7	0.971	7	7.426	16.277	80	9.122
Q8NF91	Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=4 - [SYNE1_HUMAN]	0.58	11	5	6	7	0.938	5	7.777	16.263	8797	1010.456
P83111	Serine beta-lactamase-like protein LACTB, mitochondrial OS=Homo sapiens GN=LACTB PE=1 SV=2 - [LACTB_HUMAN]	6.95	2	5	5	6	0.944	6	13.744	16.247	547	60.655
Q8N201	Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2 - [INT1_HUMAN]	3.2	5	7	7	9	1.000	9	0.000	16.245	2190	244.143
F8WAX9	Rab-like protein 3 OS=Homo sapiens GN=RABL3 PE=1 SV=1 - [F8WAX9_HUMAN]	20.75	6	1	1	6	0.973	1		16.241	53	5.647
B7ZM44	PIK3CD protein OS=Homo sapiens GN=PIK3CD PE=2 SV=1 - [B7ZM44_HUMAN]	5.37	12	5	5	6	0.956	6	25.763	16.238	1043	119.274
E9ATP7	Inosine triphosphate pyrophosphatase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4630 PE=3 SV=1 - [E9ATP7_LEIMU]	3.42	1	1	1	6	1.500	2	47.485	16.234	234	25.092
Q96GM8	Target of EGR1 protein 1 OS=Homo sapiens GN=TOE1 PE=1 SV=1 - [TOE1_HUMAN]	11.37	3	3	3	8	1.000	6	0.000	16.233	510	56.512
E9PJK1	Tetraspanin OS=Homo sapiens GN=CD81 PE=1 SV=1 - [E9PJK1_HUMAN]	15.76	9	1	2	5	1.000	4	0.000	16.188	165	17.951
H0YBX2	Putative deoxyribonuclease TATDN1 (Fragment) OS=Homo sapiens GN=TATDN1 PE=1 SV=1 - [H0YBX2_HUMAN]	13.37	11	2	3	6	0.904	3	10.190	16.169	202	22.653
Q92615	La-related protein 4B OS=Homo sapiens GN=LARP4B PE=1 SV=3 - [LAR4B_HUMAN]	9.21	4	7	7	7	0.869	7	28.109	16.168	738	80.503
A8K7A0	cDNA FLJ75753, highly similar to Homo sapiens primase, polypeptide 2A, 58kDa (PRIM2A), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K7A0_HUMAN]	5.5	5	3	3	6	1.000	6	26.024	16.162	509	58.797
A7E2F7	CAP-GLY domain containing linker protein 2 OS=Homo sapiens GN=CLIP2 PE=2 SV=1 - [A7E2F7_HUMAN]	3.36	7	2	4	6	0.945	2	8.435	16.143	1011	111.655
P25815	Protein S100-P OS=Homo sapiens GN=S100P PE=1 SV=2 - [S100P_HUMAN]	21.05	1	2	2	5	1.000	5	0.000	16.117	95	10.393
F8VRS8	CCR4-NOT transcription complex subunit 2 (Fragment) OS=Homo sapiens GN=CNOT2 PE=1 SV=1 - [F8VRS8_HUMAN]	16.67	10	4	4	8	0.935	7	11.378	16.116	276	29.906
Q9UG22	GTPase IMAP family member 2 OS=Homo sapiens GN=GIMAP2 PE=1 SV=2 - [GIMA2_HUMAN]	11.28	1	4	4	6	1.090	6	12.775	16.115	337	37.992
Q9HAC6	Aspartyl aminopeptidase, isoform CRA_g OS=Homo sapiens GN=DNPEP PE=2 SV=1 - [Q9HAC6_HUMAN]	8.61	17	3	3	6	0.884	6	32.701	16.092	267	29.693
E9PS63	Rab GTPase-activating protein 1-like (Fragment) OS=Homo sapiens GN=RABGAP1L PE=1 SV=1 - [E9PS63_HUMAN]	23.68	8	3	4	11	1.030	8	7.478	16.070	190	22.499
P46939	Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 - [UTRO_HUMAN]	2.1	4	6	7	8	0.996	6	0.638	16.050	3433	394.220
Q13636	Ras-related protein Rab-31 OS=Homo sapiens GN=RAB31 PE=1 SV=1 - [RAB31_HUMAN]	19.59	3	3	4	6	0.989	4	10.579	16.034	194	21.555
O00268	Transcription initiation factor TFIID subunit 4 OS=Homo sapiens GN=TAF4 PE=1 SV=2 - [TAF4_HUMAN]	2.76	1	2	2	5	1.000	5	0.000	16.034	1085	110.047
D6R9Y1	Polyadenylate-binding protein-interacting protein 2 OS=Homo sapiens GN=PAIP2 PE=4 SV=1 - [D6R9Y1_HUMAN]	22.39	4	2	2	7	0.841	7	21.378	16.031	67	7.694
E5RFP0	NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 - [E5RFP0_HUMAN]	15.91	2	2	2	5	0.871	5	5.186	16.025	132	14.736
Q4KMP7	TBC1 domain family member 10B OS=Homo sapiens GN=TBC1D10B PE=1 SV=3 - [TB10B_HUMAN]	7.18	2	4	4	11	1.000	9	0.000	16.008	808	87.145
Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	17.16	6	7	7	7	1.033	7	8.121	15.998	408	45.856
O00154	Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3 - [BACH_HUMAN]	9.47	4	4	4	8	1.000	8	3.676	15.995	380	41.769
B4DMD3	cDNA FLJ58174, highly similar to WW domain-binding protein 11 OS=Homo sapiens PE=2 SV=1 - [B4DMD3_HUMAN]	7.3	5	5	5	7	1.000	7	3.965	15.993	589	64.867
Q8NBN7	Retinol dehydrogenase 13 OS=Homo sapiens GN=RDH13 PE=1 SV=2 - [RDH13_HUMAN]	7.25	5	2	2	5	1.000	5	0.000	15.986	331	35.910
Q96AJ9	Vesicle transport through interaction with t-SNAREs homolog 1A OS=Homo sapiens GN=VTI1A PE=1 SV=2 - [VTI1A_HUMAN]	11.06	1	2	2	4	0.866	4	29.614	15.984	217	25.202
Q53TK4	Putative uncharacterized protein ITSN2 (Fragment) OS=Homo sapiens GN=ITSN2 PE=4 SV=1 - [Q53TK4_HUMAN]	1.81	10	2	3	7	1.141	2	0.947	15.975	1329	150.921
E7EXA6	Chromosome transmission fidelity protein 18 homolog OS=Homo sapiens GN=CHTF18 PE=1 SV=2 - [E7EXA6_HUMAN]	6.05	5	3	3	6	1.000	4	0.000	15.952	975	107.365
Q96A10	HCG2043597, isoform CRA_b OS=Homo sapiens GN=hCG_2043597 PE=2 SV=1 - [Q96A10_HUMAN]	10.81	3	2	2	6	1.022	6	15.516	15.944	74	7.860
P19838	Nuclear factor NF-kappa-B p105 subunit OS=Homo sapiens GN=NFKB1 PE=1 SV=2 - [NFKB1_HUMAN]	5.48	4	6	6	8	0.867	8	9.007	15.933	968	105.290
B4DKU1	cDNA FLJ57520, highly similar to Homo sapiens NMD3 homolog (NMD3), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DKU1_HUMAN]	13.93	5	5	5	9	1.176	9	26.262	15.928	323	37.074
K7EKE8	Nectin-2 (Fragment) OS=Homo sapiens GN=PVRL2 PE=4 SV=1 - [K7EKE8_HUMAN]	12.38	4	3	3	9	0.976	9	21.522	15.921	210	22.738
A0A087X023	Myosin-binding protein H OS=Homo sapiens GN=MYBPH PE=4 SV=1 - [A0A087X023_HUMAN]	7.56	2	2	2	7	1.000	3	0.000	15.917	476	51.959
A6PW79	Cyclic GMP-AMP synthase OS=Homo sapiens GN=MB21D1 PE=1 SV=1 - [A6PW79_HUMAN]	12.48	2	5	5	9	1.044	8	11.525	15.916	505	56.645
D6RCD0	Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens GN=HSD17B11 PE=1 SV=2 - [D6RCD0_HUMAN]	11.33	2	2	2	5	1.000	4	0.000	15.882	256	28.084
O95881	Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1 - [TXD12_HUMAN]	30.81	3	6	6	11	0.976	11	8.860	15.879	172	19.194
K7EK35	Signal transducer and activator of transcription OS=Homo sapiens GN=STAT5A PE=1 SV=1 - [K7EK35_HUMAN]	5.64	11	4	5	6	1.000	5	1.888	15.843	763	87.308
Q16643	Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 - [DREB_HUMAN]	8.63	7	4	5	6	1.199	4	24.059	15.839	649	71.385
P43897	Elongation factor Ts, mitochondrial OS=Homo sapiens GN=TSFM PE=1 SV=2 - [EFTS_HUMAN]	13.54	7	5	5	6	0.947	6	15.211	15.835	325	35.368
Q13426	DNA repair protein XRCC4 OS=Homo sapiens GN=XRCC4 PE=1 SV=2 - [XRCC4_HUMAN]	11.61	4	4	4	6	0.910	6	18.947	15.833	336	38.263
E7EMW7	E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=1 SV=1 - [E7EMW7_HUMAN]	2.15	5	6	6	6	1.000	6	18.855	15.818	2792	308.382
A9UK01	Rho GTPase activating protein OS=Homo sapiens PE=2 SV=1 - [A9UK01_HUMAN]	4.52	5	3	3	6	0.998	6	3.240	15.815	663	74.931
G5EA48	SLIT-ROBO Rho GTPase activating protein 1, isoform CRA_a OS=Homo sapiens GN=SRGAP1 PE=1 SV=1 - [G5EA48_HUMAN]	1.76	3	1	2	5	1.000	1		15.793	1022	116.768
Q8WW33	Gametocyte-specific factor 1 OS=Homo sapiens GN=GTSF1 PE=1 SV=2 - [GTSF1_HUMAN]	17.37	2	4	4	6	0.998	6	25.559	15.774	167	19.254
B4E0K5	Mitogen-activated protein kinase 14 OS=Homo sapiens GN=MAPK14 PE=1 SV=1 - [B4E0K5_HUMAN]	11.31	6	3	3	6	1.000	6	0.000	15.733	283	32.336
Q9BU23	Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 PE=1 SV=2 - [LMF2_HUMAN]	4.53	1	2	2	5	0.982	4	13.677	15.719	707	79.647
T1WHH0	Methylmalonyl-CoA mutase (Fragment) OS=Homo sapiens GN=MUT PE=2 SV=1 - [T1WHH0_HUMAN]	3.25	3	3	3	7	0.865	7	21.757	15.714	708	78.404
Q6PIU2	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3 - [NCEH1_HUMAN]	8.09	2	3	3	6	1.021	6	6.029	15.705	408	45.779
A0A087WTU3	Testis-expressed sequence 264 protein OS=Homo sapiens GN=TEX264 PE=4 SV=1 - [A0A087WTU3_HUMAN]	13.81	8	3	3	6	1.000	6	0.000	15.701	239	25.950
Q9NZL4	Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 PE=1 SV=1 - [HPBP1_HUMAN]	10.22	6	3	3	7	0.878	6	14.330	15.697	362	39.449
B7Z6J7	cDNA FLJ61662, highly similar to CCR4-NOT transcription complex subunit 3 OS=Homo sapiens PE=2 SV=1 - [B7Z6J7_HUMAN]	4.18	5	3	3	6	1.000	6	1.724	15.695	718	76.522
U3KPZ7	RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=4 SV=1 - [U3KPZ7_HUMAN]	5.55	5	5	6	7	0.965	6	6.164	15.693	1027	114.472
B7Z4Q0	cDNA FLJ55728, highly similar to ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens PE=2 SV=1 - [B7Z4Q0_HUMAN]	14.86	5	6	6	7	1.000	7	1.655	15.693	444	48.939
Q53X12	V-type proton ATPase subunit a OS=Homo sapiens PE=1 SV=1 - [Q53X12_HUMAN]	3.85	12	5	5	6	1.040	6	23.216	15.690	831	95.689
U6FVB0	Tyrosine-protein kinase receptor OS=Homo sapiens GN=CD74-Ntrk1 fusion gene PE=2 SV=1 - [U6FVB0_HUMAN]	10.05	10	5	5	9	1.000	7	26.825	15.687	627	70.290
D6RAM3	Docking protein 3 OS=Homo sapiens GN=DOK3 PE=1 SV=1 - [D6RAM3_HUMAN]	13.64	6	5	5	7	1.000	7	24.776	15.683	440	47.572
Q969E4	Transcription elongation factor A protein-like 3 OS=Homo sapiens GN=TCEAL3 PE=1 SV=1 - [TCAL3_HUMAN]	30.5	5	5	5	6	0.753	6	43.934	15.676	200	22.489
B0AZU2	cDNA FLJ55491 OS=Homo sapiens PE=2 SV=1 - [B0AZU2_HUMAN]	9.59	9	3	3	5	1.000	5	0.000	15.662	386	43.643
A6NC98	Coiled-coil domain-containing protein 88B OS=Homo sapiens GN=CCDC88B PE=1 SV=1 - [CC88B_HUMAN]	4.07	4	6	6	7	1.000	7	0.000	15.655	1476	164.710
Q8NFD5	AT-rich interactive domain-containing protein 1B OS=Homo sapiens GN=ARID1B PE=1 SV=2 - [ARI1B_HUMAN]	1.7	6	4	4	6	1.000	6	11.384	15.646	2236	235.974
Q3YEC7	Rab-like protein 6 OS=Homo sapiens GN=RABL6 PE=1 SV=2 - [RABL6_HUMAN]	4.53	10	3	3	6	0.995	6	21.240	15.639	729	79.500
C9J2P0	Ubiquitin-conjugating enzyme E2 E1 (Fragment) OS=Homo sapiens GN=UBE2E1 PE=1 SV=1 - [C9J2P0_HUMAN]	16.33	2	2	2	6	1.000	4	0.000	15.624	147	16.200
Q9H1C4	Protein unc-93 homolog B1 OS=Homo sapiens GN=UNC93B1 PE=1 SV=2 - [UN93B_HUMAN]	4.19	4	2	2	10	1.000	9	0.000	15.616	597	66.588
Q96PU4	E3 ubiquitin-protein ligase UHRF2 OS=Homo sapiens GN=UHRF2 PE=1 SV=1 - [UHRF2_HUMAN]	4.86	2	2	4	6	0.761	2	42.138	15.613	802	89.928
B4DWD1	cDNA FLJ60919, highly similar to Cytochrome b-245 heavy chain OS=Homo sapiens PE=2 SV=1 - [B4DWD1_HUMAN]	3.63	3	1	1	5	1.270	5	16.537	15.589	303	35.051
A0A024R669	Menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis), isoform CRA_b OS=Homo sapiens GN=MNAT1 PE=4 SV=1 - [A0A024R669_HUMAN]	9.74	4	2	2	4	1.000	4	0.000	15.581	267	31.129
Q9BTW9	Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2 - [TBCD_HUMAN]	3.52	5	4	4	5	1.002	5	7.615	15.576	1192	132.515
Q13951	Core-binding factor subunit beta OS=Homo sapiens GN=CBFB PE=1 SV=2 - [PEBB_HUMAN]	12.64	5	2	2	4	0.882	4	15.756	15.572	182	21.495
B4DRG7	Condensin complex subunit 2 OS=Homo sapiens PE=2 SV=1 - [B4DRG7_HUMAN]	6.83	7	5	6	7	0.907	5	14.565	15.572	717	80.079
H0YCM7	Engulfment and cell motility protein 2 (Fragment) OS=Homo sapiens GN=ELMO2 PE=1 SV=1 - [H0YCM7_HUMAN]	7.26	9	2	4	7	1.051	3	8.706	15.549	441	51.416
Q9UK45	U6 snRNA-associated Sm-like protein LSm7 OS=Homo sapiens GN=LSM7 PE=1 SV=1 - [LSM7_HUMAN]	20.39	6	2	3	6	1.006	3	1.162	15.543	103	11.595
B7Z1U1	cDNA FLJ60457, highly similar to NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial (EC 1.6.5.3) OS=Homo sapiens PE=2 SV=1 - [B7Z1U1_HUMAN]	9.34	12	3	3	7	1.000	7	15.342	15.528	182	19.773
B3KP49	RAN binding protein 10, isoform CRA_b OS=Homo sapiens GN=RANBP10 PE=2 SV=1 - [B3KP49_HUMAN]	6.65	3	2	2	5	1.000	3	0.000	15.526	391	42.878
E5RFT1	Zinc transporter ZIP14 (Fragment) OS=Homo sapiens GN=SLC39A14 PE=4 SV=3 - [E5RFT1_HUMAN]	4.46	2	1	1	6	1.000	6	3.852	15.507	202	22.599
B2R8F3	cDNA, FLJ93871, highly similar to Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8F3_HUMAN]	10.97	3	3	3	9	1.000	8	20.317	15.504	319	35.182
P62318	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1 - [SMD3_HUMAN]	24.6	2	2	2	7	1.000	5	0.000	15.489	126	13.907
Q14257	Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=1 SV=1 - [RCN2_HUMAN]	11.36	3	4	4	7	1.095	7	13.427	15.489	317	36.854
Q9HBI0	Gamma-parvin OS=Homo sapiens GN=PARVG PE=2 SV=1 - [PARVG_HUMAN]	7.85	4	2	2	5	1.070	5	10.029	15.486	331	37.462
P42574	Caspase-3 OS=Homo sapiens GN=CASP3 PE=1 SV=2 - [CASP3_HUMAN]	11.91	5	2	2	5	1.900	5	2.948	15.464	277	31.587
Q9H6W3	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 OS=Homo sapiens GN=NO66 PE=1 SV=2 - [NO66_HUMAN]	3.28	1	2	2	5	1.000	5	0.000	15.431	641	71.041
Q496C9	D-tyrosyl-tRNA(Tyr) deacylase OS=Homo sapiens GN=DTD1 PE=2 SV=1 - [Q496C9_HUMAN]	14.83	2	2	2	4	1.012	4	1.798	15.410	209	23.469
M0R3F6	SURP and G-patch domain-containing protein 2 OS=Homo sapiens GN=SUGP2 PE=1 SV=1 - [M0R3F6_HUMAN]	8.8	8	7	7	10	1.000	9	0.000	15.410	841	93.801
P09001	39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 - [RM03_HUMAN]	8.33	7	3	3	7	1.002	7	30.222	15.388	348	38.608
Q8TAE8	Growth arrest and DNA damage-inducible proteins-interacting protein 1 OS=Homo sapiens GN=GADD45GIP1 PE=1 SV=1 - [G45IP_HUMAN]	12.61	2	3	3	5	1.000	5	0.000	15.365	222	25.368
A0A024R2Z6	Guanine nucleotide binding protein-like 3 (Nucleolar), isoform CRA_b OS=Homo sapiens GN=GNL3 PE=4 SV=1 - [A0A024R2Z6_HUMAN]	9.87	5	5	5	6	0.920	6	31.534	15.362	537	60.535
B4DWE9	cDNA FLJ57216, highly similar to Homo sapiens Rho GTPase activating protein 17 (ARHGAP17), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DWE9_	4.2	10	4	4	7	0.965	7	19.032	15.358	714	77.478
B2R6U8	cDNA, FLJ93125, highly similar to Homo sapiens cleavage and polyadenylation specific factor 5, 25 kDa(CPSF5), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6U8_HUI	18.06	5	5	5	7	1.000	7	12.819	15.355	227	26.199
Q9NWU5	39S ribosomal protein L22, mitochondrial OS=Homo sapiens GN=MRPL22 PE=1 SV=1 - [RM22_HUMAN]	17.96	3	3	3	6	1.000	6	0.000	15.350	206	23.626
P01111	GTPase NRas OS=Homo sapiens GN=NRAS PE=1 SV=1 - [RASN_HUMAN]	15.34	12	3	3	6	1.003	6	9.959	15.348	189	21.216
Q9NX55	Huntingtin-interacting protein K OS=Homo sapiens GN=HYPK PE=1 SV=2 - [HYPK_HUMAN]	19.38	2	2	2	6	1.024	6	6.672	15.346	129	14.656
B7Z6M7	cDNA FLJ56248, highly similar to Vacuolar protein sorting 33B OS=Homo sapiens PE=2 SV=1 - [B7Z6M7_HUMAN]	7.87	4	5	5	7	0.971	7	6.013	15.324	572	65.339
B3KR88	cDNA FLJ33863 fis, clone CTONG2006393, highly similar to Rho-GTPase-activating protein 12 OS=Homo sapiens PE=2 SV=1 - [B3KR88_HUMAN]	6.99	6	5	5	7	1.000	5	0.000	15.319	816	92.985
Q9NR33	DNA polymerase epsilon subunit 4 OS=Homo sapiens GN=POLE4 PE=1 SV=2 - [DPOE4_HUMAN]	29.06	1	2	2	5	1.000	5	0.000	15.318	117	12.201
B0QYR6	ADP-ribosylation factor-binding protein GGA1 (Fragment) OS=Homo sapiens GN=GGA1 PE=1 SV=1 - [B0QYR6_HUMAN]	12.6	6	5	5	6	0.936	6	23.279	15.315	246	27.862
Q8WX92	Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1 - [NELFB_HUMAN]	6.03	1	3	3	6	1.000	5	3.069	15.312	580	65.655
K7EQV2	Ribonuclease P protein subunit p29 (Fragment) OS=Homo sapiens GN=POP4 PE=1 SV=1 - [K7EQV2_HUMAN]	13.33	4	1	2	5	1.000	4	0.000	15.280	150	17.418
Q13315	Serine-protein kinase ATM OS=Homo sapiens GN=ATM PE=1 SV=4 - [ATM_HUMAN]	1.37	4	4	4	6	1.000	5	0.000	15.280	3056	350.462
H0YF92	Putative sodium-coupled neutral amino acid transporter 10 (Fragment) OS=Homo sapiens GN=SLC38A10 PE=4 SV=3 - [H0YF92_HUMAN]	13.04	1	1	4	6	1.000	1		15.250	299	31.742
A8K4U4	cDNA FLJ77113 OS=Homo sapiens PE=2 SV=1 - [A8K4U4_HUMAN]	2.51	2	1	1	5	1.000	4	0.000	15.248	837	95.543
A0A024R2X6	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP4 PE=3 SV=1 - [A0A024R2X6_HUMAN]	2.84	6	1	3	7	1.000	1		15.247	916	103.892
A0A087WXN4	Integrator complex subunit 12 OS=Homo sapiens GN=INTS12 PE=4 SV=1 - [A0A087WXN4_HUMAN]	7.43	2	3	3	5	1.126	4	22.234	15.244	444	46.638
P17050	Alpha-N-acetylgalactosaminidase OS=Homo sapiens GN=NAGA PE=1 SV=2 - [NAGAB_HUMAN]	10.71	1	5	5	7	1.028	7	6.585	15.231	411	46.534
Q6ZUJ8	Phosphoinositide 3-kinase adapter protein 1 OS=Homo sapiens GN=PIK3AP1 PE=1 SV=2 - [BCAP_HUMAN]	11.68	2	7	7	10	1.000	8	1.070	15.226	805	90.341
F5H5B4	Serine/threonine-protein kinase 4 OS=Homo sapiens GN=STK4 PE=1 SV=1 - [F5H5B4_HUMAN]	7.18	6	4	4	6	1.044	6	7.162	15.191	432	49.511
S5FZ81	PHD finger protein 10 OS=Homo sapiens GN=PHF10 PE=2 SV=1 - [S5FZ81_HUMAN]	10.34	5	4	4	5	1.000	5	0.000	15.187	377	42.586
O60522	Tudor domain-containing protein 6 OS=Homo sapiens GN=TDRD6 PE=2 SV=2 - [TDRD6_HUMAN]	0.91	3	1	2	8	1.092	2	1.485	15.181	2096	236.367
H0YCR2	RalBP1-associated Eps domain-containing protein 1 (Fragment) OS=Homo sapiens GN=REPS1 PE=1 SV=1 - [H0YCR2_HUMAN]	15.79	6	2	2	5	1.000	5	0.000	15.181	152	17.019
A0A024R3N3	Amyloid beta (A4)-like protein 2, isoform CRA_a OS=Homo sapiens GN=APLP2 PE=4 SV=1 - [A0A024R3N3_HUMAN]	7.46	5	5	5	6	1.000	5	0.000	15.163	710	81.927
E9PGW7	Mediator of RNA polymerase II transcription subunit 22 (Fragment) OS=Homo sapiens GN=MED22 PE=1 SV=1 - [E9PGW7_HUMAN]	20.72	6	2	2	5	1.000	5	0.000	15.153	111	12.846
H0YLH3	Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens GN=RABGGTA PE=1 SV=1 - [H0YLH3_HUMAN]	6.37	5	3	3	5	0.919	5	22.964	15.147	424	48.970
B7Z737	cDNA FLJ52784, highly similar to Bcl-2-like 13 protein OS=Homo sapiens PE=2 SV=1 - [B7Z737_HUMAN]	9.76	7	2	2	10	0.927	10	11.273	15.139	205	21.622
H0Y5G7	Neuroblastoma-amplified sequence (Fragment) OS=Homo sapiens GN=NBAS PE=1 SV=1 - [H0Y5G7_HUMAN]	5.36	5	7	7	8	1.000	8	9.313	15.135	1419	160.424
H7C3P7	Ras-related protein Ral-A (Fragment) OS=Homo sapiens GN=RALA PE=1 SV=1 - [H7C3P7_HUMAN]	11.59	5	1	2	5	1.047	2	15.538	15.131	164	18.359
Q59ES5	Sorting nexin 9 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59ES5_HUMAN]	5.44	6	2	2	8	1.000	7	0.000	15.131	349	39.492
B4DF80	cDNA FLJ58527, highly similar to Nucleolar protein 6 OS=Homo sapiens PE=2 SV=1 - [B4DF80_HUMAN]	3.2	3	3	3	5	1.000	5	0.000	15.114	1094	121.973
Q53S08	Putative uncharacterized protein RAB6C OS=Homo sapiens GN=RAB6C PE=2 SV=1 - [Q53S08_HUMAN]	7.48	2	1	3	6	0.944	2	37.984	15.084	254	28.224
O60925	Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2 - [PFD1_HUMAN]	29.51	2	4	4	8	0.968	8	22.783	15.081	122	14.202
P22681	E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=2 - [CBL_HUMAN]	5.52	1	4	4	7	1.000	7	3.720	15.080	906	99.569
Q9NZ63	Uncharacterized protein C9orf78 OS=Homo sapiens GN=C9orf78 PE=1 SV=1 - [CI078_HUMAN]	17.3	4	6	6	8	1.000	8	11.987	15.071	289	33.667
Q9NRV9	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1 - [HEBP1_HUMAN]	28.57	3	5	5	7	1.000	7	0.000	15.065	189	21.084
A0A087WVI1	PDZ and LIM domain protein 2 OS=Homo sapiens GN=PDLIM2 PE=4 SV=1 - [A0A087WVI1_HUMAN]	14.15	10	4	4	5	0.853	5	22.247	15.064	325	34.745
A0A087WY88	Protein jagunal homolog 1 OS=Homo sapiens GN=JAGN1 PE=4 SV=1 - [A0A087WY88_HUMAN]	6.63	2	1	1	5	1.000	5	49.673	15.055	181	20.778
Q75MT5	Putative uncharacterized protein RFC2 OS=Homo sapiens GN=RFC2 PE=2 SV=1 - [Q75MT5_HUMAN]	7.19	11	2	2	4	0.805	4	26.911	15.053	320	35.221
B6ETR7	MHC class II antigen (Fragment) OS=Homo sapiens GN=HLA-DRB1 PE=4 SV=1 - [B6ETR7_HUMAN]	18.58	531	2	4	6	1.216	2	28.905	15.030	183	21.329
O96011	Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B PE=1 SV=1 - [PX11B_HUMAN]	15.44	3	4	4	7	1.000	7	5.486	15.019	259	28.413
K7EIR2	Protein QIL1 OS=Homo sapiens GN=C19orf70 PE=4 SV=1 - [K7EIR2_HUMAN]	7.95	3	1	1	6	0.995	6	5.590	15.003	88	9.694
E9B620	Putative threonyl-tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1410 PE=3 SV=1 - [E9B620_LEIMU]	5.34	1	3	4	6	1.015	3	2.160	14.995	787	89.673
E9B4H3	Putative ascorbate-dependent peroxidase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0070 PE=3 SV=1 - [E9B4H3_LEIMU]	11.88	1	3	4	8	1.195	5	5.416	14.991	303	33.599
Q5JUV4	Cytosolic purine 5'-nucleotidase (Fragment) OS=Homo sapiens GN=NT5C2 PE=1 SV=1 - [Q5JUV4_HUMAN]	13.21	8	4	4	6	0.833	6	14.102	14.981	265	30.876
Q7Z6L1	Tectonin beta-propeller repeat-containing protein 1 OS=Homo sapiens GN=TECPR1 PE=1 SV=1 - [TCPR1_HUMAN]	2.23	19	1	3	6	1.000	1		14.975	1165	129.614
O15302	CaM kinase II isoform OS=Homo sapiens PE=2 SV=1 - [O15302_HUMAN]	17.99	1	1	5	9	1.000	1		14.973	239	26.744
F6T1Q0	2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=1 - [F6T1Q0_HUMAN]	9.75	2	4	4	8	0.972	7	4.453	14.959	472	52.143
C9J6A7	Ribulose-phosphate 3-epimerase (Fragment) OS=Homo sapiens GN=RPE PE=1 SV=1 - [C9J6A7_HUMAN]	5.66	3	1	1	5	0.947	4	1.485	14.953	159	17.403
Q562E7	WD repeat-containing protein 81 OS=Homo sapiens GN=WDR81 PE=1 SV=2 - [WDR81_HUMAN]	2.99	2	4	4	6	1.000	6	1.461	14.949	1941	211.564
E9B6P8	Putative Gim5A protein (Glycosomal membrane protein) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3700 PE=4 SV=1 - [E9B6P8_LEIMU]	18.22	1	5	5	8	2.252	8	180.438	14.925	225	24.864
Q9Y639	Neuroplastin OS=Homo sapiens GN=NPTN PE=1 SV=2 - [NPTN_HUMAN]	10.3	5	4	4	5	1.000	5	0.000	14.905	398	44.360
B3KNB0	cDNA FLJ14159 fis, clone NT2RM2001360, highly similar to Homo sapiens clone C40 unknown mRNA OS=Homo sapiens PE=2 SV=1 - [B3KNB0_HUMAN]	9.01	2	3	3	5	0.973	5	4.110	14.901	322	36.080
H0Y360	AMP deaminase 2 (Fragment) OS=Homo sapiens GN=AMPD2 PE=1 SV=1 - [H0Y360_HUMAN]	4.76	7	4	4	6	0.849	5	4.246	14.898	861	98.450
E7ERU0	Dystonin OS=Homo sapiens GN=DST PE=1 SV=1 - [E7ERU0_HUMAN]	0.5	8	1	3	6	1.000	1		14.886	5375	615.272
B4DSQ7	cDNA FLJ52974, highly similar to Neural cell adhesion molecule 1, 140 kDa isoform OS=Homo sapiens PE=2 SV=1 - [B4DSQ7_HUMAN]	8.63	12	2	3	6	0.948	4	13.560	14.875	313	33.347
Q4G0N4	NAD kinase 2, mitochondrial OS=Homo sapiens GN=NADK2 PE=1 SV=2 - [NAKD2_HUMAN]	8.6	4	4	4	6	0.985	6	4.694	14.862	442	49.402
P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3 - [MA1A1_HUMAN]	4.9	3	2	3	6	0.793	3	21.304	14.858	653	72.922
P19623	Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 - [SPEE_HUMAN]	15.56	3	3	3	5	1.000	5	0.000	14.850	302	33.803
Q05BM8	GALNT1 protein OS=Homo sapiens GN=GALNT1 PE=2 SV=1 - [Q05BM8_HUMAN]	6.81	4	3	3	5	1.000	5	2.865	14.844	499	57.300
E9ANF3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0070 PE=4 SV=1 - [E9ANF3_LEIMU]	16.26	1	3	3	7	1.000	5	0.000	14.833	1562	174.296
B2R8Y6	cDNA, FLJ94121, highly similar to Homo sapiens stromal antigen 2 (STAG2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8Y6_HUMAN]	4.04	8	4	5	7	0.812	4	19.405	14.819	1162	133.976
Q8IV08	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 - [PLD3_HUMAN]	6.12	6	3	3	6	1.013	6	3.763	14.816	490	54.671
Q01658	Protein Dr1 OS=Homo sapiens GN=DR1 PE=1 SV=1 - [NC2B_HUMAN]	8.52	2	2	2	5	1.071	5	9.464	14.797	176	19.432
E9PKP0	Ribonuclease H2 subunit C OS=Homo sapiens GN=RNASEH2C PE=1 SV=1 - [E9PKP0_HUMAN]	17.28	7	1	1	4	0.681	4	67.713	14.773	81	8.951
C9J2G0	BRCA1-A complex subunit BRE (Fragment) OS=Homo sapiens GN=BRE PE=1 SV=1 - [C9J2G0_HUMAN]	9.15	4	1	1	4	1.000	4	0.000	14.772	153	17.328
Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens GN=COA6 PE=1 SV=1 - [COA6_HUMAN]	11.2	2	1	1	4	1.000	4	18.538	14.766	125	14.107
Q9NR09	Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=2 - [BIRC6_HUMAN]	1.38	3	6	6	6	1.000	5	18.055	14.762	4857	529.919
Q9NR50	Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 - [EI2BG_HUMAN]	7.74	3	3	4	6	0.647	5	53.000	14.757	452	50.208
B4DU23	cDNA FLJ53488, highly similar to Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 3 (LRCH3), mRNA OS=Homo sapiens PE=2 SV=1 -	3.21	6	2	2	6	1.000	6	0.000	14.753	623	68.473
E9B215	Prostaglandin f2-alpha synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2150 PE=4 SV=1 - [E9B215_LEIMU]	10.21	2	3	3	6	1.657	5	86.997	14.747	284	31.842

Q8IWX8	Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=3 - [CHERP_HUMAN]	4.69	5	4	4	6	0.992	6	27.820	14.743	916	103.637
B1AKD8	Rootletin (Fragment) OS=Homo sapiens GN=CROCC PE=4 SV=2 - [B1AKD8_HUMAN]	2.06	6	1	3	6	1.089	2	12.720	14.722	1311	149.086
O14949	Cytochrome b-c1 complex subunit 8 OS=Homo sapiens GN=UQCRQ PE=1 SV=4 - [QCR8_HUMAN]	30.49	2	4	4	6	1.062	6	11.777	14.688	82	9.900
C9JAB9	Cytoplasmic protein NCK1 (Fragment) OS=Homo sapiens GN=NCK1 PE=1 SV=1 - [C9JAB9_HUMAN]	18.97	3	3	3	6	1.000	5	0.000	14.687	174	20.056
P41214	Eukaryotic translation initiation factor 2D OS=Homo sapiens GN=EIF2D PE=1 SV=3 - [EIF2D_HUMAN]	6.16	4	3	3	5	1.021	5	7.319	14.683	584	64.666
A0A059QFD5	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=COX2 PE=3 SV=1 - [A0A059QFD5_HUMAN]	7.49	7	1	2	6	0.773	3	34.593	14.669	227	25.625
Q9H9Y6	DNA-directed RNA polymerase I subunit RPA2 OS=Homo sapiens GN=POLR1B PE=1 SV=2 - [RPA2_HUMAN]	2.73	10	3	3	5	0.996	5	27.054	14.662	1135	128.146
B4DJ71	cDNA FLJ58138, highly similar to Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DJ71	5.51	3	2	2	5	0.955	4	31.839	14.661	454	49.238
B2R9H3	cDNA, FLJ94391, highly similar to Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8 (SERPINB8), mRNA OS=Homo sapiens PE=2 S	12.57	5	4	5	9	1.000	7	0.000	14.655	374	42.727
B2RBM8	cDNA, FLJ95596, highly similar to Homo sapiens activity-dependent neuroprotector (ADNP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBM8_HUMAN]	2.54	4	3	3	6	1.000	6	9.080	14.654	1102	123.538
A8K6M4	cDNA FLJ75725, highly similar to Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1B (yeast) (VTI1B), mRNA OS=Homo sapiens PE=2 SV=1	24.14	8	4	5	7	0.601	5	21.867	14.643	232	26.672
E9AT12	Glyceraldehyde-3-phosphate dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2350 PE=3 SV=1 - [E9AT12_LEIMU]	6.65	2	1	2	7	1.516	1		14.633	331	35.484
Q9BTT5	Similar to NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 9 (39kD) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BTT5_HUMAN]	7.69	4	2	3	6	1.000	5	13.058	14.630	338	38.417
Q86VN1	Vacuolar protein-sorting-associated protein 36 OS=Homo sapiens GN=VPS36 PE=1 SV=1 - [VPS36_HUMAN]	8.81	2	4	4	5	1.000	5	7.271	14.571	386	43.789
B4DSQ5	cDNA FLJ53608, highly similar to Protein transport protein Sec23A OS=Homo sapiens PE=2 SV=1 - [B4DSQ5_HUMAN]	4.89	9	2	3	6	1.000	5	0.000	14.544	736	82.875
Q7LG56	Ribonucleoside-diphosphate reductase subunit M2 B OS=Homo sapiens GN=RRM2B PE=1 SV=1 - [RIR2B_HUMAN]	3.13	2	1	1	5	1.000	5	24.094	14.529	351	40.710
A8K4R1	cDNA FLJ77420, highly similar to Homo sapiens cancer susceptibility candidate 4 (CASC4), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4R1_HUMA	11.05	6	5	5	6	1.057	6	23.171	14.521	380	43.305
O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Homo sapiens GN=NDUFB4 PE=1 SV=3 - [NDUB4_HUMAN]	21.71	3	2	2	6	1.000	4	0.000	14.503	129	15.199
B3GQE6	DEAD box polypeptide 27 OS=Homo sapiens GN=DDX27 PE=2 SV=1 - [B3GQE6_HUMAN]	5.36	7	3	4	5	1.000	4	4.265	14.494	765	86.581
B3KM81	cDNA FLJ10471 fis, clone NT2RP2000045, highly similar to DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B3KM81_HUMAN]	6.18	3	2	2	5	1.000	5	0.000	14.478	453	49.552
A0A024R2G2	Fanconi anemia, complementation group D2, isoform CRA_b OS=Homo sapiens GN=FANCD2 PE=4 SV=1 - [A0A024R2G2_HUMAN]	3.86	4	5	5	6	0.910	6	14.039	14.474	1451	164.025
Q9NZD8	Maspardin OS=Homo sapiens GN=SPG21 PE=1 SV=1 - [SPG21_HUMAN]	14.94	9	4	4	6	1.004	6	0.925	14.465	308	34.938
E8NHI0	40S ribosomal protein S3a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_34_0400a_1 PE=3 SV=1 - [E8NHI0_LEIMU]	8.71	1	2	2	6	1.000	6	0.000	14.436	264	30.017
B7Z6K2	cDNA FLJ58625, highly similar to Polypeptide N-acetylgalactosaminyltransferase 2 (EC 2.4.1.41) OS=Homo sapiens PE=2 SV=1 - [B7Z6K2_HUMAN]	6.57	4	4	4	6	1.093	6	6.993	14.434	533	60.787
Q9NTX5	Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 PE=1 SV=2 - [ECHD1_HUMAN]	11.07	9	3	3	5	1.000	5	45.978	14.388	307	33.677
E9AKW4	Dihydrofolate reductase-thymidylate synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0860 PE=3 SV=1 - [E9AKW4_LEIMU]	1.15	1	1	1	7	1.083	3	18.359	14.378	520	58.488
A8K702	cDNA FLJ78285, highly similar to Homo sapiens gasdermin domain containing 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K702_HUMAN]	4.55	10	2	2	4	0.976	4	8.795	14.377	484	52.787
F8WBJ6	RNA-binding protein PNO1 OS=Homo sapiens GN=PNO1 PE=1 SV=1 - [F8WBJ6_HUMAN]	19.12	3	2	2	4	0.969	4	6.353	14.371	136	15.166
E9ATG6	Putative glycyl tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3840 PE=3 SV=1 - [E9ATG6_LEIMU]	6.21	1	4	4	6	1.966	6	131.572	14.338	628	70.218
Q29789	MHC class II HLA-DR2 (non-Dw2/non-Dw12) a-associated glycoprotein beta-chain (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q29789_HUMAN]	10.97	426	1	3	6	1.104	2	14.783	14.330	237	26.865
E9B2K8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0840 PE=4 SV=1 - [E9B2K8_LEIMU]	7.9	1	4	4	5	1.225	5	30.793	14.325	519	56.709
H0Y6J6	Splicing factor 45 (Fragment) OS=Homo sapiens GN=RBM17 PE=1 SV=1 - [H0Y6J6_HUMAN]	18.22	5	4	4	7	1.000	7	11.889	14.320	225	25.267
P78536	Disintegrin and metalloproteinase domain-containing protein 17 OS=Homo sapiens GN=ADAM17 PE=1 SV=1 - [ADA17_HUMAN]	10.19	7	7	7	8	1.000	7	4.368	14.317	824	92.961
Q53F88	General transcription factor IIE, polypeptide 1 (Alpha subunit, 56kD) variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53F88_HUMAN]	6.44	3	2	2	6	1.000	5	5.326	14.313	357	40.093
A0A087WZX2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Homo sapiens GN=NDUFB6 PE=4 SV=1 - [A0A087WZX2_HUMAN]	22.68	2	3	3	9	0.991	9	16.846	14.309	97	11.708
E9AST4	Clathrin heavy chain OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1630 PE=3 SV=1 - [E9AST4_LEIMU]	2.13	1	4	4	6	1.000	6	0.000	14.283	1693	191.106
B4DLW4	cDNA FLJ60300, highly similar to Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12C (PPP1R12C), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DLW	12.45	3	1	4	6	1.000	1		14.270	538	59.294
I3L459	Phosphatidylinositol transfer protein alpha isoform (Fragment) OS=Homo sapiens GN=PITPNA PE=1 SV=1 - [I3L459_HUMAN]	19.72	10	4	4	6	1.194	6	17.720	14.260	142	16.684
A0A087WW65	ATP-binding cassette sub-family B member 7, mitochondrial OS=Homo sapiens GN=ABCB7 PE=4 SV=1 - [A0A087WW65_HUMAN]	5.05	5	4	4	8	1.000	8	23.244	14.260	713	78.239
Q9BRV8	Suppressor of IKBKE 1 OS=Homo sapiens GN=SIKE1 PE=1 SV=1 - [SIKE1_HUMAN]	30.92	1	5	5	6	1.000	6	0.000	14.255	207	23.706
B3KSI3	Branched-chain-amino-acid aminotransferase OS=Homo sapiens GN=BCAT2 PE=1 SV=1 - [B3KSI3_HUMAN]	6.53	6	2	2	4	0.997	4	0.468	14.249	352	39.890
B7Z872	cDNA FLJ56895, highly similar to Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens PE=2 SV=1 - [B7Z872_HUMAN]	6.63	8	2	3	5	1.000	2	0.000	14.229	603	65.555
B3KM32	cDNA FLJ10124 fis, clone HEMBA1002951, highly similar to Homo sapiens EH domain binding protein 1 (EHBP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KM32_HU	8.42	4	1	2	6	1.000	1		14.228	202	23.972
Q5T8Q9	Glutathione S-transferase M5, isoform CRA_a OS=Homo sapiens GN=GSTM5 PE=3 SV=1 - [Q5T8Q9_HUMAN]	14.36	8	3	4	7	0.916	6	5.035	14.228	202	23.427
E9AK23	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0420 PE=4 SV=1 - [E9AK23_LEIMU]	6.37	1	2	2	4	1.133	4	18.628	14.216	361	39.184
Q6IB68	MYCBP protein OS=Homo sapiens GN=MYCBP PE=2 SV=1 - [Q6IB68_HUMAN]	19.42	3	2	2	5	0.971	5	16.873	14.207	103	11.945
Q12913	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3 - [PTPRJ_HUMAN]	4.64	4	6	6	7	0.950	7	5.560	14.186	1337	145.851
Q9UBK8	Methionine synthase reductase OS=Homo sapiens GN=MTRR PE=1 SV=3 - [MTRR_HUMAN]	7.72	8	3	4	5	1.000	4	0.000	14.173	725	80.359
P15848	Arylsulfatase B OS=Homo sapiens GN=ARSB PE=1 SV=1 - [ARSB_HUMAN]	7.69	2	4	4	5	0.970	5	16.524	14.162	533	59.649
B3KSG9	cDNA FLJ36188 fis, clone TESTI2027179, highly similar to Transmembrane 9 superfamily protein member 2 OS=Homo sapiens PE=2 SV=1 - [B3KSG9_HUMAN]	7.85	2	4	4	7	1.000	7	22.297	14.144	573	65.387
Q9UBF2	Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 - [COPG2_HUMAN]	5.28	5	4	5	6	0.991	5	23.469	14.131	871	97.560
B4DR72	cDNA FLJ59963, highly similar to Homo sapiens multiple substrate lipid kinase (MULK), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DR72_HUMAN]	11.89	5	4	4	6	0.950	6	12.610	14.128	244	26.862
E5KQF5	Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 PE=3 SV=1 - [E5KQF5_HUMAN]	8.89	15	5	5	7	0.786	7	36.872	14.118	742	81.457
Q5RKV6	Exosome complex component MTR3 OS=Homo sapiens GN=EXOSC6 PE=1 SV=1 - [EXOS6_HUMAN]	21.69	1	5	5	6	1.000	6	3.393	14.104	272	28.218
P56537	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 - [IF6_HUMAN]	13.06	2	2	2	5	0.989	5	9.381	14.103	245	26.582
B3KX12	Anoctamin OS=Homo sapiens PE=2 SV=1 - [B3KX12_HUMAN]	6.16	4	3	3	7	1.091	7	12.917	14.097	357	41.943
E9AS23	Glycosomal malate dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0710 PE=3 SV=1 - [E9AS23_LEIMU]	9.94	1	3	3	5	1.021	5	3.037	14.096	322	33.706
J3QQM5	LIM domain-containing protein 2 (Fragment) OS=Homo sapiens GN=LIMD2 PE=1 SV=1 - [J3QQM5_HUMAN]	15.6	4	2	2	5	1.000	5	0.000	14.089	109	12.005
Q6ZS46	Putative uncharacterized protein FLJ45840 OS=Homo sapiens PE=5 SV=2 - [YF009_HUMAN]	5.05	1	1	1	5	0.948	5	47.841	14.089	218	22.136
A8K4W5	cDNA FLJ76813, highly similar to Homo sapiens acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase), mRNA OS=Homo sapiens PE=2 SV=1 - [A8k	8.06	3	4	4	6	0.991	6	18.860	14.082	397	41.352
Q9Y3D6	Mitochondrial fission 1 protein OS=Homo sapiens GN=FIS1 PE=1 SV=2 - [FIS1_HUMAN]	17.11	1	3	3	5	0.961	5	8.326	14.074	152	16.927
K7EJE6	Formin-like protein 1 (Fragment) OS=Homo sapiens GN=FMNL1 PE=1 SV=1 - [K7EJE6_HUMAN]	10.86	3	1	5	7	1.041	1		14.070	488	55.056
P82932	28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 - [RT06_HUMAN]	21.6	1	3	3	5	1.000	5	0.000	14.014	125	14.218
A2ACR1	Proteasome subunit beta type OS=Homo sapiens GN=PSMB9 PE=1 SV=1 - [A2ACR1_HUMAN]	9.69	3	2	2	6	0.912	5	8.456	14.010	196	20.947
A0A024R4S2	Protein phosphatase 1, regulatory (Inhibitor) subunit 12C, isoform CRA_b OS=Homo sapiens GN=PPP1R12C PE=4 SV=1 - [A0A024R4S2_HUMAN]	8.1	2	1	4	6	0.994	1		14.007	778	84.715
P14384	Carboxypeptidase M OS=Homo sapiens GN=CPM PE=1 SV=2 - [CBPM_HUMAN]	8.8	3	4	4	6	1.000	6	0.106	14.000	443	50.481
Q9H446	RWD domain-containing protein 1 OS=Homo sapiens GN=RWDD1 PE=1 SV=1 - [RWDD1_HUMAN]	7.41	4	2	3	5	0.931	4	13.053	13.993	243	27.922
C9J931	GTP-binding protein Rheb OS=Homo sapiens GN=RHEB PE=1 SV=1 - [C9J931_HUMAN]	45.57	5	4	4	6	0.987	6	13.768	13.947	79	8.668
Q9NVT9	Armadillo repeat-containing protein 1 OS=Homo sapiens GN=ARMC1 PE=1 SV=1 - [ARMC1_HUMAN]	9.93	3	3	3	7	1.000	7	14.601	13.939	282	31.261
Q9NRF9	DNA polymerase epsilon subunit 3 OS=Homo sapiens GN=POLE3 PE=1 SV=1 - [DPOE3_HUMAN]	13.61	1	3	3	5	0.942	5	8.800	13.938	147	16.849
P25325	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3 - [THTM_HUMAN]	6.73	4	2	2	5	1.022	5	5.228	13.937	297	33.158
A8K564	cDNA FLJ76716, highly similar to Homo sapiens WD repeat domain 70 (WDR70), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K564_HUMAN]	7.65	3	6	6	6	0.971	6	4.441	13.919	654	73.145
Q15819	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4 - [UB2V2_HUMAN]	22.07	6	3	4	8	1.069	7	10.351	13.899	145	16.352
E9B303	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2220 PE=4 SV=1 - [E9B303_LEIMU]	4.28	1	1	1	4	1.000	4	0.000	13.892	1541	171.933
Q5SSV3	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens GN=DDAH2 PE=1 SV=1 - [Q5SSV3_HUMAN]	12.83	4	3	3	7	1.000	7	8.615	13.889	226	23.554
B1APE1	Transcription initiation factor IIB (Fragment) OS=Homo sapiens GN=GTF2B PE=1 SV=1 - [B1APE1_HUMAN]	12.95	3	3	3	4	0.770	4	31.974	13.856	224	24.972
Q59HD7	Very low-density lipoprotein receptor variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59HD7_HUMAN]	10.63	4	4	4	7	1.000	7	0.000	13.843	555	60.245
Q59F56	DJ34F7.7 (Superkiller viralicidic activity 2-like variant) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59F56_HUMAN]	6.92	10	3	4	5	1.164	4	17.953	13.842	607	67.506
Q53X93	CREB1 protein (Fragment) OS=Homo sapiens GN=CREB1 PE=2 SV=1 - [Q53X93_HUMAN]	11.62	14	2	2	5	1.000	5	0.000	13.841	327	35.115
S4R331	Coiled-coil domain-containing protein 12 (Fragment) OS=Homo sapiens GN=CCDC12 PE=1 SV=2 - [S4R331_HUMAN]	35.8	6	3	3	6	0.977	6	5.105	13.838	81	9.569
E9AVG6	Proteasome subunit alpha type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1700 PE=3 SV=1 - [E9AVG6_LEIMU]	12.99	1	3	3	5	5.503	5	54.721	13.838	231	25.073
Q8WYJ5	Protein kinase C inhibitor-2 OS=Homo sapiens PE=2 SV=1 - [Q8WYJ5_HUMAN]	19.53	3	2	2	4	0.835	4	17.732	13.831	128	13.909
Q9Y2Z2	Protein MTO1 homolog, mitochondrial OS=Homo sapiens GN=MTO1 PE=1 SV=2 - [MTO1_HUMAN]	4.04	6	3	3	6	1.000	6	0.000	13.811	717	79.914
Q96RK0	Protein capicua homolog OS=Homo sapiens GN=CIC PE=1 SV=2 - [CIC_HUMAN]	1.87	3	2	2	5	1.000	3	0.000	13.806	1608	163.719
D3DPS9	Mitochondrial ribosomal protein S15, isoform CRA_c OS=Homo sapiens GN=MRPS15 PE=3 SV=1 - [D3DPS9_HUMAN]	19.25	2	4	4	7	1.010	7	18.147	13.786	161	19.172
Q5QPJ9	Dolichol-phosphate mannosyltransferase subunit 1 (Fragment) OS=Homo sapiens GN=DPM1 PE=1 SV=2 - [Q5QPJ9_HUMAN]	6.33	4	2	2	5	1.087	5	8.609	13.785	221	25.090
C0LQF2	Deoxyribonuclease II (Fragment) OS=Homo sapiens PE=2 SV=1 - [C0LQF2_HUMAN]	7.56	4	3	3	7	0.997	7	0.483	13.783	344	38.157
X6RJS7	Lys-63-specific deubiquitinase BRCC36 (Fragment) OS=Homo sapiens GN=BRCC3 PE=1 SV=1 - [X6RJS7_HUMAN]	8.41	2	2	2	4	1.000	3	0.000	13.777	226	25.740
J3KS94	Myelin basic protein (Fragment) OS=Homo sapiens GN=MBP PE=1 SV=1 - [J3KS94_HUMAN]	15.72	4	2	2	5	1.000	5	0.000	13.769	159	17.432
F8VVX6	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial (Fragment) OS=Homo sapiens GN=COQ5 PE=1 SV=1 - [F8VVX6_HUMAN]	12.68	7	2	2	4	1.000	4	0.000	13.730	213	24.485
Q9H7M5	FLJ00045 protein (Fragment) OS=Homo sapiens GN=FLJ00045 PE=2 SV=1 - [Q9H7M5_HUMAN]	4.41	9	2	2	4	1.000	4	0.000	13.676	272	31.505
B4DZZ0	cDNA FLJ52128, highly similar to PRA1 family protein 3 OS=Homo sapiens PE=2 SV=1 - [B4DZZ0_HUMAN]	8.48	3	2	2	6	0.947	6	14.999	13.672	165	19.193
A0A024R0X0	AP1 gamma subunit binding protein 1, isoform CRA_d OS=Homo sapiens GN=AP1GBP1 PE=4 SV=1 - [A0A024R0X0_HUMAN]	3.2	3	3	3	6	1.000	5	0.000	13.671	1314	140.552
Q68CZ2	Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 - [TENS3_HUMAN]	2.49	5	3	3	5	1.000	5	0.000	13.665	1445	155.169
A0A087WTB8	Ubiquitin carboxyl-terminal esterase L3 (Ubiquitin thiolesterase), isoform CRA_d OS=Homo sapiens GN=UCHL3 PE=4 SV=1 - [A0A087WTB8_HUMAN]	17.01	3	2	3	4	1.082	2	19.553	13.658	194	21.931
U3KQ83	Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=1 - [U3KQ83_HUMAN]	21.88	8	1	1	4	1.000	3	0.000	13.657	96	11.097
Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1 - [ABHDA_HUMAN]	12.42	1	3	3	5	1.000	5	14.076	13.652	306	33.911
P31350	Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens GN=RRM2 PE=1 SV=1 - [RIR2_HUMAN]	10.28	5	4	4	5	1.026	5	45.093	13.648	389	44.849
C9JR56	One cut domain family member OS=Homo sapiens GN=SATB2 PE=3 SV=1 - [C9JR56_HUMAN]	6.53	4	3	5	6	1.183	4	43.941	13.641	674	75.988
Q9BVJ7	Dual specificity protein phosphatase 23 OS=Homo sapiens GN=DUSP23 PE=1 SV=1 - [DUS23_HUMAN]	26	1	3	3	5	1.000	5	9.878	13.587	150	16.578
Q12873	Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3 - [CHD3_HUMAN]	1.5	7	1	3	4	1.000	1		13.580	2000	226.450
F5GXX5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=1 SV=1 - [F5GXX5_HUMAN]	21.18	3	2	2	5	0.873	5	33.714	13.565	85	9.548
A8K9G9	cDNA FLJ77260, highly similar to Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9G9_H	4.72	3	5	5	5	1.038	5	8.614	13.544	1102	126.330
B4DNM0	cDNA FLJ60738, highly similar to RNA polymerase-associated protein LEO1 OS=Homo sapiens PE=2 SV=1 - [B4DNM0_HUMAN]	6.52	2	6	6	6	1.000	6	1.802	13.536	644	72.740
B4DP34	cDNA FLJ53149, highly similar to Peptidylprolyl isomerase domain and WDrepeat-containing protein 1 (EC 5.2.1.8) OS=Homo sapiens PE=2 SV=1 - [B4DP34_HUMAN]	5.53	6	3	3	4	1.092	4	25.632	13.531	506	57.398
B4DZE5	cDNA FLJ58806, highly similar to DNA-directed RNA polymerase, mitochondrial (EC 2.7.7.6) OS=Homo sapiens PE=2 SV=1 - [B4DZE5_HUMAN]	3.67	5	3	3	8	1.000	5	0.000	13.505	927	104.580
F5H1A5	Splicing factor, suppressor of white-apricot homolog OS=Homo sapiens GN=SFSWAP PE=4 SV=1 - [F5H1A5_HUMAN]	19.83	5	2	2	5	1.000	4	0.000	13.503	121	13.506
E9AVN9	Putative proteasome regulatory ATPase subunit 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0570 PE=3 SV=1 - [E9AVN9_LEIMU]	8.01	2	1	3	6	4.647	3	2.286	13.499	437	48.975
O75792	Ribonuclease H2 subunit A OS=Homo sapiens GN=RNASEH2A PE=1 SV=2 - [RNH2A_HUMAN]	13.04	3	4	4	6	0.907	6	17.830	13.498	299	33.374
Q53HI2	DEAD-box protein abstrakt variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HI2_HUMAN]	9.81	6	6	6	8	0.979	8	6.665	13.484	622	69.794
C4PGM0	Specificity protien 1 OS=Homo sapiens GN=Sp1 PE=2 SV=1 - [C4PGM0_HUMAN]	6.69	3	2	2	4	0.987	4	23.693	13.483	299	31.230
O00625	Pirin OS=Homo sapiens GN=PIR PE=1 SV=1 - [PIR_HUMAN]	9.66	1	3	3	6	1.000	5	2.005	13.479	290	32.093
Q7Z6M3	Allergin-1 OS=Homo sapiens GN=MILR1 PE=1 SV=2 - [MILR1_HUMAN]	7.58	3	3	3	5	0.984	5	7.387	13.469	343	38.710
Q92520	Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1 - [FAM3C_HUMAN]	12.33	3	3	3	6	1.116	6	12.235	13.460	227	24.665
Q8TCD1	UPF0729 protein C18orf32 OS=Homo sapiens GN=C18orf32 PE=2 SV=1 - [CR032_HUMAN]	14.47	1	2	2	4	1.231	4	29.800	13.455	76	8.664
O94766	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 OS=Homo sapiens GN=B3GAT3 PE=1 SV=2 - [B3GA3_HUMAN]	8.06	5	3	3	5	0.945	5	8.477	13.441	335	37.099
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3 - [IPO9_HUMAN]	4.23	1	5	5	6	1.088	6	15.979	13.439	1041	115.889
Q5HYI5	Putative uncharacterized protein DKFZp313C1541 OS=Homo sapiens GN=DKFZp313C1541 PE=2 SV=1 - [Q5HYI5_HUMAN]	21.53	8	1	5	8	0.985	1		13.436	209	23.405
C9J8E1	MAP kinase-activated protein kinase 3 (Fragment) OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 - [C9J8E1_HUMAN]	2.41	6	1	1	5	0.589	5	97.081	13.413	332	37.366
Q9Y3D9	28S ribosomal protein S23, mitochondrial OS=Homo sapiens GN=MRPS23 PE=1 SV=2 - [RT23_HUMAN]	17.89	2	3	3	5	1.000	5	5.951	13.404	190	21.757
O95372	Acyl-protein thioesterase 2 OS=Homo sapiens GN=LYPLA2 PE=1 SV=1 - [LYPA2_HUMAN]	21.65	7	5	5	7	1.042	7	2.577	13.397	231	24.721
O75164	Lysine-specific demethylase 4A OS=Homo sapiens GN=KDM4A PE=1 SV=2 - [KDM4A_HUMAN]	4.04	3	3	3	4	0.772	4	56.655	13.388	1064	120.585
E9B6U3	Polyadenylate-binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4130 PE=3 SV=1 - [E9B6U3_LEIMU]	4.88	1	3	3	5	1.162	5	39.862	13.385	594	65.177
Q8N5N7	39S ribosomal protein L50, mitochondrial OS=Homo sapiens GN=MRPL50 PE=1 SV=2 - [RM50_HUMAN]	15.19	1	2	2	4	1.150	4	9.607	13.368	158	18.313
E9AX57	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_2110 PE=4 SV=1 - [E9AX57_LEIMU]	8.38	3	5	5	7	5.905	7	321.509	13.367	501	55.294
B4E0R5	cDNA FLJ61517, highly similar to Homo sapiens ubiquitin associated protein 2 (UBAP2), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B4E0R5_HUMAN]	2.93	10	1	2	5	1.000	3	3.972	13.364	852	87.872
J3KND1	Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=1 - [J3KND1_HUMAN]	4.86	5	3	3	5	1.000	5	0.000	13.356	473	53.425
Q9Y5B0	RNA polymerase II subunit A C-terminal domain phosphatase OS=Homo sapiens GN=CTDP1 PE=1 SV=3 - [CTDP1_HUMAN]	3.95	2	4	4	5	1.000	4	0.000	13.350	961	104.335
H0YLF3	Beta-2-microglobulin form pI 5.3 (Fragment) OS=Homo sapiens GN=B2M PE=1 SV=1 - [H0YLF3_HUMAN]	36.62	8	3	3	7	0.956	7	12.767	13.314	71	8.493
A8KAQ6	cDNA FLJ76490, highly similar to Homo sapiens ancient ubiquitous protein 1 (AUP1), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [A8KAQ6_HUMAN]	6.34	5	3	3	6	1.009	6	4.339	13.305	410	45.777
Q96K19	E3 ubiquitin-protein ligase RNF170 OS=Homo sapiens GN=RNF170 PE=1 SV=2 - [RN170_HUMAN]	9.3	3	2	2	5	1.000	4	0.000	13.300	258	29.795
Q8WZA0	Protein LZIC OS=Homo sapiens GN=LZIC PE=1 SV=1 - [LZIC_HUMAN]	17.37	2	4	4	5	1.164	5	14.551	13.289	190	21.481
Q96QH2	PML-RARA-regulated adapter molecule 1 OS=Homo sapiens GN=PRAM1 PE=1 SV=2 - [PRAM_HUMAN]	14.62	2	3	3	5	1.000	5	0.000	13.286	718	79.196
A2ABF8	Histone-lysine N-methyltransferase EHMT2 OS=Homo sapiens GN=EHMT2 PE=1 SV=1 - [A2ABF8_HUMAN]	4.62	6	4	4	6	1.000	5	0.000	13.284	1233	135.333
Q8N1G0	Zinc finger protein 687 OS=Homo sapiens GN=ZNF687 PE=1 SV=1 - [ZN687_HUMAN]	4.61	4	3	3	4	1.000	3	0.000	13.278	1237	129.446
A8K8Z3	cDNA FLJ77613, highly similar to Homo sapiens tousled-like kinase 1 (TLK1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8Z3_HUMAN]	3.52	18	1	3	5	1.000	1		13.273	766	86.616
Q96BW5	Phosphotriesterase-related protein OS=Homo sapiens GN=PTER PE=1 SV=1 - [PTER_HUMAN]	10.03	1	4	4	5	0.992	5	1.126	13.271	349	38.993
Q5VTU3	Dynein light chain Tctex-type 1 OS=Homo sapiens GN=DYNLT1 PE=1 SV=1 - [Q5VTU3_HUMAN]	17.39	2	1	1	4	1.000	4	0.000	13.266	92	10.194
E9APM4	Proteasome subunit alpha type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0310 PE=3 SV=1 - [E9APM4_LEIMU]	3.51	1	1	1	4	3.116	4	128.369	13.257	285	32.212
A9CQZ4	Dihydropyrimidinase-like 2 long form (Fragment) OS=Homo sapiens GN=DPYSL2 PE=2 SV=1 - [A9CQZ4_HUMAN]	35.15	1	1	5	5	0.540	1		13.233	165	17.854
Q9NYJ1	Cytochrome c oxidase assembly factor 4 homolog, mitochondrial OS=Homo sapiens GN=COA4 PE=1 SV=2 - [COA4_HUMAN]	21.84	1	2	2	5	0.905	5	14.839	13.226	87	10.128
K7ERD8	Microtubule-associated protein RP/EB family member 2 (Fragment) OS=Homo sapiens GN=MAPRE2 PE=1 SV=1 - [K7ERD8_HUMAN]	26.29	6	5	5	6	0.942	6	6.661	13.226	194	21.581
B7Z2B4	cDNA FLJ53389, highly similar to Homo sapiens RAB GTPase activating protein 1 (RABGAP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z2B4_HUMAN]	4.9	2	2	2	5	1.000	5	0.000	13.225	408	48.147
O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Homo sapiens GN=NDUFS6 PE=1 SV=1 - [NDUS6_HUMAN]	23.39	2	3	3	5	1.000	5	6.717	13.212	124	13.703
Q15751	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens GN=HERC1 PE=1 SV=2 - [HERC1_HUMAN]	0.82	4	4	4	8	1.000	7	0.000	13.211	4861	531.891
Q6IAN0	Dehydrogenase/reductase SDR family member 7B OS=Homo sapiens GN=DHRS7B PE=1 SV=2 - [DRS7B_HUMAN]	5.85	2	2	2	5	1.000	5	5.786	13.199	325	35.097
Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Homo sapiens GN=PNPT1 PE=1 SV=2 - [PNPT1_HUMAN]	7.15	4	4	6	6	1.025	4	4.769	13.193	783	85.897
B2RAG5	cDNA, FLJ94903, highly similar to Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAG5_HUMAN]	5	9	4	4	5	1.000	5	14.828	13.190	680	77.257
Q53FE5	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FE5_HUMAN]	17.11	6	3	3	6	0.907	6	14.566	13.186	263	28.325
Q8NI36	WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1 - [WDR36_HUMAN]	2.73	1	2	2	4	0.917	4	12.906	13.182	951	105.255
B7ZLC8	JMJD1C protein OS=Homo sapiens GN=JMJD1C PE=2 SV=1 - [B7ZLC8_HUMAN]	1.95	4	5	5	6	1.000	6	9.220	13.181	2358	262.992
H7BYG8	E3 ubiquitin-protein ligase listerin OS=Homo sapiens GN=LTN1 PE=1 SV=1 - [H7BYG8_HUMAN]	3.08	3	2	2	4	1.000	2	0.000	13.177	813	91.346
B1AJY5	26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens GN=PSMD10 PE=1 SV=1 - [B1AJY5_HUMAN]	25.41	4	4	4	5	0.990	4	2.122	13.177	185	20.204
B2R835	cDNA, FLJ93721, highly similar to Homo sapiens NADP-dependent retinol dehydrogenase/reductase (RDHL),transcript variant C, mRNA OS=Homo sapiens PE=2 SV=1	10.34	5	4	4	6	1.124	6	2.659	13.176	319	35.214
Q15651	High mobility group nucleosome-binding domain-containing protein 3 OS=Homo sapiens GN=HMGN3 PE=1 SV=2 - [HMGN3_HUMAN]	15.15	2	2	2	6	1.038	5	8.167	13.164	99	10.660
Q9NXW2	DnaJ homolog subfamily B member 12 OS=Homo sapiens GN=DNAJB12 PE=1 SV=4 - [DJB12_HUMAN]	11.47	5	4	5	5	1.014	4	7.639	13.139	375	41.793
B7ZLW1	CAMSAP1 protein OS=Homo sapiens GN=CAMSAP1 PE=2 SV=1 - [B7ZLW1_HUMAN]	2.59	3	4	4	6	1.000	4	13.276	13.118	1467	163.157
E9AQL3	Putative orotidine-5-phosphate decarboxylase/orotate phosphoribosyltransferase (Putative ompdcase-oprtase) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103)	3.06	1	2	2	5	1.000	5	0.000	13.108	457	49.604
B4E162	cDNA FLJ56281, highly similar to 6-phosphofructokinase, muscle type (EC 2.7.1.11) OS=Homo sapiens PE=2 SV=1 - [B4E162_HUMAN]	4.28	5	1	3	5	1.000	1		13.086	607	66.741
B4DKU3	cDNA FLJ53449, highly similar to rRNA methyltransferase 3 (EC 2.1.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DKU3_HUMAN]	4.82	2	4	4	5	1.000	5	1.568	13.086	726	82.528
Q8TF42	Ubiquitin-associated and SH3 domain-containing protein B OS=Homo sapiens GN=UBASH3B PE=1 SV=2 - [UBS3B_HUMAN]	6.16	1	4	4	8	1.002	8	20.209	13.084	649	72.649
B4DVB4	cDNA FLJ54796, highly similar to Homo sapiens selenocysteine lyase (SCLY), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DVB4_HUMAN]	9.12	11	2	2	4	1.000	3	5.800	13.071	351	37.979
Q9UM54	Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=1 SV=4 - [MYO6_HUMAN]	3.25	3	3	3	4	0.709	3	14.508	13.061	1294	149.596
A0A087WXI1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=4 SV=1 - [A0A087WXI1_HUMAN]	9.47	5	4	4	5	1.002	5	17.309	13.034	380	42.819
Q0VDG4	Secernin-3 OS=Homo sapiens GN=SCRN3 PE=1 SV=1 - [SCRN3_HUMAN]	7.31	6	3	3	7	1.000	7	0.000	13.027	424	48.513
J3KRK0	Serine/threonine-protein kinase tousled-like 2 (Fragment) OS=Homo sapiens GN=TLK2 PE=1 SV=1 - [J3KRK0_HUMAN]	4.38	20	1	3	5	0.626	1		13.021	593	68.790
E9B2G6	40S ribosomal protein S2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0450 PE=3 SV=1 - [E9B2G6_LEIMU]	9.09	3	2	3	5	1.931	4	19.599	13.016	264	28.616
B4DTB9	cDNA FLJ50666, weakly similar to Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B4DTB9_HUMAN]	7.34	4	4	4	5	0.903	5	15.143	13.014	572	63.577
Q86VY4	Testis-specific Y-encoded-like protein 5 OS=Homo sapiens GN=TSPYL5 PE=1 SV=2 - [TSYL5_HUMAN]	13.67	1	5	5	5	1.000	5	0.000	13.011	417	45.116
Q5T5I6	Golgi phosphoprotein 3-like (Fragment) OS=Homo sapiens GN=GOLPH3L PE=1 SV=1 - [Q5T5I6_HUMAN]	9.67	2	2	2	4	0.918	4	10.317	13.001	269	31.109
E9AVP4	Putative proteasome regulatory ATPase subunit 5 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0620 PE=3 SV=1 - [E9AVP4_LEIMU]	4.5	1	1	2	5	1.020	1		12.998	444	49.439
H0YN22	GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMPR2 PE=4 SV=1 - [H0YN22_HUMAN]	26.09	14	2	2	5	0.912	5	13.818	12.994	69	7.633
Q8IXM3	39S ribosomal protein L41, mitochondrial OS=Homo sapiens GN=MRPL41 PE=1 SV=1 - [RM41_HUMAN]	15.33	1	2	2	4	1.159	4	11.624	12.993	137	15.373
O95721	Synaptosomal-associated protein 29 OS=Homo sapiens GN=SNAP29 PE=1 SV=1 - [SNP29_HUMAN]	20.93	2	5	5	7	0.873	7	20.360	12.990	258	28.953
Q8TC12	Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2 - [RDH11_HUMAN]	8.49	3	2	2	3	1.176	3	0.849	12.981	318	35.363
Q9Y2U8	Inner nuclear membrane protein Man1 OS=Homo sapiens GN=LEMD3 PE=1 SV=2 - [MAN1_HUMAN]	4.28	3	3	3	4	0.961	4	5.934	12.980	911	99.935
P23229	Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5 - [ITA6_HUMAN]	1.95	1	2	2	4	1.039	3	2.760	12.975	1130	126.526
A0A024R2V4	Coiled-coil domain containing 51, isoform CRA_a OS=Homo sapiens GN=CCDC51 PE=4 SV=1 - [A0A024R2V4_HUMAN]	16.23	3	4	4	4	0.979	4	3.087	12.961	302	33.636
B3KP90	cDNA FLJ31447 fis, clone NT2NE2000913, highly similar to Protein phosphatase 2C isoform beta (EC 3.1.3.16) OS=Homo sapiens PE=2 SV=1 - [B3KP90_HUMAN]	4.8	2	1	2	5	1.000	2	0.000	12.953	479	52.676
B4E2D6	cDNA FLJ61066, highly similar to Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens PE=2 SV=1 - [B4E2D6_HUMAN]	4.04	11	2	2	4	1.048	4	7.850	12.939	717	76.983
Q02040	A-kinase anchor protein 17A OS=Homo sapiens GN=AKAP17A PE=1 SV=2 - [AK17A_HUMAN]	4.89	3	3	3	5	1.000	5	0.000	12.932	695	80.686
E9AX49	3-oxoacyl-(Acyl-carrier protein) reductase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_2030 PE=3 SV=1 - [E9AX49_LEIMU]	8.11	1	2	2	4	1.000	4	0.000	12.916	259	27.065
B4DWZ5	cDNA FLJ53016, highly similar to Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens PE=2 SV=1 - [B4DWZ5_HUMAN]	9.96	3	3	3	5	0.982	5	4.396	12.913	251	27.726
Q9Y613	FH1/FH2 domain-containing protein 1 OS=Homo sapiens GN=FHOD1 PE=1 SV=3 - [FHOD1_HUMAN]	3.78	3	3	3	4	1.000	4	9.849	12.900	1164	126.473
B3KP88	cDNA FLJ31415 fis, clone NT2NE2000284, highly similar to Galectin-3-binding protein OS=Homo sapiens PE=2 SV=1 - [B3KP88_HUMAN]	6.44	14	3	3	6	0.967	6	8.828	12.896	481	54.136
A8K9E1	cDNA FLJ77957, highly similar to Homo sapiens HBS1-like (S. cerevisiae) (HBS1L), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9E1_HUMAN]	4.09	14	3	3	6	0.996	6	0.584	12.863	684	75.456
B3KUQ5	cDNA FLJ40389 fis, clone TESTI2036691, highly similar to Thioredoxin reductase 2, mitochondrial (EC 1.8.1.9) OS=Homo sapiens PE=2 SV=1 - [B3KUQ5_HUMAN]	6.26	10	3	3	5	1.461	5	11.071	12.851	463	49.972
A0A024RB10	Cyclin-dependent kinase 2, isoform CRA_a OS=Homo sapiens GN=CDK2 PE=4 SV=1 - [A0A024RB10_HUMAN]	12.5	60	2	4	7	0.933	2	26.504	12.849	264	30.016
B4DQC5	cDNA FLJ58039, highly similar to Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DQC5_HUMAN]	23.26	4	2	2	3	1.312	3	28.222	12.826	129	14.424

B4DEP8	cDNA FLJ56960, highly similar to Homo sapiens phosphatidylinositol 4-kinase type II (PI4KII), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DEP8_HUMAN]	7.8	3	3	3	5	1.000	5	23.447	12.820	449	51.102
Q9Y570	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 - [PPME1_HUMAN]	8.81	1	3	3	6	1.000	6	0.698	12.817	386	42.288
B4DIN7	E3 ubiquitin-protein ligase OS=Homo sapiens PE=2 SV=1 - [B4DIN7_HUMAN]	3.3	2	2	2	5	1.000	4	0.000	12.813	757	86.688
A0A087WW90	General transcription factor II-I repeat domain-containing protein 2B OS=Homo sapiens GN=GTF2IRD2B PE=4 SV=1 - [A0A087WW90_HUMAN]	3.43	8	1	2	5				12.799	437	47.779
Q9UBV2	Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3 - [SE1L1_HUMAN]	6.68	4	5	5	6	1.002	6	4.445	12.794	794	88.699
Q04941	Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1 - [PLP2_HUMAN]	8.55	1	1	1	5	1.036	5	22.623	12.776	152	16.680
A0A024RA66	Cell division cycle 2-like 5 (Cholinesterase-related cell division controller), isoform CRA_b OS=Homo sapiens GN=CDC2L5 PE=4 SV=1 - [A0A024RA66_HUMAN]	3.51	44	1	5	7	0.980	2	2.955	12.751	1452	158.338
E9AK75	Complete genome, chromosome 4 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0940 PE=3 SV=1 - [E9AK75_LEIMU]	6.29	1	2	3	6	1.000	2	0.000	12.745	493	51.909
Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	6.53	1	3	3	6	1.000	6	6.499	12.729	429	47.121
B3KTD2	cDNA FLJ38079 fis, clone CTONG2016056, highly similar to AT-hook-containing transcription factor 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KTD2_HUMAN]	2.54	4	2	2	4	1.018	4	4.550	12.725	906	99.607
Q16610	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2 - [ECM1_HUMAN]	5.19	2	2	2	5	1.037	4	9.068	12.701	540	60.635
B4DGP6	cDNA FLJ53865, highly similar to Succinate semialdehyde dehydrogenase, mitochondrial (EC 1.2.1.24) OS=Homo sapiens PE=2 SV=1 - [B4DGP6_HUMAN]	9.4	8	4	4	6	1.000	6	6.017	12.689	447	48.306
Q15126	Phosphomevalonate kinase OS=Homo sapiens GN=PMVK PE=1 SV=3 - [PMVK_HUMAN]	21.35	1	4	4	5	1.000	5	9.142	12.687	192	21.981
Q8TDD1	ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 - [DDX54_HUMAN]	3.75	2	4	4	5	0.925	5	36.377	12.685	881	98.534
H3BP35	Diphosphomevalonate decarboxylase (Fragment) OS=Homo sapiens GN=MVD PE=1 SV=1 - [H3BP35_HUMAN]	5.9	4	2	2	5	1.000	5	1.892	12.684	271	29.360
Q9C0H2	Protein tweety homolog 3 OS=Homo sapiens GN=TTYH3 PE=1 SV=3 - [TTYH3_HUMAN]	4.59	2	3	3	4	1.008	4	1.224	12.684	523	57.508
P18433	Receptor-type tyrosine-protein phosphatase alpha OS=Homo sapiens GN=PTPRA PE=1 SV=2 - [PTPRA_HUMAN]	3.49	12	2	3	6	1.000	2	0.000	12.672	802	90.542
I3L0Q8	Putative sodium-coupled neutral amino acid transporter 10 (Fragment) OS=Homo sapiens GN=SLC38A10 PE=4 SV=1 - [I3L0Q8_HUMAN]	16.28	1	1	4	6	1.000	1		12.653	258	27.461
Q14919	Dr1-associated corepressor OS=Homo sapiens GN=DRAP1 PE=1 SV=3 - [NC2A_HUMAN]	14.63	4	4	4	5	1.000	5	23.025	12.641	205	22.336
Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP PE=1 SV=1 - [IKIP_HUMAN]	11.14	2	5	5	7	1.000	7	9.211	12.627	350	39.285
H0YM74	Zinc finger protein 592 OS=Homo sapiens GN=ZNF592 PE=1 SV=1 - [H0YM74_HUMAN]	2.8	2	2	2	6	1.000	5	0.000	12.625	858	91.923
P20292	Arachidonate 5-lipoxygenase-activating protein OS=Homo sapiens GN=ALOX5AP PE=1 SV=2 - [AL5AP_HUMAN]	11.8	2	2	2	5	1.054	5	8.475	12.604	161	18.145
P47755	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 - [CAZA2_HUMAN]	11.89	5	2	3	7	0.861	2	22.422	12.598	286	32.929
E9PH82	Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1 - [E9PH82_HUMAN]	5.45	6	1	2	5	1.000	1		12.589	312	34.409
W0S1J7	PJA2/FER fusion protein OS=Homo sapiens GN=Pe7Fe14 PE=2 SV=1 - [W0S1J7_HUMAN]	3.38	7	2	3	4	1.000	1		12.576	858	96.218
F6IR49	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [F6IR49_HUMAN]	7.12	1	1	1	5	1.000	5	0.000	12.572	337	38.105
Q9NP72	Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 - [RAB18_HUMAN]	13.59	8	3	3	5	1.092	5	14.556	12.572	206	22.963
Q00653	Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens GN=NFKB2 PE=1 SV=4 - [NFKB2_HUMAN]	3.67	3	2	3	4	0.955	2	6.788	12.572	900	96.689
O15254	Peroxisomal acyl-coenzyme A oxidase 3 OS=Homo sapiens GN=ACOX3 PE=1 SV=2 - [ACOX3_HUMAN]	5.57	2	4	4	6	0.905	6	28.309	12.569	700	77.580
Q9Y3B4	Splicing factor 3B subunit 6 OS=Homo sapiens GN=SF3B6 PE=1 SV=1 - [SF3B6_HUMAN]	30.4	1	4	4	7	1.051	7	7.331	12.564	125	14.576
Q7Z658	Putative uncharacterized protein DKFZp779F115 (Fragment) OS=Homo sapiens GN=DKFZp779F115 PE=1 SV=1 - [Q7Z658_HUMAN]	6.75	2	2	2	5	1.000	5	7.914	12.549	252	27.038
A0A024R6R1	SHC SH2-domain binding protein 1, isoform CRA_a OS=Homo sapiens GN=SHCBP1 PE=4 SV=1 - [A0A024R6R1_HUMAN]	3.27	5	2	2	4	1.000	4	0.000	12.547	672	75.612
Q9BV73	Centrosome-associated protein CEP250 OS=Homo sapiens GN=CEP250 PE=1 SV=2 - [CP250_HUMAN]	1.23	2	2	3	6	1.000	3	0.000	12.541	2442	280.967
Q9C0B5	Palmitoyltransferase ZDHHC5 OS=Homo sapiens GN=ZDHHC5 PE=1 SV=2 - [ZDHC5_HUMAN]	4.34	7	3	3	6	1.000	6	0.000	12.534	715	77.496
Q6P1N0	Coiled-coil and C2 domain-containing protein 1A OS=Homo sapiens GN=CC2D1A PE=1 SV=1 - [C2D1A_HUMAN]	4.84	5	4	4	4	0.758	4	42.942	12.520	951	103.998
B2R5H5	cDNA, FLJ92476, highly similar to Homo sapiens LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2F	17.65	3	2	2	6	1.018	6	4.449	12.499	102	11.822
B4DE40	cDNA FLJ50114, highly similar to Spermine synthase (EC 2.5.1.22) OS=Homo sapiens PE=2 SV=1 - [B4DE40_HUMAN]	9.45	3	3	3	5	1.084	5	6.790	12.488	275	31.083
Q13564	NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1 - [ULA1_HUMAN]	7.68	1	4	4	6	1.158	6	36.458	12.481	534	60.209
E9PMI6	Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=1 SV=1 - [E9PMI6_HUMAN]	22.75	5	2	2	4	1.045	3	6.546	12.455	167	18.248
Q96IJ6	Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 - [GMPPA_HUMAN]	5.24	4	2	2	5	1.036	5	9.125	12.449	420	46.262
P45973	Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1 SV=1 - [CBX5_HUMAN]	14.14	3	3	3	5	0.879	5	8.139	12.419	191	22.211
E9B6X2	Putative mitochondrial phosphate transporter OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4430 PE=3 SV=1 - [E9B6X2_LEIMU]	13.56	1	4	4	8	1.000	8	1.600	12.397	317	34.689
E9PL24	Myomegalin OS=Homo sapiens GN=PDE4DIP PE=1 SV=2 - [E9PL24_HUMAN]	4.12	2	2	4	4	0.827	2	28.638	12.394	1116	126.871
Q9Y2R9	28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=1 SV=2 - [RT07_HUMAN]	14.88	5	3	3	4	1.039	4	5.674	12.390	242	28.116
H3BTD3	cAMP-regulated phosphoprotein 19 (Fragment) OS=Homo sapiens GN=ARPP19 PE=1 SV=1 - [H3BTD3_HUMAN]	30.56	4	1	2	5	1.607	1		12.388	72	8.122
Q13823	Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 - [NOG2_HUMAN]	5.34	3	4	4	5	0.975	5	3.751	12.382	731	83.603
Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3 OS=Homo sapiens GN=ADPRHL2 PE=1 SV=1 - [ARHL2_HUMAN]	16.25	4	5	5	5	0.785	5	19.174	12.382	363	38.922
V9GZ55	Proteasome assembly chaperone 2 (Fragment) OS=Homo sapiens GN=PSMG2 PE=1 SV=1 - [V9GZ55_HUMAN]	8.13	4	2	2	5	0.913	5	9.473	12.380	209	23.491
Q9NXY1	FLJ00004 protein (Fragment) OS=Homo sapiens GN=FLJ00004 PE=2 SV=1 - [Q9NXY1_HUMAN]	7.31	12	4	4	5	1.001	3	0.117	12.377	698	75.826
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens GN=NDUFA2 PE=1 SV=3 - [NDUA2_HUMAN]	17.17	1	2	2	5	1.041	5	26.071	12.371	99	10.915
H0YKX3	PCNA-associated factor OS=Homo sapiens GN=KIAA0101 PE=1 SV=1 - [H0YKX3_HUMAN]	39.29	4	2	2	4	1.000	4	0.000	12.368	84	9.281
D3DT21	15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=4 SV=1 - [D3DT21_HUMAN]	12.63	5	1	1	3	2.120	3	59.488	12.364	95	9.964
J3KSW8	Myosin phosphatase Rho-interacting protein (Fragment) OS=Homo sapiens GN=MPRIP PE=1 SV=1 - [J3KSW8_HUMAN]	5.09	6	1	3	5	0.996	1		12.339	844	95.870
Q9Y6M5	Zinc transporter 1 OS=Homo sapiens GN=SLC30A1 PE=1 SV=3 - [ZNT1_HUMAN]	6.31	1	3	3	6	1.000	5	5.147	12.332	507	55.264
E9B2G1	Putative ATP-dependent RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0400 PE=3 SV=1 - [E9B2G1_LEIMU]	6.43	1	2	3	5	0.748	2	45.118	12.326	622	67.745
C9JQ41	Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1 - [C9JQ41_HUMAN]	20	4	3	3	5	1.044	5	21.581	12.323	130	15.287
Q5TAL2	U1 small nuclear ribonucleoprotein C OS=Homo sapiens GN=SNRPC PE=1 SV=1 - [Q5TAL2_HUMAN]	7.63	3	1	1	4	0.966	4	9.859	12.322	118	12.343
Q9NX24	H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 - [NHP2_HUMAN]	18.95	4	3	3	4	1.048	4	17.191	12.270	153	17.190
E9PCS8	Metastasis-associated protein MTA3 OS=Homo sapiens GN=MTA3 PE=4 SV=1 - [E9PCS8_HUMAN]	5.87	17	2	3	5	0.867	3	8.020	12.229	392	44.457
Q53HC9	Protein TSSC1 OS=Homo sapiens GN=TSSC1 PE=1 SV=2 - [TSSC1_HUMAN]	10.08	8	3	3	4	1.000	4	37.491	12.227	387	43.576
Q93034	Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4 - [CUL5_HUMAN]	5.64	9	4	5	5	0.870	4	13.670	12.217	780	90.897
B4DYH7	cDNA FLJ58306, highly similar to Homo sapiens nischarin (NISCH), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DYH7_HUMAN]	5.66	4	4	4	4	1.000	3	0.000	12.202	1113	123.009
A0A024RDA1	Exocyst complex component 1, isoform CRA_a OS=Homo sapiens GN=EXOC1 PE=4 SV=1 - [A0A024RDA1_HUMAN]	5.69	3	5	5	6	1.000	6	21.864	12.190	879	100.219
B4DE96	cDNA FLJ53762, highly similar to Synaptobrevin-like protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DE96_HUMAN]	13.07	6	2	2	4	0.943	4	61.985	12.179	153	17.368
E9APL2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0190 PE=4 SV=1 - [E9APL2_LEIMU]	9.05	1	2	2	4	10.574	4	123.081	12.174	199	22.301
Q7L5D6	Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1 - [GET4_HUMAN]	5.81	4	2	2	7	1.000	7	0.000	12.174	327	36.481
H0Y2S9	Myosin phosphatase Rho-interacting protein (Fragment) OS=Homo sapiens GN=MPRIP PE=1 SV=3 - [H0Y2S9_HUMAN]	2.06	5	1	3	4	1.000	1		12.156	1794	203.360
B4DQ27	cDNA FLJ59949, highly similar to Homo sapiens sulfatase modifying factor 2 (SUMF2), transcript variant 4, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DQ27_HUMAN]	14.22	8	1	3	4	0.764	1		12.151	232	25.827
Q5R372	Rab GTPase-activating protein 1-like OS=Homo sapiens GN=RABGAP1L PE=1 SV=1 - [RBG1L_HUMAN]	4.05	2	2	3	5	1.166	3	12.470	12.146	815	92.454
Q96L92	Sorting nexin-27 OS=Homo sapiens GN=SNX27 PE=1 SV=2 - [SNX27_HUMAN]	6.84	2	4	4	7	1.056	7	8.135	12.142	541	61.226
B4DNE5	cDNA FLJ59661, highly similar to Tyrosine-protein phosphatase non-receptortype 18 (EC 3.1.3.48) OS=Homo sapiens PE=2 SV=1 - [B4DNE5_HUMAN]	18.92	3	1	1	3	1.000	3	0.000	12.140	111	11.121
Q7Z6A8	Interleukin-1 receptor associated kinase 4 mutant form 1 OS=Homo sapiens GN=IRAK4 PE=2 SV=1 - [Q7Z6A8_HUMAN]	8.22	6	3	3	5	0.833	5	27.884	12.116	292	32.683
E9B073	Putative acyl-CoA dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2510 PE=3 SV=1 - [E9B073_LEIMU]	7.15	1	4	4	4	1.176	4	17.543	12.098	629	68.959
E9AYS1	Putative proteasome alpha 7 subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0190 PE=4 SV=1 - [E9AYS1_LEIMU]	5.88	1	1	1	4	1.000	4	0.000	12.093	238	25.562
B2R4N3	cDNA, FLJ92155, highly similar to Homo sapiens ubiquitin-like 5 (UBL5), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R4N3_HUMAN]	39.73	3	3	3	5	1.131	5	2.405	12.088	73	8.542
Q9Y4W2	Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 - [LAS1L_HUMAN]	6.13	2	5	5	5	1.000	5	0.000	12.075	734	83.013
E7EWP0	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial OS=Homo sapiens GN=NDUFB5 PE=1 SV=1 - [E7EWP0_HUMAN]	9.04	6	2	2	6	1.085	6	4.269	12.071	177	20.026
E9ALV7	Tryparedoxin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1160 PE=4 SV=1 - [E9ALV7_LEIMU]	14.48	1	2	2	4	1.000	4	14.869	12.070	145	16.625
Q96PU8	Protein quaking OS=Homo sapiens GN=QKI PE=1 SV=1 - [QKI_HUMAN]	11.14	6	4	4	5	0.929	5	10.893	12.059	341	37.647
M0R2A8	Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9 PE=1 SV=1 - [M0R2A8_HUMAN]	4.44	8	2	2	5	1.000	5	11.611	12.055	518	59.032
Q9BWJ5	Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1 - [SF3B5_HUMAN]	45.35	1	3	3	4	0.868	4	6.704	12.041	86	10.129
A0A087WVZ9	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Homo sapiens GN=POLR2E PE=4 SV=1 - [A0A087WVZ9_HUMAN]	21.74	5	4	4	6	1.000	6	3.846	12.034	184	21.446
B4DKI2	cDNA FLJ60282, highly similar to Sorbitol dehydrogenase (EC 1.1.1.14) OS=Homo sapiens PE=2 SV=1 - [B4DKI2_HUMAN]	5.4	4	2	2	5	1.000	5	16.003	12.030	278	29.744
P86790	Vacuolar fusion protein CCZ1 homolog B OS=Homo sapiens GN=CCZ1B PE=1 SV=1 - [CCZ1B_HUMAN]	5.81	4	3	3	5	1.000	5	10.365	12.024	482	55.830
Q8IWV8	E3 ubiquitin-protein ligase UBR2 OS=Homo sapiens GN=UBR2 PE=1 SV=1 - [UBR2_HUMAN]	1.88	2	4	4	5	1.000	5	0.000	12.014	1755	200.408
Q59EI3	Branched chain keto acid dehydrogenase E1, alpha polypeptide variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EI3_HUMAN]	5.86	9	3	3	5	1.000	5	37.367	12.011	444	50.368
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6 - [ZZEF1_HUMAN]	1.72	2	4	5	7	1.008	4	1.199	12.002	2961	330.864
B4E3M8	cDNA FLJ52077, weakly similar to X-linked retinitis pigmentosa GTPase regulator-interacting protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E3M8_HUMAN]	2.08	16	2	3	5	1.102	3	7.783	11.991	1253	144.706
B3KU23	cDNA FLJ39097 fis, clone NTONG2000977, highly similar to Neurolysin, mitochondrial (EC 3.4.24.16) OS=Homo sapiens PE=2 SV=1 - [B3KU23_HUMAN]	6.26	9	4	4	4	1.069	4	18.689	11.988	607	69.693
Q96PV6	Leukocyte receptor cluster member 8 OS=Homo sapiens GN=LENG8 PE=1 SV=2 - [LENG8_HUMAN]	4.62	8	3	3	4	1.000	4	0.000	11.986	779	86.075
D6RBJ7	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1 - [D6RBJ7_HUMAN]	8.05	3	3	3	5	1.045	4	1.781	11.971	348	38.772
B4DM58	Dihydrofolate reductase OS=Homo sapiens GN=DHFR PE=1 SV=1 - [B4DM58_HUMAN]	15.5	6	2	2	5	1.000	5	16.911	11.963	129	14.491
H0YIN2	Methyltransferase-like protein 25 (Fragment) OS=Homo sapiens GN=METTL25 PE=4 SV=1 - [H0YIN2_HUMAN]	6.29	2	1	1	6	1.000	6	0.000	11.961	143	16.526
B4DJ39	cDNA FLJ54357, highly similar to Epidermal Langerhans cell protein LCP1 OS=Homo sapiens PE=2 SV=1 - [B4DJ39_HUMAN]	3.28	7	1	2	4	0.979	2	25.324	11.939	549	59.353
E9APC0	Katanin p60 ATPase-containing subunit A-like 2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=KATNAL2 PE=3 SV=1 - [E9APC0_LEIMU]	4.31	4	1	2	5	1.000	3	0.000	11.932	557	60.679
Q7L8L6	FAST kinase domain-containing protein 5 OS=Homo sapiens GN=FASTKD5 PE=1 SV=1 - [FAKD5_HUMAN]	3.66	2	2	3	5	1.000	4	0.000	11.931	764	86.519
B4DHS1	cDNA FLJ54983, highly similar to Sulfatase-modifying factor 1 OS=Homo sapiens PE=2 SV=1 - [B4DHS1_HUMAN]	11.16	4	2	2	4	0.953	4	29.929	11.910	242	25.662
Q96FS1	CTNND1 protein (Fragment) OS=Homo sapiens GN=CTNND1 PE=2 SV=2 - [Q96FS1_HUMAN]	5.3	8	4	4	5	1.125	5	45.322	11.901	830	92.331
Q658J0	Putative GTP cyclohydrolase 1 type 2 (Fragment) OS=Homo sapiens GN=DKFZp762L015 PE=2 SV=1 - [Q658J0_HUMAN]	9.94	9	4	4	5	0.893	5	2.394	11.896	332	37.006
F8WA11	CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=2 - [F8WA11_HUMAN]	2.84	13	4	4	5	1.000	5	0.000	11.886	1478	162.658
A8K968	cDNA FLJ77757 OS=Homo sapiens PE=2 SV=1 - [A8K968_HUMAN]	5.82	14	1	5	5	0.732	1		11.883	756	84.659
E9AQN5	Transaldolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0760 PE=3 SV=1 - [E9AQN5_LEIMU]	7.27	1	2	3	5	2.578	3	2.144	11.883	330	36.953
B4DN71	cDNA FLJ54105, highly similar to Sulfatase-modifying factor 2 OS=Homo sapiens PE=2 SV=1 - [B4DN71_HUMAN]	15.3	10	1	3	5	1.112	2	15.897	11.880	183	20.489
G1UI17	Glycogen debranching enzyme (Fragment) OS=Homo sapiens GN=AGL PE=2 SV=1 - [G1UI17_HUMAN]	1.74	2	2	2	5	1.000	5	0.000	11.873	1262	143.630
B4DRF0	cDNA FLJ56418, highly similar to WD repeat protein 26 OS=Homo sapiens PE=2 SV=1 - [B4DRF0_HUMAN]	4.43	3	2	2	5	1.000	5	0.000	11.872	451	51.500
Q96B26	Exosome complex component RRP43 OS=Homo sapiens GN=EXOSC8 PE=1 SV=1 - [EXOS8_HUMAN]	10.51	1	2	2	4	1.000	4	4.087	11.858	276	30.020
E9B5Y5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1050 PE=4 SV=1 - [E9B5Y5_LEIMU]	6.25	1	2	2	5	1.000	3	0.000	11.855	496	54.516
Q7L8J4	SH3 domain-binding protein 5-like OS=Homo sapiens GN=SH3BP5L PE=1 SV=1 - [3BP5L_HUMAN]	2.04	1	1	1	4	0.940	4	12.876	11.840	393	43.473
E5RGG1	Dynactin subunit 4 (Fragment) OS=Homo sapiens GN=DCTN4 PE=1 SV=1 - [E5RGG1_HUMAN]	27.19	4	2	2	5	0.709	4	42.265	11.837	114	13.052
B4E142	cDNA FLJ60390, highly similar to JmjC domain-containing histone demethylationprotein 3C (EC 1.14.11.-) OS=Homo sapiens PE=2 SV=1 - [B4E142_HUMAN]	2.23	5	1	1	3	1.000	2	0.000	11.831	629	70.164
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	8.33	1	3	3	4	0.772	4	32.712	11.809	432	47.455
Q7L4I2	Arginine/serine-rich coiled-coil protein 2 OS=Homo sapiens GN=RSRC2 PE=1 SV=1 - [RSRC2_HUMAN]	6.45	5	2	2	4	0.834	3	11.925	11.807	434	50.529
A0A024R5B2	MAP/microtubule affinity-regulating kinase 2, isoform CRA_c OS=Homo sapiens GN=MARK2 PE=4 SV=1 - [A0A024R5B2_HUMAN]	6.95	10	4	4	5	1.000	5	0.000	11.792	691	77.583
Q05823	2-5A-dependent ribonuclease OS=Homo sapiens GN=RNASEL PE=1 SV=2 - [RN5A_HUMAN]	4.45	2	3	3	4	1.144	4	22.301	11.787	741	83.481
Q9HC36	rRNA methyltransferase 3, mitochondrial OS=Homo sapiens GN=RNMTL1 PE=1 SV=2 - [MRM3_HUMAN]	5	3	2	2	4	1.011	4	1.516	11.773	420	46.990
B4DZQ5	cDNA FLJ51417, highly similar to Serine/threonine-protein kinase PRP4 homolog (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DZQ5_HUMAN]	2.01	3	2	3	5	1.000	4	10.829	11.771	993	115.360
A0A024QZB1	HCG1998636, isoform CRA_a OS=Homo sapiens GN=hCG_1998636 PE=4 SV=1 - [A0A024QZB1_HUMAN]	4.26	3	3	3	4	1.000	4	0.000	11.763	1010	111.421
B7ZBM3	Forkhead box protein P4 OS=Homo sapiens GN=FOXP4 PE=1 SV=1 - [B7ZBM3_HUMAN]	3.74	3	2	2	4	1.000	4	8.113	11.763	668	72.242
Q8WVM7	Cohesin subunit SA-1 OS=Homo sapiens GN=STAG1 PE=1 SV=3 - [STAG1_HUMAN]	1.91	8	1	3	6	1.000	1		11.758	1258	144.336
B4E0G6	RNA-binding protein 6 OS=Homo sapiens GN=RBM6 PE=1 SV=1 - [B4E0G6_HUMAN]	11.35	5	6	6	8	1.000	7	34.235	11.753	520	59.165
A8YXX5	Cell proliferation-inducing protein 60 OS=Homo sapiens GN=PIG60 PE=2 SV=1 - [A8YXX5_HUMAN]	8.76	10	3	3	5	1.135	5	18.889	11.750	354	38.213
Q9NVW2	E3 ubiquitin-protein ligase RLIM OS=Homo sapiens GN=RLIM PE=1 SV=3 - [RNF12_HUMAN]	3.85	1	2	2	5	1.000	2	0.000	11.746	624	68.508
Q05519	Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1 - [SRS11_HUMAN]	4.55	11	2	2	5	1.000	5	0.000	11.745	484	53.510
B4DGI7	cDNA FLJ57148, highly similar to Homo sapiens pyrroline-5-carboxylate reductase-like (PYCRL), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DGI7_HUMAN]	17.52	7	2	2	4	0.716	4	13.392	11.743	137	14.318
B3KMA8	cDNA FLJ10612 fis, clone NT2RP2005358, highly similar to Methyl-CpG-binding domain protein 3 OS=Homo sapiens PE=2 SV=1 - [B3KMA8_HUMAN]	19.28	6	3	3	6	1.000	5	3.263	11.728	223	24.907
Q494V2	Coiled-coil domain-containing protein 37 OS=Homo sapiens GN=CCDC37 PE=2 SV=1 - [CCD37_HUMAN]	1.15	1	1	1	8	1.039	7	15.547	11.695	611	71.073
Q9H089	Large subunit GTPase 1 homolog OS=Homo sapiens GN=LSG1 PE=1 SV=2 - [LSG1_HUMAN]	4.56	6	2	3	5	1.000	3	0.000	11.682	658	75.178
B7Z611	cDNA FLJ50848, highly similar to Homo sapiens suppressor of var1, 3-like 1 (S. cerevisiae) (SUPV3L1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B7Z611_HU	5.39	3	3	3	5	1.000	5	0.385	11.675	631	71.057
E9B146	Conserved TPR domain protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2740 PE=4 SV=1 - [E9B146_LEIMU]	6.97	1	3	3	5	1.000	4	0.000	11.666	402	45.132
P02679	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3 - [FIBG_HUMAN]	5.96	7	3	3	5	0.800	4	20.977	11.653	453	51.479
E9PP76	Superoxide dismutase [Cu-Zn] (Fragment) OS=Homo sapiens GN=CCS PE=1 SV=1 - [E9PP76_HUMAN]	54.41	3	4	4	4	1.076	4	22.860	11.651	68	7.281
P54278	Mismatch repair endonuclease PMS2 OS=Homo sapiens GN=PMS2 PE=1 SV=2 - [PMS2_HUMAN]	4.41	6	3	3	4	1.017	4	10.676	11.650	862	95.736
P38935	DNA-binding protein SMUBP-2 OS=Homo sapiens GN=IGHMBP2 PE=1 SV=3 - [SMBP2_HUMAN]	2.92	1	3	3	4	1.000	3	0.000	11.649	993	109.082
F8W8R3	DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1 - [F8W8R3_HUMAN]	6.15	9	3	3	4	0.792	4	48.172	11.640	455	49.581
Q99747	Gamma-soluble NSF attachment protein OS=Homo sapiens GN=NAPG PE=1 SV=1 - [SNAG_HUMAN]	18.91	4	4	4	5	0.837	4	7.679	11.639	312	34.724
A8KAH1	cDNA FLJ75839, highly similar to Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8KAH1_HUMAN]	2.96	5	2	2	5	0.949	5	3.064	11.632	473	55.431
H0Y4T6	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (Fragment) OS=Homo sapiens GN=PIN4 PE=1 SV=1 - [H0Y4T6_HUMAN]	14.29	4	2	2	7	0.983	7	4.524	11.620	91	9.537
Q96H20	Vacuolar-sorting protein SNF8 OS=Homo sapiens GN=SNF8 PE=1 SV=1 - [SNF8_HUMAN]	10.08	5	2	2	3	1.000	3	15.443	11.610	258	28.846
Q8NI45	Placental protein KG-20 OS=Homo sapiens PE=2 SV=1 - [Q8NI45_HUMAN]	15.64	8	3	3	5	0.978	5	11.757	11.608	179	20.159
A0A087X1A5	Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=4 SV=1 - [A0A087X1A5_HUMAN]	3.25	9	2	2	5	0.959	5	6.238	11.605	493	54.912
D3DSC5	Neural cell adhesion molecule 2, isoform CRA_a (Fragment) OS=Homo sapiens GN=NCAM2 PE=4 SV=1 - [D3DSC5_HUMAN]	4.16	4	4	4	5	1.005	5	12.322	11.592	818	90.995
Q53GJ1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GJ1_HUMAN]	6.7	6	2	2	4	0.851	4	34.639	11.584	448	49.850
B4E0B7	Condensin complex subunit 1 OS=Homo sapiens PE=2 SV=1 - [B4E0B7_HUMAN]	2.51	6	3	3	4	0.861	3	21.295	11.583	1356	152.141
Q8N8J7	Uncharacterized protein C4orf32 OS=Homo sapiens GN=C4orf32 PE=2 SV=2 - [CD032_HUMAN]	12.88	1	1	1	4	1.031	4	4.550	11.582	132	14.643
Q8IY37	Probable ATP-dependent RNA helicase DHX37 OS=Homo sapiens GN=DHX37 PE=1 SV=1 - [DHX37_HUMAN]	3.98	4	4	5	7	1.000	6	13.912	11.549	1157	129.464
Q8WZ82	Ovarian cancer-associated gene 2 protein OS=Homo sapiens GN=OVCA2 PE=1 SV=1 - [OVCA2_HUMAN]	5.73	1	1	1	3	1.000	3	0.000	11.544	227	24.403
Q9BUT9	Protein FAM195A OS=Homo sapiens GN=FAM195A PE=1 SV=2 - [F195A_HUMAN]	30	2	4	4	5	1.000	5	0.000	11.542	160	17.817
Q9BU61	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens GN=NDUFAF3 PE=1 SV=1 - [NDUF3_HUMAN]	5.98	1	1	1	3	0.949	3	2.027	11.533	184	20.337
B4DUD8	cDNA FLJ57597 OS=Homo sapiens PE=2 SV=1 - [B4DUD8_HUMAN]	2.41	5	2	2	4	1.032	4	22.063	11.514	789	88.959
B1AKZ5	Astrocytic phosphoprotein PEA-15 OS=Homo sapiens GN=PEA15 PE=1 SV=1 - [B1AKZ5_HUMAN]	25	3	4	4	8	0.935	8	19.019	11.510	108	12.523
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1 OS=Homo sapiens GN=UFC1 PE=1 SV=3 - [UFC1_HUMAN]	16.17	1	3	3	7	1.000	7	14.509	11.505	167	19.446
Q96GA3	Protein LTV1 homolog OS=Homo sapiens GN=LTV1 PE=1 SV=1 - [LTV1_HUMAN]	9.05	2	5	5	5	1.201	5	8.625	11.503	475	54.821
E9PF84	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial (Fragment) OS=Homo sapiens GN=IDH3G PE=1 SV=1 - [E9PF84_HUMAN]	7.37	9	2	2	4	1.000	4	0.000	11.503	285	31.402
Q96DF8	Protein DGCR14 OS=Homo sapiens GN=DGCR14 PE=1 SV=1 - [DGC14_HUMAN]	6.51	2	2	2	4	1.138	3	19.358	11.500	476	52.536
D3DP75	RAB3 GTPase activating protein subunit 1 (Catalytic), isoform CRA_a OS=Homo sapiens GN=RAB3GAP1 PE=4 SV=1 - [D3DP75_HUMAN]	5.79	2	4	4	5	0.974	4	14.374	11.497	881	99.072
O60220	Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens GN=TIMM8A PE=1 SV=1 - [TIM8A_HUMAN]	19.59	1	2	2	4	0.847	4	29.195	11.487	97	10.991
E9ANZ4	Cytochrome c oxidase subunit IV OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0670 PE=4 SV=1 - [E9ANZ4_LEIMU]	7.67	1	3	3	5	1.000	5	0.000	11.481	339	38.989
E9AX08	Putative succinate dehydrogenase flavoprotein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1630 PE=4 SV=1 - [E9AX08_LEIMU]	4.61	1	3	3	4	1.000	4	0.000	11.472	607	66.679
E9PJN1	Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA4 PE=1 SV=1 - [E9PJN1_HUMAN]	4.58	12	4	4	5	1.000	5	50.721	11.469	765	84.703
Q5HYD9	Putative uncharacterized protein DKFZp686M0619 (Fragment) OS=Homo sapiens GN=DKFZp686M0619 PE=2 SV=1 - [Q5HYD9_HUMAN]	11.21	5	1	1	5	1.223	4	30.557	11.469	107	11.866
E9AY45	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0660 PE=3 SV=1 - [E9AY45_LEIMU]	6.86	1	3	3	4	4.843	4	36.755	11.453	379	40.922
B4DJQ7	cDNA FLJ60602, moderately similar to D-dopachrome decarboxylase (EC 4.1.1.84) OS=Homo sapiens PE=2 SV=1 - [B4DJQ7_HUMAN]	13.39	6	2	2	5	0.950	5	10.837	11.446	112	11.668
E9AST2	Universal minicircle sequence binding protein,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1610 PE=4 SV=1 - [E9AST2_LEIMU]	16.52	2	3	3	7	1.000	5	0.000	11.429	115	12.585
K7ELY9	Beclin-1 (Fragment) OS=Homo sapiens GN=BECN1 PE=4 SV=1 - [K7ELY9_HUMAN]	12.23	7	3	3	4	1.077	4	19.466	11.418	229	26.878
Q96JK2	DDB1- and CUL4-associated factor 5 OS=Homo sapiens GN=DCAF5 PE=1 SV=2 - [DCAF5_HUMAN]	5.84	2	4	4	5	1.000	5	0.000	11.409	942	103.899
Q96S66	Chloride channel CLIC-like protein 1 OS=Homo sapiens GN=CLCC1 PE=1 SV=1 - [CLCC1_HUMAN]	4.54	4	2	2	3	1.000	3	0.000	11.408	551	61.983
Q9H814	Phosphorylated adapter RNA export protein OS=Homo sapiens GN=PHAX PE=1 SV=1 - [PHAX_HUMAN]	9.14	2	3	3	4	1.000	4	22.455	11.407	394	44.375
O00767	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2 - [ACOD_HUMAN]	7.24	2	2	3	5	1.184	2	25.378	11.405	359	41.496
Q9NWU2	Glucose-induced degradation protein 8 homolog OS=Homo sapiens GN=GID8 PE=1 SV=1 - [GID8_HUMAN]	23.25	2	4	4	4	0.927	3	6.738	11.397	228	26.732
B8ZZK0	Rho GTPase-activating protein 15 OS=Homo sapiens GN=ARHGAP15 PE=1 SV=1 - [B8ZZK0_HUMAN]	10.87	3	1	1	3	0.988	3	1.725	11.394	138	15.608
Q9P219	Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3 - [DAPLE_HUMAN]	1.23	2	1	4	6	1.000	1		11.391	2028	228.091
B2R9B9	cDNA, FLJ94321, highly similar to Homo sapiens eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R9B	11.67	3	1	1	4	1.000	4	0.000	11.384	120	13.003
B4E343	cDNA FLJ54249, highly similar to U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens PE=2 SV=1 - [B4E343_HUMAN]	3.21	5	2	2	4	1.000	3	0.000	11.382	717	82.148
P20929	Nebulin OS=Homo sapiens GN=NEB PE=1 SV=5 - [NEBU_HUMAN]	0.55	9	4	5	6	0.724	5	13.466	11.373	6669	772.428
J3KS17	Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=1 SV=1 - [J3KS17_HUMAN]	8.65	4	1	1	5	1.207	5	12.677	11.356	104	11.654
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	6.57	16	1	3	5	0.949	2	7.738	11.343	472	51.529
A8K3Z5	Nucleoporin NUP53 OS=Homo sapiens PE=2 SV=1 - [A8K3Z5_HUMAN]	7.67	2	2	2	3	1.014	3	84.435	11.336	326	34.793
E8NHK3	WGS CADB00000000 data, contig 50 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_14_1120a_1 PE=4 SV=1 - [E8NHK3_LEIMU]	51.79	2	2	2	4	1.028	4	11.206	11.328	753	83.516
O00244	Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 - [ATOX1_HUMAN]	38.24	4	2	2	4	1.047	4	7.186	11.326	68	7.397
B7Z7F5	cDNA FLJ51581 OS=Homo sapiens PE=2 SV=1 - [B7Z7F5_HUMAN]	7.17	5	2	2	4	1.043	4	7.167	11.325	279	30.746
O60828	Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 PE=1 SV=1 - [PQBP1_HUMAN]	13.58	4	3	3	4	0.953	4	8.305	11.310	265	30.454
D6RDK6	OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 - [D6RDK6_HUMAN]	16.2	10	3	3	4	0.946	4	14.172	11.293	179	19.977
R4GMM6	Ubiquitin-conjugating enzyme E2 E3 OS=Homo sapiens GN=UBE2E3 PE=1 SV=1 - [R4GMM6_HUMAN]	27.93	5	2	2	4	1.000	4	0.000	11.288	111	12.158
B4DJQ8	cDNA FLJ55694, highly similar to Dipeptidyl-peptidase 1 (EC 3.4.14.1) OS=Homo sapiens PE=2 SV=1 - [B4DJQ8_HUMAN]	8.74	5	3	3	5	1.000	4	0.176	11.262	446	50.119
Q9Y294	Histone chaperone ASF1A OS=Homo sapiens GN=ASF1A PE=1 SV=1 - [ASF1A_HUMAN]	9.31	4	2	2	5	0.992	5	19.618	11.260	204	22.954
H7C155	RAF proto-oncogene serine/threonine-protein kinase (Fragment) OS=Homo sapiens GN=RAF1 PE=1 SV=1 - [H7C155_HUMAN]	6.26	10	2	3	4	1.000	3	0.478	11.259	527	59.703
H7C577	Acetyl-coenzyme A transporter 1 (Fragment) OS=Homo sapiens GN=SLC33A1 PE=4 SV=1 - [H7C577_HUMAN]	5.95	3	1	1	4	1.000	4	0.000	11.252	185	20.403
Q9BSN3	NOP56 protein OS=Homo sapiens GN=NOP56 PE=2 SV=1 - [Q9BSN3_HUMAN]	17.82	3	3	3	4	1.000	4	13.996	11.250	174	19.497
B2RAT6	Galactose-1-phosphate uridylyltransferase OS=Homo sapiens PE=2 SV=1 - [B2RAT6_HUMAN]	14.25	12	5	5	5	1.022	5	33.022	11.246	379	43.320

B3KVJ8	cDNA FLJ16654 fis, clone TESTI4038284, highly similar to Chloride channel protein 7 OS=Homo sapiens PE=2 SV=1 - [B3KVJ8_HUMAN]	4.84	13	4	4	6	0.946	6	16.562	11.238	805	88.640
P16157	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3 - [ANK1_HUMAN]	2.39	3	4	4	5	0.801	4	48.545	11.237	1881	206.137
A8MYT4	Phosphatidylinositol 3-kinase OS=Homo sapiens GN=PIK3C3 PE=1 SV=2 - [A8MYT4_HUMAN]	2.31	8	2	2	5	1.000	5	0.000	11.230	824	94.340
P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 - [ACOC_HUMAN]	3.49	4	4	4	6	0.976	6	18.080	11.223	889	98.337
E9B1U9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1490 PE=4 SV=1 - [E9B1U9_LEIMU]	0.46	1	1	1	5	1.000	5	9.708	11.217	1528	160.600
A0A024R936	Neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2), isoform CRA_a OS=Homo sapiens GN=NCF2 PE=4 SV=1 - [A0A024R936_HUMAN]	11.6	4	4	4	4	1.000	3	0.000	11.204	526	59.752
Q9Y3L5	Ras-related protein Rap-2c OS=Homo sapiens GN=RAP2C PE=1 SV=1 - [RAP2C_HUMAN]	15.3	6	2	3	4	1.071	3	13.832	11.202	183	20.731
B2RA70	cDNA, FLJ94729, highly similar to Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1(YES1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RA70_HUM	4.6	55	1	3	5	1.099	2	14.094	11.199	543	60.793
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3 - [BIG2_HUMAN]	1.34	19	1	3	5	1.088	3	12.594	11.195	1785	201.909
O75420	PERQ amino acid-rich with GYF domain-containing protein 1 OS=Homo sapiens GN=GIGYF1 PE=1 SV=2 - [PERQ1_HUMAN]	2.8	2	1	3	4	1.000	1		11.174	1035	114.531
E9ARQ9	Putative prolyl-tRNA synthetase, putative,bifunctional aminoacyl-tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1220 PE=3	5.31	2	4	4	5	3.761	5	475.987	11.168	715	79.759
Q9UBB6	Neurochondrin OS=Homo sapiens GN=NCDN PE=1 SV=1 - [NCDN_HUMAN]	4.53	4	3	3	4	0.984	4	8.104	11.159	729	78.814
O95989	Diphosphoinositol polyphosphate phosphohydrolase 1 OS=Homo sapiens GN=NUDT3 PE=1 SV=1 - [NUDT3_HUMAN]	22.09	1	2	4	4	0.928	2	11.063	11.140	172	19.459
Q53F30	Aryl hydrocarbon receptor nuclear translocator isoform 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53F30_HUMAN]	11.75	7	1	3	3	0.857	1		11.139	315	34.800
Q9BTZ2	Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens GN=DHRS4 PE=1 SV=3 - [DHRS4_HUMAN]	16.19	13	5	5	5	1.000	5	20.370	11.125	278	29.518
E9AZB6	Putative RNA-binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_2100 PE=4 SV=1 - [E9AZB6_LEIMU]	5.44	1	4	4	5	1.000	4	0.000	11.106	423	46.738
B7Z4B1	cDNA FLJ50801, highly similar to Coiled-coil domain-containing protein 55 OS=Homo sapiens PE=2 SV=1 - [B7Z4B1_HUMAN]	6.94	5	3	3	5	0.802	5	33.521	11.095	490	58.803
G8JLJ2	Superoxide dismutase [Mn], mitochondrial (Fragment) OS=Homo sapiens GN=SOD2 PE=1 SV=1 - [G8JLJ2_HUMAN]	49.18	15	3	3	4	1.022	4	6.501	11.087	61	6.768
Q2M1P5	Kinesin-like protein KIF7 OS=Homo sapiens GN=KIF7 PE=1 SV=2 - [KIF7_HUMAN]	1.86	4	1	4	5	1.000	1		11.084	1343	150.495
B3KXK5	cDNA FLJ45623 fis, clone BRTHA3027957, highly similar to MKL/myocardin-like protein 2 OS=Homo sapiens PE=2 SV=1 - [B3KXK5_HUMAN]	2.25	5	1	3	6	0.914	1		11.075	578	62.203
K7EIR0	WD repeat-containing protein 18 OS=Homo sapiens GN=WDR18 PE=1 SV=1 - [K7EIR0_HUMAN]	7.33	6	3	3	4	1.150	4	37.597	11.064	409	44.809
E9AMY6	Histone H2B OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_1340 PE=3 SV=1 - [E9AMY6_LEIMU]	9.35	3	1	1	4	5.829	4	80.616	11.063	107	11.900
A0A024R8E8	Senataxin, isoform CRA_b OS=Homo sapiens GN=SETX PE=4 SV=1 - [A0A024R8E8_HUMAN]	3.83	4	5	5	6	1.000	4	12.416	11.056	1776	199.887
Q3V6T2	Girdin OS=Homo sapiens GN=CCDC88A PE=1 SV=2 - [GRDN_HUMAN]	2.08	14	3	5	7	0.947	4	8.133	11.052	1871	215.909
E9AYL4	Putative 60S ribosomal protein L35 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_2330 PE=3 SV=1 - [E9AYL4_LEIMU]	14.17	1	2	2	4	1.000	3	0.000	11.052	127	15.182
Q8NHP1	Aflatoxin B1 aldehyde reductase member 4 OS=Homo sapiens GN=AKR7L PE=2 SV=6 - [ARK74_HUMAN]	5.44	2	1	2	4	1.182	1		11.047	331	36.941
H7C4E5	Cytochrome c oxidase copper chaperone (Fragment) OS=Homo sapiens GN=COX17 PE=1 SV=1 - [H7C4E5_HUMAN]	34.48	3	2	2	5	1.000	5	31.222	11.020	58	6.408
Q92785	Zinc finger protein ubi-d4 OS=Homo sapiens GN=DPF2 PE=1 SV=2 - [REQU_HUMAN]	5.88	3	2	2	5	0.829	4	28.407	11.008	391	44.127
Q59HE6	RNA binding motif protein 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59HE6_HUMAN]	4.75	2	1	3	5	1.157	1		11.006	505	56.076
P07311	Acylphosphatase-1 OS=Homo sapiens GN=ACYP1 PE=1 SV=2 - [ACYP1_HUMAN]	20.2	2	2	2	4	0.967	4	4.096	11.003	99	11.254
Q04721	Neurogenic locus notch homolog protein 2 OS=Homo sapiens GN=NOTCH2 PE=1 SV=3 - [NOTC2_HUMAN]	1.5	7	4	4	5	1.002	5	20.361	10.978	2471	265.226
I3L2J8	Centrosomal protein of 131 kDa OS=Homo sapiens GN=CEP131 PE=1 SV=1 - [I3L2J8_HUMAN]	3.63	6	4	4	4	1.000	3	0.000	10.975	1047	117.627
B6VEX5	Abl-interactor 1 variant 72 OS=Homo sapiens PE=2 SV=1 - [B6VEX5_HUMAN]	4.64	14	2	2	4	1.035	4	23.721	10.975	388	42.611
O15078	Centrosomal protein of 290 kDa OS=Homo sapiens GN=CEP290 PE=1 SV=2 - [CE290_HUMAN]	1.33	9	3	4	5	2.120	2	156.801	10.965	2479	290.207
K7EQX8	Matrix-remodeling-associated protein 7 OS=Homo sapiens GN=MXRA7 PE=1 SV=1 - [K7EQX8_HUMAN]	73.33	3	1	2	4	1.027	3	29.739	10.955	15	1.911
D3DN94	Poly (ADP-ribose) polymerase family, member 14, isoform CRA_a OS=Homo sapiens GN=PARP14 PE=4 SV=1 - [D3DN94_HUMAN]	3.58	4	4	4	4	0.914	4	52.677	10.947	1424	160.062
D6RIY6	Exosome complex component RRP45 OS=Homo sapiens GN=EXOSC9 PE=1 SV=1 - [D6RIY6_HUMAN]	4.26	4	2	2	4	0.902	4	11.276	10.937	423	46.948
Q86Y56	HEAT repeat-containing protein 2 OS=Homo sapiens GN=HEATR2 PE=1 SV=4 - [HEAT2_HUMAN]	4.44	7	4	4	6	1.000	6	5.542	10.920	855	93.462
D6W5Z8	Kruppel-like factor 16, isoform CRA_a OS=Homo sapiens GN=KLF16 PE=4 SV=1 - [D6W5Z8_HUMAN]	17.54	2	2	2	4	1.000	3	0.000	10.893	211	21.556
B4DH44	cDNA FLJ52538, highly similar to Dual specificity mitogen-activated proteinkinase kinase 4 (EC 2.7.12.2) OS=Homo sapiens PE=2 SV=1 - [B4DH44_HUMAN]	7.18	4	3	3	5	1.039	5	10.782	10.893	376	42.518
B1ALH6	Phytanoyl-CoA dioxygenase, peroxisomal OS=Homo sapiens GN=PHYH PE=4 SV=1 - [B1ALH6_HUMAN]	5.3	5	2	2	4	1.000	4	0.000	10.879	321	36.942
Q502X7	Elongation of very long chain fatty acids protein OS=Homo sapiens GN=ELOVL1 PE=2 SV=1 - [Q502X7_HUMAN]	9.72	2	1	1	3	1.061	3	6.064	10.878	144	16.874
Q9H330	Transmembrane protein 245 OS=Homo sapiens GN=TMEM245 PE=1 SV=2 - [TM245_HUMAN]	7.03	2	2	3	5	1.063	4	9.087	10.874	911	100.881
P36507	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 - [MP2K2_HUMAN]	8	5	1	3	6	0.885	1		10.869	400	44.396
B4DQX8	cDNA FLJ51723, highly similar to DCC-interacting protein 13 alpha (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DQX8_HUMAN]	4.9	2	3	3	4	0.841	4	17.443	10.866	633	71.294
E9B1E7	Putative 60S acidic ribosomal protein P2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3730 PE=3 SV=1 - [E9B1E7_LEIMU]	19.05	1	2	2	4	1.000	4	0.000	10.862	105	10.620
P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	9.01	4	4	4	4	1.067	4	15.417	10.858	455	52.915
B2R6N3	cDNA, FLJ93032, highly similar to Homo sapiens zinc finger, A20 domain containing 3 (ZA20D3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6N3_HUMAN]	16.35	7	2	2	3	0.726	2	50.272	10.854	208	22.537
P50749	Ras association domain-containing protein 2 OS=Homo sapiens GN=RASSF2 PE=1 SV=1 - [RASF2_HUMAN]	16.26	3	2	4	5	1.000	3	0.000	10.848	326	37.767
Q96IV0	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase OS=Homo sapiens GN=NGLY1 PE=1 SV=1 - [NGLY1_HUMAN]	3.82	1	2	2	3	1.000	3	0.000	10.827	654	74.343
Q49AG2	TMED5 protein OS=Homo sapiens GN=TMED5 PE=2 SV=1 - [Q49AG2_HUMAN]	9.3	5	2	2	4	0.939	4	83.266	10.822	172	19.880
Q9Y333	U6 snRNA-associated Sm-like protein LSm2 OS=Homo sapiens GN=LSM2 PE=1 SV=1 - [LSM2_HUMAN]	46.32	1	4	4	5	1.037	5	8.858	10.819	95	10.828
B3KVL0	cDNA FLJ16691 fis, clone TRACH3000692, highly similar to Paxillin OS=Homo sapiens PE=2 SV=1 - [B3KVL0_HUMAN]	4.24	8	2	2	4	1.000	4	15.087	10.818	589	64.118
G5EA36	Cell division cycle 27, isoform CRA_c OS=Homo sapiens GN=CDC27 PE=1 SV=1 - [G5EA36_HUMAN]	3.28	9	3	3	4	0.967	4	12.397	10.812	823	91.680
Q6MZK6	Putative uncharacterized protein DKFZp686F1789 (Fragment) OS=Homo sapiens GN=DKFZp686F1789 PE=2 SV=1 - [Q6MZK6_HUMAN]	29.76	10	1	1	2				10.809	84	8.980
U3KQS7	U6 snRNA-associated Sm-like protein LSm4 (Fragment) OS=Homo sapiens GN=LSM4 PE=1 SV=1 - [U3KQS7_HUMAN]	15.6	5	2	2	5	1.051	5	7.366	10.804	109	12.447
K7ELQ0	39S ribosomal protein L4, mitochondrial OS=Homo sapiens GN=MRPL4 PE=1 SV=1 - [K7ELQ0_HUMAN]	11.36	7	2	2	5	1.000	4	2.844	10.800	220	24.431
Q5T011	Protein SZT2 OS=Homo sapiens GN=SZT2 PE=2 SV=3 - [SZT2_HUMAN]	0.64	1	2	2	6	1.000	4	0.000	10.795	3432	377.791
D6RAN1	PDZ and LIM domain protein 7 (Fragment) OS=Homo sapiens GN=PDLIM7 PE=1 SV=1 - [D6RAN1_HUMAN]	18.89	1	1	2	4	0.981	2	1.101	10.769	90	9.453
B3KW74	Phosphoglycerate dehydrogenase like 1, isoform CRA_e OS=Homo sapiens GN=PHGDHL1 PE=2 SV=1 - [B3KW74_HUMAN]	24.55	6	2	2	4	1.000	4	0.000	10.767	110	12.690
E9ARK7	Citrate synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0670 PE=3 SV=1 - [E9ARK7_LEIMU]	14.1	2	6	6	6	1.078	6	11.221	10.762	454	50.161
Q9H6E5	Speckle targeted PIP5K1A-regulated poly(A) polymerase OS=Homo sapiens GN=TUT1 PE=1 SV=2 - [STPAP_HUMAN]	4.35	2	3	3	4	1.000	3	0.000	10.754	874	93.788
F8W0Q9	Periphilin-1 OS=Homo sapiens GN=PPHLN1 PE=1 SV=1 - [F8W0Q9_HUMAN]	8.31	8	3	4	5	1.000	3	0.000	10.753	385	44.656
E9PQ73	Protocadherin Fat 3 OS=Homo sapiens GN=FAT3 PE=4 SV=1 - [E9PQ73_HUMAN]	0.81	3	3	3	5	1.002	4	13.583	10.747	4439	488.537
V9GYE3	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1 - [V9GYE3_HUMAN]	21.15	6	2	2	4	1.166	4	8.189	10.746	52	5.873
M0QYT5	Vesicle transport protein USE1 (Fragment) OS=Homo sapiens GN=USE1 PE=1 SV=1 - [M0QYT5_HUMAN]	11.8	3	2	2	3	0.879	3	14.909	10.740	161	17.788
A8KA41	cDNA FLJ75060, highly similar to Homo sapiens 2'-5'-oligoadenylate synthetase 2, 69/71kDa, mRNA OS=Homo sapiens PE=2 SV=1 - [A8KA41_HUMAN]	3.93	3	2	2	5	1.000	5	0.000	10.734	687	78.767
A8K9J6	cDNA FLJ78024 OS=Homo sapiens PE=2 SV=1 - [A8K9J6_HUMAN]	12.11	6	3	3	3	1.000	3	0.000	10.731	388	41.684
P51116	Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 - [FXR2_HUMAN]	5.94	2	3	4	5	1.000	3	0.000	10.731	673	74.178
B4DMA8	cDNA FLJ53841, highly similar to Kinesin-like protein KIFC1 OS=Homo sapiens PE=2 SV=1 - [B4DMA8_HUMAN]	7.47	3	4	4	4	0.926	4	21.585	10.717	549	60.476
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	16.95	2	1	1	5	0.868	5	11.842	10.711	59	6.644
Q9ULR0	Pre-mRNA-splicing factor ISY1 homolog OS=Homo sapiens GN=ISY1 PE=1 SV=3 - [ISY1_HUMAN]	7.72	1	2	2	4	1.000	4	0.000	10.705	285	32.972
C9JQQ5	Atlastin-2 (Fragment) OS=Homo sapiens GN=ATL2 PE=1 SV=1 - [C9JQQ5_HUMAN]	12	6	2	2	4	0.977	4	3.463	10.701	175	20.287
Q15061	WD repeat-containing protein 43 OS=Homo sapiens GN=WDR43 PE=1 SV=3 - [WDR43_HUMAN]	4.14	3	3	3	4	1.000	3	0.000	10.693	677	74.843
H0Y4S7	RanBP-type and C3HC4-type zinc finger-containing protein 1 (Fragment) OS=Homo sapiens GN=RBCK1 PE=4 SV=1 - [H0Y4S7_HUMAN]	9.02	8	2	2	3	0.890	3	32.493	10.692	255	28.398
E9AXQ3	Putative pyruvate dehydrogenase E1 beta subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1710 PE=4 SV=1 - [E9AXQ3_LEIMU]	8.57	1	2	2	4	1.037	4	4.020	10.684	350	37.849
M0R3B2	Nitric oxide synthase-interacting protein (Fragment) OS=Homo sapiens GN=NOSIP PE=1 SV=3 - [M0R3B2_HUMAN]	16.94	9	3	3	4	1.014	4	4.389	10.677	242	26.875
B4DMX4	cDNA FLJ57154, highly similar to Alpha-fetoprotein OS=Homo sapiens PE=2 SV=1 - [B4DMX4_HUMAN]	3.99	4	2	2	3	1.160	3	3.563	10.672	451	50.723
B2R9W9	cDNA, FLJ94590, highly similar to Homo sapiens craniofacial development protein 1 (CFDP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R9W9_HUMAN]	6.35	2	2	2	4	0.739	4	15.242	10.672	299	33.587
A0A087WXQ8	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=4 SV=1 - [A0A087WXQ8_HUMAN]	15.89	4	2	2	4	0.698	4	36.382	10.670	107	12.074
D3DQT1	Tripartite motif-containing 22, isoform CRA_a OS=Homo sapiens GN=TRIM22 PE=4 SV=1 - [D3DQT1_HUMAN]	3.64	8	1	2	4	1.000	1		10.663	494	56.336
Q9Y371	Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1 - [SHLB1_HUMAN]	4.38	3	1	2	4	0.330	1		10.661	365	40.771
Q9HCK8	Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens GN=CHD8 PE=1 SV=5 - [CHD8_HUMAN]	3.14	7	4	5	7	0.974	4	16.520	10.651	2581	290.338
Q8TDB6	E3 ubiquitin-protein ligase DTX3L OS=Homo sapiens GN=DTX3L PE=1 SV=1 - [DTX3L_HUMAN]	4.46	1	2	2	3	1.000	3	40.506	10.643	740	83.501
A0A087WT81	Polymerase delta-interacting protein 2 (Fragment) OS=Homo sapiens GN=POLDIP2 PE=4 SV=1 - [A0A087WT81_HUMAN]	14.71	3	2	2	4	1.124	3	0.797	10.641	170	18.561
E9AP81	40S ribosomal protein S12 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0570 PE=3 SV=1 - [E9AP81_LEIMU]	19.15	1	3	3	4	1.079	4	10.154	10.638	141	15.582
B3KSJ2	cDNA FLJ36408 fis, clone THYMU2010094, highly similar to Probable phospholipid-transporting ATPase IF (EC 3.6.3.1) OS=Homo sapiens PE=2 SV=1 - [B3KSJ2_HUM.	4.08	7	2	3	4	1.000	3	0.000	10.624	736	83.395
Q59FF4	Huntingtin variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FF4_HUMAN]	2.35	3	2	2	3	0.863	3	7.320	10.615	1147	127.012
E9AYD6	Putative thimet oligopeptidase (Metallo-peptidase, clan ma(E), family m3) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1570 PE=3 SV=1 - [	2.77	1	2	2	4	1.000	4	0.000	10.604	685	76.996
A8K304	cDNA FLJ75636, highly similar to Homo sapiens FYVE, RhoGEF and PH domain containing 2, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K304_HUMAN]	6.41	6	4	4	5	1.000	5	0.000	10.603	655	74.939
B7Z5N0	cDNA FLJ51282, highly similar to Thyroglobulin OS=Homo sapiens PE=2 SV=1 - [B7Z5N0_HUMAN]	0.78	6	1	1	5	1.000	5	0.000	10.598	901	99.250
H0Y6T7	Nicastrin (Fragment) OS=Homo sapiens GN=NCSTN PE=1 SV=1 - [H0Y6T7_HUMAN]	6.91	6	2	2	5	1.000	5	13.201	10.595	275	30.137
P48509	CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3 - [CD151_HUMAN]	6.32	8	2	2	5	0.928	4	3.536	10.563	253	28.276
O75438	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 OS=Homo sapiens GN=NDUFB1 PE=1 SV=1 - [NDUB1_HUMAN]	18.97	2	1	1	3	1.061	3	4.166	10.543	58	6.957
Q12962	Transcription initiation factor TFIID subunit 10 OS=Homo sapiens GN=TAF10 PE=1 SV=1 - [TAF10_HUMAN]	11.47	1	1	1	3	1.000	3	0.000	10.525	218	21.698
B4DTG4	cDNA FLJ56244, highly similar to Heat shock factor protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DTG4_HUMAN]	6.53	8	2	2	4	1.000	4	4.052	10.501	383	40.778
F5H4V9	Programmed cell death protein 2 OS=Homo sapiens GN=PDCD2 PE=1 SV=1 - [F5H4V9_HUMAN]	6.38	8	2	2	4	1.107	4	10.144	10.499	298	33.489
K7EM09	Transmembrane protein 205 (Fragment) OS=Homo sapiens GN=TMEM205 PE=1 SV=1 - [K7EM09_HUMAN]	14.17	4	1	1	3	1.016	3	4.815	10.497	120	13.381
B7Z8R6	cDNA FLJ51445, highly similar to AMBP protein OS=Homo sapiens PE=2 SV=1 - [B7Z8R6_HUMAN]	2.59	2	1	1	5	1.187	4	10.585	10.483	270	29.759
Q6PIW8	COG4 protein (Fragment) OS=Homo sapiens GN=COG4 PE=2 SV=1 - [Q6PIW8_HUMAN]	4.85	9	3	4	5	0.797	4	37.736	10.478	763	86.592
B4DP84	DCN1-like protein OS=Homo sapiens PE=2 SV=1 - [B4DP84_HUMAN]	17.86	4	3	3	4	1.024	4	3.533	10.466	168	20.042
A4D2E1	PERQ amino acid rich, with GYF domain 1 OS=Homo sapiens GN=PERQ1 PE=4 SV=1 - [A4D2E1_HUMAN]	4.04	1	1	3	4	1.230	1		10.463	817	89.685
E9PMH9	Putative deoxyribose-phosphate aldolase (Fragment) OS=Homo sapiens GN=DERA PE=1 SV=1 - [E9PMH9_HUMAN]	12.88	7	2	2	3	1.000	3	1.341	10.442	163	17.563
J3K000	PEPD protein OS=Homo sapiens GN=PEPD PE=2 SV=1 - [J3K000_HUMAN]	5.48	3	3	3	4	0.988	4	17.968	10.434	493	54.547
Q53TD9	Putative uncharacterized protein ZFHX1B (Fragment) OS=Homo sapiens GN=ZFHX1B PE=1 SV=1 - [Q53TD9_HUMAN]	6.58	20	6	6	6	0.985	6	11.393	10.431	1079	121.335
H7C2R6	UPF0769 protein C21orf59 (Fragment) OS=Homo sapiens GN=C21orf59 PE=4 SV=1 - [H7C2R6_HUMAN]	13.68	4	1	2	4	1.354	1		10.420	117	13.436
Q9UKL0	REST corepressor 1 OS=Homo sapiens GN=RCOR1 PE=1 SV=1 - [RCOR1_HUMAN]	7.47	2	3	3	4	1.073	4	31.346	10.418	482	52.996
H7BXY3	Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1 - [H7BXY3_HUMAN]	4.2	3	5	5	5	0.940	5	18.637	10.401	1166	130.469
E7EPF2	RNA-binding motif, single-stranded-interacting protein 1 (Fragment) OS=Homo sapiens GN=RBMS1 PE=1 SV=3 - [E7EPF2_HUMAN]	13.28	12	1	2	4	0.697	3	5.111	10.392	128	13.818
C9J2C4	DnaJ homolog subfamily B member 6 (Fragment) OS=Homo sapiens GN=DNAJB6 PE=1 SV=1 - [C9J2C4_HUMAN]	9.65	13	3	3	7	0.966	7	8.701	10.390	228	25.361
Q96EY7	Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3 - [PTCD3_HUMAN]	4.64	4	4	4	4	1.004	4	15.827	10.389	689	78.500
A0JP11	Phosphoinositide-3-kinase, regulatory subunit 4 OS=Homo sapiens GN=PIK3R4 PE=2 SV=1 - [A0JP11_HUMAN]	2.14	3	3	3	4	1.065	4	7.202	10.386	1358	153.062
E9AVE1	Putative RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1552 PE=4 SV=1 - [E9AVE1_LEIMU]	4.14	1	2	2	4	1.000	4	0.000	10.385	435	49.438
E9AVL6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0320 PE=4 SV=1 - [E9AVL6_LEIMU]	1.99	1	1	1	4	0.917	2	4.248	10.384	351	37.775
Q92522	Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1 - [H1X_HUMAN]	20.19	1	4	4	6	1.030	6	6.254	10.380	213	22.474
Q8NDD5	Putative uncharacterized protein DKFZp586L2318 OS=Homo sapiens GN=DKFZp586L2318 PE=2 SV=1 - [Q8NDD5_HUMAN]	13.28	2	2	2	5	1.008	5	6.773	10.380	128	14.089
B2RBB2	cDNA, FLJ95416, highly similar to Homo sapiens phosphatidylinositol glycan, class S (PIGS), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBB2_HUMAN]	3.06	10	2	2	4	1.004	4	6.105	10.377	555	61.647
B7Z4V7	cDNA FLJ50087 OS=Homo sapiens PE=2 SV=1 - [B7Z4V7_HUMAN]	5.99	4	4	4	6	1.000	6	0.012	10.376	568	64.185
Q08722	Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1 - [CD47_HUMAN]	5.88	1	2	2	4	1.046	4	17.074	10.375	323	35.191
Q9NYB0	Telomeric repeat-binding factor 2-interacting protein 1 OS=Homo sapiens GN=TERF2IP PE=1 SV=1 - [TE2IP_HUMAN]	7.77	1	2	2	4	1.000	3	1.940	10.361	399	44.233
H7BZH6	Quinone oxidoreductase PIG3 (Fragment) OS=Homo sapiens GN=TP53I3 PE=1 SV=1 - [H7BZH6_HUMAN]	17.13	3	3	3	6	1.006	6	3.796	10.351	216	22.640
Q8NFX3	Dual specificity phosphatase 1 OS=Homo sapiens PE=2 SV=1 - [Q8NFX3_HUMAN]	10.92	14	3	3	4	0.973	4	22.404	10.337	293	33.362
Q96DA6	Mitochondrial import inner membrane translocase subunit TIM14 OS=Homo sapiens GN=DNAJC19 PE=1 SV=3 - [TIM14_HUMAN]	14.66	1	2	2	4	1.015	4	11.970	10.333	116	12.491
B2RCD8	cDNA, FLJ96012, highly similar to Homo sapiens interferon regulatory factor 2 binding protein 1 (IRF2BP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RCD8_HUMAN]	7.88	2	4	4	4	1.000	4	0.000	10.326	584	61.675
K7EID2	Chitobiosyldiphosphodolichol beta-mannosyltransferase (Fragment) OS=Homo sapiens GN=ALG1 PE=1 SV=3 - [K7EID2_HUMAN]	11.31	2	2	2	4	0.728	4	14.865	10.320	168	19.365
A8JZZ8	cDNA FLJ77826, highly similar to Homo sapiens BCS1-like (yeast), mRNA OS=Homo sapiens PE=2 SV=1 - [A8JZZ8_HUMAN]	7.88	8	3	3	3	0.965	3	7.101	10.316	419	47.520
A0PJI7	CIR protein (Fragment) OS=Homo sapiens GN=CIR PE=2 SV=1 - [A0PJI7_HUMAN]	6.57	2	3	3	5	1.000	5	0.000	10.293	426	49.554
B1ANE3	Methionine synthase (Fragment) OS=Homo sapiens GN=MTR PE=1 SV=1 - [B1ANE3_HUMAN]	4.76	6	4	4	5	1.000	5	0.000	10.289	819	91.722
Q96BN8	Ubiquitin thioesterase otulin OS=Homo sapiens GN=OTULIN PE=1 SV=3 - [OTUL_HUMAN]	16.48	2	5	5	11	1.000	9	5.891	10.287	352	40.237
B4DUH1	cDNA FLJ51323, highly similar to Short-chain specific acyl-CoA dehydrogenase, mitochondrial (EC 1.3.99.2) OS=Homo sapiens PE=2 SV=1 - [B4DUH1_HUMAN]	8.89	5	3	3	4	1.000	4	7.198	10.285	405	43.602
J3QS45	L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=1 SV=1 - [J3QS45_HUMAN]	36	7	3	3	4	0.971	4	7.447	10.272	100	10.798
E9AVH4	40S ribosomal protein S6 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1780 PE=3 SV=1 - [E9AVH4_LEIMU]	6.43	1	1	1	4	1.000	4	0.000	10.262	249	28.245
B2RDT8	cDNA, FLJ96764, highly similar to Homo sapiens sorting nexin 8 (SNX8), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDT8_HUMAN]	4.09	6	2	2	4	1.000	4	0.000	10.257	465	52.564
E9AJN3	Putative ATP-dependent Clp protease subunit, heat shock protein 78 (HSP78) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0710 PE=4 SV=	4.04	1	2	4	6	2.405	3	17.074	10.255	817	90.910
P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2 - [S10AA_HUMAN]	13.4	3	2	2	5	1.229	5	8.951	10.253	97	11.196
Q9BYV8	Centrosomal protein of 41 kDa OS=Homo sapiens GN=CEP41 PE=1 SV=1 - [CEP41_HUMAN]	9.38	6	2	2	3	1.000	2	0.000	10.241	373	41.343
E5RK82	Centrin-3 OS=Homo sapiens GN=CETN3 PE=4 SV=1 - [E5RK82_HUMAN]	11.54	7	1	2	5	1.000	1		10.240	156	18.325
L7N2F4	Alanyl-tRNA-editing protein Aarsd1 (Fragment) OS=Homo sapiens GN=AARSD1 PE=1 SV=1 - [L7N2F4_HUMAN]	18.57	4	2	2	3	0.938	3	26.250	10.212	140	15.474
Q08945	FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 - [SSRP1_HUMAN]	5.92	4	5	6	7	0.915	5	5.470	10.203	709	81.024
K7EMZ9	Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 - [K7EMZ9_HUMAN]	4.8	7	1	2	4	0.483	2	128.199	10.188	333	36.610
E9APR1	Elongation of fatty acids protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0660 PE=3 SV=1 - [E9APR1_LEIMU]	5.28	1	1	1	4	1.000	4	0.000	10.187	284	32.477
Q5VXN0	Ribosome production factor 2 homolog (Fragment) OS=Homo sapiens GN=RPF2 PE=1 SV=1 - [Q5VXN0_HUMAN]	9.35	6	2	2	4	1.368	4	27.396	10.186	214	24.589
B4DEZ3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Homo sapiens GN=NDUFA13 PE=2 SV=1 - [B4DEZ3_HUMAN]	21.67	6	3	3	4	1.027	4	3.905	10.186	120	14.076
B7Z3R2	Two pore calcium channel protein 1 OS=Homo sapiens GN=TPCN1 PE=2 SV=1 - [B7Z3R2_HUMAN]	2.27	3	1	1	3	1.000	3	0.000	10.176	748	87.262
P46109	Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1 - [CRKL_HUMAN]	14.19	1	2	2	2	1.000	2	0.000	10.165	303	33.756
A8K4V4	cDNA FLJ76392, highly similar to Homo sapiens mitochondrial ribosomal protein L43 (MRPL43), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4V4_H	18.24	7	3	3	5	1.000	5	0.810	10.162	159	17.748
D3DXC9	Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT1 PE=3 SV=1 - [D3DXC9_HUMAN]	3.6	6	1	2	5	0.674	2	87.098	10.158	444	49.031
G5EA42	Tropomodulin 2 (Neuronal), isoform CRA_a OS=Homo sapiens GN=TMOD2 PE=4 SV=1 - [G5EA42_HUMAN]	5.21	5	1	2	5	1.120	4	16.911	10.156	307	34.471
O43715	TP53-regulated inhibitor of apoptosis 1 OS=Homo sapiens GN=TRIAP1 PE=1 SV=1 - [TRIA1_HUMAN]	19.74	1	2	2	5	1.000	5	26.666	10.153	76	8.780
B4DXU3	cDNA FLJ54989, highly similar to Mitochondrial import receptor subunit TOM34 OS=Homo sapiens PE=2 SV=1 - [B4DXU3_HUMAN]	9.33	3	3	3	4	0.869	4	9.253	10.146	268	30.174
E9PJP1	Mth938 domain-containing protein OS=Homo sapiens GN=AAMDC PE=1 SV=1 - [E9PJP1_HUMAN]	24.73	7	2	2	4	1.000	4	0.000	10.139	93	10.119
E9AZR2	40S ribosomal protein S14 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_0960 PE=3 SV=1 - [E9AZR2_LEIMU]	15.97	1	2	2	4	1.000	4	0.000	10.119	144	15.553
Q9BV20	Methylthioribose-1-phosphate isomerase OS=Homo sapiens GN=MRI1 PE=1 SV=1 - [MTNA_HUMAN]	5.15	2	2	2	4	0.940	4	6.674	10.109	369	39.125
A7E261	5-oxoprolinase (ATP-hydrolysing) OS=Homo sapiens GN=OPLAH PE=2 SV=1 - [A7E261_HUMAN]	4.04	3	4	4	4	1.031	3	26.561	10.089	1288	137.343
D6RCD9	Transmembrane protein 175 OS=Homo sapiens GN=TMEM175 PE=1 SV=1 - [D6RCD9_HUMAN]	19.44	7	2	2	3	1.000	3	0.000	10.081	72	7.903
Q9BU76	Multiple myeloma tumor-associated protein 2 OS=Homo sapiens GN=MMTAG2 PE=1 SV=1 - [MMTA2_HUMAN]	12.93	1	3	3	4	1.000	4	0.000	10.079	263	29.394
B7ZMF2	Fanconi anemia, complementation group I OS=Homo sapiens GN=FANCI PE=2 SV=1 - [B7ZMF2_HUMAN]	2.71	9	3	3	4	1.000	4	0.000	10.073	1328	149.241
B4DMI9	cDNA FLJ55894, highly similar to Discs large homolog 7 OS=Homo sapiens PE=2 SV=1 - [B4DMI9_HUMAN]	2.53	3	2	2	4	1.087	3	14.229	10.067	792	88.873
C9J8M3	Replication factor C subunit 4 (Fragment) OS=Homo sapiens GN=RFC4 PE=1 SV=1 - [C9J8M3_HUMAN]	20.09	8	4	4	5	1.142	5	19.840	10.058	214	23.634
Q8IV38	Ankyrin repeat and MYND domain-containing protein 2 OS=Homo sapiens GN=ANKMY2 PE=1 SV=1 - [ANKY2_HUMAN]	5.22	3	3	3	4	1.000	4	11.338	10.056	441	49.267
E9AZP7	Putative RNA binding protein rbp16 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_0825 PE=4 SV=1 - [E9AZP7_LEIMU]	7.75	1	1	1	3	6.709	3	100.808	10.052	142	15.132
O14519	Cyclin-dependent kinase 2-associated protein 1 OS=Homo sapiens GN=CDK2AP1 PE=1 SV=1 - [CDKA1_HUMAN]	15.65	4	2	2	4	1.000	4	2.530	10.048	115	12.357
F5GX09	Protein FAM76B OS=Homo sapiens GN=FAM76B PE=1 SV=1 - [F5GX09_HUMAN]	7.1	3	2	3	4	0.580	2	111.333	10.045	338	38.596
E9AK37	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0550 PE=4 SV=1 - [E9AK37_LEIMU]	2.39	1	3	3	8	1.336	7	19.701	10.045	1546	169.067
H0YJH0	Protein salvador homolog 1 (Fragment) OS=Homo sapiens GN=SAV1 PE=1 SV=1 - [H0YJH0_HUMAN]	5.77	3	2	2	5	1.249	4	7.975	10.043	312	36.643
Q96E11	Ribosome-recycling factor, mitochondrial OS=Homo sapiens GN=MRRF PE=1 SV=1 - [RRFM_HUMAN]	13.74	4	3	3	3	1.000	3	6.963	10.041	262	29.259
B4DSC2	Elongation of very long chain fatty acids protein OS=Homo sapiens PE=2 SV=1 - [B4DSC2_HUMAN]	2.77	3	1	1	4	1.224	4	30.827	10.039	289	34.133
E9AV10	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0430 PE=4 SV=1 - [E9AV10_LEIMU]	6.21	1	2	2	4	1.000	3	0.000	10.031	419	47.464
B4DMK6	cDNA FLJ60055, highly similar to Rattus norvegicus Ssu72 RNA polymerase II CTD phosphatase homolog, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DMK6_HUMAN]	6.18	2	1	1	4	0.940	4	42.919	10.031	178	20.247
E9B1G1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_0130 PE=4 SV=1 - [E9B1G1_LEIMU]	0.85	1	1	1	5	1.000	4	3.032	10.002	823	92.110
A0A087WXS7	ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=4 SV=1 - [A0A087WXS7_HUMAN]	9.37	4	3	3	3	1.831	3	1.125	9.997	331	37.095
Q9HCD5	Nuclear receptor coactivator 5 OS=Homo sapiens GN=NCOA5 PE=1 SV=2 - [NCOA5_HUMAN]	4.66	2	3	3	4	1.014	4	4.308	9.988	579	65.496
Q6ZWP8	FLJ00080 protein (Fragment) OS=Homo sapiens GN=FLJ00080 PE=2 SV=1 - [Q6ZWP8_HUMAN]	3.77	3	2	2	3	1.000	3	0.000	9.988	716	80.355
E9B493	Putative carboxypeptidase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2540 PE=4 SV=1 - [E9B493_LEIMU]	5.01	1	3	3	4	1.727	4	96.322	9.987	499	56.921
Q5TIH2	Vesicle transport protein SFT2B OS=Homo sapiens GN=SFT2D2 PE=1 SV=1 - [Q5TIH2_HUMAN]	10.19	2	2	2	4	0.961	4	9.622	9.985	108	11.748
K7ES67	HAUS augmin-like complex subunit 1 (Fragment) OS=Homo sapiens GN=HAUS1 PE=1 SV=3 - [K7ES67_HUMAN]	8.33	2	1	1	3	0.931	3	12.245	9.971	108	12.251
Q59H59	Hepatocyte growth factor isoform 1 preproprotein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H59_HUMAN]	3.27	3	1	1	4	1.134	4	20.323	9.969	245	27.590
E9AXC7	RNA-binding protein, putative, UPB2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0500 PE=4 SV=1 - [E9AXC7_LEIMU]	10.78	2	2	2	4	1.854	4	57.393	9.961	167	19.000
E9B2M5	Chaperonin containing t-complex protein,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_1000 PE=3 SV=1 - [E9B2M5_LEIMU]	6.51	1	3	4	5	1.141	4	19.683	9.944	538	59.263
B2RDV2	cDNA, FLJ96778, highly similar to Homo sapiens aminopeptidase-like 1 (NPEPL1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDV2_HUMAN]	2.92	3	1	1	3	1.000	3	0.000	9.943	411	43.490
P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	27.87	4	4	4	4	1.007	4	1.101	9.938	244	25.773
B3KXN9	cDNA FLJ45793 fis, clone NT2RI2009233 OS=Homo sapiens PE=2 SV=1 - [B3KXN9_HUMAN]	4.07	2	1	1	4	1.000	4	0.000	9.928	270	29.835
B4DNP0	Signal transducer and activator of transcription OS=Homo sapiens PE=2 SV=1 - [B4DNP0_HUMAN]	2.68	6	2	2	3	0.906	3	20.818	9.924	672	76.113
D3DVA3	Misato homolog 1 (Drosophila), isoform CRA_a OS=Homo sapiens GN=MSTO1 PE=4 SV=1 - [D3DVA3_HUMAN]	6.15	6	2	2	4	0.845	4	25.444	9.923	309	34.308
Q9BQ48	39S ribosomal protein L34, mitochondrial OS=Homo sapiens GN=MRPL34 PE=1 SV=1 - [RM34_HUMAN]	10.87	2	1	1	3	1.575	3	19.147	9.915	92	10.159
J3QL56	Protein SCO1 homolog, mitochondrial OS=Homo sapiens GN=SCO1 PE=1 SV=1 - [J3QL56_HUMAN]	5.93	2	2	2	4	0.920	4	24.509	9.911	270	30.160
Q9HC03	Dolichyl-phosphate beta-glucosyltransferase OS=Homo sapiens PE=2 SV=1 - [Q9HC03_HUMAN]	6.17	3	2	2	4	0.872	4	14.437	9.900	324	36.940
H7CEH5	Cathepsin K (Fragment) OS=Homo sapiens GN=CTSK PE=4 SV=1 - [H7CEH5_HUMAN]	13.46	11	1	1	4	1.026	4	4.043	9.897	52	5.873
A0A024R5N1	Purinergic receptor P2Y, G-protein coupled, 2, isoform CRA_a OS=Homo sapiens GN=P2RY2 PE=3 SV=1 - [A0A024R5N1_HUMAN]	3.45	2	2	2	4	1.000	3	0.000	9.895	377	42.209

E9B6K7	Putative 60S ribosomal subunit protein L31 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3280 PE=4 SV=1 - [E9B6K7_LEIMU]	4.79	1	2	2	4	1.000	4	0.000	9.877	188	21.396
F8VYH9	Cyclin-dependent kinase 4 (Fragment) OS=Homo sapiens GN=CDK4 PE=1 SV=1 - [F8VYH9_HUMAN]	20.59	54	2	4	6	1.000	3	27.119	9.874	170	18.674
A6PVN5	Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=1 SV=1 - [A6PVN5_HUMAN]	14.59	13	1	4	6	1.192	1		9.874	329	37.352
B7ZM73	MON2 protein OS=Homo sapiens GN=MON2 PE=2 SV=1 - [B7ZM73_HUMAN]	1.78	3	3	3	4	1.062	4	2.692	9.872	1688	187.200
Q8N4P8	GTPBP4 protein (Fragment) OS=Homo sapiens GN=GTPBP4 PE=2 SV=1 - [Q8N4P8_HUMAN]	5.38	7	4	4	5	1.162	5	2.469	9.871	632	73.663
B2RAM6	cDNA, FLJ95005, highly similar to Homo sapiens kinesin family member 11 (KIF11), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAM6_HUMAN]	2.37	3	3	3	4	0.885	4	20.834	9.867	1056	119.058
E9B128	Reticulon-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2580 PE=4 SV=1 - [E9B128_LEIMU]	13.2	1	2	2	4	1.000	4	0.000	9.867	197	22.188
Q6P4R8	Nuclear factor related to kappa-B-binding protein OS=Homo sapiens GN=NFRKB PE=1 SV=2 - [NFRKB_HUMAN]	3.39	4	3	3	4	1.000	4	15.660	9.854	1299	138.915
O00479	High mobility group nucleosome-binding domain-containing protein 4 OS=Homo sapiens GN=HMGN4 PE=1 SV=3 - [HMGN4_HUMAN]	26.67	1	2	3	5	1.354	4	27.099	9.840	90	9.533
B4DGP7	cDNA FLJ57924 OS=Homo sapiens PE=2 SV=1 - [B4DGP7_HUMAN]	11.88	7	1	2	4	1.000	2	0.000	9.838	160	18.622
F5H7F6	Microsomal glutathione S-transferase 1 (Fragment) OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [F5H7F6_HUMAN]	16.88	4	1	1	3	1.000	3	18.418	9.836	77	8.880
O15451	Proline and glutamic acid rich nuclear protein isoform (Fragment) OS=Homo sapiens PE=1 SV=2 - [O15451_HUMAN]	3.53	7	2	2	4	1.000	2	0.000	9.835	1021	109.068
J3QQJ5	Trafficking protein particle complex subunit 8 OS=Homo sapiens GN=TRAPPC8 PE=1 SV=1 - [J3QQJ5_HUMAN]	1.67	4	3	3	3	0.989	3	1.205	9.832	1381	154.887
B4DW50	Mannose-6-phosphate isomerase OS=Homo sapiens PE=2 SV=1 - [B4DW50_HUMAN]	6.97	5	2	2	3	1.000	3	0.000	9.829	373	41.121
Q99608	Necdin OS=Homo sapiens GN=NDN PE=2 SV=1 - [NECD_HUMAN]	2.8	1	1	1	5	0.835	5	3.364	9.822	321	36.063
H3BTB7	Probable glutamate--tRNA ligase, mitochondrial OS=Homo sapiens GN=EARS2 PE=1 SV=1 - [H3BTB7_HUMAN]	7.11	5	4	4	4	0.902	4	17.427	9.821	506	56.790
Q15269	Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2 - [PWP2_HUMAN]	2.94	1	2	2	3	1.079	3	11.357	9.816	919	102.387
B4DKK0	cDNA FLJ52511, highly similar to Abhydrolase domain-containing protein 14B OS=Homo sapiens PE=2 SV=1 - [B4DKK0_HUMAN]	7.69	5	1	1	3	0.830	3	8.348	9.795	130	13.902
B2RA10	Homer homolog 3 (Drosophila), isoform CRA_b OS=Homo sapiens GN=HOMER3 PE=2 SV=1 - [B2RA10_HUMAN]	5.82	6	2	2	3	1.000	3	3.228	9.794	361	39.881
B4DU07	Acyl-coenzyme A oxidase OS=Homo sapiens PE=2 SV=1 - [B4DU07_HUMAN]	2.7	4	2	2	5	1.070	5	4.666	9.775	592	66.414
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1 - [PPP6_HUMAN]	8.52	2	3	3	6	1.110	6	13.646	9.769	305	35.121
P58107	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]	3.99	3	1	3	6	1.000	1		9.759	5090	555.279
B2R5K5	cDNA, FLJ92508 OS=Homo sapiens PE=2 SV=1 - [B2R5K5_HUMAN]	18.18	3	2	2	3	1.267	3	2.561	9.756	110	12.327
B7Z3I9	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1 - [B7Z3I9_HUMAN]	10.86	4	3	3	6	0.969	6	38.877	9.751	313	34.497
P42773	Cyclin-dependent kinase 4 inhibitor C OS=Homo sapiens GN=CDKN2C PE=1 SV=1 - [CDN2C_HUMAN]	18.45	1	4	4	4	1.125	4	5.163	9.745	168	18.116
K7ENM5	Nucleolar protein 4 (Fragment) OS=Homo sapiens GN=NOL4 PE=4 SV=1 - [K7ENM5_HUMAN]	4.57	5	1	1	4	5.399	4	71.885	9.733	219	23.958
E9ANP4	Putative pyruvate phosphate dikinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_1000 PE=4 SV=1 - [E9ANP4_LEIMU]	4.16	1	4	4	6	2.366	6	189.862	9.732	914	100.944
Q2TA85	C10orf54 protein (Fragment) OS=Homo sapiens GN=C10orf54 PE=2 SV=1 - [Q2TA85_HUMAN]	5.54	2	2	2	6	1.000	6	8.160	9.715	307	33.599
J3KQ72	F-box only protein 6 (Fragment) OS=Homo sapiens GN=FBXO6 PE=1 SV=1 - [J3KQ72_HUMAN]	9.64	2	2	2	4	1.108	2	15.332	9.712	249	28.892
E9AW84	3-ketoacyl-CoA thiolase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0690 PE=1 SV=1 - [E9AW84_LEIMU]	5.44	1	2	3	4	0.808	3	42.494	9.707	441	47.342
E9ATI7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4040 PE=4 SV=1 - [E9ATI7_LEIMU]	5.81	1	2	2	4	1.041	4	4.312	9.707	430	47.058
Q9Y5S1	Transient receptor potential cation channel subfamily V member 2 OS=Homo sapiens GN=TRPV2 PE=1 SV=1 - [TRPV2_HUMAN]	4.19	2	3	3	5	1.012	5	20.897	9.705	764	85.926
Q99848	Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2 - [EBP2_HUMAN]	6.54	3	2	2	4	1.024	4	13.310	9.693	306	34.830
Q9BRK4	Leucine zipper putative tumor suppressor 2 OS=Homo sapiens GN=LZTS2 PE=1 SV=2 - [LZTS2_HUMAN]	3.89	3	1	2	5	1.000	1		9.688	669	72.715
Q8NHU6	Tudor domain-containing protein 7 OS=Homo sapiens GN=TDRD7 PE=1 SV=2 - [TDRD7_HUMAN]	1.55	1	2	2	3	1.000	3	7.350	9.676	1098	123.506
A0A024R819	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1, isoform CRA_a OS=Homo sapiens GN=NUDT1 PE=3 SV=1 - [A0A024R819_HUMAN]	7.69	3	1	1	3	0.972	3	31.942	9.672	156	17.940
Q9UQN3	Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B PE=1 SV=1 - [CHM2B_HUMAN]	15.96	3	4	4	4	0.978	4	6.529	9.671	213	23.891
X6RA56	Dynactin subunit 3 OS=Homo sapiens GN=DCTN3 PE=1 SV=1 - [X6RA56_HUMAN]	19.01	5	3	3	4	1.000	4	3.535	9.663	142	16.081
C9J8T0	Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC PE=1 SV=1 - [C9J8T0_HUMAN]	8.49	3	3	3	5	1.000	5	6.211	9.659	436	47.846
E9B6X6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4470 PE=4 SV=1 - [E9B6X6_LEIMU]	12.38	1	3	3	4	1.643	4	32.009	9.657	202	21.823
E9B600	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1210 PE=4 SV=1 - [E9B600_LEIMU]	12.79	1	3	3	4	1.000	4	0.000	9.635	219	24.456
E9AUF1	Phosphoglycerate kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_0110 PE=3 SV=1 - [E9AUF1_LEIMU]	7.91	2	4	4	4	6.262	4	79.799	9.633	417	44.824
A0A024RBU9	Nuclear receptor co-repressor 2, isoform CRA_a OS=Homo sapiens GN=NCOR2 PE=4 SV=1 - [A0A024RBU9_HUMAN]	2.06	12	4	5	6	1.000	5	9.366	9.623	2471	268.942
B7ZBB8	Protein phosphatase 1 regulatory subunit 3G OS=Homo sapiens GN=PPP1R3G PE=3 SV=1 - [PP13G_HUMAN]	3.35	1	1	1	2	1.000	2	0.000	9.622	358	37.995
O43660	Pleiotropic regulator 1 OS=Homo sapiens GN=PLRG1 PE=1 SV=1 - [PLRG1_HUMAN]	3.11	2	2	2	4	0.993	4	7.197	9.616	514	57.158
E9AVK2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0180 PE=4 SV=1 - [E9AVK2_LEIMU]	13.51	1	3	3	5	1.000	5	0.000	9.611	259	28.243
H0YG82	28S ribosomal protein S35, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS35 PE=1 SV=1 - [H0YG82_HUMAN]	9.26	3	2	2	5	1.166	4	26.169	9.611	162	18.009
Q9ULG6	Cell cycle progression protein 1 OS=Homo sapiens GN=CCPG1 PE=2 SV=3 - [CCPG1_HUMAN]	2.77	2	2	2	3	1.287	3	13.839	9.608	757	87.286
E9AJU3	Putative arginine N-methyltransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_03_0600 PE=4 SV=1 - [E9AJU3_LEIMU]	2.76	1	1	1	3	1.000	3	0.000	9.596	399	43.427
Q9BRF8	Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3 - [CPPED_HUMAN]	8.28	2	4	4	4	0.948	4	8.541	9.589	314	35.526
A0A024R3K4	Friend leukemia virus integration 1, isoform CRA_b OS=Homo sapiens GN=FLI1 PE=3 SV=1 - [A0A024R3K4_HUMAN]	7.25	15	3	3	6	0.998	6	3.185	9.588	386	43.621
Q9Y5K6	CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN]	4.69	1	3	4	6	0.945	5	8.339	9.584	639	71.407
B3KVN6	cDNA FLJ16819 fis, clone TRACH3014316, highly similar to Zinc finger with KRAB and SCAN domain-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KVN6_HU	5.02	28	1	2	4	1.000	3	50.888	9.572	299	33.561
C9JKF1	Sterile alpha motif domain-containing protein 9 (Fragment) OS=Homo sapiens GN=SAMD9 PE=1 SV=1 - [C9JKF1_HUMAN]	1.64	4	2	2	4	0.985	4	6.052	9.565	1283	148.727
E9PQW1	Caspase recruitment domain-containing protein 16 (Fragment) OS=Homo sapiens GN=CARD16 PE=1 SV=1 - [E9PQW1_HUMAN]	27.37	3	1	3	5	0.732	2	107.906	9.564	95	10.324
E9APB1	Mitochondrial processing peptidase alpha subunit,putative (Metallo-peptidase, clan me, family m16) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM	7.39	1	4	4	4	2.468	4	98.574	9.554	528	57.601
J3KTF9	ORM1-like protein 3 (Fragment) OS=Homo sapiens GN=ORMDL3 PE=4 SV=1 - [J3KTF9_HUMAN]	10.78	7	1	1	3	0.802	3	10.989	9.552	102	11.898
B7Z7D2	Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=2 SV=1 - [B7Z7D2_HUMAN]	6.39	15	3	3	4	1.077	4	10.981	9.508	391	44.483
B2RE59	cDNA, FLJ93148, highly similar to Homo sapiens RCD1 required for cell differentiation1 homolog (S. pombe) (RQCD1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RE59	9.7	4	3	3	4	1.004	4	0.574	9.507	299	33.596
Q8WXE0	Caskin-2 OS=Homo sapiens GN=CASKIN2 PE=1 SV=2 - [CSKI2_HUMAN]	1.66	2	1	2	4	0.966	1		9.482	1202	126.705
H3BTW5	C-myc promoter-binding protein (Fragment) OS=Homo sapiens GN=DENND4A PE=1 SV=1 - [H3BTW5_HUMAN]	2.7	3	2	2	3	1.000	3	0.000	9.479	1001	112.536
Q5T9B9	Endoglin (Osler-Rendu-Weber syndrome 1) OS=Homo sapiens GN=ENG PE=4 SV=1 - [Q5T9B9_HUMAN]	4	7	2	2	3	1.097	3	32.480	9.473	625	67.499
Q59FT7	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1 isoform alpha variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FT7_HUMAN]	3.7	6	2	2	3	1.000	3	0.000	9.466	648	70.221
Q9UBX3	Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2 - [DIC_HUMAN]	10.1	4	1	3	4	0.956	1		9.460	287	31.262
Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2 OS=Homo sapiens GN=RPRD2 PE=1 SV=1 - [RPRD2_HUMAN]	4.86	1	7	7	8	1.000	8	15.790	9.453	1461	155.924
Q99871	HAUS augmin-like complex subunit 7 OS=Homo sapiens GN=HAUS7 PE=1 SV=3 - [HAUS7_HUMAN]	6.52	5	2	2	3	1.000	3	0.000	9.449	368	40.752
B3KTY3	Cyclin D3, isoform CRA_c OS=Homo sapiens GN=CCND3 PE=2 SV=1 - [B3KTY3_HUMAN]	9.95	9	1	2	5	1.000	4	0.000	9.435	211	22.857
Q6BDS2	UHRF1-binding protein 1 OS=Homo sapiens GN=UHRF1BP1 PE=1 SV=1 - [URFB1_HUMAN]	1.88	3	2	2	4	1.000	4	19.065	9.433	1440	159.385
C9J7K9	Phospholipid scramblase 1 OS=Homo sapiens GN=PLSCR1 PE=1 SV=1 - [C9J7K9_HUMAN]	7.4	6	2	2	3	1.085	3	1.615	9.423	311	34.194
Q9UPU7	TBC1 domain family member 2B OS=Homo sapiens GN=TBC1D2B PE=1 SV=2 - [TBD2B_HUMAN]	3.63	3	2	2	3	1.000	2	0.000	9.418	963	109.812
Q8N1N4	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2 - [K2C78_HUMAN]	4.62	22	1	3	6	0.889	1		9.410	520	56.830
B3KM97	cDNA FLJ10554 fis, clone NT2RP2002385, highly similar to Synaptic glycoprotein SC2 OS=Homo sapiens PE=2 SV=1 - [B3KM97_HUMAN]	8.77	5	3	3	6	1.018	6	13.934	9.408	308	36.030
A0A087WY66	Dachshund homolog 1 OS=Homo sapiens GN=DACH1 PE=4 SV=1 - [A0A087WY66_HUMAN]	1.59	4	1	1	3	1.000	3	0.000	9.395	504	51.859
Q8NEZ4	Histone-lysine N-methyltransferase 2C OS=Homo sapiens GN=KMT2C PE=1 SV=3 - [KMT2C_HUMAN]	0.39	19	2	3	4	0.991	2	14.159	9.394	4911	541.029
B4DED6	cDNA FLJ56545, highly similar to ATP-dependent RNA helicase DDX50 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DED6_HUMAN]	3.58	7	2	2	3	1.000	3	10.332	9.394	643	72.113
Q0EFC6	HSR1 protein OS=Homo sapiens GN=HSR1 PE=4 SV=1 - [Q0EFC6_HUMAN]	5.87	10	3	3	4	1.001	4	0.203	9.379	545	62.097
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1 - [TIM13_HUMAN]	33.68	2	3	3	5	1.000	5	0.000	9.369	95	10.493
G5E9B5	TCF3 (E2A) fusion partner (In childhood Leukemia), isoform CRA_b OS=Homo sapiens GN=TFPT PE=1 SV=1 - [G5E9B5_HUMAN]	12.3	4	2	2	3	1.196	2	27.041	9.363	244	27.188
B3KMP2	cDNA FLJ11747 fis, clone HEMBA1005530, highly similar to Anaphase-promoting complex subunit 7 OS=Homo sapiens PE=2 SV=1 - [B3KMP2_HUMAN]	6.96	7	3	3	3	0.907	3	11.382	9.356	503	56.278
D6RFJ5	FYN-binding protein (Fragment) OS=Homo sapiens GN=FYB PE=1 SV=1 - [D6RFJ5_HUMAN]	7.47	4	1	1	3	1.000	3	0.000	9.352	174	18.474
E9AQ94	Putative 40S ribosomal protein S3 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0950 PE=3 SV=1 - [E9AQ94_LEIMU]	8.22	1	2	2	3	1.110	3	58.015	9.349	219	24.456
P20702	Integrin alpha-X OS=Homo sapiens GN=ITGAX PE=1 SV=3 - [ITAX_HUMAN]	2.32	5	2	3	4	1.160	3	17.601	9.338	1163	127.749
B4DLX5	Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens PE=2 SV=1 - [B4DLX5_HUMAN]	12.59	5	1	4	6	1.000	1		9.333	397	43.867
A0A087WW70	WAS/WASL-interacting protein family member 1 OS=Homo sapiens GN=WIPF1 PE=4 SV=1 - [A0A087WW70_HUMAN]	6.3	9	3	3	5	1.000	5	21.047	9.330	492	50.383
Q3T7B4	tRNA dimethylallyltransferase, mitochondrial OS=Homo sapiens GN=TRIT1 PE=1 SV=1 - [Q3T7B4_HUMAN]	21.18	7	2	2	3	1.315	3	33.818	9.328	85	9.782
Q6GMQ7	VPS16 protein OS=Homo sapiens GN=VPS16 PE=2 SV=1 - [Q6GMQ7_HUMAN]	6.11	5	3	3	4	0.885	4	8.387	9.325	524	59.179
B2RDP6	cDNA, FLJ96709, highly similar to Homo sapiens glutamate rich WD repeat protein GRWD (GRWD), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDP6_HUMAN]	11.66	5	3	3	5	1.209	4	9.160	9.322	446	49.358
B7Z6I6	cDNA FLJ54059, highly similar to Glycogen (starch) synthase, muscle (EC 2.4.1.11) OS=Homo sapiens PE=2 SV=1 - [B7Z6I6_HUMAN]	2.79	6	2	2	3	1.000	3	0.000	9.321	681	77.507
Q15070	Mitochondrial inner membrane protein OXA1L OS=Homo sapiens GN=OXA1L PE=1 SV=3 - [OXA1L_HUMAN]	7.36	6	3	3	6	1.053	6	13.534	9.320	435	48.517
E9AMI0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_1100 PE=4 SV=1 - [E9AMI0_LEIMU]	10.41	1	5	5	5	1.000	5	0.000	9.313	365	42.184
Q05BW9	PAPSS1 protein (Fragment) OS=Homo sapiens GN=PAPSS1 PE=2 SV=1 - [Q05BW9_HUMAN]	5.6	4	3	3	3	0.893	3	0.028	9.305	571	64.466
Q13884	Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3 - [SNTB1_HUMAN]	6.32	1	2	2	3	1.000	3	0.000	9.303	538	58.025
B7Z9D5	cDNA FLJ50387 OS=Homo sapiens PE=2 SV=1 - [B7Z9D5_HUMAN]	2.08	3	1	1	3	0.591	3	16.765	9.298	433	49.347
Q9BYD2	39S ribosomal protein L9, mitochondrial OS=Homo sapiens GN=MRPL9 PE=1 SV=2 - [RM09_HUMAN]	7.49	4	3	3	6	1.025	6	8.432	9.298	267	30.224
B3KUM4	cDNA FLJ40239 fis, clone TESTI2023436, highly similar to Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8) OS=Homo sapiens PE=2 SV=1 - [B3KUM4	24.14	4	3	3	3	1.103	3	17.094	9.296	145	16.120
E9APP0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0450 PE=4 SV=1 - [E9APP0_LEIMU]	9.01	4	2	4	4	1.960	2	105.833	9.279	322	36.469
Q10589	Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1 - [BST2_HUMAN]	10	2	2	2	3	1.151	3	2.395	9.274	180	19.756
A0A024R172	Leukotriene B4 12-hydroxydehydrogenase, isoform CRA_a OS=Homo sapiens GN=LTB4DH PE=4 SV=1 - [A0A024R172_HUMAN]	6.69	2	2	2	4	1.013	4	10.302	9.271	329	35.863
R4GMN1	Motile sperm domain-containing protein 2 OS=Homo sapiens GN=MOSPD2 PE=1 SV=1 - [R4GMN1_HUMAN]	10.29	3	5	5	5	1.000	4	9.862	9.270	486	55.644
B4E213	cDNA FLJ61051, highly similar to HpaII tinys locus 9c protein OS=Homo sapiens PE=2 SV=1 - [B4E213_HUMAN]	4.6	3	2	2	4	1.000	3	0.000	9.264	261	28.985
O95470	Sphingosine-1-phosphate lyase 1 OS=Homo sapiens GN=SGPL1 PE=1 SV=3 - [SGPL1_HUMAN]	3.35	3	2	2	3	2.150	3	0.769	9.253	568	63.483
P78362	SRSF protein kinase 2 OS=Homo sapiens GN=SRPK2 PE=1 SV=3 - [SRPK2_HUMAN]	3.49	10	1	3	4	0.668	2	276.254	9.238	688	77.478
A6NML8	Diaphanous homolog 2 (Drosophila), isoform CRA_c OS=Homo sapiens GN=DIAPH2 PE=1 SV=3 - [A6NML8_HUMAN]	3.1	16	3	4	4	0.949	3	7.839	9.220	1096	124.775
E9AXG9	Peptidyl-prolyl cis-trans isomerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0910 PE=3 SV=1 - [E9AXG9_LEIMU]	8.47	1	2	2	4	2.115	3	140.648	9.220	177	18.782
B7Z2P6	cDNA FLJ55296, highly similar to Homo sapiens WD repeat domain 42A (WDR42A), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z2P6_HUMAN]	8.66	10	2	5	5	1.184	2	25.447	9.217	751	84.726
Q5EBM0	UMP-CMP kinase 2, mitochondrial OS=Homo sapiens GN=CMPK2 PE=1 SV=3 - [CMPK2_HUMAN]	6.46	1	2	2	3	1.000	3	0.000	9.207	449	49.417
Q8IUI8	Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 PE=1 SV=2 - [CRLF3_HUMAN]	7.47	3	3	3	4	1.000	4	0.000	9.205	442	49.735
E9B701	Putative glycine cleavage system H protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4720 PE=3 SV=1 - [E9B701_LEIMU]	14.02	1	2	2	3	7.081	3	140.943	9.204	107	11.573
Q9ULC4	Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1 - [MCTS1_HUMAN]	9.94	1	2	2	3	0.911	3	10.099	9.201	181	20.542
Q15311	RalA-binding protein 1 OS=Homo sapiens GN=RALBP1 PE=1 SV=3 - [RBP1_HUMAN]	3.51	6	3	3	4	1.150	4	24.732	9.194	655	76.016
B3KVN4	cDNA FLJ16812 fis, clone THYMU3025865, highly similar to Zinc finger protein GFI-1 OS=Homo sapiens PE=2 SV=1 - [B3KVN4_HUMAN]	2.61	2	1	1	3	0.816	2	30.814	9.181	422	45.295
B2R514	cDNA, FLJ92300, Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kD) (COPS6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R514_HUMAN]	8.75	3	2	2	3	1.000	3	0.000	9.180	297	33.554
Q8IWR0	Zinc finger CCCH domain-containing protein 7A OS=Homo sapiens GN=ZC3H7A PE=1 SV=1 - [Z3H7A_HUMAN]	3.19	4	3	3	3	1.000	3	0.000	9.170	971	110.466
Q8N3C0	Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3 - [ASCC3_HUMAN]	2.32	1	3	4	4	1.363	3	56.476	9.159	2202	251.301
Q8N972	Zinc finger protein 709 OS=Homo sapiens GN=ZNF709 PE=2 SV=1 - [ZN709_HUMAN]	15.13	218	1	4	5	1.267	1		9.143	641	74.603
A8K6D4	cDNA FLJ77769, highly similar to Homo sapiens NAD kinase, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6D4_HUMAN]	6.05	3	2	2	5	1.000	4	0.000	9.142	446	49.220
I6L9C8	Zinc finger protein 428 OS=Homo sapiens GN=ZNF428 PE=2 SV=1 - [I6L9C8_HUMAN]	14.89	3	1	2	3	1.101	1		9.142	188	20.454
E9AS61	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1100 PE=4 SV=1 - [E9AS61_LEIMU]	1.6	1	1	2	4	1.045	1		9.139	1311	138.244
P42345	Serine/threonine-protein kinase mTOR OS=Homo sapiens GN=MTOR PE=1 SV=1 - [MTOR_HUMAN]	1.37	6	4	4	5	0.773	5	23.058	9.139	2549	288.707
A8K4A8	cDNA FLJ76156, highly similar to Homo sapiens aspartyl-tRNA synthetase 2 (DARS2), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4A8_HUMAN]	3.41	5	2	3	4	0.732	2	26.792	9.128	645	73.528
Q9H2L5	Ras association domain-containing protein 4 OS=Homo sapiens GN=RASSF4 PE=1 SV=2 - [RASF4_HUMAN]	10.28	5	2	3	4	1.000	3	86.702	9.127	321	36.725
Q9NXH8	Torsin-4A OS=Homo sapiens GN=TOR4A PE=1 SV=2 - [TOR4A_HUMAN]	8.04	2	3	4	4	0.722	3	13.353	9.126	423	46.885
O43513	Mediator of RNA polymerase II transcription subunit 7 OS=Homo sapiens GN=MED7 PE=1 SV=1 - [MED7_HUMAN]	9.44	1	2	2	2	1.000	2	0.000	9.119	233	27.228
Q5JX58	Copine-1 (Fragment) OS=Homo sapiens GN=CPNE1 PE=1 SV=3 - [Q5JX58_HUMAN]	13.86	19	3	3	3	0.943	3	7.002	9.112	202	22.663
C9J7P5	Protein TBRG4 (Fragment) OS=Homo sapiens GN=TBRG4 PE=1 SV=1 - [C9J7P5_HUMAN]	7.26	9	2	2	3	0.774	3	2.443	9.108	248	28.362
P30414	NK-tumor recognition protein OS=Homo sapiens GN=NKTR PE=1 SV=2 - [NKTR_HUMAN]	2.46	3	4	4	5	1.000	5	0.000	9.106	1462	165.577
B7Z4Y0	cDNA FLJ52711, highly similar to Homo sapiens thioredoxin domain containing 14 (TXNDC14), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z4Y0_HUMAN]	26.24	3	5	5	6	1.104	6	12.614	9.104	202	23.331
Q9NPA8	Transcription and mRNA export factor ENY2 OS=Homo sapiens GN=ENY2 PE=1 SV=1 - [ENY2_HUMAN]	14.85	6	2	2	4	0.976	4	11.951	9.100	101	11.521
I3L0N7	Serine/arginine repetitive matrix protein 2 (Fragment) OS=Homo sapiens GN=SRRM2 PE=1 SV=1 - [I3L0N7_HUMAN]	26.96	4	1	4	5	1.000	1		9.099	115	13.372
Q53R16	Putative uncharacterized protein KIAA0053 (Fragment) OS=Homo sapiens GN=KIAA0053 PE=4 SV=1 - [Q53R16_HUMAN]	11.47	8	5	5	5	1.095	4	53.184	9.097	558	63.012
E9ALU9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1240 PE=4 SV=1 - [E9ALU9_LEIMU]	4.41	2	3	4	4	1.000	3	0.000	9.081	725	79.643
H0YHS6	Tyrosine--tRNA ligase, mitochondrial (Fragment) OS=Homo sapiens GN=YARS2 PE=1 SV=1 - [H0YHS6_HUMAN]	5.84	2	2	2	4	1.070	4	10.038	9.076	291	32.165
O75376	Nuclear receptor corepressor 1 OS=Homo sapiens GN=NCOR1 PE=1 SV=2 - [NCOR1_HUMAN]	2.05	24	4	5	5	0.967	4	8.687	9.067	2440	270.044
B4DHJ9	cDNA FLJ61262, highly similar to Ubiquitin-protein ligase E3C (EC 6.3.2.-) OS=Homo sapiens PE=2 SV=1 - [B4DHJ9_HUMAN]	2.46	2	2	2	4	1.051	4	7.388	9.066	936	106.456
M0R1L7	Charged multivesicular body protein 2a (Fragment) OS=Homo sapiens GN=CHMP2A PE=1 SV=1 - [M0R1L7_HUMAN]	20.13	8	3	4	8	1.000	6	14.241	9.066	159	18.727
Q9NZ45	CDGSH iron-sulfur domain-containing protein 1 OS=Homo sapiens GN=CISD1 PE=1 SV=1 - [CISD1_HUMAN]	24.07	1	2	2	5	1.000	5	4.272	9.064	108	12.191
Q9BZ95	Histone-lysine N-methyltransferase NSD3 OS=Homo sapiens GN=WHSC1L1 PE=1 SV=1 - [NSD3_HUMAN]	1.39	2	2	2	5	1.000	5	1.332	9.045	1437	161.509
B4DGL1	cDNA FLJ59001, highly similar to CpG-binding protein OS=Homo sapiens PE=2 SV=1 - [B4DGL1_HUMAN]	9.13	7	2	2	5	0.999	4	0.099	9.038	219	24.275
Q8TEH6	FLJ00221 protein (Fragment) OS=Homo sapiens GN=FLJ00221 PE=2 SV=1 - [Q8TEH6_HUMAN]	8.39	4	3	3	5	0.894	3	2.952	9.028	298	33.148
Q59GH5	COP9 signalosome subunit 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GH5_HUMAN]	6.88	3	2	2	4	0.850	4	4.660	9.023	276	31.239
Q7KZA3	Ferrochelatase OS=Homo sapiens GN=DKFZp686P18130 PE=2 SV=1 - [Q7KZA3_HUMAN]	6.25	9	3	3	4	1.052	4	29.195	9.002	416	47.102
Q9UHB7	AF4/FMR2 family member 4 OS=Homo sapiens GN=AFF4 PE=1 SV=1 - [AFF4_HUMAN]	2.75	2	3	3	5	1.000	5	10.310	9.002	1163	127.382
B4DVF9	cDNA FLJ54388, highly similar to Tax1-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DVF9_HUMAN]	4.73	5	4	4	4	0.986	4	2.107	9.001	697	80.549
Q9UL26	Ras-related protein Rab-22A OS=Homo sapiens GN=RAB22A PE=1 SV=2 - [RB22A_HUMAN]	12.89	2	1	2	4	0.925	2	11.517	9.000	194	21.841
Q7Z773	2-hydroxyacyl-CoA lyase 1 OS=Homo sapiens GN=HACL1 PE=1 SV=1 - [Q7Z773_HUMAN]	7.56	7	1	1	3	1.091	3	17.948	8.997	119	12.491
Q9NQ81	Uridine diphospho-glucose dehydrogenase (Fragment) OS=Homo sapiens GN=GDH PE=4 SV=1 - [Q9NQ81_HUMAN]	12.2	5	2	2	3	0.854	3	36.731	8.995	164	17.826
A8MWD9	Putative small nuclear ribonucleoprotein G-like protein 15 OS=Homo sapiens GN=SNRPGP15 PE=5 SV=2 - [RUXGL_HUMAN]	25	5	2	2	7	0.993	7	8.333	8.994	76	8.538
B7ZMD6	IRGQ protein OS=Homo sapiens GN=IRGQ PE=2 SV=1 - [B7ZMD6_HUMAN]	6.1	3	3	3	3	0.753	2	21.318	8.992	623	62.635
Q96JB2	Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3 - [COG3_HUMAN]	3.38	3	3	3	3	1.000	3	8.443	8.992	828	94.036
Q53TK7	Acylphosphatase (Fragment) OS=Homo sapiens GN=ACYP2 PE=3 SV=1 - [Q53TK7_HUMAN]	34.43	7	2	2	3	1.193	3	17.926	8.988	61	6.695
Q9NVV4	Poly(A) RNA polymerase, mitochondrial OS=Homo sapiens GN=MTPAP PE=1 SV=1 - [PAPD1_HUMAN]	5.67	2	3	3	3	0.802	3	29.652	8.982	582	66.130
Q96J73	NNP3 OS=Homo sapiens PE=2 SV=1 - [Q96J73_HUMAN]	12.8	5	4	4	4	0.972	4	4.157	8.977	328	36.995
B7Z3E4	cDNA FLJ50538, highly similar to Retinoic acid receptor RXR-beta OS=Homo sapiens PE=2 SV=1 - [B7Z3E4_HUMAN]	16.08	7	2	3	3	1.000	2	0.000	8.972	286	30.076
Q14004	Cyclin-dependent kinase 13 OS=Homo sapiens GN=CDK13 PE=1 SV=2 - [CDK13_HUMAN]	3.31	44	1	5	6	0.847	1		8.958	1512	164.823
H7BZ52	Zinc finger SWIM domain-containing protein 8 OS=Homo sapiens GN=ZSWIM8 PE=1 SV=2 - [H7BZ52_HUMAN]	1.65	5	2	2	3	1.000	2	0.000	8.954	1336	143.793
Q6P3W7	SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1 - [SCYL2_HUMAN]	0.75	1	1	1	3	1.000	3	2.134	8.948	929	103.642
A7E2C0	CASP8AP2 protein OS=Homo sapiens GN=CASP8AP2 PE=2 SV=1 - [A7E2C0_HUMAN]	2.07	3	3	3	3	0.916	2	13.124	8.941	1981	222.383
A4FVC0	Protein argonaute (Fragment) OS=Homo sapiens GN=EIF2C2 PE=2 SV=1 - [A4FVC0_HUMAN]	5.45	2	3	4	4	1.000	3	0.000	8.938	808	91.438
B4E1P2	cDNA FLJ59223, highly similar to C-Rel proto-oncogene protein OS=Homo sapiens PE=2 SV=1 - [B4E1P2_HUMAN]	4.77	2	2	2	4	1.000	4	0.000	8.933	587	65.118
Q15172	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform OS=Homo sapiens GN=PPP2R5A PE=1 SV=1 - [2A5A_HUMAN]	2.88	13	1	2	7	1.273	1		8.930	486	56.158
E9B6Q4	Putative 60S ribosomal protein L27A/L29 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3760 PE=3 SV=1 - [E9B6Q4_LEIMU]	11.72	1	1	2	10	1.000	1		8.921	145	16.059
Q5T7U1	General transcription factor 3C polypeptide 5 OS=Homo sapiens GN=GTF3C5 PE=1 SV=1 - [Q5T7U1_HUMAN]	4.81	5	2	2	3	1.000	3	0.000	8.908	457	52.257
F8VV32	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [F8VV32_HUMAN]	8.65	2	1	1	3	1.000	3	10.390	8.900	104	11.481
B0I1S1	DNAH10 variant protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [B0I1S1_HUMAN]	0.45	2	2	2	4	1.000	3	0.000	8.889	3319	380.551
Q59HA2	Ariadne homolog 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59HA2_HUMAN]	9.43	4	3	3	3	1.000	3	0.000	8.888	318	37.987
Q7Z3K3	Pogo transposable element with ZNF domain OS=Homo sapiens GN=POGZ PE=1 SV=2 - [POGZ_HUMAN]	3.33	6	2	3	3	1.287	2	14.718	8.883	1410	155.245
B0FTY2	NudC-like protein OS=Homo sapiens PE=2 SV=1 - [B0FTY2_HUMAN]	5.82	16	3	3	4	0.937	4	34.083	8.881	361	40.754
J3QQU0	Protein IMPACT (Fragment) OS=Homo sapiens GN=IMPACT PE=1 SV=1 - [J3QQU0_HUMAN]	10.38	3	1	1	2	1.205	2	0.065	8.880	106	11.819
K7EJ61	Uncharacterized protein KIAA1328 OS=Homo sapiens GN=KIAA1328 PE=1 SV=1 - [K7EJ61_HUMAN]	11.66	7	1	2	4				8.869	163	18.403
B2R7F8	cDNA, FLJ93426, highly similar to Homo sapiens plasminogen (PLG), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7F8_HUMAN]	4.32	14	4	4	7	1.316	4	12.999	8.868	810	90.480
G5E9R5	Acid phosphatase 1, soluble, isoform CRA_d OS=Homo sapiens GN=ACP1 PE=1 SV=1 - [G5E9R5_HUMAN]	22.5	3	1	1	2	1.000	2	0.000	8.867	80	8.965
C9JE56	WD repeat-containing protein 76 (Fragment) OS=Homo sapiens GN=WDR76 PE=4 SV=1 - [C9JE56_HUMAN]	3.95	2	1	1	3	1.000	3	0.000	8.859	228	25.202
H7C5E4	5'-3' exoribonuclease 1 (Fragment) OS=Homo sapiens GN=XRN1 PE=1 SV=1 - [H7C5E4_HUMAN]	2.76	3	2	2	3	1.033	2	4.861	8.850	1160	130.107
B4E046	cDNA FLJ52911, highly similar to Max-like protein X OS=Homo sapiens PE=2 SV=1 - [B4E046_HUMAN]	9.26	2	1	1	3	1.000	3	0.000	8.844	162	18.730
E9AXQ9	Putative 3-oxo-5-alpha-steroid 4-dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1770 PE=4 SV=1 - [E9AXQ9_LEIMU]	11.11	1	3	3	4	2.704	4	209.220	8.835	306	34.114
Q9UKK6	NTF2-related export protein 1 OS=Homo sapiens GN=NXT1 PE=1 SV=1 - [NXT1_HUMAN]	10.71	2	2	2	4	0.908	4	21.666	8.834	140	15.837
E9B001	Putative replication factor A, 51kDa subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1820 PE=4 SV=1 - [E9B001_LEIMU]	5.78	1	2	2	3	1.217	2	29.734	8.831	467	52.353
E9AMV3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_1010 PE=4 SV=1 - [E9AMV3_LEIMU]	1.46	1	1	1	3	1.000	3	0.000	8.831	616	67.348
B2RA34	cDNA, FLJ94678, highly similar to Homo sapiens BCL2-associated athanogene 4 (BAG4), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RA34_HUMAN]	5.25	3	2	2	4	0.689	4	59.590	8.825	457	49.573
Q59FI6	Calcium/calmodulin-dependent protein kinase II gamma isoform 6 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FI6_HUMAN]	14.19	14	1	2	4	1.000	1		8.820	155	16.750
E9B2V9	Superoxide dismutase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_1820 PE=3 SV=1 - [E9B2V9_LEIMU]	15.38	3	3	3	5	1.000	3	0.000	8.819	195	21.709
B3KN49	cDNA FLJ13562 fis, clone PLACE1008080, highly similar to Homo sapiens hexamethylene bis-acetamide inducible 1 (HEXIM1), mRNA OS=Homo sapiens PE=2 SV=1 -	10.03	3	4	4	5	1.000	5	15.588	8.817	359	40.582
Q9H993	UPF0364 protein C6orf211 OS=Homo sapiens GN=C6orf211 PE=1 SV=1 - [CF211_HUMAN]	2.49	1	2	2	3	1.070	3	10.077	8.814	441	51.140
Q8TDX6	Chondroitin sulfate N-acetylgalactosaminyltransferase 1 OS=Homo sapiens GN=CSGALNACT1 PE=1 SV=2 - [CGAT1_HUMAN]	2.44	7	1	2	4	1.268	1		8.810	532	61.255
X5D7P8	Serine threonine kinase 39 isoform D (Fragment) OS=Homo sapiens GN=STK39 PE=2 SV=1 - [X5D7P8_HUMAN]	6.74	7	2	3	3	0.947	2	8.100	8.797	475	52.233
B4DFP7	Transcription termination factor 4, mitochondrial OS=Homo sapiens GN=MTERF4 PE=1 SV=1 - [B4DFP7_HUMAN]	11.92	6	2	2	3	1.000	3	0.000	8.792	193	22.746
K7EN04	Coiled-coil domain-containing protein 68 (Fragment) OS=Homo sapiens GN=CCDC68 PE=4 SV=1 - [K7EN04_HUMAN]	4.93	2	1	1	6	1.000	6	0.000	8.791	203	23.865
Q8IXG0	Crn protein OS=Homo sapiens GN=crn PE=2 SV=1 - [Q8IXG0_HUMAN]	7.71	4	5	5	6	1.000	6	10.476	8.789	687	83.087
D3DPG0	Titin, isoform CRA_a OS=Homo sapiens GN=TTN PE=4 SV=1 - [D3DPG0_HUMAN]	0.16	14	4	6	6	0.924	4	13.058	8.788	34942	3878.844

Q9BUP3	Oxidoreductase HTATIP2 OS=Homo sapiens GN=HTATIP2 PE=1 SV=2 - [HTAI2_HUMAN]	10.74	1	1	3	4	1.079	2	14.267	8.785	242	27.032
E9B361	Proteasome regulatory non-ATP-ase subunit,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2820 PE=4 SV=1 - [E9B361_LEIMU]	4.41	1	2	2	3	1.000	3	0.000	8.785	408	46.270
H0YKH0	Lipopolysaccharide-induced tumor necrosis factor-alpha factor OS=Homo sapiens GN=LITAF PE=4 SV=1 - [H0YKH0_HUMAN]	5.84	12	3	3	4	0.724	4	60.658	8.775	445	47.732
Q6PK69	CCDC25 protein (Fragment) OS=Homo sapiens GN=CCDC25 PE=2 SV=1 - [Q6PK69_HUMAN]	27.62	3	3	3	3	0.973	3	0.112	8.774	105	12.289
Q96P11	Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens GN=NSUN5 PE=1 SV=2 - [NSUN5_HUMAN]	2.56	2	1	1	3	0.886	3	18.017	8.772	429	46.662
E7ESG2	Claspin OS=Homo sapiens GN=CLSPN PE=1 SV=1 - [E7ESG2_HUMAN]	1.24	4	2	2	3	1.000	3	79.893	8.768	1286	145.228
I3L1M4	Fatty aldehyde dehydrogenase (Fragment) OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [I3L1M4_HUMAN]	12.35	6	2	2	3	0.937	3	0.752	8.764	162	18.471
Q9Y217	Myotubularin-related protein 6 OS=Homo sapiens GN=MTMR6 PE=1 SV=3 - [MTMR6_HUMAN]	3.7	3	2	2	3	1.000	3	0.000	8.754	621	71.922
Q9Y508	E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 - [RN114_HUMAN]	14.47	3	3	3	5	0.855	5	13.340	8.746	228	25.677
F8WF15	Ubiquitin-conjugating enzyme E2 E2 OS=Homo sapiens GN=UBE2E2 PE=1 SV=1 - [F8WF15_HUMAN]	29.21	4	2	2	3	1.000	3	0.000	8.736	89	9.697
Q32P44	Echinoderm microtubule-associated protein-like 3 OS=Homo sapiens GN=EML3 PE=1 SV=1 - [EMAL3_HUMAN]	3.46	9	3	3	3	1.000	3	51.898	8.732	896	95.138
Q9H3U5	Major facilitator superfamily domain-containing protein 1 OS=Homo sapiens GN=MFSD1 PE=2 SV=2 - [MFSD1_HUMAN]	3.66	1	2	2	3	1.183	3	25.307	8.730	465	51.174
B2R4C9	cDNA, FLJ92044, highly similar to Homo sapiens death-associated protein (DAP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R4C9_HUMAN]	15.69	3	2	2	5	0.933	5	10.275	8.727	102	11.177
A0A024RBQ5	2'-5'-oligoadenylate synthetase 3, 100kDa, isoform CRA_a OS=Homo sapiens GN=OAS3 PE=4 SV=1 - [A0A024RBQ5_HUMAN]	2.58	5	3	3	4	0.971	4	28.507	8.722	1087	121.095
Q9C010	cAMP-dependent protein kinase inhibitor beta OS=Homo sapiens GN=PKIB PE=2 SV=1 - [IPKB_HUMAN]	26.92	2	1	2	4	1.000	2	0.000	8.719	78	8.463
B4DSX6	cDNA FLJ57427, highly similar to Glycogenin-1 (EC 2.4.1.186) OS=Homo sapiens PE=2 SV=1 - [B4DSX6_HUMAN]	10.36	8	2	2	3	1.104	3	2.321	8.718	193	21.466
A0A024R3R7	HEAT repeat containing 1, isoform CRA_b OS=Homo sapiens GN=HEATR1 PE=4 SV=1 - [A0A024R3R7_HUMAN]	1.13	10	2	2	3	1.000	3	0.000	8.716	2036	230.399
H6UKR8	TOX2 variant 5 OS=Homo sapiens PE=2 SV=1 - [H6UKR8_HUMAN]	4.57	7	1	2	4	1.000	2	0.000	8.708	350	37.472
B4E265	cDNA FLJ61059, highly similar to Homo sapiens SMC5 structural maintenance of chromosomes 5-like 1 (SMC5L1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4E265_HU	3.16	13	2	3	4	1.000	2	0.000	8.701	729	85.451
A8K3B8	cDNA FLJ77684 OS=Homo sapiens PE=2 SV=1 - [A8K3B8_HUMAN]	6.31	3	2	2	3	1.000	2	0.000	8.700	444	50.360
E9PHV5	Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2 PE=1 SV=1 - [E9PHV5_HUMAN]	1.86	5	2	2	3	1.000	3	0.000	8.691	1237	136.054
O75569	Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=1 SV=1 - [PRKRA_HUMAN]	9.9	5	3	3	4	1.273	4	36.974	8.686	313	34.383
O43598	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 OS=Homo sapiens GN=DNPH1 PE=1 SV=1 - [DNPH1_HUMAN]	8.62	2	2	2	4	1.000	4	0.000	8.685	174	19.097
B7Z2F5	cDNA FLJ55918, highly similar to Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens PE=2 SV=1 - [B7Z2F5_HUMAN]	6.44	1	1	2	4				8.679	807	87.184
B8ZZZ7	DNA polymerase-transactivated protein 6, isoform CRA_b OS=Homo sapiens GN=SPATS2L PE=1 SV=1 - [B8ZZZ7_HUMAN]	8.43	3	4	4	4	1.078	4	10.463	8.675	498	54.911
E9AWG1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1410 PE=4 SV=1 - [E9AWG1_LEIMU]	14.57	1	3	3	3	1.000	3	0.000	8.671	247	27.285
B2RDW9	cDNA, FLJ96803, highly similar to Homo sapiens GTP binding protein 1 (GTPBP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDW9_HUMAN]	3.6	5	2	2	4	0.902	4	3.765	8.669	584	63.438
Q86UL3	Glycerol-3-phosphate acyltransferase 4 OS=Homo sapiens GN=AGPAT6 PE=1 SV=1 - [GPAT4_HUMAN]	6.58	4	3	3	4	0.919	4	18.154	8.668	456	52.037
B3KSS4	cDNA FLJ36858 fis, clone ASTRO2015185, highly similar to POLIOVIRUS RECEPTOR OS=Homo sapiens PE=2 SV=1 - [B3KSS4_HUMAN]	3.87	3	1	1	4	1.000	2	0.000	8.668	362	39.555
Q6LEE1	4a-carbinolamine dehydratase (Fragment) OS=Homo sapiens PE=4 SV=1 - [Q6LEE1_HUMAN]	25.93	5	1	1	4	0.915	4	6.735	8.662	27	3.248
B4DIG4	cDNA FLJ57115, highly similar to 39S ribosomal protein L19, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B4DIG4_HUMAN]	8.76	5	2	2	4	0.823	4	21.005	8.644	194	22.781
C9J0I9	Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 - [C9J0I9_HUMAN]	6.75	3	2	2	4	1.000	3	0.000	8.641	459	50.530
E9PI87	Oxidoreductase HTATIP2 OS=Homo sapiens GN=HTATIP2 PE=1 SV=1 - [E9PI87_HUMAN]	13.78	1	1	3	4	0.926	2	24.582	8.641	196	21.962
Q9NPJ3	Acyl-coenzyme A thioesterase 13 OS=Homo sapiens GN=ACOT13 PE=1 SV=1 - [ACO13_HUMAN]	7.14	1	1	1	3	1.129	3	14.298	8.631	140	14.951
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens GN=UBE2V1 PE=1 SV=2 - [UB2V1_HUMAN]	17.69	5	2	3	4	0.925	3	13.493	8.630	147	16.484
H3BVG8	UPF0505 protein C16orf62 OS=Homo sapiens GN=C16orf62 PE=1 SV=2 - [H3BVG8_HUMAN]	5.76	11	3	3	4	1.000	4	5.434	8.622	451	50.572
Q8TCG1	Protein CIP2A OS=Homo sapiens GN=KIAA1524 PE=1 SV=2 - [CIP2A_HUMAN]	4.31	2	5	5	5	1.000	5	7.628	8.621	905	102.121
Q05DA4	P4HA2 protein OS=Homo sapiens GN=P4HA2 PE=2 SV=1 - [Q05DA4_HUMAN]	6.15	3	3	3	3	0.940	3	9.166	8.621	504	57.342
O00425	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2 - [IF2B3_HUMAN]	5.53	1	3	3	3	0.945	2	8.421	8.611	579	63.666
Q9BRG1	Vacuolar protein-sorting-associated protein 25 OS=Homo sapiens GN=VPS25 PE=1 SV=1 - [VPS25_HUMAN]	15.34	3	3	3	4	1.004	4	11.432	8.611	176	20.735
P28289	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1 - [TMOD1_HUMAN]	4.18	1	1	2	4	0.970	1		8.611	359	40.544
Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	8.91	2	3	3	3	1.286	3	27.709	8.609	303	32.524
P30043	Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	11.65	3	2	2	3	1.165	3	1.496	8.600	206	22.105
C9J6S2	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1 - [C9J6S2_HUMAN]	16.85	4	2	2	4	1.113	4	2.458	8.596	89	9.962
Q8ND04	Protein SMG8 OS=Homo sapiens GN=SMG8 PE=1 SV=1 - [SMG8_HUMAN]	5.95	2	4	4	5	1.000	3	0.000	8.596	991	109.614
B2RB94	cDNA, FLJ95380, highly similar to Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B2RB94_HUM	2.22	5	2	2	4	1.000	4	0.000	8.587	854	98.485
E9ALM8	Putative fumarate hydratase (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1960 PE=4 SV=1 - [E9ALM8_LEIMU]	5.48	1	1	1	3	1.000	3	0.000	8.584	219	24.501
E9AQ74	ABC1 transporter-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0760 PE=3 SV=1 - [E9AQ74_LEIMU]	0.56	1	2	2	7	1.000	7	0.000	8.578	2679	291.301
D3DVF0	F11 receptor, isoform CRA_a OS=Homo sapiens GN=F11R PE=4 SV=1 - [D3DVF0_HUMAN]	8.11	4	3	3	4	1.028	4	26.242	8.571	296	32.207
P49903	Selenide, water dikinase 1 OS=Homo sapiens GN=SEPHS1 PE=1 SV=2 - [SPS1_HUMAN]	6.63	6	2	3	4	0.887	3	22.013	8.559	392	42.883
K7EQV7	Zinc finger protein 700 OS=Homo sapiens GN=ZNF700 PE=4 SV=1 - [K7EQV7_HUMAN]	14.23	131	1	3	3	0.835	1		8.551	724	84.203
E9AXT3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_2010 PE=4 SV=1 - [E9AXT3_LEIMU]	8.24	1	2	2	3	3.571	3	15.324	8.549	279	30.322
B2RD00	cDNA, FLJ96396, highly similar to Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RD00_HUMAN]	4.71	4	1	2	3	1.025	1		8.542	467	53.485
A0A087WVF1	Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=4 SV=1 - [A0A087WVF1_HUMAN]	10.91	4	2	2	3	1.000	2	0.000	8.541	275	29.628
C9JTD3	StAR-related lipid transfer protein 7, mitochondrial (Fragment) OS=Homo sapiens GN=STARD7 PE=1 SV=1 - [C9JTD3_HUMAN]	10.2	4	2	2	3	1.000	3	0.000	8.534	147	17.786
E9AJY2	Elongation initiation factor 2 alpha subunit,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_03_0980 PE=4 SV=1 - [E9AJY2_LEIMU]	4.36	5	1	2	4	1.306	1		8.533	413	46.594
O60502	Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=1 SV=2 - [NCOAT_HUMAN]	3.49	4	3	3	3	1.017	3	6.103	8.502	916	102.849
Q96DZ1	Endoplasmic reticulum lectin 1 OS=Homo sapiens GN=ERLEC1 PE=1 SV=1 - [ERLEC_HUMAN]	12.22	1	5	5	5	1.044	5	6.348	8.500	483	54.823
Q08AM6	Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=1 SV=1 - [VAC14_HUMAN]	4.73	4	4	4	4	0.974	4	9.477	8.498	782	87.917
Q5T160	Probable arginine--tRNA ligase, mitochondrial OS=Homo sapiens GN=RARS2 PE=1 SV=1 - [SYRM_HUMAN]	7.44	3	4	4	5	0.957	5	15.016	8.495	578	65.464
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1 OS=Homo sapiens GN=PTRHD1 PE=1 SV=1 - [PTRD1_HUMAN]	22.14	1	3	3	3	1.084	3	23.492	8.491	140	15.795
E9AW04	Peroxidoxin (Tryparedoxin peroxidase) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0040 PE=4 SV=1 - [E9AW04_LEIMU]	6.64	1	2	2	4	2.210	4	102.311	8.490	226	25.357
Q9NWQ8	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1 OS=Homo sapiens GN=PAG1 PE=1 SV=2 - [PHAG1_HUMAN]	6.71	1	2	2	3	1.000	3	0.000	8.487	432	46.951
C9J1C6	E3 ubiquitin-protein ligase RNF181 OS=Homo sapiens GN=RNF181 PE=4 SV=1 - [C9J1C6_HUMAN]	16.55	2	2	2	3	1.000	3	0.000	8.475	139	16.021
P56377	AP-1 complex subunit sigma-2 OS=Homo sapiens GN=AP1S2 PE=1 SV=1 - [AP1S2_HUMAN]	10.19	2	1	1	2	1.009	2	3.497	8.472	157	18.603
E9B1E9	Putative 5-methyltetrahydropteroyltriglutamate--homocyst ei nemethyltransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_0010 PE=3 S	2.86	1	2	2	4	1.000	4	21.506	8.471	770	86.053
Q9H7E9	UPF0488 protein C8orf33 OS=Homo sapiens GN=C8orf33 PE=1 SV=1 - [CH033_HUMAN]	6.99	1	1	1	2	0.913	2	2.232	8.469	229	24.977
Q13233	Mitogen-activated protein kinase kinase kinase 1 OS=Homo sapiens GN=MAP3K1 PE=1 SV=4 - [M3K1_HUMAN]	3.11	1	3	3	3	1.000	3	0.000	8.445	1512	164.366
P98172	Ephrin-B1 OS=Homo sapiens GN=EFNB1 PE=1 SV=1 - [EFNB1_HUMAN]	2.02	1	1	1	4	1.052	4	10.519	8.444	346	37.982
E9AVY4	Putative 40S ribosomal protein L14 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_1520 PE=4 SV=1 - [E9AVY4_LEIMU]	20	1	4	4	5	1.000	5	0.000	8.443	175	19.973
Q86SX6	Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 - [GLRX5_HUMAN]	8.92	1	1	1	3	1.000	3	0.000	8.435	157	16.618
Q7Z2Z2	Elongation factor Tu GTP-binding domain-containing protein 1 OS=Homo sapiens GN=EFTUD1 PE=1 SV=2 - [ETUD1_HUMAN]	4.2	3	3	3	3	0.847	3	25.024	8.429	1120	125.350
Q9NQS1	Cell death regulator Aven OS=Homo sapiens GN=AVEN PE=1 SV=1 - [AVEN_HUMAN]	8.56	1	3	3	4	1.000	3	0.000	8.419	362	38.483
P23258	Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2 - [TBG1_HUMAN]	2.22	1	1	1	4	1.000	4	0.000	8.418	451	51.138
B2R6K2	cDNA, FLJ92993, highly similar to Homo sapiens F-box and leucine-rich repeat protein 20 (FBXL20), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6K2_HUMAN]	4.13	7	2	2	3	0.895	3	12.507	8.417	436	48.320
H3BN64	Abscission/NoCut checkpoint regulator (Fragment) OS=Homo sapiens GN=ZFYVE19 PE=1 SV=1 - [H3BN64_HUMAN]	9.96	5	2	3	4	1.000	3	0.000	8.406	271	29.679
B2R8X4	cDNA, FLJ94105, highly similar to Homo sapiens GA binding protein transcription factor, alpha subunit 60kDa (GABPA), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8X4	5.95	4	3	3	4	0.964	4	11.609	8.405	454	51.235
B4DQI6	Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=1 SV=1 - [B4DQI6_HUMAN]	16.11	2	3	4	4	1.166	3	4.056	8.402	180	20.577
A8K8E1	TBC1 domain family, member 15, isoform CRA_d OS=Homo sapiens GN=TBC1D15 PE=2 SV=1 - [A8K8E1_HUMAN]	4.94	3	2	2	3	1.071	3	10.207	8.400	445	51.628
E9ALG1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2630 PE=4 SV=1 - [E9ALG1_LEIMU]	4.13	1	2	3	3	1.000	2	0.000	8.385	1236	132.360
B4DIA5	cDNA FLJ59531, highly similar to Transcription factor E3 OS=Homo sapiens PE=2 SV=1 - [B4DIA5_HUMAN]	4.89	10	1	3	4	0.945	1		8.379	470	50.599
H0YJJ8	Translation initiation factor eIF-2B subunit beta (Fragment) OS=Homo sapiens GN=EIF2B2 PE=1 SV=1 - [H0YJJ8_HUMAN]	8	4	1	1	3	1.392	2	31.741	8.358	200	22.616
H3BRE8	RNA polymerase II-associated protein 1 OS=Homo sapiens GN=RPAP1 PE=1 SV=1 - [H3BRE8_HUMAN]	1.6	3	1	1	2	1.000	2	0.000	8.349	1128	122.991
Q96PY5	Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=1 SV=3 - [FMNL2_HUMAN]	2.76	10	2	4	6	1.000	3	0.000	8.348	1086	123.243
E9AP56	Putative small Rab GTP binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0220 PE=3 SV=1 - [E9AP56_LEIMU]	6.16	1	1	1	3				8.339	211	22.924
Q9NXE4	Sphingomyelin phosphodiesterase 4 OS=Homo sapiens GN=SMPD4 PE=1 SV=2 - [NSMA3_HUMAN]	3.02	14	3	3	4	1.000	4	17.272	8.337	827	93.292
Q9P0H6	AD-012 protein OS=Homo sapiens PE=2 SV=1 - [Q9P0H6_HUMAN]	3.6	3	1	2	3	2.424	1		8.328	583	60.668
Q8IYS2	Uncharacterized protein KIAA2013 OS=Homo sapiens GN=KIAA2013 PE=2 SV=1 - [K2013_HUMAN]	4.1	2	2	2	3	0.965	2	46.227	8.314	634	69.113
E9ALU2	Putative carnitine/choline acetyltransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1310 PE=3 SV=1 - [E9ALU2_LEIMU]	3.67	1	2	2	3	0.793	3	3.052	8.313	627	68.534
A0PJK4	NUP43 protein (Fragment) OS=Homo sapiens GN=NUP43 PE=2 SV=1 - [A0PJK4_HUMAN]	8.36	4	2	2	3	0.422	3	38.394	8.311	287	31.594
X6RA14	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=1 - [X6RA14_HUMAN]	6.72	4	2	2	5	1.103	5	25.145	8.311	253	28.208
A8MZH8	Pituitary tumor-transforming gene 1 protein-interacting protein OS=Homo sapiens GN=PTTG1IP PE=4 SV=1 - [A8MZH8_HUMAN]	13.08	6	2	2	3	1.037	3	2.688	8.310	107	11.591
Q6XYC5	LP6054 OS=Homo sapiens GN=RP3-402G11.12 PE=2 SV=1 - [Q6XYC5_HUMAN]	4.11	3	1	1	3	0.931	3	7.086	8.303	292	33.160
E9B617	Mitochondrial processing peptidase, beta subunit,putative,metallo-peptidase, Clan ME, Family M16 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM	5.92	1	3	3	4	1.220	4	48.284	8.296	490	54.607
E9AMR8	Putative prefoldin subunit 2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0670 PE=4 SV=1 - [E9AMR8_LEIMU]	14.49	1	1	1	2	1.000	2	0.000	8.277	138	15.357
E9AXP1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1610 PE=4 SV=1 - [E9AXP1_LEIMU]	6.75	1	2	2	3	1.000	3	0.000	8.274	326	36.737
O94915	Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=1 SV=2 - [FRYL_HUMAN]	1	9	2	3	3	1.000	2	0.000	8.268	3013	339.383
A0A087WWP8	Round spermatid basic protein 1 OS=Homo sapiens GN=RSBN1 PE=4 SV=1 - [A0A087WWP8_HUMAN]	3.58	2	2	2	3	1.054	3	31.278	8.264	754	84.923
Q14011	Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=1 SV=1 - [CIRBP_HUMAN]	11.63	6	2	2	3	0.866	3	17.209	8.264	172	18.637
I6L976	Chromosome 6 open reading frame 57 OS=Homo sapiens GN=C6orf57 PE=2 SV=1 - [I6L976_HUMAN]	17.59	2	2	2	3	1.000	3	11.725	8.263	108	12.208
Q8NHP8	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2 - [PLBL2_HUMAN]	1.53	1	1	1	3	1.078	3	11.239	8.250	589	65.430
E9ARV4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0020 PE=4 SV=1 - [E9ARV4_LEIMU]	5.61	1	2	2	3	1.000	3	0.000	8.240	374	40.574
B4DW31	cDNA FLJ54186, highly similar to Nuclear receptor-binding protein OS=Homo sapiens PE=2 SV=1 - [B4DW31_HUMAN]	2.33	3	1	1	3	1.000	3	0.000	8.224	515	57.921
A0A087WWA4	UBX domain-containing protein 8 (Fragment) OS=Homo sapiens GN=UBXN8 PE=4 SV=1 - [A0A087WWA4_HUMAN]	8.51	5	1	1	3	1.000	3	24.759	8.219	94	11.170
Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase OS=Homo sapiens GN=AASDHPPT PE=1 SV=2 - [ADPPT_HUMAN]	7.12	3	2	2	5	1.000	5	0.000	8.184	309	35.753
P27144	Adenylate kinase 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 - [KAD4_HUMAN]	20.18	2	4	4	4	0.911	4	21.148	8.171	223	25.252
Q16626	Male-enhanced antigen 1 OS=Homo sapiens GN=MEA1 PE=1 SV=2 - [MEA1_HUMAN]	10.81	1	2	2	3	1.000	3	0.000	8.170	185	19.892
Q9UHP3	Ubiquitin carboxyl-terminal hydrolase 25 OS=Homo sapiens GN=USP25 PE=1 SV=4 - [UBP25_HUMAN]	1.9	3	2	2	3	1.000	3	2.840	8.159	1055	122.142
Q59F59	Importin 8 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59F59_HUMAN]	8.66	2	3	3	3	1.000	2	0.000	8.154	485	55.487
H3BMZ1	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 (Fragment) OS=Homo sapiens GN=PTPLAD1 PE=1 SV=1 - [H3BMZ1_HUMAN]	10.07	5	1	1	2	0.913	2	7.928	8.153	139	16.153
A0A024R776	CCR4-NOT transcription complex, subunit 4, isoform CRA_a OS=Homo sapiens GN=CNOT4 PE=4 SV=1 - [A0A024R776_HUMAN]	3.15	4	2	2	3	1.000	3	43.033	8.153	572	63.022
Q5T6V7	Chromosome 9 open reading frame 64, isoform CRA_c OS=Homo sapiens GN=C9orf64 PE=1 SV=1 - [Q5T6V7_HUMAN]	13.5	3	3	3	6	0.992	6	7.091	8.150	200	23.260
Q96H29	ER lumen protein-retaining receptor OS=Homo sapiens PE=2 SV=1 - [Q96H29_HUMAN]	4.21	4	1	1	3	0.946	3	2.323	8.132	190	21.897
H0YCS3	Protein EMSY (Fragment) OS=Homo sapiens GN=C11orf30 PE=4 SV=3 - [H0YCS3_HUMAN]	5.05	7	1	1	3	1.000	3	0.000	8.128	218	23.350
B7Z9D0	cDNA FLJ57097, highly similar to Homo sapiens acyl-Coenzyme A binding domain containing 5 (ACBD5), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z9D0_HUMAN]	5.05	7	2	2	3	1.000	3	5.575	8.117	416	46.257
E7EWE1	Ubiquitin-like modifier-activating enzyme 5 OS=Homo sapiens GN=UBA5 PE=1 SV=1 - [E7EWE1_HUMAN]	10.95	6	4	4	6	1.000	6	0.518	8.105	347	38.728
M0R2S3	Coiled-coil domain-containing protein 94 (Fragment) OS=Homo sapiens GN=CCDC94 PE=1 SV=3 - [M0R2S3_HUMAN]	9.94	2	1	1	2	0.848	2	24.735	8.103	161	19.418
Q8TEW0	Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2 - [PARD3_HUMAN]	3.83	7	3	3	6	1.000	3	0.000	8.100	1356	151.330
E9B6V8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4280 PE=4 SV=1 - [E9B6V8_LEIMU]	1.83	3	2	2	4	0.936	2	9.798	8.085	818	90.007
Q8NBT6	cDNA FLJ90758 fis, clone SKNMC1000082, highly similar to Mitochondrial deoxynucleotide carrier OS=Homo sapiens PE=2 SV=1 - [Q8NBT6_HUMAN]	8.13	4	3	3	3	1.078	3	7.653	8.080	320	35.445
Q15059	Bromodomain-containing protein 3 OS=Homo sapiens GN=BRD3 PE=1 SV=1 - [BRD3_HUMAN]	4.82	2	2	3	3	0.705	2	81.758	8.075	726	79.492
P26885	Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Homo sapiens GN=FKBP2 PE=1 SV=2 - [FKBP2_HUMAN]	14.08	2	3	3	4	1.010	4	5.253	8.073	142	15.639
E9B687	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2090 PE=3 SV=1 - [E9B687_LEIMU]	3.18	1	2	2	3	1.000	3	0.000	8.069	691	75.979
E9AN28	Putative mitogen-activated protein kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0200 PE=4 SV=1 - [E9AN28_LEIMU]	1.97	1	1	1	4	1.133	1		8.068	407	46.286
D3DVA4	KIAA0907, isoform CRA_a OS=Homo sapiens GN=KIAA0907 PE=4 SV=1 - [D3DVA4_HUMAN]	2.75	3	1	1	3	0.940	2	7.195	8.068	327	34.490
A7MAV4	UBE2Q1 protein (Fragment) OS=Homo sapiens GN=UBE2Q1 PE=2 SV=2 - [A7MAV4_HUMAN]	4.94	6	2	2	3	1.196	3	16.187	8.055	344	38.249
A6NM15	Putative COBW domain-containing protein 7 OS=Homo sapiens GN=CBWD7 PE=5 SV=3 - [CBWD7_HUMAN]	17.41	21	3	3	5	0.874	5	20.145	8.054	247	28.215
B4DNL7	cDNA FLJ60737, highly similar to Cysteine desulfurase, mitochondrial (EC 2.8.1.7) OS=Homo sapiens PE=2 SV=1 - [B4DNL7_HUMAN]	8.24	6	2	2	3	1.000	3	0.000	8.053	255	28.194
B4DI03	SEC11-like 3 (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=SEC11L3 PE=2 SV=1 - [B4DI03_HUMAN]	5.77	3	1	1	4	1.000	4	0.000	8.037	156	17.393
Q9NUU6	Inactive ubiquitin thioesterase FAM105A OS=Homo sapiens GN=FAM105A PE=2 SV=1 - [F105A_HUMAN]	4.49	1	2	2	3	1.000	3	8.460	8.034	356	42.169
B3KQ33	cDNA FLJ32715 fis, clone TESTI2000784, highly similar to Importin-4 OS=Homo sapiens PE=2 SV=1 - [B3KQ33_HUMAN]	3.7	19	4	4	4	0.840	4	14.783	8.030	1081	118.651
B4DGM5	cDNA FLJ53983, highly similar to IWS1 homolog OS=Homo sapiens PE=2 SV=1 - [B4DGM5_HUMAN]	5.49	4	4	4	5	1.000	5	0.000	8.027	729	82.072
M0QZ21	AP-2 complex subunit sigma OS=Homo sapiens GN=AP2S1 PE=1 SV=1 - [M0QZ21_HUMAN]	11.48	6	2	2	4	0.965	4	5.332	8.025	122	14.547
Q9NZJ9	Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Homo sapiens GN=NUDT4 PE=1 SV=2 - [NUDT4_HUMAN]	16.67	7	2	3	3	1.025	2	3.682	8.018	180	20.293
H7C2F4	Xyloside xylosyltransferase 1 (Fragment) OS=Homo sapiens GN=XXYLT1 PE=4 SV=1 - [H7C2F4_HUMAN]	17.54	2	2	2	3	1.004	3	12.172	8.011	114	12.071
C9JE02	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 - [C9JE02_HUMAN]	10	8	2	2	4	0.970	4	4.475	7.997	160	17.935
Q2NLD4	PURA protein (Fragment) OS=Homo sapiens GN=PURA PE=2 SV=1 - [Q2NLD4_HUMAN]	8.77	5	3	3	4	1.018	4	13.521	7.992	285	31.995
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16_HUMAN]	10.67	6	2	2	3	1.001	3	30.600	7.988	178	21.175
B3KMC8	cDNA FLJ10695 fis, clone NT2RP3000403, highly similar to WW domain-binding protein 4 OS=Homo sapiens PE=2 SV=1 - [B3KMC8_HUMAN]	8.78	3	3	3	5	1.000	5	0.000	7.981	376	42.478
B3KSR8	cDNA FLJ36832 fis, clone ASTRO2010799, highly similar to ALPHA-1 CATENIN OS=Homo sapiens PE=2 SV=1 - [B3KSR8_HUMAN]	5.27	7	3	3	4	0.896	4	24.663	7.980	588	65.162
Q7Z3Y7	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN]	7.76	11	1	3	6	1.012	1		7.978	464	50.536
F8WF93	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase OS=Homo sapiens GN=ALG3 PE=1 SV=1 - [F8WF93_HUMAN]	18.46	5	1	1	2	0.953	2	7.150	7.977	65	7.446
E9AZ29	Putative T-complex protein 1, beta subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1260 PE=3 SV=1 - [E9AZ29_LEIMU]	8.13	1	4	4	4	1.377	4	36.082	7.970	529	57.698
B3KST9	cDNA FLJ36938 fis, clone BRACE2005434, highly similar to Histone RNA hairpin-binding protein OS=Homo sapiens PE=2 SV=1 - [B3KST9_HUMAN]	13.33	8	3	3	3	1.000	3	4.914	7.969	270	31.265
H0YMB1	Regulator of microtubule dynamics protein 3 (Fragment) OS=Homo sapiens GN=RMDN3 PE=1 SV=1 - [H0YMB1_HUMAN]	10.78	6	4	4	5	1.074	4	10.257	7.963	306	34.127
B4E3G4	cDNA FLJ50383, highly similar to CRSP complex subunit 3 OS=Homo sapiens PE=2 SV=1 - [B4E3G4_HUMAN]	1.68	6	2	2	3	0.869	3	9.152	7.960	1009	115.516
Q9Y4L6	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9Y4L6_HUMAN]	14.56	3	1	1	2	1.000	1		7.953	158	17.208
K7ENK9	Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=4 SV=1 - [K7ENK9_HUMAN]	35.29	12	2	2	5	1.000	5	20.221	7.952	68	7.770
B4DHJ4	cDNA FLJ57931, highly similar to MORC family CW-type zinc finger 3 OS=Homo sapiens PE=2 SV=1 - [B4DHJ4_HUMAN]	4.95	7	4	4	4	1.044	4	4.609	7.952	868	99.215
Q69YM4	Putative uncharacterized protein DKFZp667A184 (Fragment) OS=Homo sapiens GN=DKFZp667A184 PE=2 SV=1 - [Q69YM4_HUMAN]	10.91	4	1	1	3	1.019	3	18.043	7.947	110	11.601
Q00535	Cyclin-dependent-like kinase 5 OS=Homo sapiens GN=CDK5 PE=1 SV=3 - [CDK5_HUMAN]	8.22	45	1	2	3	0.602	1		7.937	292	33.283
Q9Y3D7	Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens GN=PAM16 PE=1 SV=2 - [TIM16_HUMAN]	18.4	4	3	3	4	0.925	4	25.404	7.935	125	13.816
I3L1P8	Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=1 SV=1 - [I3L1P8_HUMAN]	5.74	2	2	2	3	1.138	3	18.881	7.935	296	32.162
Q6ZS11	Ras and Rab interactor-like protein OS=Homo sapiens GN=RINL PE=2 SV=2 - [RINL_HUMAN]	4.42	1	2	2	3	1.000	2	0.000	7.928	566	62.428
E9B5F8	Vacuolar ATP synthase catalytic subunit A,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3670 PE=3 SV=1 - [E9B5F8_LEIMU]	3.61	1	1	2	3	1.299	2	40.288	7.917	610	67.769
Q9H368	PRO1670 OS=Homo sapiens PE=2 SV=1 - [Q9H368_HUMAN]	4.04	2	1	1	3	0.767	3	11.117	7.897	223	25.530
O43422	52 kDa repressor of the inhibitor of the protein kinase OS=Homo sapiens GN=PRKRIR PE=1 SV=2 - [P52K_HUMAN]	2.23	3	2	3	3	0.928	2	11.044	7.897	761	87.648
B7ZLC9	GEMIN5 protein OS=Homo sapiens GN=GEMIN5 PE=2 SV=1 - [B7ZLC9_HUMAN]	1.79	3	3	3	3	1.000	3	13.403	7.893	1507	168.326
B4E2J1	cDNA FLJ54240, highly similar to ATPase family AAA domain-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E2J1_HUMAN]	9.52	2	3	3	3	1.136	3	84.137	7.892	273	30.615
Q14684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 - [RRP1B_HUMAN]	3.96	2	2	2	2	0.969	2	4.737	7.890	758	84.375
A0A087WVD7	Transcription initiation factor TFIID subunit 9 OS=Homo sapiens GN=TAF9 PE=4 SV=1 - [A0A087WVD7_HUMAN]	8.26	3	1	1	3	0.985	3	8.839	7.882	109	12.537
Q5JR04	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=MOV10 PE=1 SV=1 - [Q5JR04_HUMAN]	4.12	5	3	3	3	0.955	3	5.625	7.880	947	107.142
Q96SK2	Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 - [TM209_HUMAN]	4.46	1	2	2	3	1.000	3	0.000	7.871	561	62.881
Q9BV79	Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR PE=1 SV=2 - [MECR_HUMAN]	7.77	3	3	3	5	1.000	5	39.283	7.867	373	40.436
H7C5M9	Programmed cell death protein 10 (Fragment) OS=Homo sapiens GN=PDCD10 PE=1 SV=1 - [H7C5M9_HUMAN]	25.41	3	3	3	4	1.016	4	9.461	7.867	122	14.218
H3BMS0	RNA-binding protein with serine-rich domain 1 OS=Homo sapiens GN=RNPS1 PE=1 SV=1 - [H3BMS0_HUMAN]	11.67	14	3	3	3	1.000	3	11.393	7.862	257	27.415
Q8IYI6	Exocyst complex component 8 OS=Homo sapiens GN=EXOC8 PE=1 SV=2 - [EXOC8_HUMAN]	3.45	1	2	2	3	1.000	3	0.000	7.860	725	81.747
E9ALJ3	Enoyl-CoA hydratase/isomerase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2310 PE=3 SV=1 - [E9ALJ3_LEIMU]	9.74	1	1	2	5	0.804	1		7.850	267	29.087
Q8TAX8	MYC associated factor X OS=Homo sapiens GN=MAX PE=2 SV=1 - [Q8TAX8_HUMAN]	13.25	9	2	2	3	0.818	3	19.654	7.848	151	17.237
A0JLS5	TBL3 protein (Fragment) OS=Homo sapiens GN=TBL3 PE=2 SV=1 - [A0JLS5_HUMAN]	2.98	4	2	2	3	1.000	3	11.595	7.848	570	63.052
E9ATN0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4460 PE=4 SV=1 - [E9ATN0_LEIMU]	18.13	1	3	3	3	1.417	3	55.322	7.847	160	17.307
P48060	Glioma pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR1 PE=1 SV=3 - [GLIP1_HUMAN]	4.51	1	1	1	2	0.980	2	3.060	7.845	266	30.346
P36405	ADP-ribosylation factor-like protein 3 OS=Homo sapiens GN=ARL3 PE=1 SV=2 - [ARL3_HUMAN]	8.79	1	2	2	3	1.044	3	6.512	7.843	182	20.443
Q9C005	Protein dpy-30 homolog OS=Homo sapiens GN=DPY30 PE=1 SV=1 - [DPY30_HUMAN]	11.11	2	2	2	3	0.913	3	2.372	7.839	99	11.243
L0R6H6	Alternative protein GRINL1A OS=Homo sapiens GN=GRINL1A PE=4 SV=1 - [L0R6H6_HUMAN]	30.23	2	1	1	2				7.827	86	8.822
Q15080	Neutrophil cytosol factor 4 OS=Homo sapiens GN=NCF4 PE=1 SV=2 - [NCF4_HUMAN]	5.6	4	2	2	3	0.870	3	1.577	7.819	339	39.007
E9ANH0	Proteasome subunit alpha type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0240 PE=3 SV=1 - [E9ANH0_LEIMU]	9.31	1	3	3	3	1.790	3	27.782	7.818	247	27.762
Q8TF32	Zinc finger protein 431 OS=Homo sapiens GN=ZNF431 PE=2 SV=2 - [ZN431_HUMAN]	18.75	175	1	3	6	1.000	3	0.000	7.817	576	67.173
Q8WYL5	Protein phosphatase Slingshot homolog 1 OS=Homo sapiens GN=SSH1 PE=1 SV=2 - [SSH1_HUMAN]	2	1	2	2	3	1.042	3	6.140	7.813	1049	115.439
B4DFG6	cDNA FLJ54285, highly similar to 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B4DFG6_HUMAN]	16.53	2	2	2	3	1.000	3	9.893	7.804	121	14.039
Q9UID3	Vacuolar protein sorting-associated protein 51 homolog OS=Homo sapiens GN=VPS51 PE=1 SV=2 - [VPS51_HUMAN]	2.69	4	2	2	3	1.000	3	0.000	7.796	782	85.988
Q9Y6X9	MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2 - [MORC2_HUMAN]	2.33	1	3	3	3	0.824	3	8.633	7.785	1032	117.750
B7Z1N3	cDNA FLJ51050, highly similar to GPI transamidase component PIG-T OS=Homo sapiens PE=1 SV=1 - [B7Z1N3_HUMAN]	12.03	8	3	3	4	0.925	4	18.683	7.782	316	36.030
B4DKR0	Syntaxin 5A, isoform CRA_c OS=Homo sapiens GN=STX5A PE=2 SV=1 - [B4DKR0_HUMAN]	6.18	4	2	2	3	0.828	3	4.543	7.776	259	29.215
E9AKR8	Putative 60S ribosomal protein L19 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0410 PE=3 SV=1 - [E9AKR8_LEIMU]	7.69	1	3	3	3	1.165	3	22.925	7.771	247	28.185
A0A087WUX8	MICOS complex subunit MIC27 OS=Homo sapiens GN=APOOL PE=4 SV=1 - [A0A087WUX8_HUMAN]	10.27	4	2	2	3	1.000	3	0.000	7.770	263	28.743
B2RDG9	cDNA, FLJ96603, highly similar to Homo sapiens actin-related protein 10 homolog (S. cerevisiae) (ACTR10), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDG9_HUMAN	4.32	13	2	2	4	1.000	4	10.346	7.760	417	46.247
V5NW03	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1 - [V5NW03_HUMAN]	10.84	3	1	1	3	1.000	3	0.000	7.757	83	9.319
Q96GX2	Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 - [A7L3B_HUMAN]	10.31	1	1	1	3	0.947	3	9.068	7.755	97	10.764

B4E1V0	cDNA FLJ54839, highly similar to Lactotransferrin (EC 3.4.21.-) OS=Homo sapiens PE=2 SV=1 - [B4E1V0_HUMAN]	7	12	2	2	4	1.003	4	7.488	7.743	300	33.004
Q9NUN5	Probable lysosomal cobalamin transporter OS=Homo sapiens GN=LMBRD1 PE=1 SV=1 - [LMBD1_HUMAN]	2.78	1	1	1	2	1.000	2	0.000	7.736	540	61.349
E9B6K2	Putative cystathione gamma lyase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3230 PE=3 SV=1 - [E9B6K2_LEIMU]	6.34	1	3	3	5	1.000	5	0.000	7.732	410	44.418
E9AM68	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0110 PE=4 SV=1 - [E9AM68_LEIMU]	0.81	13	1	3	3	1.000	1		7.719	2840	324.725
B4DY33	cDNA FLJ55600, highly similar to Homo sapiens forkhead box K1 (FOXK1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DY33_HUMAN]	5.49	10	2	3	4	0.972	2	4.199	7.716	583	61.928
B4DKX3	cDNA FLJ51228, highly similar to Probable ATP-dependent RNA helicase DDX10 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DKX3_HUMAN]	1.92	2	1	1	3	1.000	3	0.000	7.709	781	90.260
Q8TE77	Protein phosphatase Slingshot homolog 3 OS=Homo sapiens GN=SSH3 PE=1 SV=2 - [SSH3_HUMAN]	5.46	3	3	3	3	1.000	3	4.911	7.708	659	72.951
E9PJF0	Mitogen-activated protein kinase OS=Homo sapiens GN=MAPK3 PE=1 SV=1 - [E9PJF0_HUMAN]	5.7	7	1	2	3	0.874	1		7.701	316	35.714
Q7Z2W9	39S ribosomal protein L21, mitochondrial OS=Homo sapiens GN=MRPL21 PE=1 SV=2 - [RM21_HUMAN]	12.2	5	3	3	3	1.092	3	15.342	7.701	205	22.800
Q4G176	Acyl-CoA synthetase family member 3, mitochondrial OS=Homo sapiens GN=ACSF3 PE=1 SV=3 - [ACSF3_HUMAN]	5.38	8	3	3	3	1.888	3	6.333	7.700	576	64.089
B3KUH0	cDNA FLJ39883 fis, clone SPLEN2016268, highly similar to Protein CHMP7 OS=Homo sapiens PE=2 SV=1 - [B3KUH0_HUMAN]	4.42	6	2	2	3	0.705	2	55.508	7.678	453	50.907
Q9HA77	Probable cysteine--tRNA ligase, mitochondrial OS=Homo sapiens GN=CARS2 PE=1 SV=1 - [SYCM_HUMAN]	4.96	6	3	3	3	0.880	3	15.032	7.675	564	62.185
A0A087WX16	Alpha-1,2-mannosyltransferase ALG9 OS=Homo sapiens GN=ALG9 PE=4 SV=1 - [A0A087WX16_HUMAN]	14.71	7	1	1	2	1.000	2	0.000	7.665	102	11.352
Q9Y3Q3	Transmembrane emp24 domain-containing protein 3 OS=Homo sapiens GN=TMED3 PE=1 SV=1 - [TMED3_HUMAN]	10.14	7	2	2	2	0.687	2	43.056	7.650	217	24.761
B4DHI5	cDNA FLJ51844, highly similar to Serine incorporator 3 OS=Homo sapiens PE=2 SV=1 - [B4DHI5_HUMAN]	3.64	4	2	2	3	1.000	3	0.000	7.650	440	49.270
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta OS=Homo sapiens GN=BUB1B PE=1 SV=3 - [BUB1B_HUMAN]	3.05	1	3	3	3	0.787	2	36.723	7.650	1050	119.470
Q5SRE5	Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1 - [NU188_HUMAN]	3.66	2	5	5	5	0.991	5	17.500	7.648	1749	195.917
B3KPM6	cDNA FLJ31963 fis, clone NT2RP7007610, highly similar to Homo sapiens DDHD domain containing 2 (DDHD2), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KPM6_HUI	2.95	4	3	3	3	1.000	3	0.000	7.648	711	80.910
E9AYB7	Prefoldin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1380 PE=4 SV=1 - [E9AYB7_LEIMU]	9.79	1	2	2	3	1.756	3	28.608	7.641	194	22.177
Q8N122	Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1 - [RPTOR_HUMAN]	1.8	1	2	2	2	1.028	2	11.520	7.638	1335	148.942
Q8WWC4	Uncharacterized protein C2orf47, mitochondrial OS=Homo sapiens GN=C2orf47 PE=1 SV=1 - [CB047_HUMAN]	8.25	2	3	3	3	1.024	3	9.190	7.629	291	32.524
B4DDK7	cDNA FLJ51792, highly similar to Smad nuclear-interacting protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DDK7_HUMAN]	5.79	3	2	2	2	1.000	2	0.000	7.628	380	43.927
B4DQK1	cDNA FLJ53475, highly similar to Autophagy-related protein 7 OS=Homo sapiens PE=2 SV=1 - [B4DQK1_HUMAN]	2.79	8	2	2	3	1.211	3	2.342	7.624	681	75.458
H3BRI5	Snurportin-1 (Fragment) OS=Homo sapiens GN=SNUPN PE=1 SV=3 - [H3BRI5_HUMAN]	8.1	7	2	2	3	0.746	3	12.419	7.622	210	24.402
B5LY64	Orotidine 5'-phosphate decarboxylase OS=Homo sapiens GN=UMPS PE=2 SV=1 - [B5LY64_HUMAN]	9.93	7	3	3	4	0.877	4	19.705	7.622	302	33.030
B4E1C9	cDNA FLJ52963, highly similar to Synapse-associated protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E1C9_HUMAN]	12.89	5	5	5	5	0.954	5	51.646	7.620	318	36.736
H7C459	Mitogen-activated protein kinase kinase kinase 13 (Fragment) OS=Homo sapiens GN=MAP3K13 PE=4 SV=1 - [H7C459_HUMAN]	4.07	4	1	1	3	1.000	2	0.000	7.619	246	28.602
P19793	Retinoic acid receptor RXR-alpha OS=Homo sapiens GN=RXRA PE=1 SV=1 - [RXRA_HUMAN]	8.87	5	1	3	3	1.000	1		7.619	462	50.778
E9APD3	Putative proteasome regulatory ATPase subunit 2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1090 PE=3 SV=1 - [E9APD3_LEIMU]	4.11	1	1	2	3	1.000	1		7.617	438	49.233
O14548	Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Homo sapiens GN=COX7A2L PE=1 SV=2 - [COX7R_HUMAN]	19.3	3	2	2	2	1.113	2	18.004	7.615	114	12.607
B2RDK5	cDNA, FLJ96655, highly similar to Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDK5_HUMAN]	3.41	6	2	2	3	0.968	3	0.631	7.611	440	47.678
F5GY90	Porphobilinogen deaminase (Fragment) OS=Homo sapiens GN=HMBS PE=1 SV=1 - [F5GY90_HUMAN]	10.7	4	2	2	3	0.971	3	3.396	7.610	187	20.879
E9B257	Ubiquinol-cytochrome-c reductase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2580 PE=4 SV=1 - [E9B257_LEIMU]	6.67	1	1	1	2	6.504	2	3.869	7.610	135	14.774
Q4VB87	EPB41 protein (Fragment) OS=Homo sapiens GN=EPB41 PE=2 SV=1 - [Q4VB87_HUMAN]	5.37	8	2	3	3	0.651	2	70.754	7.603	615	68.366
A0A087WTJ2	GTPase IMAP family member 5 OS=Homo sapiens GN=GIMAP5 PE=4 SV=1 - [A0A087WTJ2_HUMAN]	4.11	4	2	2	3	0.820	3	21.149	7.598	511	57.016
A0A087WV26	Sjoegren syndrome nuclear autoantigen 1 OS=Homo sapiens GN=SSNA1 PE=4 SV=1 - [A0A087WV26_HUMAN]	22.22	2	3	3	3	1.014	3	2.210	7.586	81	9.190
Q96HD4	Similar to adducin 2 (Beta) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96HD4_HUMAN]	8.16	3	2	2	3	1.000	3	0.000	7.575	282	30.941
B3KVD5	cDNA FLJ16430 fis, clone BRACE3009044, highly similar to Centaurin-gamma 1 OS=Homo sapiens PE=2 SV=1 - [B3KVD5_HUMAN]	2	5	1	2	3	0.879	2	6.578	7.561	848	91.134
Q6QBN8	V-type proton ATPase subunit a (Fragment) OS=Homo sapiens GN=TCIRG1 PE=2 SV=1 - [Q6QBN8_HUMAN]	11.2	6	2	2	3	1.244	3	24.163	7.556	125	14.262
E9ATK1	Putative oxidoreductase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4170 PE=4 SV=1 - [E9ATK1_LEIMU]	4.71	1	1	1	2	0.906	2	2.293	7.547	340	36.069
E9AV93	T-complex protein 1 subunit delta OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1090 PE=3 SV=1 - [E9AV93_LEIMU]	5.63	1	3	3	3	1.539	3	10.936	7.543	551	59.667
Q86YS7	C2 domain-containing protein 5 OS=Homo sapiens GN=C2CD5 PE=1 SV=1 - [C2CD5_HUMAN]	2	5	2	2	3	1.000	3	0.000	7.540	1000	110.377
F6U1T9	Calcineurin subunit B type 1 OS=Homo sapiens GN=PPP3R1 PE=4 SV=1 - [F6U1T9_HUMAN]	13.75	5	2	2	4	1.117	4	2.166	7.538	160	18.196
A0A024R972	Laminin, gamma 1 (Formerly LAMB2), isoform CRA_a OS=Homo sapiens GN=LAMC1 PE=4 SV=1 - [A0A024R972_HUMAN]	1.72	2	2	2	2	1.032	2	4.727	7.527	1573	173.900
E7EVH9	Pseudouridine-5'-monophosphatase (Fragment) OS=Homo sapiens GN=HDHD1 PE=1 SV=1 - [E7EVH9_HUMAN]	5.24	2	1	1	2	0.879	2	3.338	7.525	191	21.452
C9JNP9	Ubiquitin fusion degradation protein 1 homolog (Fragment) OS=Homo sapiens GN=UFD1L PE=1 SV=1 - [C9JNP9_HUMAN]	14.47	4	2	2	3	0.987	3	22.605	7.513	159	17.542
F5H8E2	Succinate dehydrogenase assembly factor 2, mitochondrial OS=Homo sapiens GN=SDHAF2 PE=4 SV=1 - [F5H8E2_HUMAN]	19.32	8	2	2	3	1.040	2	36.158	7.513	88	10.142
H7C3J0	All-trans-retinol 13,14-reductase (Fragment) OS=Homo sapiens GN=RETSAT PE=1 SV=1 - [H7C3J0_HUMAN]	3.01	3	1	1	2	0.958	2	6.424	7.507	399	43.789
Q9BRT3	Migration and invasion enhancer 1 OS=Homo sapiens GN=MIEN1 PE=1 SV=1 - [MIEN1_HUMAN]	23.48	2	3	3	3	0.903	3	24.476	7.506	115	12.395
B4DVB0	Oxysterol-binding protein OS=Homo sapiens GN=OSBPL5 PE=1 SV=1 - [B4DVB0_HUMAN]	4.3	10	3	3	3	0.754	3	43.746	7.503	790	88.379
D6RCL3	Probable dimethyladenosine transferase OS=Homo sapiens GN=DIMT1 PE=1 SV=1 - [D6RCL3_HUMAN]	5.84	4	1	1	3	0.831	2	4.841	7.496	154	17.059
Q6ZMI0	Protein phosphatase 1 regulatory subunit 21 OS=Homo sapiens GN=PPP1R21 PE=1 SV=1 - [PPR21_HUMAN]	3.85	2	3	4	4	0.961	3	5.951	7.496	780	88.260
B2R9R2	cDNA, FLJ94517, highly similar to Homo sapiens baculoviral IAP repeat-containing 4 (BIRC4), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R9R2_HUMAN]	4.83	2	2	2	3	1.000	3	0.000	7.493	497	56.587
F2Z2Y4	Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1 - [F2Z2Y4_HUMAN]	3.68	2	2	2	3	1.017	3	2.539	7.489	272	30.619
B2R894	Mitochondrial ribosomal protein L38, isoform CRA_b OS=Homo sapiens GN=MRPL38 PE=2 SV=1 - [B2R894_HUMAN]	8.96	2	3	3	4	1.009	4	1.449	7.488	346	40.731
E9B2B1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_3110 PE=4 SV=1 - [E9B2B1_LEIMU]	2.01	1	3	3	4	0.921	4	17.004	7.479	846	95.907
Q6U7I7	Arylamine N-acetyltransferase 1 variant (Fragment) OS=Homo sapiens GN=NAT1 PE=3 SV=1 - [Q6U7I7_HUMAN]	6.67	6	2	2	3	1.241	3	15.632	7.478	270	31.454
A8K201	cDNA FLJ75605, highly similar to Homo sapiens CGI-115 protein (CGI-115), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K201_HUMAN]	5.02	2	1	1	2	0.951	2	7.456	7.468	259	28.897
Q5TBA9	Protein furry homolog OS=Homo sapiens GN=FRY PE=1 SV=1 - [FRY_HUMAN]	1.76	8	4	5	5	1.168	3	19.106	7.467	3013	338.659
Q8N142	Adenylosuccinate synthetase isozyme 1 OS=Homo sapiens GN=ADSSL1 PE=2 SV=1 - [PURA1_HUMAN]	3.72	4	1	2	3	1.000	1		7.462	457	50.177
B4DQ03	cDNA FLJ57859, highly similar to Ras-related GTP-binding protein C OS=Homo sapiens PE=2 SV=1 - [B4DQ03_HUMAN]	7.89	6	2	2	3	1.000	3	0.000	7.462	279	31.675
E9AN29	Putative nucleolar protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0210 PE=4 SV=1 - [E9AN29_LEIMU]	2.53	1	1	1	2	1.216	2	29.671	7.455	474	52.692
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	4.44	1	3	3	3	0.956	3	12.247	7.449	563	61.681
J3KNG9	Anion exchange protein 2 OS=Homo sapiens GN=SLC4A2 PE=1 SV=1 - [J3KNG9_HUMAN]	3.45	12	2	2	2	0.994	2	0.957	7.447	1159	127.568
H0Y6I0	Golgin subfamily A member 4 (Fragment) OS=Homo sapiens GN=GOLGA4 PE=1 SV=1 - [H0Y6I0_HUMAN]	0.76	5	2	2	5	1.000	5	0.000	7.445	2099	246.456
E9AWB6	Small hydrophilic endoplasmic reticulum-associated protein (Sherp) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1050 PE=4 SV=1 - [E9AW	29.82	1	1	1	2	1.000	2	0.000	7.442	57	5.943
B4E072	cDNA FLJ61196, highly similar to 3-ketoacyl-CoA thiolase, peroxisomal (EC 2.3.1.16) OS=Homo sapiens PE=2 SV=1 - [B4E072_HUMAN]	7.14	6	1	1	4	1.000	4	9.563	7.436	126	13.491
E9AQT2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1210 PE=4 SV=1 - [E9AQT2_LEIMU]	1.05	1	2	2	4	1.130	4	17.327	7.435	1242	132.348
B3KMR3	cDNA FLJ12391 fis, clone MAMMA1002684, highly similar to Transmembrane GTPase MFN2 (EC 3.6.5.-) OS=Homo sapiens PE=2 SV=1 - [B3KMR3_HUMAN]	4.71	5	2	2	4	1.000	3	0.000	7.425	382	44.000
A8K335	cDNA FLJ76254, highly similar to Homo sapiens gamma-glutamyl hydrolase (GGH), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K335_HUMAN]	4.72	3	2	2	3	1.032	3	18.985	7.411	318	36.024
A8K0B6	cDNA FLJ77858, highly similar to Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, mRNA OS=Homo sapiens PE=2 S	6.84	10	3	3	3	1.015	3	2.263	7.409	395	44.645
B4DJ85	cDNA FLJ60587, highly similar to Glomulin OS=Homo sapiens PE=2 SV=1 - [B4DJ85_HUMAN]	4.31	3	3	3	3	0.926	3	11.472	7.406	580	66.667
F2FB34	SOGA OS=Homo sapiens PE=2 SV=1 - [F2FB34_HUMAN]	2.44	5	3	3	3	1.000	3	3.336	7.392	1351	151.155
O95298	NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Homo sapiens GN=NDUFC2 PE=1 SV=1 - [NDUC2_HUMAN]	15.97	7	1	2	3	1.176	2	77.041	7.391	119	14.178
B4E3L5	cDNA FLJ54656, highly similar to Aryl hydrocarbon receptor nuclear translocator OS=Homo sapiens PE=2 SV=1 - [B4E3L5_HUMAN]	5	3	1	3	3				7.391	740	82.264
E9AMB3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0340 PE=4 SV=1 - [E9AMB3_LEIMU]	0.15	1	1	1	3	1.004	3	0.597	7.384	4776	508.298
B4DIP7	cDNA FLJ57114, highly similar to Niemann-Pick C1 protein OS=Homo sapiens PE=2 SV=1 - [B4DIP7_HUMAN]	2.32	5	2	2	3	1.134	2	7.744	7.375	776	86.302
E9AR47	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0700 PE=4 SV=1 - [E9AR47_LEIMU]	1.25	1	1	1	5	0.883	5	8.674	7.373	480	52.387
Q8WXA9	Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens GN=SREK1 PE=1 SV=1 - [SREK1_HUMAN]	14.57	4	5	5	8	0.904	6	21.387	7.370	508	59.345
B4DXW2	cDNA FLJ60947, highly similar to Coiled-coil domain-containing protein 9 OS=Homo sapiens PE=2 SV=1 - [B4DXW2_HUMAN]	5.65	5	2	2	3	1.000	3	0.000	7.362	513	57.978
Q9BVI4	Nucleolar complex protein 4 homolog OS=Homo sapiens GN=NOC4L PE=1 SV=1 - [NOC4L_HUMAN]	3.29	2	2	2	3	1.000	3	0.000	7.357	516	58.431
B4DQJ4	cDNA FLJ59213, highly similar to Nuclear valosin-containing protein-like OS=Homo sapiens PE=2 SV=1 - [B4DQJ4_HUMAN]	6.28	6	3	3	3	1.070	2	0.798	7.352	589	64.873
U3KQ85	Protein C10 OS=Homo sapiens GN=C12orf57 PE=1 SV=1 - [U3KQ85_HUMAN]	24.18	3	2	2	3	1.000	3	0.000	7.346	91	9.633
E9B165	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2920 PE=4 SV=1 - [E9B165_LEIMU]	4.86	4	1	2	3	1.000	2	0.000	7.322	453	49.479
A0A087WZ32	Pleckstrin homology domain-containing family A member 2 OS=Homo sapiens GN=PLEKHA2 PE=4 SV=1 - [A0A087WZ32_HUMAN]	4.8	6	2	2	3	1.000	3	0.000	7.311	375	41.184
Q15814	Tubulin-specific chaperone C OS=Homo sapiens GN=TBCC PE=1 SV=2 - [TBCC_HUMAN]	2.31	1	2	2	3	1.085	3	7.481	7.306	346	39.224
C9K0G7	D-beta-hydroxybutyrate dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens GN=BDH1 PE=3 SV=1 - [C9K0G7_HUMAN]	14.46	6	3	3	4	0.842	4	16.264	7.305	166	18.432
P11388	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN]	0.72	1	1	1	2	1.373	2	49.780	7.296	1531	174.276
A8K2I7	cDNA FLJ76072, highly similar to Homo sapiens GIPC PDZ domain containing family, member 1 (GIPC1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A	6.01	7	1	2	3	1.000	1		7.278	333	36.017
A0A087WUR6	Calcium/calmodulin-dependent protein kinase type 1D OS=Homo sapiens GN=CAMK1D PE=4 SV=1 - [A0A087WUR6_HUMAN]	6.19	6	2	2	3	0.801	3	36.809	7.271	291	32.452
Q03111	Protein ENL OS=Homo sapiens GN=MLLT1 PE=1 SV=2 - [ENL_HUMAN]	3.76	1	2	2	3	1.000	3	0.000	7.269	559	62.018
A8K5Q1	cDNA FLJ77548, highly similar to Homo sapiens bin3, bicoid-interacting 3, homolog (Drosophila) (BCDIN3), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5Q1_HUMAN]	3.92	2	2	2	3	0.723	2	51.037	7.264	689	74.282
Q59F54	Solute carrier family 2 (Facilitated glucose transporter), member 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59F54_HUMAN]	3.81	6	1	1	3	1.000	2	0.000	7.259	289	31.853
E5KRP6	Spastin OS=Homo sapiens GN=SPAST PE=3 SV=1 - [E5KRP6_HUMAN]	8.05	2	3	3	5	1.000	5	0.000	7.256	584	63.567
O95155	Ubiquitin conjugation factor E4 B OS=Homo sapiens GN=UBE4B PE=1 SV=1 - [UBE4B_HUMAN]	2.15	3	3	3	3	0.919	3	43.152	7.253	1302	146.092
E9PC90	G2/mitotic-specific cyclin-B1 (Fragment) OS=Homo sapiens GN=CCNB1 PE=1 SV=1 - [E9PC90_HUMAN]	6.98	4	3	3	3	0.908	3	0.329	7.238	401	44.903
H7C0V9	Amyloid beta A4 protein (Fragment) OS=Homo sapiens GN=APP PE=1 SV=1 - [H7C0V9_HUMAN]	5.15	7	2	2	2	0.949	2	7.723	7.225	485	55.057
Q96KM6	Zinc finger protein 512B OS=Homo sapiens GN=ZNF512B PE=1 SV=1 - [Z512B_HUMAN]	3.03	1	1	2	3	1.000	1		7.220	892	97.202
Q92551	Inositol hexakisphosphate kinase 1 OS=Homo sapiens GN=IP6K1 PE=1 SV=3 - [IP6K1_HUMAN]	5.44	2	2	2	3	0.631	3	36.616	7.219	441	50.204
H3BTK3	Calcium-regulated heat stable protein 1 (Fragment) OS=Homo sapiens GN=CARHSP1 PE=1 SV=1 - [H3BTK3_HUMAN]	11.27	7	1	1	3	0.909	3	11.851	7.218	71	7.665
E9AP54	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0200 PE=4 SV=1 - [E9AP54_LEIMU]	3.02	1	2	2	4	1.000	4	0.000	7.203	761	83.542
O43159	Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 - [RRP8_HUMAN]	8.77	3	3	3	3	0.866	3	21.664	7.196	456	50.683
P84157	Matrix-remodeling-associated protein 7 OS=Homo sapiens GN=MXRA7 PE=1 SV=1 - [MXRA7_HUMAN]	9.31	2	2	3	3	1.154	2	21.495	7.196	204	21.452
G9FP35	Guanine nucleotide binding protein OS=Homo sapiens GN=GNAQ PE=2 SV=1 - [G9FP35_HUMAN]	4.18	114	1	2	3	1.018	2	2.709	7.191	359	42.084
A9Z1Z3	Fer-1-like protein 4 OS=Homo sapiens GN=FER1L4 PE=2 SV=1 - [FR1L4_HUMAN]	0.84	2	1	2	3				7.191	1794	200.854
D6RAR7	Dysbindin (Fragment) OS=Homo sapiens GN=DTNBP1 PE=4 SV=1 - [D6RAR7_HUMAN]	11.27	5	1	1	4	1.000	4	0.000	7.190	142	15.819
Q53TG4	Putative uncharacterized protein NCK2 (Fragment) OS=Homo sapiens GN=NCK2 PE=4 SV=1 - [Q53TG4_HUMAN]	7.89	2	2	2	3	1.000	3	0.000	7.184	304	33.943
Q5W0V3	Protein FAM160B1 OS=Homo sapiens GN=FAM160B1 PE=2 SV=1 - [F16B1_HUMAN]	1.7	1	1	1	2	1.146	2	20.430	7.175	765	86.503
A2IDC7	39S ribosomal protein L28, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL28 PE=1 SV=1 - [A2IDC7_HUMAN]	9.79	6	1	2	3	1.000	2	0.000	7.174	194	23.131
A0A087WZ88	Retinoic acid receptor RXR-gamma OS=Homo sapiens GN=RXRG PE=4 SV=1 - [A0A087WZ88_HUMAN]	9.71	4	1	3	3	0.842	1		7.170	340	38.583
Q9NVK3	cDNA FLJ10678 fis, clone NT2RP2006472 OS=Homo sapiens PE=2 SV=1 - [Q9NVK3_HUMAN]	2.12	7	1	2	3	0.692	1		7.166	707	80.405
Q10469	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT2 PE=1 SV=1 - [MGAT2_HUMAN]	3.13	2	2	2	3	1.172	3	3.707	7.166	447	51.517
E5RIA9	Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens GN=MSRA PE=3 SV=1 - [E5RIA9_HUMAN]	3.76	2	1	1	3	0.887	3	10.354	7.164	213	23.581
B3KQJ8	CKLF-like MARVEL transmembrane domain containing 3, isoform CRA_b OS=Homo sapiens GN=CMTM3 PE=2 SV=1 - [B3KQJ8_HUMAN]	12.5	4	1	1	2	0.987	2	1.947	7.159	96	10.632
H0UI99	Zinc finger, CCCH-type with G patch domain, isoform CRA_b OS=Homo sapiens GN=ZGPAT PE=4 SV=1 - [H0UI99_HUMAN]	9.16	5	3	3	4	1.000	3	10.811	7.156	502	54.640
Q9UMX5	Neudesin OS=Homo sapiens GN=NENF PE=1 SV=1 - [NENF_HUMAN]	19.77	1	3	3	3	1.108	2	0.675	7.154	172	18.845
H0Y5R6	Uroporphyrinogen decarboxylase (Fragment) OS=Homo sapiens GN=UROD PE=1 SV=1 - [H0Y5R6_HUMAN]	10.53	5	2	2	2	0.941	2	9.009	7.150	228	25.408
A8K255	cDNA FLJ78322 OS=Homo sapiens PE=2 SV=1 - [A8K255_HUMAN]	5.4	3	1	2	3				7.146	278	31.821
E9AKQ4	Putative 5'-3' exonuclease OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0260 PE=4 SV=1 - [E9AKQ4_LEIMU]	1.31	1	2	2	3	1.000	3	0.000	7.133	1527	170.046
P26010	Integrin beta-7 OS=Homo sapiens GN=ITGB7 PE=1 SV=1 - [ITB7_HUMAN]	8.02	11	4	5	6	0.621	3	59.599	7.130	798	86.847
P36551	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 - [HEM6_HUMAN]	9.25	3	3	3	3	1.292	3	42.692	7.128	454	50.120
A8K8N3	cDNA FLJ78740, highly similar to Homo sapiens sperm associated antigen 5 (SPAG5), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8N3_HUMAN]	2.18	4	2	2	3	0.918	3	12.769	7.127	1193	134.312
B4DXX1	cDNA FLJ56040 OS=Homo sapiens PE=2 SV=1 - [B4DXX1_HUMAN]	6.76	4	4	4	4	1.008	4	1.226	7.118	577	64.992
O95167	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 OS=Homo sapiens GN=NDUFA3 PE=1 SV=1 - [NDUA3_HUMAN]	21.43	7	2	2	3	0.905	3	6.907	7.104	84	9.273
Q9NPB8	Glycerophosphocholine phosphodiesterase GPCPD1 OS=Homo sapiens GN=GPCPD1 PE=1 SV=2 - [GPCP1_HUMAN]	2.08	1	1	1	2	1.000	2	0.000	7.103	672	75.986
H0YDP7	39S ribosomal protein L49, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL49 PE=1 SV=1 - [H0YDP7_HUMAN]	11.02	3	1	1	2	1.242	2	10.959	7.100	127	14.673
E9B1F6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_0080 PE=4 SV=1 - [E9B1F6_LEIMU]	8.75	1	2	2	4	1.210	4	28.816	7.091	240	26.703
Q96A19	Coiled-coil domain-containing protein 102A OS=Homo sapiens GN=CCDC102A PE=1 SV=2 - [C102A_HUMAN]	3.27	8	1	3	3	3.116	1		7.087	550	62.558
B3KW34	cDNA FLJ42071 fis, clone SYNOV2014157, highly similar to Protein YIPF5 OS=Homo sapiens PE=2 SV=1 - [B3KW34_HUMAN]	4.67	2	1	1	2	1.099	2	39.300	7.087	257	28.013
Q6NX55	Chromosome 19 open reading frame 2 OS=Homo sapiens GN=C19orf2 PE=2 SV=1 - [Q6NX55_HUMAN]	5.67	4	3	3	4	1.063	4	29.591	7.081	494	55.434
E9B4B5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2750 PE=4 SV=1 - [E9B4B5_LEIMU]	1.66	1	1	1	2	1.000	2	0.000	7.080	1145	121.527
Q14BN4	Sarcolemmal membrane-associated protein OS=Homo sapiens GN=SLMAP PE=1 SV=1 - [SLMAP_HUMAN]	3.62	8	4	4	4	1.000	4	0.000	7.078	828	95.140
B3KRS1	cDNA FLJ34794 fis, clone NT2NE2005676, highly similar to Gamma-tubulin complex component 2 OS=Homo sapiens PE=2 SV=1 - [B3KRS1_HUMAN]	4.85	6	2	2	3	1.000	3	19.293	7.075	721	82.524
E9AXW8	Putative serine/threonine-protein kinase (Putative protein kinase) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_2340 PE=4 SV=1 - [E9AXWi	7.97	1	2	2	2	1.000	2	0.000	7.072	389	44.441
B4DSE2	cDNA FLJ57277, highly similar to Tripeptidyl-peptidase 1 (EC 3.4.14.9) OS=Homo sapiens PE=2 SV=1 - [B4DSE2_HUMAN]	5.45	8	2	2	3	0.905	3	2.897	7.070	385	41.650
H0YGV7	alpha-1,2-Mannosidase OS=Homo sapiens GN=MAN1B1 PE=3 SV=2 - [H0YGV7_HUMAN]	2.36	10	1	2	3	0.812	1		7.066	550	62.360
Q24JR3	SEMA6C protein OS=Homo sapiens GN=SEMA6C PE=2 SV=1 - [Q24JR3_HUMAN]	3.16	6	2	2	3	0.953	3	46.282	7.055	474	51.817
Q5JSH3	WD repeat-containing protein 44 OS=Homo sapiens GN=WDR44 PE=1 SV=1 - [WDR44_HUMAN]	0.88	1	1	1	3	0.769	3	23.265	7.053	913	101.304
Q8N4C8	Misshapen-like kinase 1 OS=Homo sapiens GN=MINK1 PE=1 SV=2 - [MINK1_HUMAN]	2.4	3	3	3	3	1.000	3	23.485	7.039	1332	149.729
Q6NXS2	PPP1R2 protein OS=Homo sapiens GN=PPP1R2 PE=2 SV=1 - [Q6NXS2_HUMAN]	19.48	6	1	1	4	1.000	3	0.000	7.039	77	8.586
C9JQV3	Serine/threonine-protein kinase 11-interacting protein OS=Homo sapiens GN=STK11IP PE=1 SV=1 - [C9JQV3_HUMAN]	2.02	5	1	2	2	0.953	1		7.035	1088	120.184
B4DYE2	cDNA FLJ61467, highly similar to Chromosome-associated kinesin KIF4A OS=Homo sapiens PE=2 SV=1 - [B4DYE2_HUMAN]	2.03	6	1	3	4	0.943	2	8.666	7.035	1234	139.817
O00273	DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1 - [DFFA_HUMAN]	3.32	2	1	1	2	0.962	2	5.822	7.034	331	36.500
Q8N5G2	Macoilin OS=Homo sapiens GN=TMEM57 PE=1 SV=1 - [MACOI_HUMAN]	4.22	1	3	3	3	1.000	2	0.000	7.033	664	76.130
E9AQ39	Putative 60S acidic ribosomal protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0370 PE=3 SV=1 - [E9AQ39_LEIMU]	10.28	1	1	1	2	5.088	2	1.252	7.023	107	10.100
E9AV21	Putative la RNA binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0540 PE=4 SV=1 - [E9AV21_LEIMU]	5.01	1	2	2	2	1.000	2	0.000	7.023	339	37.183
B3KMM9	cDNA FLJ11635 fis, clone HEMBA1004286, highly similar to Homo sapiens transforming growth factor, beta receptor associated protein 1 (TGFBRAP1), mRNA OS=Hom	3.17	2	1	1	2	1.756	2	100.387	7.018	315	35.662
B4DR76	cDNA FLJ58249, highly similar to Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens PE=2 SV=1 - [B4DR76_HUMAN]	4.69	3	3	3	3	0.833	2	35.181	7.016	640	68.889
A6XGL3	Protease serine 1 OS=Homo sapiens GN=PRSS1 PE=2 SV=1 - [A6XGL3_HUMAN]	3.38	9	1	1	4	1.015	4	13.183	7.012	237	25.383
Q9H1A4	Anaphase-promoting complex subunit 1 OS=Homo sapiens GN=ANAPC1 PE=1 SV=1 - [APC1_HUMAN]	0.82	2	2	2	3	1.172	3	23.800	7.011	1944	216.361
Q9BQ70	Transcription factor 25 OS=Homo sapiens GN=TCF25 PE=1 SV=1 - [TCF25_HUMAN]	4.14	10	3	3	3	1.185	3	25.156	7.010	676	76.619
Q6ZNK5	FLJ00293 protein (Fragment) OS=Homo sapiens GN=FLJ00293 PE=1 SV=1 - [Q6ZNK5_HUMAN]	2.34	2	2	2	4	1.000	3	6.412	7.005	812	92.760
E9AKR5	Putative glutamine synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0370 PE=3 SV=1 - [E9AKR5_LEIMU]	6.33	1	2	2	3	1.355	3	72.103	7.005	379	42.266
E9AN57	GP63, leishmanolysin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0470 PE=4 SV=1 - [E9AN57_LEIMU]	6.81	6	3	4	4	1.000	3	0.000	7.000	602	63.617
Q9UKW4	Guanine nucleotide exchange factor VAV3 OS=Homo sapiens GN=VAV3 PE=1 SV=1 - [VAV3_HUMAN]	2.13	12	1	2	4	1.000	1		6.998	847	97.713
Q92747	Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2 - [ARC1A_HUMAN]	6.49	5	3	3	3	1.037	3	13.880	6.996	370	41.543
C9JVY5	A-kinase anchor protein 2 (Fragment) OS=Homo sapiens GN=AKAP2 PE=1 SV=1 - [C9JVY5_HUMAN]	2.83	5	1	1	2	1.000	2	0.000	6.991	778	85.231
A8K2Z3	cDNA FLJ76092, highly similar to Homo sapiens 5'-nucleotidase, cytosolic II-like 1 (NT5C2L1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2Z3_HUMAN]	2.64	2	1	1	2	0.978	2	4.355	6.991	455	51.826
Q59H44	Lymphocyte antigen 75 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H44_HUMAN]	2.46	2	3	3	4	1.089	4	21.153	6.991	1340	154.497
G3V2F4	Tyrosyl-DNA phosphodiesterase 1 OS=Homo sapiens GN=TDP1 PE=1 SV=1 - [G3V2F4_HUMAN]	6.4	15	4	4	4	0.793	4	25.178	6.987	578	64.786
A0A024QZR3	HCG2002731, isoform CRA_a OS=Homo sapiens GN=hCG_2002731 PE=4 SV=1 - [A0A024QZR3_HUMAN]	3.9	3	1	1	2	1.486	2	64.192	6.987	385	43.350
E9B1C6	S-adenosylmethionine synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3500 PE=3 SV=1 - [E9B1C6_LEIMU]	6.89	3	2	3	4	1.000	3	0.000	6.983	392	43.102
B3KRZ6	cDNA FLJ35174 fis, clone PLACE6013386, highly similar to Beta-1,4-galactosyltransferase 3 (EC 2.4.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KRZ6_HUMAN]	6.22	5	2	2	2	1.200	2	27.495	6.979	370	41.461
Q9ULM3	YEATS domain-containing protein 2 OS=Homo sapiens GN=YEATS2 PE=1 SV=2 - [YETS2_HUMAN]	1.2	4	1	2	3	1.000	1		6.973	1422	150.689
Q5HYI7	Metaxin-3 OS=Homo sapiens GN=MTX3 PE=1 SV=2 - [MTX3_HUMAN]	8.97	1	2	2	3	1.000	3	0.515	6.965	312	35.071
H7C1U3	Coiled-coil and C2 domain-containing protein 1B (Fragment) OS=Homo sapiens GN=CC2D1B PE=1 SV=2 - [H7C1U3_HUMAN]	5.65	3	4	4	4	0.579	4	88.579	6.964	672	74.559
H7BZ93	Histone-lysine N-methyltransferase SETD2 (Fragment) OS=Homo sapiens GN=SETD2 PE=1 SV=1 - [H7BZ93_HUMAN]	1.55	5	2	2	3	1.000	3	0.000	6.963	1290	145.478
Q9H9B1	Histone-lysine N-methyltransferase EHMT1 OS=Homo sapiens GN=EHMT1 PE=1 SV=4 - [EHMT1_HUMAN]	4.31	2	3	3	4	1.000	3	0.000	6.956	1298	141.377
Q7Z7K6	Centromere protein V OS=Homo sapiens GN=CENPV PE=1 SV=1 - [CENPV_HUMAN]	10.55	1	3	3	6	1.030	6	4.461	6.956	275	29.927
P50238	Cysteine-rich protein 1 OS=Homo sapiens GN=CRIP1 PE=1 SV=3 - [CRIP1_HUMAN]	16.88	5	2	2	4	0.790	4	4.220	6.952	77	8.527
E9B3Q4	60S ribosomal protein L6 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_0720 PE=3 SV=1 - [E9B3Q4_LEIMU]	12.82	2	3	3	3	1.346	3	100.715	6.938	195	21.129
H3BM63	Armadillo repeat-containing X-linked protein 3 (Fragment) OS=Homo sapiens GN=ARMCX3 PE=1 SV=1 - [H3BM63_HUMAN]	30.16	3	1	1	2	1.000	2	0.000	6.938	63	6.762
B4E367	cDNA FLJ61564, highly similar to Plexin domain-containing protein 2 OS=Homo sapiens PE=2 SV=1 - [B4E367_HUMAN]	5.44	4	3	3	3	1.000	3	11.438	6.934	515	58.147
B3KX74	cDNA FLJ44929 fis, clone BRAMY3015547, highly similar to Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10-like, transcript variant 1, mRNA OS=Homo	1.92	5	2	2	3	1.126	2	17.698	6.914	1040	114.254
H9ZYI9	GA binding protein transcription factor beta subunit 1 transcript variant gamma-2 OS=Homo sapiens GN=GABPB1 PE=1 SV=1 - [H9ZYI9_HUMAN]	4.61	8	2	2	4	1.044	4	11.253	6.905	347	36.828
Q3LIE7	Putative uncharacterized protein Nbla03646 OS=Homo sapiens GN=Nbla03646 PE=2 SV=1 - [Q3LIE7_HUMAN]	3.51	4	2	2	3	0.926	3	4.791	6.901	427	49.404
E9AU41	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6060 PE=4 SV=1 - [E9AU41_LEIMU]	4.18	1	2	2	2	1.383	2	50.973	6.899	765	84.528
P28749	Retinoblastoma-like protein 1 OS=Homo sapiens GN=RBL1 PE=1 SV=3 - [RBL1_HUMAN]	1.03	1	1	1	2	0.751	2	44.432	6.898	1068	120.770
S4R3P0	Aldo-keto reductase family 1 member C2 (Fragment) OS=Homo sapiens GN=AKR1C2 PE=4 SV=1 - [S4R3P0_HUMAN]	12	14	2	2	2	0.612	2	48.216	6.885	200	22.617
H7C2D3	Round spermatid basic protein 1-like protein (Fragment) OS=Homo sapiens GN=RSBN1L PE=4 SV=1 - [H7C2D3_HUMAN]	12.43	4	2	2	2	0.871	2	20.632	6.884	177	20.212
Q9NYU1	UDP-glucose:glycoprotein glucosyltransferase 2 OS=Homo sapiens GN=UGGT2 PE=1 SV=4 - [UGGG2_HUMAN]	1.32	2	1	3	4	0.696	1		6.883	1516	174.624
F8W0R1	Relaxin-3 (Fragment) OS=Homo sapiens GN=RLN3 PE=4 SV=1 - [F8W0R1_HUMAN]	6.98	7	1	1	4	1.000	4	0.000	6.877	172	19.497
E9AMM0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0210 PE=4 SV=1 - [E9AMM0_LEIMU]	4.26	2	1	2	3	1.000	1		6.869	305	33.076
Q96J01	THO complex subunit 3 OS=Homo sapiens GN=THOC3 PE=1 SV=1 - [THOC3_HUMAN]	7.98	2	3	3	3	1.000	3	0.000	6.866	351	38.747
Q9UHD2	Serine/threonine-protein kinase TBK1 OS=Homo sapiens GN=TBK1 PE=1 SV=1 - [TBK1_HUMAN]	2.88	2	2	2	2	0.847	2	8.163	6.854	729	83.589
E9AXF0	Eukaryotic translation initiation factor 5A OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0720 PE=1 SV=1 - [IF5A_LEIMU]	10.24	1	2	2	4	0.926	4	13.152	6.846	166	17.817
O14672	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1 - [ADA10_HUMAN]	3.88	2	2	2	2	0.874	2	30.294	6.830	748	84.088
G3V5K2	Transmembrane protein 194A OS=Homo sapiens GN=TMEM194A PE=4 SV=1 - [G3V5K2_HUMAN]	8.18	2	1	1	2	0.780	2	10.262	6.828	110	12.019
Q9Y5P6	Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 - [GMPPB_HUMAN]	8.33	2	3	3	3	0.826	3	5.380	6.820	360	39.809

E9B709	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4810 PE=4 SV=1 - [E9B709_LEIMU]	3.66	1	1	1	2	1.000	2	0.000	6.818	382	42.202
O15091	Mitochondrial ribonuclease P protein 3 OS=Homo sapiens GN=KIAA0391 PE=1 SV=2 - [MRRP3_HUMAN]	4.8	1	3	3	3	1.000	3	0.000	6.811	583	67.272
Q6NSK7	RIN3 protein OS=Homo sapiens GN=RIN3 PE=2 SV=1 - [Q6NSK7_HUMAN]	1.32	5	1	1	2	0.845	1		6.807	908	100.090
A6H8Z4	NOL8 protein OS=Homo sapiens GN=NOL8 PE=2 SV=1 - [A6H8Z4_HUMAN]	2.73	1	1	3	3	1.000	1		6.807	1099	123.716
Q3ZAQ7	Vacuolar ATPase assembly integral membrane protein VMA21 OS=Homo sapiens GN=VMA21 PE=1 SV=1 - [VMA21_HUMAN]	21.78	1	2	2	3	1.148	3	6.312	6.805	101	11.347
Q96D21	GTP-binding protein Rhes OS=Homo sapiens GN=RASD2 PE=1 SV=1 - [RHES_HUMAN]	5.26	1	1	1	3	0.854	3	25.529	6.798	266	30.346
A8K9A5	cDNA FLJ78114, highly similar to Homo sapiens thymidylate synthetase, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9A5_HUMAN]	8.31	3	2	2	2	0.949	2	7.753	6.798	313	35.792
A0A087WTT6	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=4 SV=1 - [A0A087WTT6_HUMAN]	15.09	2	2	2	3	1.000	3	0.000	6.796	53	6.111
Q8TDJ6	DmX-like protein 2 OS=Homo sapiens GN=DMXL2 PE=1 SV=2 - [DMXL2_HUMAN]	0.82	3	2	2	2	0.927	2	11.252	6.787	3036	339.427
F8VQ24	Transcription factor SOX-6 (Fragment) OS=Homo sapiens GN=SOX6 PE=4 SV=1 - [F8VQ24_HUMAN]	11.8	4	1	1	2	1.000	1		6.786	178	18.436
B2RDE0	cDNA, FLJ96567, highly similar to Homo sapiens propionyl Coenzyme A carboxylase, alpha polypeptide(PCCA), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDE0_HUM	3.13	3	2	2	2	1.000	2	0.000	6.764	703	77.365
E9B0K2	Putative 4-methyl-5(Beta-hydroxyethyl)-thiazole monophosphate synthesis protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_0750 PE=4	13.27	1	3	3	3	1.000	3	0.000	6.763	196	20.657
Q8NDE9	Putative uncharacterized protein DKFZp434J2412 (Fragment) OS=Homo sapiens GN=DKFZp434J2412 PE=2 SV=1 - [Q8NDE9_HUMAN]	3.91	5	2	2	3	1.000	3	15.187	6.763	614	66.700
E5RFE4	N-acetyltransferase ESCO2 OS=Homo sapiens GN=ESCO2 PE=1 SV=1 - [E5RFE4_HUMAN]	5.17	2	1	1	2	1.000	2	0.000	6.744	290	33.177
Q9Y655	Myelin gene expression factor 2 OS=Homo sapiens PE=2 SV=1 - [Q9Y655_HUMAN]	4.94	5	3	3	5	1.000	3	0.000	6.739	547	58.632
Q9ULZ2	Signal-transducing adaptor protein 1 OS=Homo sapiens GN=STAP1 PE=1 SV=1 - [STAP1_HUMAN]	3.73	1	1	1	2	1.114	2	16.072	6.738	295	34.270
J3KMY1	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial (Fragment) OS=Homo sapiens GN=GATC PE=4 SV=1 - [J3KMY1_HUMAN]	40.43	3	1	1	1	0.310	1		6.737	47	5.322
Q96BR5	Cytochrome c oxidase assembly factor 7 OS=Homo sapiens GN=COA7 PE=1 SV=2 - [COA7_HUMAN]	9.09	1	2	2	2	1.221	2	37.389	6.730	231	25.692
Q6IA86	Elongator complex protein 2 OS=Homo sapiens GN=ELP2 PE=1 SV=2 - [ELP2_HUMAN]	2.42	1	2	2	2	1.000	2	0.000	6.730	826	92.441
A0A087WVF8	Myomegalin OS=Homo sapiens GN=PDE4DIP PE=4 SV=1 - [A0A087WVF8_HUMAN]	1.16	7	1	3	3	1.000	1		6.725	2240	253.914
H7C1M5	Deoxynucleotidyltransferase terminal-interacting protein 1 (Fragment) OS=Homo sapiens GN=DNTTIP1 PE=1 SV=1 - [H7C1M5_HUMAN]	6.07	3	2	2	3	1.884	3	23.454	6.725	280	31.754
Q8NDV7	Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2 - [TNR6A_HUMAN]	1.53	6	2	3	5	1.000	2	0.000	6.724	1962	210.169
H0YII4	Protein DDI1 homolog 2 (Fragment) OS=Homo sapiens GN=DDI2 PE=1 SV=1 - [H0YII4_HUMAN]	15.15	3	2	2	3	1.069	2	9.886	6.715	99	11.249
Q66GS9	Centrosomal protein of 135 kDa OS=Homo sapiens GN=CEP135 PE=1 SV=2 - [CP135_HUMAN]	1.14	7	1	2	3	2.439	1		6.708	1140	133.408
B2RDT9	cDNA, FLJ96765 OS=Homo sapiens PE=2 SV=1 - [B2RDT9_HUMAN]	7.76	2	2	2	2	0.865	2	21.728	6.696	348	39.360
Q5TBQ0	Protein LSM14 homolog B (Fragment) OS=Homo sapiens GN=LSM14B PE=1 SV=1 - [Q5TBQ0_HUMAN]	12.5	9	2	3	4	0.753	1		6.688	296	32.059
Q8WUW1	Protein BRICK1 OS=Homo sapiens GN=BRK1 PE=1 SV=1 - [BRK1_HUMAN]	12	1	1	1	3	1.000	3	0.000	6.685	75	8.739
Q9HBF4	Zinc finger FYVE domain-containing protein 1 OS=Homo sapiens GN=ZFYVE1 PE=1 SV=1 - [ZFYV1_HUMAN]	3.09	2	3	3	3	1.000	3	0.000	6.682	777	87.120
A0A024R2H7	tRNA nucleotidyl transferase, CCA-adding, 1, isoform CRA_b OS=Homo sapiens GN=TRNT1 PE=3 SV=1 - [A0A024R2H7_HUMAN]	3.92	2	2	2	3	0.822	3	9.164	6.680	434	50.112
H3BTA8	Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein (Fragment) OS=Homo sapiens GN=HERPUD1 PE=1 SV=1 - [H3BTA8_	11.93	10	1	1	2	1.000	2	0.000	6.680	109	12.365
E9B6Q7	Putative 60S ribosomal protein L23 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3790 PE=3 SV=1 - [E9B6Q7_LEIMU]	7.19	1	1	1	2	4.733	2	10.391	6.669	139	14.947
J3QQW9	Polycomb protein SUZ12 OS=Homo sapiens GN=SUZ12 PE=1 SV=1 - [J3QQW9_HUMAN]	2.93	3	2	2	2	0.935	2	2.267	6.668	716	80.271
A8K134	cDNA FLJ75245, highly similar to Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K134_HUMAN]	1.47	8	1	3	3	0.965	1		6.665	1500	164.764
E7EVE9	TFIIH basal transcription factor complex helicase XPD subunit OS=Homo sapiens GN=ERCC2 PE=1 SV=1 - [E7EVE9_HUMAN]	2.2	6	1	2	3				6.662	682	77.873
P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	15.69	4	2	3	4	1.018	2	2.591	6.655	376	42.594
F5GZY7	Gamma-aminobutyric acid receptor-associated protein-like 1 (Fragment) OS=Homo sapiens GN=GABARAPL1 PE=1 SV=1 - [F5GZY7_HUMAN]	10	8	1	1	3	0.945	1		6.654	70	8.572
Q9UNY4	Transcription termination factor 2 OS=Homo sapiens GN=TTF2 PE=1 SV=2 - [TTF2_HUMAN]	3.44	2	2	3	3				6.653	1162	129.508
B4DLW6	cDNA FLJ58198, moderately similar to Adrenal medulla 50 kDa protein OS=Homo sapiens PE=2 SV=1 - [B4DLW6_HUMAN]	6.3	3	2	2	3	1.000	1		6.644	270	29.799
E9ALZ5	Cysteine peptidase C (CPC) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0820 PE=3 SV=1 - [E9ALZ5_LEIMU]	8.82	1	2	2	3	1.000	3	0.000	6.637	340	37.154
E9AVY6	Alanine--tRNA ligase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_1540 PE=3 SV=1 - [E9AVY6_LEIMU]	2.7	1	3	3	3	1.000	3	0.000	6.635	962	106.098
E5RHF4	39S ribosomal protein L15, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL15 PE=1 SV=1 - [E5RHF4_HUMAN]	9.09	4	2	2	3	0.880	2	23.281	6.632	198	21.930
J3QRX6	Coordinator of PRMT5 and differentiation stimulator (Fragment) OS=Homo sapiens GN=COPRS PE=4 SV=1 - [J3QRX6_HUMAN]	11.65	3	1	1	3	1.000	3	0.000	6.631	103	11.412
A8K9L2	cDNA FLJ76729, highly similar to Homo sapiens vaccinia related kinase 2 isoform 6 (VRK2) mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9L2_HUMAN]	6.31	4	3	3	3	1.000	3	9.095	6.627	396	44.991
D3DTH7	Myosin IC, isoform CRA_a OS=Homo sapiens GN=MYO1C PE=4 SV=1 - [D3DTH7_HUMAN]	3.02	6	3	3	6	1.125	6	32.673	6.624	862	98.872
B1AMN7	CTTNBP2 N-terminal-like protein (Fragment) OS=Homo sapiens GN=CTTNBP2NL PE=1 SV=1 - [B1AMN7_HUMAN]	6.27	2	2	2	4	1.000	3	7.672	6.616	271	31.758
E8NHJ5	WGS CADB00000000 data, contig 43 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_24_1500a_1 PE=4 SV=1 - [E8NHJ5_LEIMU]	8.82	2	2	2	3	3.730	3	12.797	6.616	170	19.305
Q9BTK6	PAXIP1-associated glutamate-rich protein 1 OS=Homo sapiens GN=PAGR1 PE=1 SV=1 - [PAGR1_HUMAN]	5.51	1	1	1	2	1.058	2	14.739	6.610	254	27.699
A0A087WVQ2	PHD finger protein 23 OS=Homo sapiens GN=PHF23 PE=4 SV=1 - [A0A087WVQ2_HUMAN]	8.23	5	1	1	2	1.000	2	0.000	6.610	158	17.081
Q2LAE2	Intersectin 1 short form (Fragment) OS=Homo sapiens GN=ITSN1 PE=2 SV=1 - [Q2LAE2_HUMAN]	1.86	12	2	2	3	1.000	3	0.000	6.609	1076	121.570
Q9HAU5	Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 PE=1 SV=1 - [RENT2_HUMAN]	3.54	1	4	5	5	1.000	4	0.000	6.602	1272	147.717
Q14191	Werner syndrome ATP-dependent helicase OS=Homo sapiens GN=WRN PE=1 SV=2 - [WRN_HUMAN]	2.37	2	3	3	3	1.000	3	0.000	6.601	1432	162.357
H0YD13	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2 - [H0YD13_HUMAN]	11.65	14	2	2	2	1.045	2	8.028	6.600	206	22.669
E5RIS3	AN1-type zinc finger protein 1 OS=Homo sapiens GN=ZFAND1 PE=1 SV=1 - [E5RIS3_HUMAN]	12.73	11	2	2	2	1.272	2	6.766	6.595	165	18.835
D3DQ38	Chromosome 1 open reading frame 123, isoform CRA_a OS=Homo sapiens GN=C1orf123 PE=4 SV=1 - [D3DQ38_HUMAN]	20	3	3	3	3	1.000	3	6.189	6.595	130	14.538
Q05CP8	CCDC6 protein (Fragment) OS=Homo sapiens GN=CCDC6 PE=2 SV=1 - [Q05CP8_HUMAN]	10.48	3	4	4	5	1.000	5	2.117	6.591	334	38.140
E9AZ75	Putative dynein heavy chain OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1750 PE=4 SV=1 - [E9AZ75_LEIMU]	0.18	1	1	1	3	0.924	3	16.990	6.590	4470	500.458
O60293	Zinc finger C3H1 domain-containing protein OS=Homo sapiens GN=ZFC3H1 PE=1 SV=3 - [ZC3H1_HUMAN]	1.61	1	3	3	3	1.000	3	0.000	6.590	1989	226.214
E9B050	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2290 PE=4 SV=1 - [E9B050_LEIMU]	0.84	1	1	1	4	1.000	4	0.000	6.584	833	90.233
E9AW79	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0640 PE=4 SV=1 - [E9AW79_LEIMU]	3.29	1	2	2	2	1.000	2	0.000	6.583	608	70.095
Q15024	Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 - [EXOS7_HUMAN]	8.59	3	3	3	4	0.901	4	9.382	6.582	291	31.801
Q9NUM4	Transmembrane protein 106B OS=Homo sapiens GN=TMEM106B PE=1 SV=2 - [T106B_HUMAN]	7.66	4	2	2	3	1.205	3	28.203	6.582	274	31.108
A6NN14	Zinc finger protein 729 OS=Homo sapiens GN=ZNF729 PE=2 SV=4 - [ZN729_HUMAN]	14.22	57	1	3	3	1.000	1		6.576	1252	144.926
Q13144	Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=1 SV=3 - [EI2BE_HUMAN]	4.58	5	3	3	4	0.988	3	1.775	6.575	721	80.329
Q9H8H0	Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=1 SV=1 - [NOL11_HUMAN]	1.39	1	1	1	2	1.024	2	374.225	6.572	719	81.072
B4DHU6	cDNA FLJ55785, highly similar to Serine/threonine-protein kinase PCTAIRE-3 (EC 2.7.11.22) OS=Homo sapiens PE=2 SV=1 - [B4DHU6_HUMAN]	6.15	72	2	3	4	0.915	2	11.987	6.569	374	42.731
Q59FI2	Protein tyrosine phosphatase, receptor type, F isoform 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FI2_HUMAN]	2.96	8	4	4	5	1.000	5	0.000	6.566	1552	174.769
P27701	CD82 antigen OS=Homo sapiens GN=CD82 PE=1 SV=1 - [CD82_HUMAN]	3.75	2	1	1	2	1.136	2	30.135	6.560	267	29.606
E9ATH0	Eukaryotic translation initiation factor 3 subunit I OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3880 PE=3 SV=1 - [E9ATH0_LEIMU]	3.37	1	1	1	2	1.527	2	44.082	6.558	356	38.577
B3KME0	Protein argonaute OS=Homo sapiens PE=2 SV=1 - [B3KME0_HUMAN]	4.48	9	2	3	3	0.926	2	3.226	6.556	782	88.663
B4DYH4	cDNA FLJ51571, moderately similar to Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DYH4_HUMAN]	1.39	2	2	3	4	1.000	3	0.000	6.555	1655	178.638
E9AJC9	Complete genome, chromosome 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_01_0410 PE=4 SV=1 - [E9AJC9_LEIMU]	9.5	1	2	2	4	1.000	4	0.000	6.547	200	23.836
Q9H1J1	Regulator of nonsense transcripts 3A OS=Homo sapiens GN=UPF3A PE=1 SV=1 - [REN3A_HUMAN]	9.45	6	3	3	3	0.735	2	48.235	6.546	476	54.663
A6ND91	Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2 - [ASPD_HUMAN]	2.83	1	1	1	3	0.780	2	26.846	6.543	283	29.927
Q9BUL9	Ribonuclease P protein subunit p25 OS=Homo sapiens GN=RPP25 PE=1 SV=1 - [RPP25_HUMAN]	6.53	1	1	1	2	0.899	2	26.604	6.534	199	20.620
Q5T280	Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 - [CI114_HUMAN]	4.79	3	2	2	3	0.925	3	10.048	6.521	376	41.982
Q8N8A2	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B OS=Homo sapiens GN=ANKRD44 PE=1 SV=3 - [ANR44_HUMAN]	3.42	4	3	3	3	1.000	3	0.000	6.520	993	107.535
A8K9F5	cDNA FLJ77771, highly similar to Homo sapiens replication initiator 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9F5_HUMAN]	8.11	5	3	3	3	1.000	3	0.000	6.519	567	63.576
E9AS68	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1170 PE=4 SV=1 - [E9AS68_LEIMU]	0.7	2	1	1	3	0.909	2	12.626	6.504	998	101.503
B7Z3K1	cDNA FLJ51973 OS=Homo sapiens PE=2 SV=1 - [B7Z3K1_HUMAN]	10.61	3	1	1	3	1.000	3	0.000	6.500	132	14.937
I3L4X3	NF-kappa-B inhibitor beta (Fragment) OS=Homo sapiens GN=NFKBIB PE=4 SV=3 - [I3L4X3_HUMAN]	11.97	5	2	2	2	0.962	2	20.863	6.499	234	25.161
A6NJ78	Probable methyltransferase-like protein 15 OS=Homo sapiens GN=METTL15 PE=2 SV=1 - [MET15_HUMAN]	6.63	3	2	2	2	1.000	2	0.000	6.497	407	46.092
P16455	Methylated-DNA--protein-cysteine methyltransferase OS=Homo sapiens GN=MGMT PE=1 SV=1 - [MGMT_HUMAN]	6.28	2	1	1	3	1.000	1		6.486	207	21.632
A0A024R557	HCG2039447, isoform CRA_a OS=Homo sapiens GN=hCG_2039447 PE=4 SV=1 - [A0A024R557_HUMAN]	5.08	5	2	2	3	1.000	3	0.000	6.473	354	39.969
B3KX06	cDNA FLJ44413 fis, clone UTERU1000337, highly similar to Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16) OS=Homo sapiens PE=2 SV=1 - [B	6.29	5	1	1	2	0.998	2	0.348	6.468	286	31.287
A8K9U1	cDNA FLJ76468, highly similar to Homo sapiens cullin 7 (CUL7), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9U1_HUMAN]	0.88	2	1	1	2	1.000	2	0.000	6.466	1698	191.039
E9B6M8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3490 PE=4 SV=1 - [E9B6M8_LEIMU]	5.63	1	2	2	3	0.995	3	0.701	6.461	426	49.664
Q59GI3	I-kappa-B-related protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GI3_HUMAN]	1.34	2	1	1	2	0.780	2	19.588	6.459	897	97.010
Q9Y312	Protein AAR2 homolog OS=Homo sapiens GN=AAR2 PE=1 SV=2 - [AAR2_HUMAN]	6.51	2	2	2	3	1.000	3	19.959	6.454	384	43.444
Q15911	Zinc finger homeobox protein 3 OS=Homo sapiens GN=ZFHX3 PE=1 SV=2 - [ZFHX3_HUMAN]	0.41	3	2	2	3	0.986	3	26.571	6.432	3703	404.165
Q86TP0	SP3 protein (Fragment) OS=Homo sapiens GN=SP3 PE=2 SV=2 - [Q86TP0_HUMAN]	4.46	8	1	1	2	1.000	2	0.000	6.432	359	39.154
Q9UL15	BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 PE=1 SV=1 - [BAG5_HUMAN]	5.82	3	3	3	3	0.897	3	5.487	6.430	447	51.168
E9AVL4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0300 PE=4 SV=1 - [E9AVL4_LEIMU]	3.56	1	2	2	2	1.000	2	0.000	6.426	562	61.193
E9B063	Putative 2-oxoglutarate dehydrogenase, E2 component,dihydrolipoamide succinyltransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_:	4.88	1	1	2	4	1.000	2	0.000	6.420	389	41.711
E5RIH5	TELO2-interacting protein 2 OS=Homo sapiens GN=TTI2 PE=1 SV=1 - [E5RIH5_HUMAN]	7.97	2	3	3	3	1.000	3	0.000	6.419	477	53.272
H0YBS3	Inositol monophosphatase 3 (Fragment) OS=Homo sapiens GN=IMPAD1 PE=1 SV=1 - [H0YBS3_HUMAN]	29.27	2	3	3	3	1.025	3	10.270	6.413	82	9.268
D6RDJ3	DNA-directed RNA polymerases I and III subunit RPAC1 (Fragment) OS=Homo sapiens GN=POLR1C PE=1 SV=1 - [D6RDJ3_HUMAN]	23.39	6	2	2	2	1.000	1		6.413	124	14.196
B3KPM8	cDNA FLJ31974 fis, clone NT2RP7008167, weakly similar to 85.1 kDa PROTEIN IN GREB-FEOA INTERGENIC REGION OS=Homo sapiens PE=2 SV=1 - [B3KPM8_HU	2.01	2	2	2	3	1.046	3	6.662	6.412	995	111.675
O95295	SNARE-associated protein Snapin OS=Homo sapiens GN=SNAPIN PE=1 SV=1 - [SNAPN_HUMAN]	8.82	1	1	1	2	0.929	2	11.003	6.410	136	14.865
O95551	Tyrosyl-DNA phosphodiesterase 2 OS=Homo sapiens GN=TDP2 PE=1 SV=1 - [TYDP2_HUMAN]	6.35	3	2	2	2	1.033	2	34.297	6.409	362	40.903
Q59F16	Alpha 1 type VII collagen variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59F16_HUMAN]	1.36	3	2	2	3	1.000	3	2.707	6.399	1027	96.749
K7EIJ0	WW domain-binding protein 2 (Fragment) OS=Homo sapiens GN=WBP2 PE=1 SV=1 - [K7EIJ0_HUMAN]	19.76	12	4	4	4	1.024	4	5.173	6.389	167	18.212
X6R3N0	Long-chain fatty acid transport protein 3 OS=Homo sapiens GN=SLC27A3 PE=4 SV=1 - [X6R3N0_HUMAN]	4.32	2	1	2	2	1.000	1		6.387	811	87.269
E9B5U7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0670 PE=4 SV=1 - [E9B5U7_LEIMU]	0.55	1	1	3	3	1.190	1		6.384	4170	456.012
Q584P1	Putative uncharacterized protein PCYOX1 (Fragment) OS=Homo sapiens GN=PCYOX1 PE=4 SV=1 - [Q584P1_HUMAN]	5.03	8	2	2	3	0.844	3	3.416	6.384	398	45.110
B3KSN1	cDNA FLJ36670 fis, clone UTERU2004037, highly similar to Conserved oligomeric Golgi complex component 7 OS=Homo sapiens PE=2 SV=1 - [B3KSN1_HUMAN]	1.95	2	1	1	2	1.000	2	0.000	6.378	614	68.856
Q9NRC6	Spectrin beta chain, non-erythrocytic 5 OS=Homo sapiens GN=SPTBN5 PE=1 SV=2 - [SPTN5_HUMAN]	0.68	3	3	3	4	0.884	4	20.934	6.371	3674	416.493
Q9BSD7	Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 - [NTPCR_HUMAN]	10.53	2	2	2	3	0.848	2	17.742	6.366	190	20.700
Q3SYG4	Protein PTHB1 OS=Homo sapiens GN=BBS9 PE=1 SV=1 - [PTHB1_HUMAN]	2.25	6	2	3	4	1.111	3	15.697	6.358	887	99.217
Q5JUE6	Rap guanine nucleotide exchange factor 1 (Fragment) OS=Homo sapiens GN=RAPGEF1 PE=1 SV=1 - [Q5JUE6_HUMAN]	2.25	5	2	2	3	0.598	3	55.812	6.353	1023	113.537
Q96MW1	Coiled-coil domain-containing protein 43 OS=Homo sapiens GN=CCDC43 PE=1 SV=2 - [CCD43_HUMAN]	7.14	2	2	2	2	0.893	2	13.811	6.350	224	25.233
Q99856	AT-rich interactive domain-containing protein 3A OS=Homo sapiens GN=ARID3A PE=1 SV=2 - [ARI3A_HUMAN]	2.19	1	1	1	4	1.000	3	0.000	6.348	593	62.850
P49454	Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2 - [CENPF_HUMAN]	1.31	1	4	4	4	1.000	4	4.544	6.347	3210	367.537
E9B658	Trypanin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1810 PE=4 SV=1 - [E9B658_LEIMU]	3.9	1	2	3	4	1.000	3	0.000	6.345	461	53.937
E9B6B5	Putative aminopeptidase P OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2350 PE=3 SV=1 - [E9B6B5_LEIMU]	4.75	1	2	2	2	1.045	2	6.573	6.342	484	53.745
O95239	Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3 - [KIF4A_HUMAN]	2.44	4	1	3	3	1.056	1		6.342	1232	139.794
O15541	RING finger protein 113A OS=Homo sapiens GN=RNF113A PE=1 SV=1 - [R113A_HUMAN]	6.71	1	2	2	3	1.531	2	213.698	6.333	343	38.763
H0Y4V6	Serine/threonine-protein kinase Chk2 (Fragment) OS=Homo sapiens GN=CHEK2 PE=4 SV=1 - [H0Y4V6_HUMAN]	7.64	4	1	1	2	1.243	2	34.224	6.329	144	16.307
A0A087X0I4	Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=4 SV=1 - [A0A087X0I4_HUMAN]	4.89	5	2	2	3	1.000	3	10.144	6.324	307	34.488
I3L2Z5	Myc-associated zinc finger protein (Fragment) OS=Homo sapiens GN=MAZ PE=1 SV=1 - [I3L2Z5_HUMAN]	17.33	9	2	4	6	1.009	2	1.395	6.310	202	22.173
B4DXS5	cDNA FLJ57802, highly similar to Zinc finger protein 225 OS=Homo sapiens PE=2 SV=1 - [B4DXS5_HUMAN]	11.79	109	1	5	5	1.293	1		6.307	670	78.128
B4DGE7	cDNA FLJ61235, weakly similar to WD repeat protein YBL104C OS=Homo sapiens PE=2 SV=1 - [B4DGE7_HUMAN]	2.74	2	2	2	2	0.995	2	4.800	6.305	875	98.574
H0Y3N9	Histone lysine demethylase PHF8 (Fragment) OS=Homo sapiens GN=PHF8 PE=1 SV=1 - [H0Y3N9_HUMAN]	2.2	6	1	2	2	1.000	1		6.304	953	105.900
H3BNN4	Protein FAM188B2 (Fragment) OS=Homo sapiens GN=FAM188B2 PE=4 SV=1 - [H3BNN4_HUMAN]	2.21	2	1	1	3	1.064	3	19.216	6.297	272	31.096
Q9UHV7	Mediator of RNA polymerase II transcription subunit 13 OS=Homo sapiens GN=MED13 PE=1 SV=3 - [MED13_HUMAN]	1.24	1	2	2	2	0.985	2	2.201	6.295	2174	239.144
E9B465	Glycosyl hydrolase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2260 PE=4 SV=1 - [E9B465_LEIMU]	1.95	1	2	2	3	1.000	2	0.000	6.294	1433	154.265
L8E853	von Willebrand factor OS=Homo sapiens GN=VWF PE=4 SV=1 - [L8E853_HUMAN]	0.59	4	1	2	3	1.258	1		6.291	2715	298.181
F5H3K2	Uncharacterized protein C12orf43 (Fragment) OS=Homo sapiens GN=C12orf43 PE=1 SV=1 - [F5H3K2_HUMAN]	14.36	10	2	2	2	1.277	2	37.516	6.276	188	20.487
Q9UDW1	Cytochrome b-c1 complex subunit 9 OS=Homo sapiens GN=UQCR10 PE=1 SV=3 - [QCR9_HUMAN]	26.98	1	1	1	2	1.000	2	0.000	6.273	63	7.304
P78345	Ribonuclease P protein subunit p38 OS=Homo sapiens GN=RPP38 PE=1 SV=2 - [RPP38_HUMAN]	9.54	2	2	2	2	1.000	2	0.000	6.259	283	31.815
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	8.12	3	2	2	2	1.065	2	22.778	6.250	234	25.882
P49715	CCAAT/enhancer-binding protein alpha OS=Homo sapiens GN=CEBPA PE=1 SV=3 - [CEBPA_HUMAN]	9.78	2	4	4	4	1.041	4	3.178	6.242	358	37.538
O15085	Rho guanine nucleotide exchange factor 11 OS=Homo sapiens GN=ARHGEF11 PE=1 SV=1 - [ARHGB_HUMAN]	2.1	2	3	3	5	1.006	5	0.946	6.241	1522	167.601
F8WAX7	Selenoprotein K OS=Homo sapiens GN=SELK PE=4 SV=1 - [F8WAX7_HUMAN]	12.50	4	1	1	3	0.150	3	3.000	6.240	72.00	8.300
Q9BUT1	3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens GN=BDH2 PE=1 SV=2 - [BDH2_HUMAN]	7.35	9	2	2	2	1.081	2	5.634	6.237	245	26.707
Q6PD74	Alpha- and gamma-adaptin-binding protein p34 OS=Homo sapiens GN=AAGAB PE=1 SV=1 - [AAGAB_HUMAN]	5.4	4	2	2	3	0.956	3	4.723	6.234	315	34.572
C9JRP1	Sodium bicarbonate cotransporter 3 (Fragment) OS=Homo sapiens GN=SLC4A7 PE=1 SV=1 - [C9JRP1_HUMAN]	2.95	5	3	3	3	1.000	3	0.000	6.222	1051	118.387
Q9UPY3	Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3 - [DICER_HUMAN]	0.62	1	1	1	2	0.702	2	92.912	6.220	1922	218.542
V5J9V0	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [V5J9V0_HUMAN]	6.63	184	0	2	3				6.219	181	21.136
Q6NYC1	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Homo sapiens GN=JMJD6 PE=1 SV=1 - [JMJD6_HUMAN]	7.44	4	2	2	2	1.452	2	59.759	6.218	403	46.433
Q9H0F6	Sharpin OS=Homo sapiens GN=SHARPIN PE=1 SV=1 - [SHRPN_HUMAN]	6.98	3	2	2	2	1.145	1		6.217	387	39.924
Q53FD1	Zinc finger, HIT domain containing 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FD1_HUMAN]	2.98	3	1	1	2	0.895	2	16.600	6.216	403	42.887
B4DJF7	cDNA FLJ56915 OS=Homo sapiens PE=2 SV=1 - [B4DJF7_HUMAN]	2.37	3	1	1	2	0.780	2	11.892	6.216	380	43.428
E9AJH9	Phosphatidylinositol 3-kinase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0120 PE=4 SV=1 - [E9AJH9_LEIMU]	0.59	1	3	3	4	1.000	3	0.000	6.210	4922	526.203
J3KSJ7	Chromosome transmission fidelity protein 8 homolog isoform 2 (Fragment) OS=Homo sapiens GN=CHTF8 PE=4 SV=1 - [J3KSJ7_HUMAN]	20	4	1	1	2	1.000	2	0.000	6.206	65	7.376
E9AK64	Pescadillo homolog OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0810 PE=3 SV=1 - [E9AK64_LEIMU]	1.04	1	1	1	3	0.907	1		6.203	671	77.302
Q96GC5	39S ribosomal protein L48, mitochondrial OS=Homo sapiens GN=MRPL48 PE=1 SV=2 - [RM48_HUMAN]	15.09	3	4	4	5	0.910	5	15.600	6.194	212	23.920
Q96HQ2	CDKN2AIP N-terminal-like protein OS=Homo sapiens GN=CDKN2AIPNL PE=1 SV=1 - [C2AIL_HUMAN]	6.03	1	1	1	3	1.000	3	23.402	6.194	116	13.187
B2RBA0	cDNA, FLJ95388, highly similar to Homo sapiens step II splicing factor SLU7 (SLU7), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBA0_HUMAN]	3.58	3	2	2	2	1.029	2	4.213	6.194	586	68.314
Q75MY8	MX2 (Fragment) OS=Homo sapiens GN=MX2 PE=4 SV=1 - [Q75MY8_HUMAN]	4.72	2	2	2	2	1.714	2	24.668	6.187	424	49.823
Q9H2R8	CGI16-iso OS=Homo sapiens PE=2 SV=1 - [Q9H2R8_HUMAN]	11.11	3	2	2	2	1.056	2	8.134	6.186	189	21.627
B4DDI1	cDNA FLJ59835, highly similar to NifU-like N-terminal domain-containing protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B4DDI1_HUMAN]	11.04	7	2	2	4	1.000	4	5.784	6.185	154	16.568
F8W9L8	PHD finger protein 20-like protein 1 OS=Homo sapiens GN=PHF20L1 PE=1 SV=1 - [F8W9L8_HUMAN]	2.72	9	1	3	4	1.000	1		6.180	992	112.295
J3QSH4	Vascular endothelial zinc finger 1 OS=Homo sapiens GN=VEZF1 PE=1 SV=1 - [J3QSH4_HUMAN]	5.27	3	1	3	5	1.000	1		6.170	512	55.758
E9PEW5	Unconventional myosin-X OS=Homo sapiens GN=MYO10 PE=1 SV=1 - [E9PEW5_HUMAN]	1.15	7	1	2	6	1.000	1		6.170	1397	161.389
P59768	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2 OS=Homo sapiens GN=GNG2 PE=1 SV=2 - [GBG2_HUMAN]	22.54	3	1	1	3	1.000	3	0.000	6.163	71	7.845
Q9HCM7	Fibrosin-1-like protein OS=Homo sapiens GN=FBRSL1 PE=1 SV=4 - [FBSL_HUMAN]	1.15	1	1	2	3	0.661	2	67.537	6.161	1045	110.839
I6L899	Golgin subfamily A member 8R OS=Homo sapiens GN=GOLGA8R PE=3 SV=1 - [GOG8R_HUMAN]	4.91	6	3	3	3	1.000	3	1.057	6.157	631	71.446
B4DHM6	cDNA FLJ54808, highly similar to TBC1 domain family member 13 OS=Homo sapiens PE=2 SV=1 - [B4DHM6_HUMAN]	5.86	4	2	2	2	1.074	2	15.933	6.155	324	37.736
E9AWI0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1480 PE=3 SV=1 - [E9AWI0_LEIMU]	5.71	1	2	2	3	1.000	3	0.000	6.153	245	27.269
O75379	Vesicle-associated membrane protein 4 OS=Homo sapiens GN=VAMP4 PE=1 SV=2 - [VAMP4_HUMAN]	18.44	1	2	2	2	0.588	2	82.697	6.151	141	16.387
Q8NDX1	PH and SEC7 domain-containing protein 4 OS=Homo sapiens GN=PSD4 PE=1 SV=2 - [PSD4_HUMAN]	4.45	4	4	4	5	0.989	4	1.699	6.148	1056	116.177
E9AXH7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0990 PE=4 SV=1 - [E9AXH7_LEIMU]	3.7	8	1	1	3	0.971	2	4.407	6.148	162	18.416
B3KUS6	cDNA FLJ40512 fis, clone TESTI2046439, highly similar to Serine/threonine-protein kinase MAK (EC 2.7.11.22) OS=Homo sapiens PE=2 SV=1 - [B3KUS6_HUMAN]	6.25	46	1	2	3	1.000	1		6.142	288	33.617
H0Y764	Neurobeachin-like protein 2 (Fragment) OS=Homo sapiens GN=NBEAL2 PE=1 SV=1 - [H0Y764_HUMAN]	1.22	6	3	3	3	0.892	3	17.523	6.140	2042	224.444
B7Z6H4	DNA-directed RNA polymerase OS=Homo sapiens PE=2 SV=1 - [B7Z6H4_HUMAN]	2.12	6	2	3	3	0.964	2	5.506	6.137	1369	153.412
B7Z768	cDNA FLJ52138, highly similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 8 (EC 1.6.5.3) OS=Homo sapiens PE=2 SV=1 - [B7Z768_HUMAN]	6.25	2	1	1	3	0.985	3	3.016	6.135	128	14.953
Q6P6C2	RNA demethylase ALKBH5 OS=Homo sapiens GN=ALKBH5 PE=1 SV=2 - [ALKB5_HUMAN]	7.11	2	2	2	4	1.000	4	0.000	6.132	394	44.229
P61964	WD repeat-containing protein 5 OS=Homo sapiens GN=WDR5 PE=1 SV=1 - [WDR5_HUMAN]	6.59	3	2	2	3	1.000	3	0.000	6.132	334	36.565
Q9H061	Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=1 SV=1 - [T126A_HUMAN]	9.74	2	2	2	2	1.083	2	9.390	6.118	195	21.513
E9AP43	Putative carboxypeptidase (Metallo-peptidase, clan ma(E), family 32) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0090 PE=4 SV=1 - [E9A	4.57	1	2	2	3	1.151	3	91.646	6.102	503	57.214
B7Z341	cDNA FLJ54521, highly similar to Protein NDRG3 OS=Homo sapiens PE=2 SV=1 - [B7Z341_HUMAN]	8.12	6	1	1	2	0.935	1		6.101	271	29.702
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	7.6	2	2	2	2	0.907	2	35.925	6.086	263	28.462
Q03405	Urokinase plasminogen activator surface receptor OS=Homo sapiens GN=PLAUR PE=1 SV=1 - [UPAR_HUMAN]	5.67	7	2	2	4	1.568	4	36.139	6.083	335	36.953
Q9Y3X7	Putative uncharacterized protein DKFZp586C1620 (Fragment) OS=Homo sapiens GN=DKFZp586C1620 PE=2 SV=1 - [Q9Y3X7_HUMAN]	23.3	6	2	2	3	1.000	3	0.000	6.082	103	12.244
E9ALB7	RNA binding protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_1000 PE=4 SV=1 - [E9ALB7_LEIMU]	3.01	1	1	1	2	1.000	2	0.000	6.081	366	38.520
P61966	AP-1 complex subunit sigma-1A OS=Homo sapiens GN=AP1S1 PE=1 SV=1 - [AP1S1_HUMAN]	10.13	2	1	1	1	1.000	1		6.075	158	18.721
Q9HB72	PNAS-106 OS=Homo sapiens PE=2 SV=1 - [Q9HB72_HUMAN]	17.11	2	2	2	3	0.932	3	6.137	6.071	76	8.463
B3KS28	cDNA FLJ35355 fis, clone PUAEN2000152, moderately similar to N-terminal acetyltransferase C complexcatalytic subunit MAK3 (EC 2.3.1.88) OS=Homo sapiens PE=2 !	3.59	2	1	1	2	0.945	1		6.066	362	39.219
E9AS50	4-coumarate:coa ligase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0995 PE=4 SV=1 - [E9AS50_LEIMU]	1.74	2	1	1	2	1.276	2	37.318	6.063	633	68.586
C9JE12	Transmembrane and ubiquitin-like domain-containing protein 1 (Fragment) OS=Homo sapiens GN=TMUB1 PE=1 SV=1 - [C9JE12_HUMAN]	7.89	3	1	1	2	0.903	2	16.991	6.057	152	16.110
E7EX41	ATP-dependent RNA helicase DDX55 OS=Homo sapiens GN=DDX55 PE=1 SV=2 - [E7EX41_HUMAN]	10.47	5	2	2	2	0.990	2	11.254	6.050	191	21.601
E9AS06	Methionine aminopeptidase 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0550 PE=3 SV=1 - [E9AS06_LEIMU]	5.99	1	2	2	2	1.000	2	0.000	6.041	401	44.886
Q658U3	Putative uncharacterized protein DKFZp666D023 (Fragment) OS=Homo sapiens GN=DKFZp666D023 PE=2 SV=1 - [Q658U3_HUMAN]	5.92	10	1	1	2	1.021	2	1.807	6.040	169	18.711
E9AWS6	Triosephosphate isomerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0850 PE=3 SV=1 - [E9AWS6_LEIMU]	7.57	1	2	2	3	1.000	3	0.000	6.035	251	27.037
Q9H939	Proline-serine-threonine phosphatase-interacting protein 2 OS=Homo sapiens GN=PSTPIP2 PE=1 SV=4 - [PPIP2_HUMAN]	6.89	1	2	2	2	1.044	2	6.377	6.035	334	38.834
O76080	AN1-type zinc finger protein 5 OS=Homo sapiens GN=ZFAND5 PE=1 SV=1 - [ZFAN5_HUMAN]	14.55	2	2	2	2	1.057	2	8.295	6.030	213	23.117
A8K4P8	cDNA FLJ75337 OS=Homo sapiens PE=2 SV=1 - [A8K4P8_HUMAN]	0.66	2	1	1	2	0.961	2	5.918	6.030	1524	170.406
Q6P2H3	Centrosomal protein of 85 kDa OS=Homo sapiens GN=CEP85 PE=1 SV=1 - [CEP85_HUMAN]	1.31	1	1	1	2	1.000	2	0.000	6.022	762	85.586
O60287	Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens GN=URB1 PE=1 SV=4 - [NPA1P_HUMAN]	1.32	1	3	3	3	1.000	3	15.643	6.020	2271	254.227

J3KP75	Phosphatase and actin regulator OS=Homo sapiens GN=PHACTR2 PE=1 SV=1 - [J3KP75_HUMAN]	4.18	4	2	2	2	1.054	2	7.782	6.011	622	68.255
A0A024R0Q9	AarF domain containing kinase 4, isoform CRA_b OS=Homo sapiens GN=ADCK4 PE=4 SV=1 - [A0A024R0Q9_HUMAN]	4.37	3	2	2	2	1.444	2	7.439	6.004	503	55.817
D6RBJ9	Deoxycytidylate deaminase (Fragment) OS=Homo sapiens GN=DCTD PE=1 SV=1 - [D6RBJ9_HUMAN]	17.16	8	2	2	2	1.000	2	0.000	5.999	169	18.964
A0A024DBG3	Integrin beta-2 (Fragment) OS=Homo sapiens GN=ITGB2 PE=4 SV=1 - [A0A024DBG3_HUMAN]	38.81	1	1	2	2	0.875	1		5.996	67	7.492
E9PP42	Small integral membrane protein 7 OS=Homo sapiens GN=SMIM7 PE=1 SV=1 - [E9PP42_HUMAN]	21.28	8	1	1	2	1.014	2	2.097	5.993	47	5.155
H7C0W2	Negative elongation factor A (Fragment) OS=Homo sapiens GN=NELFA PE=1 SV=1 - [H7C0W2_HUMAN]	4.81	10	1	1	2	0.873	2	17.059	5.988	187	20.688
E9ALD3	Peptide methionine sulfoxide reductase-like (Putative peptide met(O) reductase) (Putative methionine-s-sulfoxide reductase) OS=Leishmania mexicana (strain MHOM/GT	10.8	1	2	2	2	3.273	2	107.615	5.987	176	19.742
Q96CN7	Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3 - [ISOC1_HUMAN]	3.69	1	1	1	2	1.068	2	0.953	5.987	298	32.216
B4DRF3	cDNA FLJ53020, highly similar to Homo sapiens timeless-interacting protein, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DRF3_HUMAN]	4.5	3	1	1	2	0.942	2	8.863	5.985	200	23.284
Q05D32	CTD small phosphatase-like protein 2 OS=Homo sapiens GN=CTDSPL2 PE=1 SV=2 - [CTSL2_HUMAN]	5.36	5	2	2	2	0.892	2	19.996	5.980	466	52.966
H0YKP9	MAP/microtubule affinity-regulating kinase 3 (Fragment) OS=Homo sapiens GN=MARK3 PE=1 SV=1 - [H0YKP9_HUMAN]	18.47	8	3	3	4	1.000	4	0.000	5.967	222	24.265
A8KAG1	cDNA FLJ77219 OS=Homo sapiens PE=2 SV=1 - [A8KAG1_HUMAN]	16.37	7	6	6	6	0.943	6	12.939	5.957	446	50.381
B4DW96	cDNA FLJ51119, highly similar to Ras and Rab interactor 1 OS=Homo sapiens PE=2 SV=1 - [B4DW96_HUMAN]	11.35	5	2	2	2	1.000	1		5.955	414	44.762
K7EQ07	GPI ethanolamine phosphate transferase 1 (Fragment) OS=Homo sapiens GN=PIGN PE=4 SV=1 - [K7EQ07_HUMAN]	10.68	8	1	1	2	1.261	2	84.222	5.952	103	11.726
P50583	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] OS=Homo sapiens GN=NUDT2 PE=1 SV=3 - [AP4A_HUMAN]	14.97	1	2	2	2	1.853	2	194.988	5.941	147	16.819
Q9NXN4	Ganglioside-induced differentiation-associated protein 2 OS=Homo sapiens GN=GDAP2 PE=1 SV=1 - [GDAP2_HUMAN]	2.41	1	1	1	2	1.033	2	4.850	5.939	497	56.189
H0YB49	Piezo-type mechanosensitive ion channel component 1 (Fragment) OS=Homo sapiens GN=PIEZO1 PE=4 SV=3 - [H0YB49_HUMAN]	16.48	3	1	1	2	1.000	2	0.000	5.938	182	20.518
B7Z507	cDNA FLJ51036, highly similar to Matrix metalloproteinase-9 (EC3.4.24.35) OS=Homo sapiens PE=2 SV=1 - [B7Z507_HUMAN]	3.09	2	1	1	2	1.139	2	21.581	5.937	648	71.509
E9B0B3	Glutamate dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2910 PE=3 SV=1 - [E9B0B3_LEIMU]	6.19	1	2	2	2	1.410	2	54.487	5.932	452	49.048
M0QYH2	Bifunctional polynucleotide phosphatase/kinase OS=Homo sapiens GN=PNKP PE=1 SV=1 - [M0QYH2_HUMAN]	2.65	2	1	1	2	1.260	2	50.073	5.926	490	53.607
E9APB2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0880 PE=4 SV=1 - [E9APB2_LEIMU]	3	1	2	2	2	1.185	2	25.544	5.919	699	76.931
C9J8X5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related (Fragment) OS=Homo sapiens GN=HMG20B PE=4 SV=1 - [C9	14.42	7	3	3	4	1.033	4	40.601	5.919	215	24.406
Q53H75	Chromosome 14 open reading frame 133 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53H75_HUMAN]	6.69	4	3	3	3	1.000	3	8.903	5.911	493	56.987
Q1RMZ3	NCOA6 protein (Fragment) OS=Homo sapiens GN=NCOA6 PE=2 SV=1 - [Q1RMZ3_HUMAN]	1.68	6	1	1	6	0.358	1		5.906	357	39.527
B4DZG6	cDNA FLJ53254, highly similar to Nucleoporin NDC1 OS=Homo sapiens PE=2 SV=1 - [B4DZG6_HUMAN]	7.08	2	2	2	2	1.128	2	37.407	5.904	339	37.904
Q53FP0	Pyridoxine 5'-phosphate oxidase variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53FP0_HUMAN]	9.2	2	2	2	2	1.067	2	9.658	5.901	261	29.897
Q8TBM3	V-type proton ATPase subunit a OS=Homo sapiens GN=ATP6V0A2 PE=2 SV=1 - [Q8TBM3_HUMAN]	2.96	2	1	1	2	0.909	2	14.173	5.897	372	43.148
Q15973	Zinc finger protein 124 OS=Homo sapiens GN=ZNF124 PE=2 SV=2 - [ZN124_HUMAN]	7.41	46	1	2	2	1.424	1		5.896	351	40.191
B4DLL6	cDNA FLJ54961, highly similar to Interferon-gamma receptor alpha chain OS=Homo sapiens PE=2 SV=1 - [B4DLL6_HUMAN]	3.04	10	2	2	3	0.938	3	16.600	5.890	461	51.503
O76095	Protein JTB OS=Homo sapiens GN=JTB PE=1 SV=1 - [JTB_HUMAN]	13.7	1	2	2	2	1.041	2	7.682	5.888	146	16.347
Q9BRU9	rRNA-processing protein UTP23 homolog OS=Homo sapiens GN=UTP23 PE=1 SV=2 - [UTP23_HUMAN]	4.82	1	1	1	2	1.036	2	5.277	5.884	249	28.384
Q9ULC3	Ras-related protein Rab-23 OS=Homo sapiens GN=RAB23 PE=1 SV=1 - [RAB23_HUMAN]	12.66	1	3	3	4	1.069	4	9.897	5.880	237	26.643
Q86TT1	Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1 - [Q86TT1_HUMAN]	8.53	6	3	3	4	0.935	4	9.986	5.873	375	41.247
M0R0F9	Cdc42-interacting protein 4 OS=Homo sapiens GN=TRIP10 PE=1 SV=1 - [M0R0F9_HUMAN]	7.78	5	2	2	2	1.004	2	0.658	5.872	437	49.682
E5RJ08	Coiled-coil-helix-coiled-coil-helix domain-containing protein 7 (Fragment) OS=Homo sapiens GN=CHCHD7 PE=4 SV=1 - [E5RJ08_HUMAN]	61.36	6	2	2	2	1.000	2	0.000	5.858	44	5.228
P50336	Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1 - [PPOX_HUMAN]	4.19	8	1	2	4	1.537	1		5.852	477	50.734
E9AJF5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_01_0680 PE=4 SV=1 - [E9AJF5_LEIMU]	4.35	6	1	2	4	1.000	1		5.852	804	83.570
A8K6L3	cDNA FLJ76883, highly similar to Homo sapiens FKSG44 gene (FKSG44), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6L3_HUMAN]	4.31	2	1	1	1	1.000	1		5.849	464	51.133
P50748	Kinetochore-associated protein 1 OS=Homo sapiens GN=KNTC1 PE=1 SV=1 - [KNTC1_HUMAN]	0.95	3	2	2	2	0.966	2	5.073	5.848	2209	250.588
O14933	Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens GN=UBE2L6 PE=1 SV=4 - [UB2L6_HUMAN]	4.58	1	1	1	2	1.120	2	3.413	5.845	153	17.757
A0A024R341	Ngg1 interacting factor 3 like 1 binding protein 1, isoform CRA_b OS=Homo sapiens GN=NIF3L1BP1 PE=4 SV=1 - [A0A024R341_HUMAN]	11.18	3	2	2	3	1.000	3	0.258	5.844	152	17.845
Q5T8J1	G1/S-specific cyclin-D3 OS=Homo sapiens GN=CCND3 PE=1 SV=1 - [Q5T8J1_HUMAN]	8.68	7	1	2	3	1.000	1		5.843	242	26.216
G3XAC1	Solute carrier family 26 member 6 OS=Homo sapiens GN=SLC26A6 PE=1 SV=1 - [G3XAC1_HUMAN]	2.15	3	2	2	3	0.891	3	17.212	5.841	651	71.490
B2R704	cDNA, FLJ93207, highly similar to Homo sapiens microtubule-associated protein 7 (MAP7), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R704_HUMAN]	2.67	6	2	2	3	1.000	3	0.000	5.841	749	83.932
Q9H7Z3	Protein NRDE2 homolog OS=Homo sapiens GN=NRDE2 PE=1 SV=3 - [NRDE2_HUMAN]	2.58	3	2	2	3	0.837	2	43.529	5.838	1164	132.589
G1UI18	Proteasome activator complex subunit 4 (Fragment) OS=Homo sapiens GN=PSME4 PE=2 SV=1 - [G1UI18_HUMAN]	3.64	3	3	4	5	0.921	4	13.764	5.837	1125	128.572
Q8N4H5	Mitochondrial import receptor subunit TOM5 homolog OS=Homo sapiens GN=TOMM5 PE=1 SV=1 - [TOM5_HUMAN]	29.41	2	3	3	4	0.959	4	5.843	5.835	51	6.031
D3DR32	M-phase phosphoprotein 1, isoform CRA_a OS=Homo sapiens GN=MPHOSPH1 PE=3 SV=1 - [D3DR32_HUMAN]	1.07	2	1	2	2	1.000	1		5.834	1780	206.034
Q8TCI2	CDNA FLJ23859 fis, clone LNG08092 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TCI2_HUMAN]	8.22	1	1	1	2	1.000	2	0.000	5.832	146	16.423
E9ARX6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0250 PE=4 SV=1 - [E9ARX6_LEIMU]	1.03	1	1	1	3	0.858	3	22.943	5.832	875	94.957
Q9H974	Queuine tRNA-ribosyltransferase subunit QTRTD1 OS=Homo sapiens GN=QTRTD1 PE=1 SV=1 - [QTRD1_HUMAN]	1.93	1	1	1	2	1.000	2	0.000	5.830	415	46.683
E9ANZ0	Putative alanine aminotransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0630 PE=4 SV=1 - [E9ANZ0_LEIMU]	2.01	1	1	1	2	1.000	2	0.000	5.828	497	54.945
B4DYQ3	cDNA FLJ60974, highly similar to Mediator of RNA polymerase II transcription subunit 12 OS=Homo sapiens PE=2 SV=1 - [B4DYQ3_HUMAN]	1.15	3	2	2	2	1.000	2	0.000	5.828	2000	222.292
Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9 OS=Homo sapiens GN=TIMM9 PE=1 SV=1 - [TIM9_HUMAN]	25.84	3	2	2	2	1.037	2	7.467	5.821	89	10.371
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3 - [UBP24_HUMAN]	1.11	2	2	3	3				5.817	2620	294.178
E9B085	Putative coatomer gamma subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2620 PE=4 SV=1 - [E9B085_LEIMU]	1.39	1	2	2	3	1.000	3	0.000	5.814	865	95.721
A7E1Z6	WD repeat and FYVE domain containing 3 OS=Homo sapiens GN=WDFY3 PE=2 SV=1 - [A7E1Z6_HUMAN]	4.63	4	1	1	2	1.000	2	0.000	5.813	281	31.678
E9AZN1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_0700 PE=4 SV=1 - [E9AZN1_LEIMU]	2.11	1	1	1	3	1.054	3	2.734	5.803	475	49.934
E9ATG7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3850 PE=4 SV=1 - [E9ATG7_LEIMU]	4.89	1	1	1	2	1.000	2	0.000	5.802	225	25.547
E9AZM3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_0620 PE=4 SV=1 - [E9AZM3_LEIMU]	0.53	1	1	1	4	1.067	4	8.878	5.790	1315	143.466
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	5.42	5	3	3	3	0.915	3	1.854	5.786	535	57.803
P51151	Ras-related protein Rab-9A OS=Homo sapiens GN=RAB9A PE=1 SV=1 - [RAB9A_HUMAN]	12.44	2	2	2	2	0.905	2	14.939	5.783	201	22.823
Q8N108	Mesoderm induction early response protein 1 OS=Homo sapiens GN=MIER1 PE=1 SV=2 - [MIER1_HUMAN]	1.56	1	1	1	2	0.810	2	18.114	5.782	512	57.948
E9AKB4	Serine/threonine-protein phosphatase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0100 PE=3 SV=1 - [E9AKB4_LEIMU]	4.24	1	2	2	2	1.045	2	6.531	5.779	637	71.800
Q9NUQ3	Gamma-taxilin OS=Homo sapiens GN=TXLNG PE=1 SV=2 - [TXLNG_HUMAN]	3.22	2	1	2	5	1.000	1		5.767	528	60.548
B4DEG9	cDNA FLJ58448, highly similar to Bromodomain-containing protein 8 OS=Homo sapiens PE=2 SV=1 - [B4DEG9_HUMAN]	2.03	16	1	2	2	1.393	1		5.757	837	91.023
L0R588	Alternative protein C11orf48 OS=Homo sapiens GN=C11orf48 PE=4 SV=1 - [L0R588_HUMAN]	8.18	1	1	1	2	0.967	2	10.089	5.756	159	18.384
A7E2Y5	DnaJ (Hsp40) homolog, subfamily C, member 13 OS=Homo sapiens GN=DNAJC13 PE=2 SV=1 - [A7E2Y5_HUMAN]	1.87	4	3	3	3	1.101	3	1.261	5.755	2243	254.291
A0A087WYF1	Laminin subunit alpha-2 OS=Homo sapiens GN=LAMA2 PE=4 SV=1 - [A0A087WYF1_HUMAN]	0.22	3	1	1	3	0.977	3	11.507	5.753	3118	343.196
D3DT96	Integrator complex subunit 7, isoform CRA_a OS=Homo sapiens GN=INTS7 PE=4 SV=1 - [D3DT96_HUMAN]	1.59	2	1	1	2	0.883	2	18.544	5.752	694	76.385
F6KRQ8	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [F6KRQ8_HUMAN]	5.52	2	1	1	2	1.052	2	7.557	5.751	181	21.155
A0A024R3J2	Solute carrier family 37 (Glycerol-3-phosphate transporter), member 2, isoform CRA_b OS=Homo sapiens GN=SLC37A2 PE=4 SV=1 - [A0A024R3J2_HUMAN]	2.34	2	1	1	2	1.078	2	27.026	5.751	385	42.896
Q9H617	Transmembrane protein 164 OS=Homo sapiens GN=RP13-360B22.2 PE=2 SV=1 - [Q9H617_HUMAN]	6.98	2	1	1	2	1.000	2	0.000	5.744	258	29.212
E9PJZ4	Mediator of RNA polymerase II transcription subunit 17 (Fragment) OS=Homo sapiens GN=MED17 PE=1 SV=1 - [E9PJZ4_HUMAN]	6.29	5	1	1	2	1.337	2	45.154	5.742	143	16.261
B1Q2B0	URCC5 OS=Homo sapiens GN=URCC5 PE=2 SV=1 - [B1Q2B0_HUMAN]	6.81	3	3	3	3	1.000	3	0.000	5.734	911	101.244
A0A024R2W4	Dystroglycan 1 (Dystrophin-associated glycoprotein 1), isoform CRA_a OS=Homo sapiens GN=DAG1 PE=4 SV=1 - [A0A024R2W4_HUMAN]	4.25	5	4	4	4	1.000	3	16.278	5.733	895	97.480
E9AKR9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0412 PE=4 SV=1 - [E9AKR9_LEIMU]	3.7	1	1	1	3	1.013	2	30.064	5.731	189	20.192
E7EP22	E3 ubiquitin-protein ligase RNF14 (Fragment) OS=Homo sapiens GN=RNF14 PE=4 SV=3 - [E7EP22_HUMAN]	28.1	12	3	3	3	1.000	3	8.370	5.729	153	17.651
D6RBD9	Thioredoxin domain-containing protein 15 (Fragment) OS=Homo sapiens GN=TXNDC15 PE=4 SV=1 - [D6RBD9_HUMAN]	12.26	6	1	1	2	1.000	2	0.000	5.728	155	16.871
Q53EP0	Fibronectin type III domain-containing protein 3B OS=Homo sapiens GN=FNDC3B PE=1 SV=2 - [FND3B_HUMAN]	1.91	1	2	2	2	1.406	2	53.862	5.724	1204	132.803
D6RBR7	Zinc finger protein 330 (Fragment) OS=Homo sapiens GN=ZNF330 PE=1 SV=1 - [D6RBR7_HUMAN]	12.66	7	3	3	3	0.927	3	11.318	5.718	229	25.815
P0CAP2	DNA-directed RNA polymerase II subunit GRINL1A OS=Homo sapiens GN=POLR2M PE=1 SV=1 - [GRL1A_HUMAN]	2.99	4	1	1	2	1.000	2	0.000	5.709	368	41.714
E9B6H7	Putative chaperone protein DNAj OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2980 PE=3 SV=1 - [E9B6H7_LEIMU]	4.8	1	1	2	2	1.000	1		5.709	479	51.001
B3KS10	cDNA FLJ35237 fis, clone PROST2001676, highly similar to M-PHASE PHOSPHOPROTEIN 8 OS=Homo sapiens PE=2 SV=1 - [B3KS10_HUMAN]	1.33	2	1	1	2	1.000	1		5.701	602	69.202
P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]	10	1	1	1	3	0.732	3	34.108	5.695	110	11.277
O15243	Leptin receptor gene-related protein OS=Homo sapiens GN=LEPROT PE=1 SV=1 - [OBRG_HUMAN]	10.69	2	2	2	2	0.981	2	2.846	5.694	131	14.244
Q86SF2	N-acetylgalactosaminyltransferase 7 OS=Homo sapiens GN=GALNT7 PE=1 SV=1 - [GALT7_HUMAN]	5.94	5	4	4	4	0.911	4	35.361	5.693	657	75.341
P43155	Carnitine O-acetyltransferase OS=Homo sapiens GN=CRAT PE=1 SV=5 - [CACP_HUMAN]	1.44	1	1	1	2	0.742	2	0.804	5.691	626	70.812
Q8IWC1	MAP7 domain-containing protein 3 OS=Homo sapiens GN=MAP7D3 PE=1 SV=2 - [MA7D3_HUMAN]	2.05	2	1	2	4	1.000	1		5.690	876	98.368
A0A087WWI0	Leucine-rich repeat-containing protein C10orf11 OS=Homo sapiens GN=C10orf11 PE=4 SV=1 - [A0A087WWI0_HUMAN]	10.62	2	2	2	2	1.012	2	1.772	5.687	226	25.673
S4R3D7	Calcium uptake protein 1, mitochondrial (Fragment) OS=Homo sapiens GN=MICU1 PE=4 SV=1 - [S4R3D7_HUMAN]	14.15	4	3	3	3	0.906	3	15.512	5.684	212	24.122
E9PPI7	Forkhead box protein K2 (Fragment) OS=Homo sapiens GN=FOXK2 PE=1 SV=4 - [E9PPI7_HUMAN]	10.24	9	2	3	3	0.941	2	8.998	5.684	254	27.769
X6R8P6	SOSS complex subunit C OS=Homo sapiens GN=INIP PE=4 SV=1 - [X6R8P6_HUMAN]	17.57	2	1	1	3	0.936	3	4.859	5.680	74	8.107
K7EIY6	E3 ubiquitin-protein ligase RNF126 (Fragment) OS=Homo sapiens GN=RNF126 PE=1 SV=2 - [K7EIY6_HUMAN]	7.75	8	2	2	2	0.961	2	5.900	5.668	284	30.853
C9JNK6	Metaxin-2 OS=Homo sapiens GN=MTX2 PE=1 SV=1 - [C9JNK6_HUMAN]	11.11	5	2	2	2	0.948	2	7.893	5.666	207	23.628
H7BZ50	Mitotic-spindle organizing protein 2B (Fragment) OS=Homo sapiens GN=MZT2B PE=1 SV=1 - [H7BZ50_HUMAN]	18.18	6	1	1	2	1.000	2	0.000	5.662	121	12.379
I3L505	Acyl carrier protein (Fragment) OS=Homo sapiens GN=NDUFAB1 PE=1 SV=1 - [I3L505_HUMAN]	8.57	3	1	1	3	1.000	3	16.612	5.659	70	8.055
B4E2L8	cDNA FLJ53487, highly similar to Coagulation factor XIII A chain (EC 2.3.2.13) OS=Homo sapiens PE=2 SV=1 - [B4E2L8_HUMAN]	1.44	3	1	1	2	1.000	2	0.000	5.659	626	70.299
B3KVH4	cDNA FLJ16549 fis, clone PLACE7003657, highly similar to RAC-alpha serine/threonine-protein kinase (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B3KVH4_HUMAN	9.17	34	3	5	7	1.000	5	0.000	5.656	480	55.594
Q8WVF3	RAB28 protein OS=Homo sapiens GN=RAB28 PE=1 SV=1 - [Q8WVF3_HUMAN]	11.58	2	1	1	2	1.000	1		5.653	95	10.602
H3BRY6	von Willebrand factor A domain-containing protein 9 OS=Homo sapiens GN=VWA9 PE=1 SV=1 - [H3BRY6_HUMAN]	4.49	5	2	2	2	1.056	2	408.181	5.650	468	51.551
B3KSW0	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (Phosphatidylinositol synthase), isoform CRA_b OS=Homo sapiens GN=CDIPT PE=2 SV=1 - [B3KSW0_HUMAN]	5.41	4	1	1	4	1.100	4	7.479	5.649	185	20.232
Q96D99	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96D99_HUMAN]	25.81	1	1	1	3	1.000	3	0.000	5.645	31	3.308
Q5TEJ7	Replication protein A 32 kDa subunit (Fragment) OS=Homo sapiens GN=RPA2 PE=1 SV=1 - [Q5TEJ7_HUMAN]	11.17	3	2	2	2	0.942	2	25.805	5.641	179	19.421
O75940	Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 - [SPF30_HUMAN]	9.24	1	2	2	2	1.955	2	88.792	5.639	238	26.694
Q96L52	PP2A B56 gamma 2 OS=Homo sapiens PE=4 SV=1 - [Q96L52_HUMAN]	2.11	4	1	1	2	1.562	2	74.091	5.627	475	55.520
Q504W7	Oculocerebrorenal syndrome of Lowe OS=Homo sapiens GN=OCRL PE=2 SV=1 - [Q504W7_HUMAN]	2.46	2	2	2	2	0.789	2	36.175	5.625	893	103.115
E9ASL7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0970 PE=4 SV=1 - [E9ASL7_LEIMU]	5.05	1	1	1	2	1.151	2	8.969	5.624	198	22.449
Q59H97	Zinc finger protein ZNF-U69274 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H97_HUMAN]	3.14	2	1	1	2	1.000	1		5.622	700	79.374
E9B1W3	Putative 3-ketoacyl-CoA thiolase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1630 PE=3 SV=1 - [E9B1W3_LEIMU]	6.02	2	1	2	2	1.000	1		5.621	399	42.969
B4DQD1	cDNA FLJ57138, highly similar to Metal-regulatory transcription factor 1 OS=Homo sapiens PE=2 SV=1 - [B4DQD1_HUMAN]	5.41	2	1	1	2	1.000	2	0.000	5.610	222	23.310
P23458	Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2 - [JAK1_HUMAN]	1.56	3	1	2	2	1.206	1		5.610	1154	133.191
Q92833	Protein Jumonji OS=Homo sapiens GN=JARID2 PE=1 SV=2 - [JARD2_HUMAN]	3.05	2	2	3	3				5.610	1246	138.648
P42684	Abelson tyrosine-protein kinase 2 OS=Homo sapiens GN=ABL2 PE=1 SV=1 - [ABL2_HUMAN]	1.95	1	2	2	2	2.255	1		5.606	1182	128.263
A8K610	cDNA FLJ76619 OS=Homo sapiens PE=2 SV=1 - [A8K610_HUMAN]	14.42	6	3	3	4	1.067	3	9.604	5.601	208	23.084
B4E2V5	cDNA FLJ52062, highly similar to Erythrocyte band 7 integral membrane protein OS=Homo sapiens PE=1 SV=1 - [B4E2V5_HUMAN]	5.06	3	1	1	2	1.244	2	20.222	5.599	237	25.948
H0YA43	Aryl hydrocarbon receptor repressor (Fragment) OS=Homo sapiens GN=AHRR PE=4 SV=1 - [H0YA43_HUMAN]	4.65	5	1	1	2	0.766	2	41.115	5.594	215	23.298
O95248	Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=1 SV=3 - [MTMR5_HUMAN]	1.77	3	2	2	3	1.000	3	0.000	5.589	1867	208.184
A8K4A1	cDNA FLJ76790 OS=Homo sapiens PE=2 SV=1 - [A8K4A1_HUMAN]	3.53	4	3	3	3	1.000	3	9.906	5.585	963	108.086
B7ZLB7	C5orf44 protein (Fragment) OS=Homo sapiens GN=C5orf44 PE=2 SV=1 - [B7ZLB7_HUMAN]	2.25	3	1	1	2	1.175	2	29.114	5.581	400	44.603
H0YB62	UPF0317 protein C14orf159, mitochondrial (Fragment) OS=Homo sapiens GN=C14orf159 PE=1 SV=1 - [H0YB62_HUMAN]	4.55	11	2	2	3	1.000	3	4.999	5.577	506	54.275
E9B2L9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0950 PE=4 SV=1 - [E9B2L9_LEIMU]	1.5	1	1	1	2	1.072	2	10.395	5.573	934	102.185
B4DYN3	cDNA FLJ55634, highly similar to Autophagy-related protein 9A OS=Homo sapiens PE=2 SV=1 - [B4DYN3_HUMAN]	5.4	5	3	3	3	1.000	3	0.000	5.569	778	87.228
P19397	Leukocyte surface antigen CD53 OS=Homo sapiens GN=CD53 PE=1 SV=1 - [CD53_HUMAN]	3.65	1	2	2	2	1.067	2	21.450	5.564	219	24.325
I3L3G9	Nuclear distribution protein nudE homolog 1 OS=Homo sapiens GN=NDE1 PE=4 SV=1 - [I3L3G9_HUMAN]	15.87	13	2	2	2	0.920	2	12.346	5.549	126	15.134
E9PL10	Transcription factor BTF3 homolog 4 OS=Homo sapiens GN=BTF3L4 PE=1 SV=1 - [E9PL10_HUMAN]	9.66	3	1	3	7	0.924	1		5.549	145	15.769
H0UIA1	Acyl-CoA synthetase short-chain family member 2, isoform CRA_c OS=Homo sapiens GN=ACSS2 PE=4 SV=1 - [H0UIA1_HUMAN]	2.9	12	2	2	2	1.015	2	2.146	5.545	655	73.224
A0A087WUE1	Protein TANC2 OS=Homo sapiens GN=TANC2 PE=4 SV=1 - [A0A087WUE1_HUMAN]	0.91	3	1	1	2	0.808	2	49.669	5.545	1100	120.445
P51580	Thiopurine S-methyltransferase OS=Homo sapiens GN=TPMT PE=1 SV=1 - [TPMT_HUMAN]	9.8	3	2	2	2	0.987	2	33.850	5.540	245	28.162
B4DE70	cDNA FLJ52253, highly similar to Mus musculus syntaxin 3 (Stx3), transcript variant C, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DE70_HUMAN]	4.44	4	1	1	2	1.052	2	7.471	5.535	180	20.705
Q86T29	Zinc finger protein 605 OS=Homo sapiens GN=ZNF605 PE=2 SV=1 - [ZN605_HUMAN]	4.68	4	1	2	3	0.795	2	17.261	5.531	641	74.328
C9JX77	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4 (Fragment) OS=Homo sapiens GN=PFKFB4 PE=4 SV=1 - [C9JX77_HUMAN]	11.43	6	2	2	2	1.142	2	20.057	5.527	175	20.178
Q3LIF3	Putative uncharacterized protein Nbla10388 (Fragment) OS=Homo sapiens GN=Nbla10388 PE=2 SV=1 - [Q3LIF3_HUMAN]	3.61	4	2	2	3	1.029	2	12.126	5.520	581	63.452
Q9H0A8	COMM domain-containing protein 4 OS=Homo sapiens GN=COMMD4 PE=1 SV=1 - [COMD4_HUMAN]	11.06	2	1	1	2	1.000	2	0.000	5.519	199	21.750
E9PQL5	Uncharacterized protein C11orf57 (Fragment) OS=Homo sapiens GN=C11orf57 PE=4 SV=1 - [E9PQL5_HUMAN]	10.99	5	1	1	2	0.839	2	26.448	5.519	91	10.883
Q75MP1	Putative uncharacterized protein PRKAR2B (Fragment) OS=Homo sapiens GN=PRKAR2B PE=4 SV=1 - [Q75MP1_HUMAN]	11.44	4	3	3	3	1.173	2	23.985	5.519	306	34.097
B7Z2Y2	Conserved oligomeric Golgi complex subunit 2 OS=Homo sapiens GN=COG2 PE=1 SV=1 - [B7Z2Y2_HUMAN]	2.5	4	2	2	2	1.044	2	6.360	5.516	679	76.032
Q8IWS0	PHD finger protein 6 OS=Homo sapiens GN=PHF6 PE=1 SV=1 - [PHF6_HUMAN]	7.95	3	2	2	4	0.922	4	12.156	5.514	365	41.264
I3L2C7	Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=1 SV=1 - [I3L2C7_HUMAN]	1.05	5	1	1	2	1.000	2	0.000	5.513	1047	118.745
B2R7B1	cDNA, FLJ93361, highly similar to Homo sapiens membrane interacting protein of RGS16 (MIR16), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7B1_HUMAN]	6.65	6	2	2	2	0.869	2	12.555	5.508	331	37.708
H3BPD7	Cirhin (Fragment) OS=Homo sapiens GN=CIRH1A PE=4 SV=2 - [H3BPD7_HUMAN]	6.76	4	1	1	2	1.000	2	0.000	5.507	148	16.753
E9B356	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2770 PE=4 SV=1 - [E9B356_LEIMU]	2.31	1	2	2	3	1.000	3	0.000	5.502	954	99.043
F5GXF5	Nucleosome-remodeling factor subunit BPTF (Fragment) OS=Homo sapiens GN=BPTF PE=1 SV=2 - [F5GXF5_HUMAN]	1.06	4	3	3	3	1.084	3	4.520	5.497	2457	271.364
B3KPZ7	cDNA FLJ32517 fis, clone SMINT1000117, highly similar to Pyruvate dehydrogenase (lipoamide)-phosphatase 1 (EC 3.1.3.43) OS=Homo sapiens PE=2 SV=1 - [B3KPZ7	4.49	6	2	2	2	1.060	2	8.714	5.495	535	60.758
B5MCB5	Cellular retinoic acid-binding protein 1 (Fragment) OS=Homo sapiens GN=CRABP1 PE=4 SV=2 - [B5MCB5_HUMAN]	19.47	2	2	2	2	1.036	2	12.450	5.490	113	12.262
E9ARC2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0010 PE=4 SV=1 - [E9ARC2_LEIMU]	1.16	1	1	1	2	1.000	2	0.000	5.486	774	87.574
B7Z448	cDNA FLJ51886, highly similar to Tryptophanyl-tRNA synthetase, mitochondrial (EC 6.1.1.2) OS=Homo sapiens PE=2 SV=1 - [B7Z448_HUMAN]	5.21	3	1	1	2	0.990	2	2.878	5.482	192	21.478
Q12972	Nuclear inhibitor of protein phosphatase 1 OS=Homo sapiens GN=PPP1R8 PE=1 SV=2 - [PP1R8_HUMAN]	6.27	4	2	2	3	1.011	3	44.604	5.478	351	38.455
E9AMC1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0420 PE=4 SV=1 - [E9AMC1_LEIMU]	0.56	1	1	1	2	1.000	2	0.000	5.472	1960	210.350
H0YGL0	Armadillo repeat-containing protein 6 (Fragment) OS=Homo sapiens GN=ARMC6 PE=1 SV=1 - [H0YGL0_HUMAN]	8.64	4	1	1	2	1.167	2	32.578	5.465	81	8.829
Q9NW15	Anoctamin-10 OS=Homo sapiens GN=ANO10 PE=1 SV=2 - [ANO10_HUMAN]	2.27	8	1	2	3	1.000	1		5.458	660	76.280
A0A087WZE6	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7 OS=Homo sapiens GN=GCNT7 PE=4 SV=1 - [A0A087WZE6_HUMAN]	1.63	1	1	1	4	1.000	4	0.000	5.457	429	49.159
Q96JJ8	KIAA1829 protein (Fragment) OS=Homo sapiens GN=KIAA1829 PE=2 SV=1 - [Q96JJ8_HUMAN]	4.67	70	0	2	2				5.439	557	64.655
B4E0M5	cDNA FLJ58823, highly similar to Thromboxane-A synthase (EC 5.3.99.5) OS=Homo sapiens PE=2 SV=1 - [B4E0M5_HUMAN]	4.83	6	2	2	2	1.055	2	7.967	5.437	414	46.985
J3KS73	Thymidine kinase 2, mitochondrial (Fragment) OS=Homo sapiens GN=TK2 PE=4 SV=1 - [J3KS73_HUMAN]	6.92	9	1	1	2	1.000	2	0.000	5.419	130	15.748
Q8ND23	Leucine-rich repeat-containing protein 16B OS=Homo sapiens GN=LRRC16B PE=2 SV=2 - [LR16B_HUMAN]	0.51	1	1	1	2	1.304	2	66.474	5.418	1372	150.137
A0A024RC67	Protein regulator of cytokinesis 1, isoform CRA_e OS=Homo sapiens GN=PRC1 PE=4 SV=1 - [A0A024RC67_HUMAN]	3.23	4	2	2	2	1.114	2	16.061	5.417	620	71.620
E9AM67	Proteasome regulatory non-ATPase subunit,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0120 PE=4 SV=1 - [E9AM67_LEIMU]	2.09	1	2	2	2	1.660	2	147.047	5.410	909	99.251
G3V4M9	Inositol 1,3,4-triphosphate 5/6 kinase, isoform CRA_c OS=Homo sapiens GN=ITPK1 PE=1 SV=1 - [G3V4M9_HUMAN]	6.44	4	2	2	2	1.007	2	1.046	5.406	295	31.697
H7BYN4	Kinesin-like protein KIF23 OS=Homo sapiens GN=KIF23 PE=1 SV=1 - [H7BYN4_HUMAN]	2.31	3	2	2	2	1.180	2	24.907	5.404	952	109.061
F2Z2Y6	U6 snRNA-associated Sm-like protein LSm8 OS=Homo sapiens GN=LSM8 PE=1 SV=1 - [F2Z2Y6_HUMAN]	25.37	4	2	2	2	1.105	2	17.446	5.404	67	7.367
Q7Z434	Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2 - [MAVS_HUMAN]	2.41	1	1	1	2	1.023	2	0.930	5.403	540	56.493
E9B490	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2510 PE=4 SV=1 - [E9B490_LEIMU]	0.89	1	1	1	3	1.000	3	7.806	5.403	677	75.156
Q6PN88	Hematopoietic stem/progenitor cell induced protein 2 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6PN88_HUMAN]	6.03	1	1	1	3	0.921	3	9.982	5.398	116	12.047
O43709	Probable 18S rRNA (guanine-N(7))-methyltransferase OS=Homo sapiens GN=WBSCR22 PE=1 SV=2 - [WBS22_HUMAN]	10.32	7	2	2	2	0.984	2	2.396	5.394	281	31.860
P28330	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADL PE=2 SV=2 - [ACADL_HUMAN]	4.65	2	2	2	2	1.000	2	0.000	5.393	430	47.625
E9AVP9	Prefoldin 5-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0670 PE=4 SV=1 - [E9AVP9_LEIMU]	5.13	1	1	1	2	1.000	2	0.000	5.388	156	17.738
H0YBG5	Protein Spindly (Fragment) OS=Homo sapiens GN=SPDL1 PE=4 SV=1 - [H0YBG5_HUMAN]	3.53	2	1	1	2	1.000	2	0.000	5.386	312	36.667
B4DWA9	cDNA FLJ57214, highly similar to TBC1 domain family member 22A OS=Homo sapiens PE=2 SV=1 - [B4DWA9_HUMAN]	2.48	5	1	1	2	1.000	1		5.382	403	47.070
B9ZVV8	Histone-lysine N-methyltransferase (Fragment) OS=Homo sapiens GN=SETMAR PE=1 SV=2 - [B9ZVV8_HUMAN]	10.85	4	2	2	2	1.000	2	0.000	5.380	212	23.764
E5RJH0	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=4 SV=1 - [E5RJH0_HUMAN]	6.32	5	1	2	2	1.000	1		5.371	253	28.188
A0A087WVI0	Uncharacterized aarF domain-containing protein kinase 1 OS=Homo sapiens GN=ADCK1 PE=4 SV=1 - [A0A087WVI0_HUMAN]	1.17	4	1	1	4	0.995	2	0.750	5.369	940	104.721
S4R3D6	Methylthioribulose-1-phosphate dehydratase OS=Homo sapiens GN=APIP PE=1 SV=1 - [S4R3D6_HUMAN]	4.62	3	1	1	2	0.898	2	10.479	5.368	195	21.942
Q6P589	Tumor necrosis factor alpha-induced protein 8-like protein 2 OS=Homo sapiens GN=TNFAIP8L2 PE=1 SV=1 - [TP8L2_HUMAN]	4.35	1	1	1	2	0.865	2	3.020	5.363	184	20.543
A0A024R872	Chromosome 9 open reading frame 88, isoform CRA_a OS=Homo sapiens GN=C9orf88 PE=4 SV=1 - [A0A024R872_HUMAN]	2.32	3	2	2	2	1.659	2	214.401	5.362	733	82.631
P51828	Adenylate cyclase type 7 OS=Homo sapiens GN=ADCY7 PE=2 SV=1 - [ADCY7_HUMAN]	2.31	3	1	2	2	0.553	1		5.361	1080	120.230
Q7L7X3	Serine/threonine-protein kinase TAO1 OS=Homo sapiens GN=TAOK1 PE=1 SV=1 - [TAOK1_HUMAN]	3.5	1	2	4	4	1.000	2	0.000	5.357	1001	115.997
E9B106	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2330 PE=4 SV=1 - [E9B106_LEIMU]	4.3	1	1	1	2	1.038	2	5.515	5.357	349	37.668
C9JK45	Solute carrier family 35 member E1 (Fragment) OS=Homo sapiens GN=SLC35E1 PE=4 SV=1 - [C9JK45_HUMAN]	6.9	3	1	1	2	0.989	2	1.635	5.352	116	12.984
K7EIN4	Transmembrane emp24 domain-containing protein 1 OS=Homo sapiens GN=TMED1 PE=1 SV=1 - [K7EIN4_HUMAN]	19.51	3	2	2	2	0.935	2	124.906	5.352	82	9.629
K7ESE8	Bleomycin hydrolase (Fragment) OS=Homo sapiens GN=BLMH PE=1 SV=1 - [K7ESE8_HUMAN]	8.23	5	2	2	2	0.920	2	12.897	5.349	231	26.721
Q5JSY7	Transducin-like enhancer protein 4 (Fragment) OS=Homo sapiens GN=TLE4 PE=1 SV=1 - [Q5JSY7_HUMAN]	5.9	11	2	2	2	0.558	2	109.489	5.341	322	35.856
B3KW52	cDNA FLJ42145 fis, clone TESTI4000228, highly similar to Mus musculus ubiquitin family domain containing 1 (Ubfd1), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KW52	10.22	4	2	2	3	0.726	3	19.145	5.336	186	21.133
E9AMS8	Oligopeptidase b OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0770 PE=4 SV=1 - [E9AMS8_LEIMU]	3.97	1	2	2	2	0.907	2	17.225	5.333	731	83.534
Q96Q62	Mitochondrial ribosomal protein S11 (Fragment) OS=Homo sapiens GN=MRPS11 PE=4 SV=1 - [Q96Q62_HUMAN]	92.86	4	2	2	3	0.738	3	0.250	5.328	14	1.584
E9B5Q2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0140 PE=4 SV=1 - [E9B5Q2_LEIMU]	16.81	1	2	2	2	1.605	2	22.219	5.324	119	14.437
E9PMS3	Peroxisomal membrane protein PEX16 OS=Homo sapiens GN=PEX16 PE=4 SV=1 - [E9PMS3_HUMAN]	38.46	4	2	2	2	0.608	2	76.585	5.324	52	5.853
B1ALB4	Protein SMG7 (Fragment) OS=Homo sapiens GN=SMG7 PE=1 SV=3 - [B1ALB4_HUMAN]	1.45	6	1	1	2	1.000	2	0.000	5.309	757	84.891
C9JF62	NEDD8-conjugating enzyme UBE2F (Fragment) OS=Homo sapiens GN=UBE2F PE=3 SV=1 - [C9JF62_HUMAN]	16.55	14	2	2	2	0.997	2	0.489	5.309	139	15.664

Q499L9	Serine/threonine protein kinase MST4 OS=Homo sapiens GN=MST4 PE=2 SV=1 - [Q499L9_HUMAN]	7.69	6	3	3	3	0.798	3	34.336	5.301	416	46.501
C9JYL6	Extracellular cell-membrane-anchored RET cadherin 120 kDa fragment (Fragment) OS=Homo sapiens GN=RET PE=4 SV=1 - [C9JYL6_HUMAN]	8.84	8	1	1	1	1.000	1		5.295	181	19.347
J3KN59	BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 - [J3KN59_HUMAN]	1.84	1	1	1	2	0.923	2	11.969	5.294	435	48.814
E9ANM6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0820 PE=4 SV=1 - [E9ANM6_LEIMU]	8.9	1	2	2	2	0.799	2	34.158	5.291	337	37.423
Q9BTS4	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BTS4_HUMAN]	5.94	6	2	2	2	0.827	2	6.581	5.290	286	32.494
O94888	UBX domain-containing protein 7 OS=Homo sapiens GN=UBXN7 PE=1 SV=2 - [UBXN7_HUMAN]	3.68	3	2	2	3	1.023	3	32.851	5.287	489	54.828
C9J9Y9	BAG family molecular chaperone regulator 1 (Fragment) OS=Homo sapiens GN=BAG1 PE=4 SV=2 - [C9J9Y9_HUMAN]	25	5	1	1	2	1.135	2	18.894	5.285	48	5.607
E9B182	Putative homoserine kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3080 PE=3 SV=1 - [E9B182_LEIMU]	3.23	1	1	1	2	0.958	2	6.370	5.283	341	36.171
Q96QE2	Proton myo-inositol cotransporter OS=Homo sapiens GN=SLC2A13 PE=1 SV=3 - [MYCT_HUMAN]	2.01	1	1	1	2	1.000	1		5.283	648	70.326
Q5T2E7	UPF0668 protein C10orf76 OS=Homo sapiens GN=C10orf76 PE=4 SV=1 - [Q5T2E7_HUMAN]	5.56	3	1	1	2	1.025	2	10.896	5.278	198	22.911
Q9BXV9	Uncharacterized protein C14orf142 OS=Homo sapiens GN=C14orf142 PE=1 SV=2 - [CN142_HUMAN]	26	1	1	1	3	1.000	3	0.000	5.276	100	10.852
A8K6F4	cDNA FLJ77991, highly similar to Homo sapiens zinc finger and BTB domain containing 7B, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6F4_HUMAN]	5.19	2	2	2	2	1.000	2	0.000	5.275	539	58.017
B3KRT9	cDNA FLJ34915 fis, clone NT2RP7001283, highly similar to Homo sapiens mSin3A-associated protein 130 (SAP130), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KRT9_	1.31	3	1	1	2	0.869	2	17.085	5.274	685	72.829
B7ZKY8	ADP-ribosylation factor related protein 1 OS=Homo sapiens GN=ARFRP1 PE=2 SV=1 - [B7ZKY8_HUMAN]	8.46	5	2	2	2	0.693	2	20.470	5.263	201	22.470
Q8NBM8	Prenylcysteine oxidase-like OS=Homo sapiens GN=PCYOX1L PE=1 SV=2 - [PCYXL_HUMAN]	3.64	4	2	2	2	0.942	2	24.123	5.261	494	54.612
B2R9X3	cDNA, FLJ94599, highly similar to Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R9X3_HUMAN]	4.03	2	2	2	2	1.176	2	24.408	5.258	372	41.824
B9EK47	HEAT repeat containing 5B OS=Homo sapiens GN=HEATR5B PE=2 SV=1 - [B9EK47_HUMAN]	0.77	2	2	2	2	0.982	2	2.668	5.257	2071	224.133
B4E2I4	cDNA FLJ58227, highly similar to Glutamate--cysteine ligase catalytic subunit (EC 6.3.2.2) OS=Homo sapiens PE=2 SV=1 - [B4E2I4_HUMAN]	3.42	3	2	2	2	1.095	2	14.008	5.253	584	66.421
H0YM19	Uncharacterized protein C15orf57 OS=Homo sapiens GN=C15orf57 PE=1 SV=1 - [H0YM19_HUMAN]	6.04	5	1	1	2	0.746	2	51.673	5.252	149	16.541
B4E1G1	Derlin-1 OS=Homo sapiens GN=DERL1 PE=1 SV=1 - [B4E1G1_HUMAN]	14.57	3	2	2	2	0.866	2	27.295	5.248	151	17.022
Q9UKD2	mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2 - [MRT4_HUMAN]	10.46	3	2	3	3	0.946	2	10.430	5.239	239	27.543
Q96A35	39S ribosomal protein L24, mitochondrial OS=Homo sapiens GN=MRPL24 PE=1 SV=1 - [RM24_HUMAN]	7.87	2	2	2	2	0.862	2	6.183	5.237	216	24.899
A8K1E1	cDNA FLJ75589, highly similar to Homo sapiens mutS homolog 3 (E. coli) (MSH3), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K1E1_HUMAN]	1.95	2	2	2	2	0.979	2	74.607	5.237	1128	126.685
A0A087WUZ8	28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=4 SV=1 - [A0A087WUZ8_HUMAN]	11.93	4	2	2	2	0.965	2	5.269	5.233	176	20.650
G3V2T4	Legumain (Fragment) OS=Homo sapiens GN=LGMN PE=1 SV=1 - [G3V2T4_HUMAN]	15.56	10	2	2	2	0.794	2	90.969	5.232	135	14.626
C9JM82	Uncharacterized protein OS=Homo sapiens GN=SEPT5 PE=1 SV=1 - [C9JM82_HUMAN]	6.31	19	2	2	2	0.780	2	38.161	5.225	301	34.651
B4DP12	cDNA FLJ55119, highly similar to Homo sapiens ZW10 interactor (ZWINT), transcript variant 3, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DP12_HUMAN]	4.35	3	1	1	3	1.000	3	0.000	5.220	230	25.574
Q8N609	Translocating chain-associated membrane protein 1-like 1 OS=Homo sapiens GN=TRAM1L1 PE=2 SV=2 - [TR1L1_HUMAN]	3.25	1	1	1	2	0.799	2	34.266	5.218	369	42.135
Q9NX00	Transmembrane protein 160 OS=Homo sapiens GN=TMEM160 PE=1 SV=1 - [TM160_HUMAN]	12.23	1	2	2	3	1.020	3	11.506	5.218	188	19.645
O00241	Signal-regulatory protein beta-1 OS=Homo sapiens GN=SIRPB1 PE=1 SV=5 - [SIRB1_HUMAN]	6.03	8	1	2	2	1.000	1		5.205	398	43.184
E9PPK2	Phosphofurin acidic cluster sorting protein 1 (Fragment) OS=Homo sapiens GN=PACS1 PE=4 SV=1 - [E9PPK2_HUMAN]	6.02	2	1	1	2	1.097	2	13.843	5.199	166	18.556
B4DE48	cDNA FLJ53824, highly similar to Sorting nexin-17 OS=Homo sapiens PE=2 SV=1 - [B4DE48_HUMAN]	3.41	9	2	2	3	1.000	3	0.000	5.195	440	49.724
Q9P0B4	HSPC267 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9P0B4_HUMAN]	6.91	3	1	1	2	1.043	2	6.268	5.194	188	22.378
E9AV01	Mitochondrial processing peptidase alpha subunit,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0340 PE=3 SV=1 - [E9AV01_LEIMI	4.5	1	2	2	2	2.463	2	222.922	5.190	467	51.427
Q13643	Four and a half LIM domains protein 3 OS=Homo sapiens GN=FHL3 PE=1 SV=4 - [FHL3_HUMAN]	7.14	3	2	2	2	0.917	2	12.834	5.188	280	31.171
A5YP36	SEC15-like protein 3 OS=Homo sapiens GN=SEC15L3 PE=2 SV=1 - [A5YP36_HUMAN]	2.57	11	2	2	2	1.032	2	4.648	5.184	701	81.827
A8K245	cDNA FLJ75441, highly similar to Homo sapiens vaccinia related kinase 1 (VRK1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K245_HUMAN]	6.31	4	3	3	5	1.000	5	0.411	5.182	396	45.417
B2R4I8	cDNA, FLJ92106, highly similar to Homo sapiens adaptor-related protein complex 3, sigma 1 subunit(AP3S1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R4I8_HUMAN]	5.7	2	1	1	2	0.784	2	7.547	5.181	193	21.691
X6R7M0	CWF19-like protein 1 OS=Homo sapiens GN=CWF19L1 PE=1 SV=1 - [X6R7M0_HUMAN]	7.91	3	2	2	2	1.055	2	133.935	5.171	253	29.004
Q96CN4	EVI5-like protein OS=Homo sapiens GN=EVI5L PE=1 SV=1 - [EVI5L_HUMAN]	2.02	2	1	2	2	1.000	1		5.171	794	91.318
Q9P0B6	Coiled-coil domain-containing protein 167 OS=Homo sapiens GN=CCDC167 PE=1 SV=2 - [CC167_HUMAN]	8.25	2	1	1	2	0.952	2	14.816	5.170	97	11.452
Q6MZZ4	Putative uncharacterized protein DKFZp686H0575 OS=Homo sapiens GN=DKFZp686H0575 PE=2 SV=1 - [Q6MZZ4_HUMAN]	4.99	2	1	1	3	1.000	3	0.000	5.168	361	38.972
E9AMJ6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_1225 PE=4 SV=1 - [E9AMJ6_LEIMU]	10.08	1	2	2	2	1.958	2	118.181	5.168	238	25.979
B4DM91	cDNA FLJ60085, highly similar to Nucleolar protein 8 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DM91_HUMAN]	3.32	11	1	3	3	0.409	1		5.167	933	104.144
E8NHJ8	Putative 60S acidic ribosomal subunit protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1380 PE=3 SV=1 - [E8NHJ8_LEIMU]	5.59	2	1	2	2	1.000	1		5.167	322	34.614
B4DI15	cDNA FLJ60550, weakly similar to Exosome complex exonuclease RRP44 (EC 3.1.13.-) OS=Homo sapiens PE=2 SV=1 - [B4DI15_HUMAN]	2.81	3	1	2	2	1.000	1		5.165	675	75.555
Q86XV5	AGAP3 protein (Fragment) OS=Homo sapiens GN=AGAP3 PE=2 SV=1 - [Q86XV5_HUMAN]	2.98	6	1	1	2	1.000	2	0.000	5.163	403	43.321
A0A024RC75	Chromodomain helicase DNA binding protein 2, isoform CRA_a OS=Homo sapiens GN=CHD2 PE=4 SV=1 - [A0A024RC75_HUMAN]	0.98	8	2	2	2	1.112	2	15.779	5.162	1739	200.438
Q13136	Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1 PE=1 SV=1 - [LIPA1_HUMAN]	1.25	5	2	2	2	0.723	2	58.863	5.160	1202	135.695
Q6P587	Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens GN=FAHD1 PE=1 SV=2 - [FAHD1_HUMAN]	3.13	1	1	1	2	1.223	2	13.060	5.157	224	24.827
Q9BVV7	Mitochondrial import inner membrane translocase subunit Tim21 OS=Homo sapiens GN=TIMM21 PE=1 SV=1 - [TIM21_HUMAN]	8.47	2	2	2	3	1.000	3	33.837	5.157	248	28.185
E9PKN0	Pre-mRNA cleavage complex 2 protein Pcf11 (Fragment) OS=Homo sapiens GN=PCF11 PE=1 SV=1 - [E9PKN0_HUMAN]	2.17	5	2	2	2	1.032	2	19.747	5.156	784	88.932
B4E0U7	cDNA FLJ54264, highly similar to Exocyst complex component 5 OS=Homo sapiens PE=2 SV=1 - [B4E0U7_HUMAN]	2.49	6	1	2	2	1.180	1		5.153	643	74.267
B3KY99	cDNA FLJ16244 fis, clone HCHON2000508, highly similar to TBC1 domain family member 2 OS=Homo sapiens PE=2 SV=1 - [B3KY99_HUMAN]	1.14	2	1	1	2	1.072	2	37.797	5.151	787	88.116
B2R6P3	cDNA, FLJ93047, highly similar to Homo sapiens matrix metallopeptidase 14 (membrane-inserted) (MMP14), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6P3_HUMAN]	1.37	3	1	1	2	1.039	2	8.847	5.146	582	65.807
I3L268	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ACAP1 PE=4 SV=1 - [I3L268_HUMAN]	11.88	3	1	1	2	1.000	1		5.140	101	11.413
A0A024RAM7	Rho-related BTB domain containing 3, isoform CRA_a OS=Homo sapiens GN=RHOBTB3 PE=4 SV=1 - [A0A024RAM7_HUMAN]	2.64	2	1	1	2	0.852	2	16.462	5.138	417	47.999
B4DHE5	cDNA FLJ54675, highly similar to Homo sapiens leucine zipper protein 5 (LUZP5), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DHE5_HUMAN]	4.03	6	2	2	5	1.000	5	0.000	5.133	571	64.741
Q05DU1	GNL3L protein (Fragment) OS=Homo sapiens GN=GNL3L PE=2 SV=1 - [Q05DU1_HUMAN]	3.3	2	2	2	2	0.914	2	26.015	5.130	575	65.311
E9ARL1	Putative elongation factor Tu OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0740 PE=4 SV=1 - [E9ARL1_LEIMU]	6.87	1	3	3	3	0.951	3	82.835	5.125	466	51.649
P36954	DNA-directed RNA polymerase II subunit RPB9 OS=Homo sapiens GN=POLR2I PE=1 SV=1 - [RPB9_HUMAN]	15.2	2	2	2	2	0.993	2	1.023	5.123	125	14.514
E9B0N6	Succinate dehydrogenase assembly factor 2, mitochondrial OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1070 PE=3 SV=1 - [E9B0N6_LEIN	4.68	1	1	1	2	1.000	2	0.000	5.118	235	25.851
E9AY02	Protein pelota homolog OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0200 PE=3 SV=1 - [E9AY02_LEIMU]	1.48	1	1	1	4	0.865	3	21.081	5.115	406	45.662
B3KN82	cDNA FLJ13913 fis, clone Y79AA1000231, highly similar to Nucleolar protein NOP5 OS=Homo sapiens PE=2 SV=1 - [B3KN82_HUMAN]	5.79	3	2	2	3	0.972	2	4.243	5.111	466	52.256
A3KMF9	PDCD7 protein (Fragment) OS=Homo sapiens GN=PDCD7 PE=2 SV=1 - [A3KMF9_HUMAN]	5.93	3	1	2	2	1.147	1		5.109	270	31.954
F5H731	Pleckstrin homology domain-containing family G member 6 OS=Homo sapiens GN=PLEKHG6 PE=4 SV=1 - [F5H731_HUMAN]	4.85	3	2	2	2	1.000	2	0.000	5.108	495	55.760
B2RBH9	cDNA, FLJ95516 OS=Homo sapiens PE=2 SV=1 - [B2RBH9_HUMAN]	4.23	4	2	2	2	0.778	2	38.564	5.107	544	64.021
Q9H9J2	39S ribosomal protein L44, mitochondrial OS=Homo sapiens GN=MRPL44 PE=1 SV=1 - [RM44_HUMAN]	4.52	1	2	2	2	1.032	2	17.527	5.107	332	37.512
B2RBJ7	cDNA, FLJ95547, highly similar to Homo sapiens nuclear receptor coactivator 6 interacting protein (NCOA6IP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RBJ7_HUMAI	2.46	3	2	2	2	1.565	2	74.427	5.106	853	96.514
E9AJY9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0050 PE=4 SV=1 - [E9AJY9_LEIMU]	2.1	1	1	1	2	1.000	2	0.000	5.102	524	58.520
A8K818	cDNA FLJ75784, highly similar to Homo sapiens CD3E antigen, epsilon polypeptide associated protein (CD3EAP), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K818_HUI	9.22	4	2	2	3	1.000	2	0.000	5.101	510	54.924
H0Y430	Sulfhydryl oxidase (Fragment) OS=Homo sapiens GN=QSOX2 PE=4 SV=1 - [H0Y430_HUMAN]	3.87	4	1	1	2	0.912	2	91.561	5.083	284	32.548
Q5JV73	FERM and PDZ domain-containing protein 3 OS=Homo sapiens GN=FRMPD3 PE=2 SV=2 - [FRPD3_HUMAN]	0.94	1	2	2	2	0.808	2	32.513	5.082	1810	199.085
Q05BY4	C1orf167 protein (Fragment) OS=Homo sapiens GN=C1orf167 PE=2 SV=1 - [Q05BY4_HUMAN]	1.51	5	1	1	2	0.928	2	4.792	5.080	531	59.124
Q8NBH6	Fibulin-1 OS=Homo sapiens PE=2 SV=1 - [Q8NBH6_HUMAN]	1.57	4	1	1	2	0.874	2	86.260	5.073	638	70.531
Q8TBM8	DnaJ homolog subfamily B member 14 OS=Homo sapiens GN=DNAJB14 PE=1 SV=1 - [DJB14_HUMAN]	5.28	5	2	2	2	0.966	2	5.107	5.072	379	42.489
Q7Z4S6	Kinesin-like protein KIF21A OS=Homo sapiens GN=KIF21A PE=1 SV=2 - [KI21A_HUMAN]	1.97	6	3	3	3	1.000	2	0.000	5.070	1674	187.063
Q86SE9	Polycomb group RING finger protein 5 OS=Homo sapiens GN=PCGF5 PE=1 SV=1 - [PCGF5_HUMAN]	6.25	1	1	1	1	0.940	1		5.060	256	29.694
B4E321	Olfactory receptor 7D2 OS=Homo sapiens GN=OR7D2 PE=2 SV=1 - [B4E321_HUMAN]	2.71	1	1	1	2	1.000	1		5.058	406	46.273
Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein OS=Homo sapiens GN=GPD1L PE=1 SV=1 - [GPD1L_HUMAN]	6.27	4	2	2	2	0.996	2	0.602	5.057	351	38.394
A0A087WTY1	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Homo sapiens GN=POLR1D PE=4 SV=1 - [A0A087WTY1_HUMAN]	7.45	1	1	1	2	0.852	2	21.844	5.045	94	11.012
Q9NQ50	39S ribosomal protein L40, mitochondrial OS=Homo sapiens GN=MRPL40 PE=1 SV=1 - [RM40_HUMAN]	10.19	1	2	2	2	0.914	2	15.115	5.041	206	24.475
Q6YP21	Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens GN=CCBL2 PE=1 SV=1 - [KAT3_HUMAN]	3.3	1	2	2	3	1.154	3	27.061	5.040	454	51.368
B2R548	Prefoldin subunit 4 OS=Homo sapiens PE=2 SV=1 - [B2R548_HUMAN]	11.19	3	1	1	1	0.941	1		5.030	134	15.293
Q92733	Proline-rich protein PRCC OS=Homo sapiens GN=PRCC PE=1 SV=1 - [PRCC_HUMAN]	7.94	4	3	3	3	1.000	3	3.219	5.024	491	52.386
H0YBR0	Trafficking protein particle complex subunit 9 (Fragment) OS=Homo sapiens GN=TRAPPC9 PE=1 SV=1 - [H0YBR0_HUMAN]	2.02	4	1	2	2	0.843	1		5.023	992	110.130
I3L2K0	Exportin-6 (Fragment) OS=Homo sapiens GN=XPO6 PE=1 SV=1 - [I3L2K0_HUMAN]	3.92	3	1	1	2	0.983	2	66.141	5.018	255	29.003
Q2PD61	Aspartate aminotransferase OS=Leishmania aethiopica GN=asat PE=4 SV=1 - [Q2PD61_9TRYP]	2.91	1	1	1	2	1.000	2	0.000	5.004	412	45.886
C9JP01	Protein RFT1 homolog (Fragment) OS=Homo sapiens GN=RFT1 PE=4 SV=3 - [C9JP01_HUMAN]	3.08	2	1	1	2	0.896	2	16.345	4.997	292	32.963
A2RUS2	DENN domain-containing protein 3 OS=Homo sapiens GN=DENND3 PE=1 SV=2 - [DEND3_HUMAN]	2.17	6	3	3	3	0.829	3	13.493	4.994	1198	135.802
Q6P392	PPIL4 protein (Fragment) OS=Homo sapiens GN=PPIL4 PE=2 SV=1 - [Q6P392_HUMAN]	3.92	7	2	2	2	0.809	2	9.792	4.994	434	49.991
B4E2F1	cDNA FLJ51459, highly similar to Guanylate-binding protein 4 OS=Homo sapiens PE=2 SV=1 - [B4E2F1_HUMAN]	15.15	4	2	2	2	0.801	2	52.385	4.992	132	15.764
Q6IC98	GRAM domain-containing protein 4 OS=Homo sapiens GN=GRAMD4 PE=1 SV=1 - [GRAM4_HUMAN]	1.9	1	1	1	3	1.000	2	0.000	4.992	578	66.366
Q96RG4	Insulin receptor substrate 2 insertion mutant (Fragment) OS=Homo sapiens GN=IRS2 PE=4 SV=1 - [Q96RG4_HUMAN]	2.77	3	2	2	2	1.000	2	0.000	4.989	1338	137.234
Q9NXV2	BTB/POZ domain-containing protein KCTD5 OS=Homo sapiens GN=KCTD5 PE=1 SV=1 - [KCTD5_HUMAN]	2.99	1	1	1	2	0.969	2	20.848	4.982	234	26.076
Q05DQ6	NDC80 protein (Fragment) OS=Homo sapiens GN=NDC80 PE=2 SV=1 - [Q05DQ6_HUMAN]	1.72	2	1	1	2	1.410	2	22.334	4.978	524	60.270
Q7Z5E5	Medulloblastoma antigen MU-MB-20.240 (Fragment) OS=Homo sapiens GN=ANKRD11 PE=2 SV=1 - [Q7Z5E5_HUMAN]	1.15	1	1	1	2	1.260	2	43.909	4.968	611	71.553
E7EPJ7	Triple functional domain protein (Fragment) OS=Homo sapiens GN=TRIO PE=1 SV=2 - [E7EPJ7_HUMAN]	0.59	2	1	1	2	1.039	2	0.865	4.966	2546	285.633
Q59FF5	Myosin Va variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FF5_HUMAN]	1.56	14	1	2	2	1.000	1		4.962	1409	164.816
Q05DQ0	PIK3R3 protein (Fragment) OS=Homo sapiens GN=PIK3R3 PE=2 SV=1 - [Q05DQ0_HUMAN]	7.77	12	1	2	2	1.235	1		4.961	283	33.732
R4GMM1	Protein MINOS1-NBL1 (Fragment) OS=Homo sapiens GN=MINOS1-NBL1 PE=4 SV=1 - [R4GMM1_HUMAN]	17.39	4	1	1	2	1.003	2	6.399	4.960	46	5.150
B3KMD7	cDNA FLJ10753 fis, clone NT2RP3004539, highly similar to Pentatricopeptide repeat protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KMD7_HUMAN]	3.99	8	2	2	2	1.276	2	1.358	4.951	526	60.187
Q6PJG6	BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 - [BRAT1_HUMAN]	4.14	2	3	3	3	1.491	3	21.785	4.947	821	88.063
D3DQV2	Guanine nucleotide-binding protein subunit gamma OS=Homo sapiens GN=hCG_1992840 PE=3 SV=1 - [D3DQV2_HUMAN]	32.35	3	2	2	2	0.886	2	18.162	4.945	68	7.158
Q86SZ2	Trafficking protein particle complex subunit 6B OS=Homo sapiens GN=TRAPPC6B PE=1 SV=1 - [TPC6B_HUMAN]	12.66	4	1	2	2	1.000	1		4.944	158	17.971
H3BPN3	Trafficking protein particle complex subunit 2-like protein OS=Homo sapiens GN=TRAPPC2L PE=1 SV=1 - [H3BPN3_HUMAN]	12	3	1	1	2	0.997	2	12.118	4.943	75	8.715
B2MUD5	Neutrophil elastase (Fragment) OS=Homo sapiens GN=ELA2 PE=3 SV=1 - [B2MUD5_HUMAN]	10.42	2	2	2	2	0.783	2	5.399	4.943	192	20.649
C9J7B1	Protein NipSnap homolog 2 (Fragment) OS=Homo sapiens GN=GBAS PE=1 SV=1 - [C9J7B1_HUMAN]	47.69	2	1	3	3	1.232	1		4.941	65	7.934
E9B0D4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_0090 PE=4 SV=1 - [E9B0D4_LEIMU]	8.33	1	3	3	3	1.000	2	0.000	4.935	228	27.588
A8K0G7	cDNA FLJ78425, highly similar to Homo sapiens zinc fingers and homeoboxes 1 (ZHX1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K0G7_HUMAN]	2.86	2	2	2	2	0.841	1		4.934	873	98.012
Q9NPF0	CD320 antigen OS=Homo sapiens GN=CD320 PE=1 SV=1 - [CD320_HUMAN]	6.03	1	1	1	2	1.000	2	0.000	4.933	282	28.972
M0QZQ8	Trafficking protein particle complex subunit 5 OS=Homo sapiens GN=TRAPPC5 PE=1 SV=1 - [M0QZQ8_HUMAN]	10.74	2	1	1	2	0.967	2	10.309	4.933	121	13.511
H7C1G1	Transmembrane protein 87B (Fragment) OS=Homo sapiens GN=TMEM87B PE=4 SV=1 - [H7C1G1_HUMAN]	7.14	3	1	1	2	1.291	2	8.865	4.932	112	13.137
E9B552	Putative ATP-dependent DNA helicase (Putative ruvb dna helicase-like protein) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2610 PE=4 SV	4.76	1	1	2	2	1.000	1		4.922	483	53.684
E9ANT8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0110 PE=4 SV=1 - [E9ANT8_LEIMU]	1.97	1	2	2	2	0.779	2	27.828	4.920	813	91.719
Q969E2	Secretory carrier-associated membrane protein 4 OS=Homo sapiens GN=SCAMP4 PE=2 SV=1 - [SCAM4_HUMAN]	3.49	1	1	1	2	1.048	2	6.293	4.917	229	25.711
H0YFJ7	Cell division cycle and apoptosis regulator protein 1 (Fragment) OS=Homo sapiens GN=CCAR1 PE=1 SV=1 - [H0YFJ7_HUMAN]	7.24	1	1	3	4	0.919	2	63.273	4.911	290	34.760
Q9UP83	Conserved oligomeric Golgi complex subunit 5 OS=Homo sapiens GN=COG5 PE=1 SV=3 - [COG5_HUMAN]	2.26	2	2	2	3	0.929	3	2.086	4.910	839	92.685
G3XAL9	Solute carrier family 12 (Sodium/potassium/chloride transporters), member 2, isoform CRA_a OS=Homo sapiens GN=SLC12A2 PE=1 SV=1 - [G3XAL9_HUMAN]	2.52	3	2	2	2	1.014	2	21.330	4.905	1150	124.513
Q9NQT5	Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 - [EXOS3_HUMAN]	8	1	2	2	2	0.924	2	11.688	4.899	275	29.553
P62877	E3 ubiquitin-protein ligase RBX1 OS=Homo sapiens GN=RBX1 PE=1 SV=1 - [RBX1_HUMAN]	7.41	1	1	1	2	1.001	2	17.034	4.898	108	12.266
R4GNC5	Stromal interaction molecule 2 (Fragment) OS=Homo sapiens GN=STIM2 PE=4 SV=1 - [R4GNC5_HUMAN]	10.34	9	1	1	3	1.052	3	8.413	4.896	87	10.467
C9JNU9	Ubiquitin carboxyl-terminal hydrolase 4 OS=Homo sapiens GN=USP4 PE=1 SV=1 - [C9JNU9_HUMAN]	4.41	2	1	2	4	1.000	1		4.895	363	41.792
A0A024RDZ9	Uncharacterized protein OS=Homo sapiens GN=RP11-98F14.6 PE=4 SV=1 - [A0A024RDZ9_HUMAN]	2.74	4	1	1	2	0.911	2	13.853	4.894	292	33.761
A5PKX9	INADL protein OS=Homo sapiens GN=INADL PE=2 SV=1 - [A5PKX9_HUMAN]	0.51	4	1	1	2	1.273	2	26.891	4.893	1181	129.719
E9ATF9	Nascent polypeptide-associated complex subunit beta OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3770 PE=3 SV=1 - [E9ATF9_LEIMU]	7.77	1	1	1	2	1.150	2	28.518	4.892	103	11.643
J3QRL9	Desmocollin-3 (Fragment) OS=Homo sapiens GN=DSC3 PE=4 SV=1 - [J3QRL9_HUMAN]	3.27	2	1	1	2	0.999	1		4.889	214	23.113
Q9C0F3	Zinc finger protein 436 OS=Homo sapiens GN=ZNF436 PE=1 SV=2 - [ZN436_HUMAN]	4.47	26	1	2	2	1.000	1		4.886	470	54.242
E9AQL8	Putative carbamoyl-phosphate synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0590 PE=3 SV=1 - [E9AQL8_LEIMU]	1.09	1	1	2	2	1.000	1		4.886	1842	205.892
P22692	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2 - [IBP4_HUMAN]	3.88	1	1	1	2	0.694	2	58.449	4.881	258	27.915
I3L1K7	Golgi SNAP receptor complex member 2 OS=Homo sapiens GN=GOSR2 PE=4 SV=1 - [I3L1K7_HUMAN]	15.38	7	2	2	3	0.909	3	14.222	4.877	143	16.752
E9ANC1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_1110 PE=4 SV=1 - [E9ANC1_LEIMU]	2.28	1	1	1	2	1.000	2	0.000	4.874	527	56.877
B2R5N4	cDNA, FLJ92544, highly similar to Homo sapiens lectin, mannose-binding 2-like (LMAN2L), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5N4_HUMAN]	5.75	6	2	2	2	1.044	2	4.619	4.862	348	39.667
Q8TF64	PDZ domain-containing protein GIPC3 OS=Homo sapiens GN=GIPC3 PE=1 SV=1 - [GIPC3_HUMAN]	8.01	1	2	2	3	1.043	2	6.204	4.861	312	33.960
Q6P2P2	Putative protein arginine N-methyltransferase 9 OS=Homo sapiens GN=PRMT9 PE=2 SV=1 - [ANM9_HUMAN]	1.18	1	1	1	2	0.836	2	27.002	4.855	845	94.441
E9PHS0	LanC-like protein 1 (Fragment) OS=Homo sapiens GN=LANCL1 PE=1 SV=1 - [E9PHS0_HUMAN]	9.69	7	2	2	2	0.703	2	42.666	4.854	196	22.028
Q9BQC6	Ribosomal protein 63, mitochondrial OS=Homo sapiens GN=MRPL57 PE=1 SV=1 - [RT63_HUMAN]	6.86	1	1	1	2	0.896	2	7.358	4.851	102	12.259
Q8IXZ2	Zinc finger CCCH domain-containing protein 3 OS=Homo sapiens GN=ZC3H3 PE=1 SV=3 - [ZC3H3_HUMAN]	2.64	1	2	2	2	1.000	2	0.000	4.845	948	101.878
B4DRZ6	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens GN=CIAO1 PE=2 SV=1 - [B4DRZ6_HUMAN]	2.65	3	1	1	2	0.969	2	3.197	4.845	302	33.732
B4DNL1	cDNA FLJ51512, highly similar to Periodic tryptophan protein 1 homolog OS=Homo sapiens PE=2 SV=1 - [B4DNL1_HUMAN]	2.43	5	1	1	2	1.468	2	21.946	4.844	412	45.784
Q5SYT8	Protein NAMPTL (Fragment) OS=Homo sapiens GN=NAMPTL PE=4 SV=1 - [Q5SYT8_HUMAN]	4.45	4	2	2	2	1.403	2	26.801	4.837	472	53.360
A0A024R9Q1	Thrombospondin 1, isoform CRA_a OS=Homo sapiens GN=THBS1 PE=4 SV=1 - [A0A024R9Q1_HUMAN]	1.28	4	1	2	2				4.836	1170	129.270
E9B259	Putative calreticulin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2600 PE=3 SV=1 - [E9B259_LEIMU]	4.55	1	2	2	2	1.929	2	137.159	4.832	396	44.728
H7C0U0	P-beta (Fragment) OS=Homo sapiens GN=PARL PE=4 SV=1 - [H7C0U0_HUMAN]	7.55	4	2	2	2	1.295	2	114.014	4.831	159	17.707
A0JNW5	UHRF1-binding protein 1-like OS=Homo sapiens GN=UHRF1BP1L PE=1 SV=2 - [UH1BL_HUMAN]	3.28	2	2	3	3	1.000	1		4.829	1464	164.095
E9B2J9	Putative RNA binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0750 PE=4 SV=1 - [E9B2J9_LEIMU]	13.62	1	2	3	3	2.244	2	178.907	4.829	235	25.234
F5H1U6	M-phase phosphoprotein 9 (Fragment) OS=Homo sapiens GN=MPHOSPH9 PE=1 SV=2 - [F5H1U6_HUMAN]	15.35	5	3	3	4	1.113	4	10.889	4.827	215	24.354
A0A024R8I4	Caspase recruitment domain family, member 9, isoform CRA_a OS=Homo sapiens GN=CARD9 PE=4 SV=1 - [A0A024R8I4_HUMAN]	8.47	3	3	3	3	0.797	3	0.022	4.826	366	42.926
Q13568	Interferon regulatory factor 5 OS=Homo sapiens GN=IRF5 PE=1 SV=2 - [IRF5_HUMAN]	4.62	16	1	2	2	0.788	1		4.824	498	56.009
H0YIM9	Protein CHURC1-FNTB (Fragment) OS=Homo sapiens GN=CHURC1-FNTB PE=4 SV=1 - [H0YIM9_HUMAN]	15.29	2	1	1	2	1.103	2	14.638	4.820	85	9.818
B4DT07	cDNA FLJ58407, highly similar to Lymphocyte cytosolic protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DT07_HUMAN]	15.16	6	7	7	10	1.000	10	5.652	4.819	488	54.788
O75607	Nucleoplasmin-3 OS=Homo sapiens GN=NPM3 PE=1 SV=3 - [NPM3_HUMAN]	12.92	1	2	2	3	1.028	3	1.202	4.817	178	19.331
Q9BWG4	Single-stranded DNA-binding protein 4 OS=Homo sapiens GN=SSBP4 PE=1 SV=1 - [SSBP4_HUMAN]	5.45	5	2	2	2	0.930	2	10.731	4.815	385	39.362
E9B5Y1	Putative casein kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1010 PE=3 SV=1 - [E9B5Y1_LEIMU]	6.21	1	2	2	3	1.000	3	6.689	4.813	354	39.908
A8K8X0	cDNA FLJ75187, highly similar to Homo sapiens nap1 P120 OS=Homo sapiens PE=2 SV=1 - [A8K8X0_HUMAN]	0.93	2	1	1	2	1.021	2	3.131	4.813	972	112.123
Q6ZRR7	Leucine-rich repeat-containing protein 9 OS=Homo sapiens GN=LRRC9 PE=2 SV=2 - [LRRC9_HUMAN]	0.62	1	1	1	2	0.816	2	42.708	4.811	1453	166.805
E9AZW6	Putative ATPase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1460 PE=4 SV=1 - [E9AZW6_LEIMU]	1.82	1	1	1	2	1.000	2	0.000	4.810	771	83.442
P23610	Factor VIII intron 22 protein OS=Homo sapiens GN=F8A1 PE=1 SV=2 - [F8I2_HUMAN]	3.77	1	1	1	1	1.053	1		4.809	371	39.079
A0A087WXZ7	HEAT repeat-containing protein 6 OS=Homo sapiens GN=HEATR6 PE=4 SV=1 - [A0A087WXZ7_HUMAN]	2.51	5	1	2	2	1.000	1		4.809	916	99.603
B8ZZA3	Kynureninase OS=Homo sapiens GN=KYNU PE=1 SV=1 - [B8ZZA3_HUMAN]	19.59	10	3	3	3	1.030	2	19.461	4.804	148	16.721
B2R9P8	cDNA, FLJ94500 OS=Homo sapiens PE=2 SV=1 - [B2R9P8_HUMAN]	1.95	2	1	1	2	1.000	2	0.000	4.804	461	52.261
A8K369	cDNA FLJ76707, highly similar to Homo sapiens transmembrane protein 87A, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K369_HUMAN]	1.42	5	1	1	2	0.822	2	24.983	4.801	494	56.679
J3KNN7	BRCA1-associated protein OS=Homo sapiens GN=BRAP PE=1 SV=1 - [J3KNN7_HUMAN]	3.38	4	2	2	2	0.838	2	38.657	4.800	562	64.239
Q9H204	Mediator of RNA polymerase II transcription subunit 28 OS=Homo sapiens GN=MED28 PE=1 SV=1 - [MED28_HUMAN]	8.99	3	1	2	2	1.082	1		4.796	178	19.508
E9AP13	NADH:flavin oxidoreductase/NADH oxidase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_1130 PE=4 SV=1 - [E9AP13_LEIMU]	5.21	1	2	2	2	1.536	2	70.624	4.783	384	41.380
Q9NTC5	Putative uncharacterized protein DKFZp434I1926 (Fragment) OS=Homo sapiens GN=DKFZp434I1926 PE=2 SV=1 - [Q9NTC5_HUMAN]	5.61	3	1	1	2	1.000	2	0.000	4.779	214	23.934
Q9HD33	39S ribosomal protein L47, mitochondrial OS=Homo sapiens GN=MRPL47 PE=1 SV=2 - [RM47_HUMAN]	11.2	1	3	3	3	1.000	3	2.151	4.766	250	29.432
E9AXZ3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0075 PE=4 SV=1 - [E9AXZ3_LEIMU]	2.98	1	1	1	2	0.903	1		4.766	235	26.278
Q9H5X1	MIP18 family protein FAM96A OS=Homo sapiens GN=FAM96A PE=1 SV=1 - [FA96A_HUMAN]	6.88	1	1	1	2	1.067	2	18.070	4.762	160	18.343
E9AZE0	Obg-like ATPase 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_2330 PE=3 SV=1 - [E9AZE0_LEIMU]	4.85	1	1	2	3	1.302	1		4.757	392	43.975
H0YA20	Diacylglycerol kinase (Fragment) OS=Homo sapiens GN=DGKQ PE=3 SV=1 - [H0YA20_HUMAN]	2.51	5	2	2	2	1.000	2	0.000	4.757	876	94.878
E9ASR7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1470 PE=4 SV=1 - [E9ASR7_LEIMU]	0.55	1	1	1	4	1.081	4	11.449	4.755	1100	120.440
F2WW55	Catechol-O-methyltransferase (Fragment) OS=Homo sapiens GN=COMT PE=4 SV=1 - [F2WW55_HUMAN]	88.89	1	1	2	2	1.144	1		4.753	27	3.049
C9JBI3	Phosphoserine phosphatase (Fragment) OS=Homo sapiens GN=PSPH PE=1 SV=1 - [C9JBI3_HUMAN]	11.23	6	2	2	2	0.979	2	3.115	4.753	187	20.732
A8K124	cDNA FLJ76213, highly similar to Homo sapiens suppressor of hairy wing homolog 4 (Drosophila) (SUHW4), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 -	3.62	7	3	3	3	1.000	3	0.000	4.741	966	107.823
E9B442	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2040 PE=4 SV=1 - [E9B442_LEIMU]	0.76	1	1	1	2	1.148	2	20.693	4.737	787	86.429
Q9NRP2	COX assembly mitochondrial protein 2 homolog OS=Homo sapiens GN=CMC2 PE=1 SV=1 - [COXM2_HUMAN]	8.86	1	1	1	2	1.171	2	23.778	4.736	79	9.454
Q9P2K8	Eukaryotic translation initiation factor 2-alpha kinase 4 OS=Homo sapiens GN=EIF2AK4 PE=1 SV=3 - [E2AK4_HUMAN]	1.33	4	2	2	3	1.000	3	0.000	4.732	1649	186.794
Q96IB4	DIP2B protein (Fragment) OS=Homo sapiens GN=DIP2B PE=2 SV=2 - [Q96IB4_HUMAN]	0.96	2	1	1	2	1.726	2	13.724	4.727	936	101.657
H0Y7Y8	AT-rich interactive domain-containing protein 4B (Fragment) OS=Homo sapiens GN=ARID4B PE=1 SV=2 - [H0Y7Y8_HUMAN]	1.81	4	1	1	2	1.000	2	0.000	4.723	553	61.446
Q86YT6	E3 ubiquitin-protein ligase MIB1 OS=Homo sapiens GN=MIB1 PE=1 SV=1 - [MIB1_HUMAN]	2.68	2	2	2	2	1.000	2	0.000	4.716	1006	110.066
E9APE3	Adenylosuccinate synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1190 PE=3 SV=1 - [E9APE3_LEIMU]	1.26	1	1	1	2	3.612	2	13.393	4.715	712	78.334
E9AX53	40S ribosomal protein S8 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_2070 PE=3 SV=1 - [E9AX53_LEIMU]	12.84	1	3	3	3	1.013	3	0.599	4.709	218	24.672
Q96I23	Protein preY, mitochondrial OS=Homo sapiens GN=PYURF PE=1 SV=1 - [PREY_HUMAN]	7.02	1	1	1	2	0.820	2	8.416	4.705	114	12.647
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens GN=RPRD1B PE=1 SV=1 - [RPR1B_HUMAN]	8.9	4	3	3	3	0.979	2	6.198	4.704	326	36.877
Q3SYF1	Sorting nexin 12 OS=Homo sapiens GN=SNX12 PE=2 SV=1 - [Q3SYF1_HUMAN]	17.9	3	2	3	3	0.993	2	15.266	4.703	162	18.873
Q96BX8	MOB kinase activator 3A OS=Homo sapiens GN=MOB3A PE=1 SV=1 - [MOB3A_HUMAN]	10.14	10	3	3	4	1.084	4	9.219	4.702	217	25.448
E7EV89	Lysine-specific demethylase 5A (Fragment) OS=Homo sapiens GN=KDM5A PE=4 SV=1 - [E7EV89_HUMAN]	2.8	7	2	2	2	1.000	1		4.702	715	81.447
E9AKT9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0600 PE=4 SV=1 - [E9AKT9_LEIMU]	0.56	1	1	1	2	0.865	1		4.701	1435	148.479

E9AKC9	Putative viscerotropic leishmaniasis antigen OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0241 PE=4 SV=1 - [E9AKC9_LEIMU]	13.25	2	1	1	2	2.859	2	185.576	4.698	1411	153.468
Q16296	Microtubule-associated protein (Fragment) OS=Homo sapiens GN=4R-MAP2 PE=2 SV=1 - [Q16296_HUMAN]	6.4	7	1	1	2	0.993	2	2.680	4.696	125	13.486
E9PQA7	BSD domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BSDC1 PE=1 SV=3 - [E9PQA7_HUMAN]	5.62	4	1	1	2	1.000	1		4.696	178	19.766
Q5JV99	Serine/threonine-protein kinase 24 12 kDa subunit (Fragment) OS=Homo sapiens GN=STK24 PE=1 SV=1 - [Q5JV99_HUMAN]	10.56	9	1	1	1	1.000	1		4.695	142	15.759
A6NMZ7	Collagen alpha-6(VI) chain OS=Homo sapiens GN=COL6A6 PE=1 SV=2 - [CO6A6_HUMAN]	0.62	1	1	2	2	0.926	1		4.694	2263	247.019
E9B4M7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0580 PE=4 SV=1 - [E9B4M7_LEIMU]	13.93	1	2	2	3	3.523	3	89.334	4.692	122	14.071
Q6P9B9	Integrator complex subunit 5 OS=Homo sapiens GN=INTS5 PE=1 SV=1 - [INT5_HUMAN]	2.16	1	2	2	2	0.697	2	57.702	4.691	1019	107.927
H3BMM5	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [H3BMM5_HUMAN]	2.42	5	2	2	2	1.084	2	18.686	4.684	538	61.200
P46531	Neurogenic locus notch homolog protein 1 OS=Homo sapiens GN=NOTCH1 PE=1 SV=4 - [NOTC1_HUMAN]	1.72	1	4	4	5	1.013	5	1.891	4.683	2555	272.323
Q96SU4	Oxysterol-binding protein-related protein 9 OS=Homo sapiens GN=OSBPL9 PE=1 SV=2 - [OSBL9_HUMAN]	2.17	7	1	2	2	1.000	1		4.682	736	83.132
E9B544	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2530 PE=4 SV=1 - [E9B544_LEIMU]	1.06	1	1	2	2	1.129	1		4.681	2269	251.125
E9ATH1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3890 PE=4 SV=1 - [E9ATH1_LEIMU]	1.77	1	1	1	2	1.000	2	0.000	4.673	395	43.748
B2R9K5	cDNA, FLJ94435 OS=Homo sapiens PE=2 SV=1 - [B2R9K5_HUMAN]	4.25	2	1	1	1	1.000	1		4.672	259	29.869
E9AZA4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_2000 PE=4 SV=1 - [E9AZA4_LEIMU]	6.6	1	1	1	1	1.277	1		4.672	197	22.298
B7Z972	cDNA FLJ57779, highly similar to Protein-L-isoaspartate(D-aspartate)O-methyltransferase (EC 2.1.1.77) OS=Homo sapiens PE=1 SV=1 - [B7Z972_HUMAN]	7.81	5	2	2	2	0.849	2	0.554	4.669	192	20.670
I3XIE4	Mutant R430X UPF3B (Fragment) OS=Homo sapiens GN=UPF3B PE=4 SV=1 - [I3XIE4_HUMAN]	13.98	3	1	1	1	1.380	1		4.664	93	11.731
E9PKN8	Tudor and KH domain-containing protein (Fragment) OS=Homo sapiens GN=TDRKH PE=4 SV=1 - [E9PKN8_HUMAN]	14.5	7	2	2	2	1.008	2	1.250	4.659	131	14.619
B4DM62	cDNA FLJ51244, highly similar to Homeobox protein OTX1 OS=Homo sapiens PE=2 SV=1 - [B4DM62_HUMAN]	3.47	3	1	1	2	1.000	1		4.658	288	29.825
P20248	Cyclin-A2 OS=Homo sapiens GN=CCNA2 PE=1 SV=2 - [CCNA2_HUMAN]	5.56	1	3	3	3	0.779	3	27.272	4.654	432	48.520
Q86Y91	Kinesin-like protein KIF18B OS=Homo sapiens GN=KIF18B PE=1 SV=3 - [KI18B_HUMAN]	1.85	3	2	2	3	0.925	2	11.669	4.654	864	94.164
P17026	Zinc finger protein 22 OS=Homo sapiens GN=ZNF22 PE=1 SV=3 - [ZNF22_HUMAN]	21.88	71	2	4	5	1.116	2	16.418	4.653	224	25.899
E9B5P5	Putative prohibitin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0070 PE=4 SV=1 - [E9B5P5_LEIMU]	7.19	1	2	2	2	1.582	2	76.679	4.651	292	32.307
C9JA85	Sn1-specific diacylglycerol lipase beta (Fragment) OS=Homo sapiens GN=DAGLB PE=1 SV=1 - [C9JA85_HUMAN]	6.04	3	1	1	2	0.181	2	117.110	4.651	149	16.427
O94819	Kelch repeat and BTB domain-containing protein 11 OS=Homo sapiens GN=KBTBD11 PE=1 SV=1 - [KBTBB_HUMAN]	4.82	1	2	2	2	1.021	2	3.078	4.648	623	65.679
B4DP10	cDNA FLJ55118, highly similar to Secretory carrier-associated membrane protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DP10_HUMAN]	9.27	8	2	2	2	1.007	2	1.079	4.648	259	28.409
E9B4J1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0230 PE=4 SV=1 - [E9B4J1_LEIMU]	1.95	1	2	2	2	1.000	1		4.648	719	81.890
Q14232	Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=1 SV=1 - [EI2BA_HUMAN]	11.15	3	3	3	3	0.945	3	20.624	4.648	305	33.691
D3YTG3	Target of Nesh-SH3 OS=Homo sapiens GN=ABI3BP PE=4 SV=1 - [D3YTG3_HUMAN]	0.62	1	1	1	2	1.000	1		4.646	1777	195.204
B4DKV8	cDNA FLJ56665, highly similar to Nucleoporin Nup37 OS=Homo sapiens PE=2 SV=1 - [B4DKV8_HUMAN]	4.97	3	1	1	2	1.324	2	43.538	4.646	181	20.393
B7Z785	cDNA FLJ52789, highly similar to Uridine/cytidine kinase-like 1 OS=Homo sapiens PE=2 SV=1 - [B7Z785_HUMAN]	9.27	3	1	1	2	1.000	2	0.000	4.645	151	16.194
Q5F1R6	DnaJ homolog subfamily C member 21 OS=Homo sapiens GN=DNAJC21 PE=1 SV=2 - [DJC21_HUMAN]	6.59	1	4	4	4	0.943	4	8.778	4.641	531	61.989
P20132	L-serine dehydratase/L-threonine deaminase OS=Homo sapiens GN=SDS PE=1 SV=2 - [SDHL_HUMAN]	4.88	1	2	2	2	0.933	2	10.258	4.640	328	34.603
H7BZT2	Kinesin-like protein KIF15 (Fragment) OS=Homo sapiens GN=KIF15 PE=1 SV=1 - [H7BZT2_HUMAN]	9.79	3	2	2	2	1.144	2	5.252	4.638	194	23.360
F6VD24	Cip1-interacting zinc finger protein (Fragment) OS=Homo sapiens GN=CIZ1 PE=4 SV=1 - [F6VD24_HUMAN]	5.56	9	1	1	2	1.000	2	0.000	4.638	252	27.559
E9PJ60	Probable ATP-dependent RNA helicase DDX20 OS=Homo sapiens GN=DDX20 PE=1 SV=1 - [E9PJ60_HUMAN]	3.94	5	2	2	2	1.467	2	82.776	4.632	432	49.344
E9AU28	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5930 PE=4 SV=1 - [E9AU28_LEIMU]	2.4	2	1	1	2	1.000	2	0.000	4.631	292	33.919
E5RK48	Retinol dehydrogenase 10 OS=Homo sapiens GN=RDH10 PE=1 SV=1 - [E5RK48_HUMAN]	5.11	2	1	1	2				4.630	176	19.780
C9JBW0	Basic helix-loop-helix domain-containing protein KIAA2018 OS=Homo sapiens GN=KIAA2018 PE=4 SV=1 - [C9JBW0_HUMAN]	14.77	2	1	1	2	0.726	2	50.354	4.627	88	10.269
B4DIT7	cDNA FLJ58187, highly similar to Protein-glutamine gamma-glutamyltransferase 2(EC 2.3.2.13) OS=Homo sapiens PE=2 SV=1 - [B4DIT7_HUMAN]	3.96	10	2	2	2	0.870	2	20.895	4.627	606	68.605
Q9P2D1	Chromodomain-helicase-DNA-binding protein 7 OS=Homo sapiens GN=CHD7 PE=1 SV=3 - [CHD7_HUMAN]	1.17	8	2	3	4	1.000	1		4.618	2997	335.717
Q8N6N3	UPF0690 protein C1orf52 OS=Homo sapiens GN=C1orf52 PE=1 SV=1 - [CA052_HUMAN]	12.64	1	2	2	2	1.042	2	6.172	4.617	182	20.586
B7Z1D3	cDNA FLJ54585 OS=Homo sapiens PE=2 SV=1 - [B7Z1D3_HUMAN]	7.93	3	2	2	3	1.589	3	9.372	4.615	328	37.746
A8K297	cDNA FLJ75611, highly similar to Homo sapiens LIM domain kinase 1 (LIMK1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K297_HUMAN]	4.79	4	3	3	3	1.000	3	0.000	4.608	647	72.566
H7C1S6	Mis18-binding protein 1 (Fragment) OS=Homo sapiens GN=MIS18BP1 PE=1 SV=1 - [H7C1S6_HUMAN]	8.21	3	2	2	2	1.000	1		4.607	195	21.746
H0YE28	Selenoprotein H (Fragment) OS=Homo sapiens GN=C11orf31 PE=1 SV=1 - [H0YE28_HUMAN]	9.57	3	1	1	2	0.950	2	7.577	4.605	94	10.434
E9PL41	Hypoxia-inducible factor 1-alpha inhibitor (Fragment) OS=Homo sapiens GN=HIF1AN PE=1 SV=2 - [E9PL41_HUMAN]	6.81	3	1	1	1	0.520	1		4.602	191	22.721
E9AR42	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0650 PE=4 SV=1 - [E9AR42_LEIMU]	0.5	1	1	1	2	1.000	2	0.000	4.600	1195	126.201
Q2PH59	Histidase (Fragment) OS=Homo sapiens GN=HAL PE=4 SV=1 - [Q2PH59_HUMAN]	14.63	6	1	1	4	0.945	1		4.598	41	4.531
D6RC27	RNA polymerase II elongation factor ELL2 (Fragment) OS=Homo sapiens GN=ELL2 PE=4 SV=1 - [D6RC27_HUMAN]	4.64	3	1	1	2	0.600	2	75.142	4.598	151	16.846
A0A087WVF6	Tubulin polyglutamylase TTLL11 (Fragment) OS=Homo sapiens GN=TTLL11 PE=4 SV=1 - [A0A087WVF6_HUMAN]	2.93	3	1	1	2	1.184	2	3.367	4.596	239	24.730
A0A024R273	Tyrosine-protein kinase OS=Homo sapiens GN=SYK PE=3 SV=1 - [A0A024R273_HUMAN]	3.59	5	3	3	3	1.000	3	0.000	4.595	612	69.466
E9AP80	Putative 60S ribosomal protein L18 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0560 PE=4 SV=1 - [E9AP80_LEIMU]	3.54	2	1	1	2	1.013	2	1.986	4.592	198	22.093
B4DEB2	cDNA FLJ56491, highly similar to DNA-repair protein XRCC1 OS=Homo sapiens PE=2 SV=1 - [B4DEB2_HUMAN]	8.75	11	3	3	3	1.000	3	0.000	4.589	400	43.194
L0R6Q1	Alternative protein SLC35A4 OS=Homo sapiens GN=SLC35A4 PE=4 SV=1 - [L0R6Q1_HUMAN]	7.77	1	1	1	2	1.391	2	7.553	4.585	103	11.126
E9AQB0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_1200 PE=4 SV=1 - [E9AQB0_LEIMU]	0.3	1	1	1	2	0.975	2	3.768	4.585	2700	287.109
E9B074	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2520 PE=4 SV=1 - [E9B074_LEIMU]	2.19	1	1	1	2				4.580	640	69.781
B3KMI0	cDNA FLJ11050 fis, clone PLACE1004564, highly similar to Cleavage and polyadenylation specificity factor 100 kDa subunit OS=Homo sapiens PE=2 SV=1 - [B3KMI0_H	2.33	3	1	1	1	0.559	1		4.580	644	72.967
H0YBF7	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ASAP1 PE=1 SV=1 - [H0YBF7_HUMAN]	3.68	4	3	3	3	1.000	3	11.765	4.579	950	105.178
Q6ZRY6	cDNA FLJ45974 fis, clone PLACE7018452 OS=Homo sapiens PE=2 SV=1 - [Q6ZRY6_HUMAN]	6.9	1	1	1	2	1.000	2	0.000	4.578	174	19.095
B4DQA8	Golgi SNAP receptor complex member 1 OS=Homo sapiens GN=GOSR1 PE=1 SV=1 - [B4DQA8_HUMAN]	9.2	9	2	2	2	0.994	2	24.424	4.578	174	20.033
E9AW03	Putative beta propeller protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0030 PE=4 SV=1 - [E9AW03_LEIMU]	1.46	1	1	1	2	1.264	2	7.109	4.575	478	54.129
Q13395	Probable methyltransferase TARBP1 OS=Homo sapiens GN=TARBP1 PE=1 SV=1 - [TARB1_HUMAN]	1.3	1	2	2	2	1.125	2	44.389	4.573	1621	181.559
A0A024QYV8	CP110 protein, isoform CRA_a OS=Homo sapiens GN=CP110 PE=4 SV=1 - [A0A024QYV8_HUMAN]	1.51	4	1	2	2	1.613	1		4.561	991	111.171
H7BYX6	Neural cell adhesion molecule 1 OS=Homo sapiens GN=NCAM1 PE=4 SV=2 - [H7BYX6_HUMAN]	2.76	6	1	2	3	0.992	2	1.246	4.560	725	80.233
E9B052	Eukaryotic translation initiation factor 3 subunit E OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2310 PE=3 SV=1 - [E9B052_LEIMU]	3.7	1	1	1	1	1.000	1		4.547	405	46.346
Q9BWH2	FUN14 domain-containing protein 2 OS=Homo sapiens GN=FUNDC2 PE=1 SV=2 - [FUND2_HUMAN]	5.29	1	1	1	2	0.930	2	13.614	4.543	189	20.663
E9AS98	Mitogen-activated protein kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1440 PE=4 SV=1 - [E9AS98_LEIMU]	4.41	1	1	1	2	1.101	2	43.480	4.538	363	41.521
A1A5D9	Bicaudal D-related protein 2 OS=Homo sapiens GN=CCDC64B PE=2 SV=2 - [BICR2_HUMAN]	2.56	1	1	2	2	1.000	1		4.534	508	56.800
E2QRE5	Uncharacterized protein OS=Homo sapiens GN=TRAF3IP3 PE=4 SV=1 - [E2QRE5_HUMAN]	4.46	9	1	2	4	1.000	3	13.199	4.532	404	46.520
Q59EZ2	Telomerase protein component 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EZ2_HUMAN]	1.52	5	2	2	2	0.940	2	9.198	4.528	1903	207.657
A5PLL2	FUT8 protein OS=Homo sapiens GN=FUT8 PE=2 SV=1 - [A5PLL2_HUMAN]	2.92	3	1	1	2	0.745	2	21.505	4.519	308	35.798
E9AMD5	Translation initiation factor-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0550 PE=4 SV=1 - [E9AMD5_LEIMU]	4.36	1	1	1	1	1.000	1		4.511	344	37.983
Q5QTR6	FWP010 OS=Homo sapiens PE=2 SV=1 - [Q5QTR6_HUMAN]	4.21	2	1	1	2	0.961	2	6.932	4.508	190	20.936
Q86WV4	MRPS9 protein (Fragment) OS=Homo sapiens GN=MRPS9 PE=2 SV=1 - [Q86WV4_HUMAN]	6.29	2	2	2	2	0.994	2	0.954	4.506	302	35.126
O60476	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB OS=Homo sapiens GN=MAN1A2 PE=1 SV=1 - [MA1A2_HUMAN]	1.56	1	1	1	2	1.091	2	12.903	4.499	641	72.957
Q8NDT2	Putative RNA-binding protein 15B OS=Homo sapiens GN=RBM15B PE=1 SV=3 - [RB15B_HUMAN]	2.47	1	1	2	2	1.000	1		4.499	890	97.147
B5MC59	Replication protein A 14 kDa subunit OS=Homo sapiens GN=RPA3 PE=1 SV=1 - [B5MC59_HUMAN]	12.2	2	1	1	2	0.966	2	30.760	4.497	82	9.165
D6RAN8	39S ribosomal protein L27, mitochondrial OS=Homo sapiens GN=MRPL27 PE=1 SV=1 - [D6RAN8_HUMAN]	36.56	5	3	3	3	0.941	3	8.917	4.494	93	10.468
E9AMI2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_1120 PE=4 SV=1 - [E9AMI2_LEIMU]	1.05	1	1	1	2	0.995	2	0.694	4.479	861	95.808
Q6TFL4	Kelch-like protein 24 OS=Homo sapiens GN=KLHL24 PE=2 SV=1 - [KLH24_HUMAN]	2.17	1	2	2	2	0.971	2	4.375	4.477	600	68.317
B5TY35	Interleukin 16 OS=Homo sapiens GN=IL16 PE=1 SV=1 - [B5TY35_HUMAN]	2.86	10	2	2	2	0.863	2	46.174	4.474	560	59.309
H0YFN7	Protein RIC1 (Fragment) OS=Homo sapiens GN=RIC1 PE=1 SV=1 - [H0YFN7_HUMAN]	0.76	2	1	1	2	1.006	2	3.178	4.471	1315	147.146
P15289	Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3 - [ARSA_HUMAN]	1.78	3	1	1	2	1.129	2	13.370	4.468	507	53.554
Q93098	Protein Wnt-8b OS=Homo sapiens GN=WNT8B PE=2 SV=3 - [WNT8B_HUMAN]	3.42	1	1	1	2	1.000	2	0.000	4.466	351	38.696
A0A087WU62	39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=4 SV=1 - [A0A087WU62_HUMAN]	6.64	4	2	2	2	1.140	2	1.943	4.465	256	29.329
Q9UBV8	Peflin OS=Homo sapiens GN=PEF1 PE=1 SV=1 - [PEF1_HUMAN]	7.39	1	2	2	3	1.000	3	0.000	4.462	284	30.361
Q9BZK3	Putative nascent polypeptide-associated complex subunit alpha-like protein OS=Homo sapiens GN=NACAP1 PE=5 SV=1 - [NACP1_HUMAN]	7.04	1	1	1	1	1.000	1		4.462	213	23.292
Q5T0Q6	Dihydropyrimidinase-related protein 4 OS=Homo sapiens GN=DPYSL4 PE=4 SV=1 - [Q5T0Q6_HUMAN]	5.83	3	2	2	2	0.907	2	5.633	4.455	412	44.168
E9AY66	Putative 40S ribosomal protein S16 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0880 PE=3 SV=1 - [E9AY66_LEIMU]	4.7	1	1	1	2	1.202	2	27.835	4.453	149	16.663
B4DYB1	cDNA FLJ60956, highly similar to DNA-directed RNA polymerase I-associated factor 53 kDa subunit (EC 2.7.7.6) OS=Homo sapiens PE=2 SV=1 - [B4DYB1_HUMAN]	12.21	4	2	2	2	0.675	2	40.428	4.451	172	19.272
D3DX93	HCG1745555, isoform CRA_b OS=Homo sapiens GN=hCG_1745555 PE=4 SV=1 - [D3DX93_HUMAN]	1.73	3	4	4	4	1.038	4	5.599	4.448	3184	353.399
Q96GD0	Pyridoxal phosphate phosphatase OS=Homo sapiens GN=PDXP PE=1 SV=2 - [PLPP_HUMAN]	4.73	1	1	1	2	0.891	2	29.737	4.447	296	31.678
B3KUR4	cDNA FLJ40462 fis, clone TESTI2042062, highly similar to Transcription initiation factor TFIID subunit 6 OS=Homo sapiens PE=2 SV=1 - [B3KUR4_HUMAN]	3.33	4	1	2	2	1.000	1		4.446	601	64.178
A0A024R1D9	Neurofibromin 2 (Bilateral acoustic neuroma), isoform CRA_d OS=Homo sapiens GN=NF2 PE=4 SV=1 - [A0A024R1D9_HUMAN]	1.97	5	1	1	2	1.000	2	0.000	4.446	507	59.059
Q86XZ2	PPP2R5E protein (Fragment) OS=Homo sapiens GN=PPP2R5E PE=2 SV=1 - [Q86XZ2_HUMAN]	3.22	10	2	2	2	1.000	2	0.000	4.444	435	50.705
Q9NWY4	UPF0609 protein C4orf27 OS=Homo sapiens GN=C4orf27 PE=1 SV=2 - [CD027_HUMAN]	4.91	1	2	2	2	1.074	2	10.548	4.439	346	39.411
Q59GZ0	KIAA0182 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GZ0_HUMAN]	1.63	5	2	2	2	0.986	2	2.119	4.438	980	110.331
E9AZ36	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1300 PE=4 SV=1 - [E9AZ36_LEIMU]	5.1	1	3	3	3	1.002	3	0.253	4.437	529	59.970
P20594	Atrial natriuretic peptide receptor 2 OS=Homo sapiens GN=NPR2 PE=1 SV=1 - [ANPRB_HUMAN]	2.96	2	2	2	2	1.075	2	10.693	4.436	1047	116.948
B3KUM0	cDNA FLJ40205 fis, clone TESTI2020840, highly similar to Homo sapiens NOL1/NOP2/Sun domain family, member 4 (NSUN4), mRNA OS=Homo sapiens PE=2 SV=1 -	6.77	3	2	2	2	0.602	2	153.412	4.435	251	28.043
Q96GS4	Uncharacterized protein C17orf59 OS=Homo sapiens GN=C17orf59 PE=1 SV=2 - [CQ059_HUMAN]	4.2	1	1	1	1	1.000	1		4.429	357	37.204
H7C500	UTP--glucose-1-phosphate uridylyltransferase (Fragment) OS=Homo sapiens GN=UGP2 PE=4 SV=1 - [H7C500_HUMAN]	27.59	2	1	1	2	0.539	2	86.631	4.427	29	2.771
B2RBZ5	cDNA, FLJ95778, highly similar to Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 (SERPINA10), mRNA OS=Homo sap	1.35	1	1	1	2	1.000	2	0.000	4.426	444	50.642
A8K3N4	Tyrosine-protein phosphatase non-receptor type OS=Homo sapiens GN=PTPN2 PE=2 SV=1 - [A8K3N4_HUMAN]	4.13	10	2	2	3	1.033	3	15.655	4.424	387	45.140
E9AST1	Proteasome subunit alpha type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1600 PE=3 SV=1 - [E9AST1_LEIMU]	7.58	1	2	2	2	1.000	2	0.000	4.424	264	29.737
E8NHN3	Putative uncharacterized protein LmxM_28_2750_1 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_28_2750_1 PE=4 SV=1 - [E8NHN	9.84	3	1	1	1	1.000	1		4.424	122	13.649
D6R9C7	RWD domain-containing protein 4 (Fragment) OS=Homo sapiens GN=RWDD4 PE=1 SV=1 - [D6R9C7_HUMAN]	23.26	5	1	1	2	1.146	2	20.363	4.423	43	5.020
E9AYV2	Putative calpain-like cysteine peptidase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0510 PE=4 SV=1 - [E9AYV2_LEIMU]	0.35	1	1	2	2	3.141	1		4.422	4341	488.809
E9AVL0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0270 PE=4 SV=1 - [E9AVL0_LEIMU]	8	4	1	1	2	1.322	2	43.219	4.421	75	8.826
E9ALW5	Putative ribosomal protein L1a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1070 PE=4 SV=1 - [E9ALW5_LEIMU]	2.68	2	1	1	2	1.223	2	30.513	4.419	373	41.081
H0Y941	Coiled-coil and C2 domain-containing protein 2A (Fragment) OS=Homo sapiens GN=CC2D2A PE=4 SV=1 - [H0Y941_HUMAN]	0.66	2	1	1	2	0.852	2	24.055	4.412	903	102.728
P51808	Dynein light chain Tctex-type 3 OS=Homo sapiens GN=DYNLT3 PE=1 SV=1 - [DYLT3_HUMAN]	14.66	2	1	1	1	1.058	1		4.410	116	13.053
P56937	3-keto-steroid reductase OS=Homo sapiens GN=HSD17B7 PE=1 SV=1 - [DHB7_HUMAN]	5.57	5	2	2	2	0.950	2	7.653	4.408	341	38.182
Q92766	Ras-responsive element-binding protein 1 OS=Homo sapiens GN=RREB1 PE=1 SV=3 - [RREB1_HUMAN]	2.37	2	3	3	3	1.000	3	0.000	4.403	1687	181.306
Q9P0U0	PC326 protein OS=Homo sapiens GN=PC326 PE=2 SV=1 - [Q9P0U0_HUMAN]	2.44	2	1	1	1	1.000	1		4.400	533	58.938
E9B632	Putative reiske iron-sulfur protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1540 PE=4 SV=1 - [E9B632_LEIMU]	2.69	1	1	1	2	2.101	2	128.365	4.399	297	33.703
Q9H4G0	Band 4.1-like protein 1 OS=Homo sapiens GN=EPB41L1 PE=1 SV=2 - [E41L1_HUMAN]	2.38	9	2	2	2	1.091	2	12.916	4.399	881	98.442
H0YEM5	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 6 (Fragment) OS=Homo sapiens GN=ALKBH6 PE=4 SV=1 - [H0YEM5_HUMAN]	8.33	1	1	1	2	1.023	2	3.377	4.397	72	8.207
I3L0D1	HCG1647537, isoform CRA_b OS=Homo sapiens GN=RBAK-RBAKDN PE=4 SV=1 - [I3L0D1_HUMAN]	5.76	2	1	2	2	0.675	1		4.394	243	27.448
Q99584	Protein S100-A13 OS=Homo sapiens GN=S100A13 PE=1 SV=1 - [S10AD_HUMAN]	8.16	1	1	1	2	0.709	2	54.582	4.391	98	11.464
E9B472	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2330 PE=4 SV=1 - [E9B472_LEIMU]	0.75	1	1	1	2	1.106	2	14.993	4.386	1060	114.321
E9AMJ7	Complete genome, chromosome 8 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_1228 PE=4 SV=1 - [E9AMJ7_LEIMU]	1.78	11	2	2	2	1.079	1		4.385	845	93.318
R4GN43	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens GN=NDUFA6 PE=1 SV=1 - [R4GN43_HUMAN]	11.27	2	1	1	2	1.000	2	0.000	4.384	71	8.504
H7C446	Suppressor of SWI4 1 homolog (Fragment) OS=Homo sapiens GN=PPAN PE=1 SV=1 - [H7C446_HUMAN]	12.5	3	2	3	4	1.000	3	0.000	4.380	208	23.204
Q13502	Phosphotyrosine independent ligand p62B for the Lck SH2 domain B-cell isoform (Fragment) OS=Homo sapiens GN=OSIL PE=2 SV=1 - [Q13502_HUMAN]	8.33	6	1	2	2	1.000	1		4.379	420	45.693
H7C0R7	NADH-cytochrome b5 reductase 1 (Fragment) OS=Homo sapiens GN=CYB5R1 PE=1 SV=1 - [H7C0R7_HUMAN]	12.39	2	3	3	3	1.025	3	10.627	4.376	226	24.888
B4DTX1	cDNA FLJ53196, highly similar to SAM and SH3 domain-containing protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DTX1_HUMAN]	1.29	3	1	1	2	0.922	2	0.611	4.374	695	76.454
Q8NB15	Zinc finger protein 511 OS=Homo sapiens GN=ZNF511 PE=2 SV=1 - [ZN511_HUMAN]	10.69	3	2	2	3	1.000	3	0.000	4.373	262	29.409
Q68DZ5	Beta-arrestin-2 OS=Homo sapiens GN=DKFZp686L0365 PE=2 SV=1 - [Q68DZ5_HUMAN]	9.22	11	1	2	2	1.000	1		4.372	217	24.347
Q7Z4G1	COMM domain-containing protein 6 OS=Homo sapiens GN=COMMD6 PE=1 SV=1 - [COMD6_HUMAN]	23.53	2	2	2	2	0.806	2	15.020	4.371	85	9.632
Q6ZRH9	Uncharacterized protein FLJ46347 OS=Homo sapiens PE=2 SV=1 - [YB011_HUMAN]	1.94	1	1	1	2	1.000	2	0.000	4.370	516	53.584
Q4ZG76	Putative uncharacterized protein TANK (Fragment) OS=Homo sapiens GN=TANK PE=4 SV=1 - [Q4ZG76_HUMAN]	3.83	12	2	2	2	1.003	2	0.449	4.368	392	43.947
B4DZK6	cDNA FLJ53375, highly similar to Hyaluronan mediated motility receptor OS=Homo sapiens PE=2 SV=1 - [B4DZK6_HUMAN]	3.42	9	3	3	3	1.036	3	16.337	4.367	701	81.545
Q9BQS8	FYVE and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=FYCO1 PE=1 SV=3 - [FYCO1_HUMAN]	0.95	1	1	1	1	1.000	1		4.364	1478	166.879
A8K3R2	Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=2 SV=1 - [A8K3R2_HUMAN]	2.01	3	1	1	1	0.984	1		4.360	746	83.518
E9B476	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2370 PE=4 SV=1 - [E9B476_LEIMU]	1.6	1	1	1	2	1.000	2	0.000	4.359	563	60.791
Q59GC9	Syntaxin binding protein 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GC9_HUMAN]	7.49	6	2	3	3	0.842	2	25.871	4.352	414	47.305
Q5T6K7	Nuclear transcription factor Y subunit gamma (Fragment) OS=Homo sapiens GN=NFYC PE=1 SV=1 - [Q5T6K7_HUMAN]	15.5	6	2	2	3	1.243	3	35.485	4.351	129	14.900
E9AXU6	Putative succinyl-CoA synthetase alpha subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_2130 PE=3 SV=1 - [E9AXU6_LEIMU]	8.7	2	2	3	4	2.085	3	150.797	4.347	299	30.890
E9AVY7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_1550 PE=4 SV=1 - [E9AVY7_LEIMU]	1.62	1	1	1	2	1.035	2	0.713	4.346	616	68.235
E9AUZ2	Hexokinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0250 PE=3 SV=1 - [E9AUZ2_LEIMU]	3.61	2	1	1	1	1.801	1		4.341	471	51.637
A0A024RCZ7	Chromosome 6 open reading frame 49, isoform CRA_c OS=Homo sapiens GN=C6orf49 PE=4 SV=1 - [A0A024RCZ7_HUMAN]	2.88	1	1	1	2	0.881	2	20.930	4.340	312	33.311
H0Y849	Actin-related protein 8 (Fragment) OS=Homo sapiens GN=ACTR8 PE=1 SV=1 - [H0Y849_HUMAN]	3.44	2	1	1	1	1.000	1		4.338	378	42.525
B4DG55	cDNA FLJ53905, highly similar to Phosphatidylinositol-4-phosphate 3-kinase C2domain-containing alpha polypeptide (EC 2.7.1.154) OS=Homo sapiens PE=2 SV=1 - [B4	2.07	3	2	2	2	0.820	2	30.058	4.338	1306	148.281
A6ZJA2	Lactation elevated protein 1 (Fragment) OS=Homo sapiens GN=LACE1 PE=4 SV=1 - [A6ZJA2_HUMAN]	6.88	2	1	1	1	0.824	1		4.335	160	18.560
E9PN86	Eukaryotic translation initiation factor 3 subunit M (Fragment) OS=Homo sapiens GN=EIF3M PE=1 SV=1 - [E9PN86_HUMAN]	27.45	3	2	2	2	1.000	1		4.335	102	11.725
Q9NU23	LYR motif-containing protein 2 OS=Homo sapiens GN=LYRM2 PE=1 SV=1 - [LYRM2_HUMAN]	19.32	4	2	2	2	0.932	2	10.448	4.334	88	10.443
E5RJI7	39S ribosomal protein L13, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL13 PE=1 SV=3 - [E5RJI7_HUMAN]	11.49	2	2	2	2	0.939	2	9.309	4.332	148	17.065
E9AQM6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0670 PE=4 SV=1 - [E9AQM6_LEIMU]	1.21	1	1	1	2	1.000	2	0.000	4.331	663	70.137
G8JLD3	ELKS/Rab6-interacting/CAST family member 1 OS=Homo sapiens GN=ERC1 PE=1 SV=1 - [G8JLD3_HUMAN]	1.66	7	1	2	2	1.644	1		4.330	1086	124.743
Q15388	Mitochondrial import receptor subunit TOM20 homolog OS=Homo sapiens GN=TOMM20 PE=1 SV=1 - [TOM20_HUMAN]	4.83	1	1	1	2	1.001	2	1.015	4.328	145	16.288
A0A075B746	28S ribosomal protein S21, mitochondrial OS=Homo sapiens GN=MRPS21 PE=1 SV=1 - [A0A075B746_HUMAN]	16.09	2	1	1	1	1.213	1		4.325	87	10.681
P82909	28S ribosomal protein S36, mitochondrial OS=Homo sapiens GN=MRPS36 PE=1 SV=2 - [RT36_HUMAN]	11.65	1	1	1	2	1.362	2	17.843	4.320	103	11.459
E9B627	Arginase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1480 PE=3 SV=1 - [E9B627_LEIMU]	4.86	1	2	2	3	1.000	3	0.000	4.320	329	36.058
H7C3A5	Lanosterol synthase (Fragment) OS=Homo sapiens GN=LSS PE=1 SV=1 - [H7C3A5_HUMAN]	5.15	1	1	1	2	1.000	2	0.000	4.318	136	15.358
E9PNT2	Rho GTPase-activating protein 27 OS=Homo sapiens GN=ARHGAP27 PE=4 SV=1 - [E9PNT2_HUMAN]	3.9	5	2	2	2	1.169	2	23.462	4.318	667	74.984
H3BUD2	Dynactin subunit 5 OS=Homo sapiens GN=DCTN5 PE=1 SV=1 - [H3BUD2_HUMAN]	20.75	5	1	1	1	0.980	1		4.313	53	6.020
E9PRK2	Probable asparagine--tRNA ligase, mitochondrial (Fragment) OS=Homo sapiens GN=NARS2 PE=1 SV=1 - [E9PRK2_HUMAN]	4.98	3	1	1	2	1.000	2	0.000	4.310	241	27.188
B4DZI7	cDNA FLJ57241, highly similar to Exocyst complex component 2 OS=Homo sapiens PE=2 SV=1 - [B4DZI7_HUMAN]	3.08	3	2	2	2	1.060	2	8.671	4.309	519	58.637
A0A024R2C4	B-cell CLL/lymphoma 2, isoform CRA_b OS=Homo sapiens GN=BCL2 PE=4 SV=1 - [A0A024R2C4_HUMAN]	3.9	3	1	1	2	1.109	2	18.713	4.308	205	22.323
A0A024R0Q1	Zinc finger protein 45, isoform CRA_a OS=Homo sapiens GN=ZNF45 PE=4 SV=1 - [A0A024R0Q1_HUMAN]	17.01	233	1	4	5	1.000	1		4.305	682	78.165
Q53GL1	Nicotinamide nucleotide adenylyltransferase 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GL1_HUMAN]	6.09	4	2	2	2	0.912	1		4.305	279	31.901
A0A087WZP7	Myotubularin-related protein 13 OS=Homo sapiens GN=SBF2 PE=4 SV=1 - [A0A087WZP7_HUMAN]	1.11	3	1	2	2	1.000	1		4.303	1802	203.018
B7Z201	cDNA FLJ61224 OS=Homo sapiens PE=2 SV=1 - [B7Z201_HUMAN]	2.2	4	1	1	2	1.000	2	0.000	4.301	500	56.903
B4DM43	cDNA FLJ59342, highly similar to Positive cofactor 2glutamine/Q-rich-associated protein OS=Homo sapiens PE=2 SV=1 - [B4DM43_HUMAN]	9.52	7	1	1	1	1.000	1		4.298	189	21.709
Q96P23	Myofibrillogenesis regulator MR-2 OS=Homo sapiens PE=2 SV=1 - [Q96P23_HUMAN]	18.31	2	2	2	2	1.000	2	0.000	4.295	142	15.560
A6NP24	Quinone oxidoreductase (Fragment) OS=Homo sapiens GN=CRYZ PE=1 SV=1 - [A6NP24_HUMAN]	12.35	3	3	3	3	1.043	3	6.181	4.291	243	25.966
J3QQZ1	Sodium channel protein OS=Homo sapiens GN=SCN4A PE=3 SV=1 - [J3QQZ1_HUMAN]	0.33	2	1	1	2	1.035	2	5.049	4.284	1836	208.042
E9API9	Putative dynein heavy chain OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1650 PE=4 SV=1 - [E9API9_LEIMU]	0.77	1	2	3	4	1.000	3	0.000	4.282	4667	529.889
O95450	A disintegrin and metalloproteinase with thrombospondin motifs 2 OS=Homo sapiens GN=ADAMTS2 PE=2 SV=2 - [ATS2_HUMAN]	1.4	1	2	2	2	1.073	1		4.282	1211	134.668
Q8N6M0	OTU domain-containing protein 6B OS=Homo sapiens GN=OTUD6B PE=1 SV=1 - [OTU6B_HUMAN]	6.14	2	2	2	2	0.703	2	62.510	4.276	293	33.791
A0A024R248	Chromosome 9 open reading frame 89, isoform CRA_b OS=Homo sapiens GN=C9orf89 PE=4 SV=1 - [A0A024R248_HUMAN]	8.2	2	2	2	2	1.000	2	0.000	4.273	183	20.613
Q5T097	Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=1 - [Q5T097_HUMAN]	1.92	3	1	2	2	1.312	1		4.271	988	113.282
Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens GN=UBLCP1 PE=1 SV=2 - [UBCP1_HUMAN]	2.83	1	1	1	2	1.192	2	35.991	4.266	318	36.781
E9AUW1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_1600 PE=4 SV=1 - [E9AUW1_LEIMU]	1.79	1	1	1	2	1.000	2	0.000	4.262	1005	108.937
B4DXH2	cDNA FLJ51138, highly similar to Arfaptin-2 OS=Homo sapiens PE=2 SV=1 - [B4DXH2_HUMAN]	5.33	4	1	2	2	0.823	1		4.258	319	35.736
Q16587	Zinc finger protein 74 OS=Homo sapiens GN=ZNF74 PE=2 SV=3 - [ZNF74_HUMAN]	6.37	126	1	4	5	1.000	1		4.251	644	72.160
Q6P4A7	Sideroflexin-4 OS=Homo sapiens GN=SFXN4 PE=1 SV=1 - [SFXN4_HUMAN]	7.72	2	2	2	2	1.000	2	0.000	4.248	337	37.974
O75923	Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1 - [DYSF_HUMAN]	0.63	4	1	2	2	0.813	1		4.247	2080	237.144
E9AUS4	Coatomer subunit beta OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_1350 PE=4 SV=1 - [E9AUS4_LEIMU]	2.7	1	2	2	2	0.932	2	10.477	4.245	999	109.583
D6R954	tRNA methyltransferase 10 homolog A (Fragment) OS=Homo sapiens GN=TRMT10A PE=4 SV=3 - [D6R954_HUMAN]	7	3	1	1	1	1.373	1		4.243	200	23.971
B3KTI0	cDNA FLJ38283 fis, clone FCBBF3007077 OS=Homo sapiens PE=2 SV=1 - [B3KTI0_HUMAN]	2.26	2	1	1	2	0.696	2	28.219	4.242	354	40.386
B4DET6	cDNA FLJ59314, highly similar to UV radiation resistance-associated gene protein OS=Homo sapiens PE=2 SV=1 - [B4DET6_HUMAN]	1.17	6	1	1	3	1.085	3	63.657	4.241	598	66.984
E9AQW5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1520 PE=4 SV=1 - [E9AQW5_LEIMU]	0.7	1	1	1	2	1.041	2	0.063	4.241	1148	126.882
A0A024RAJ7	G elongation factor, mitochondrial 2, isoform CRA_c OS=Homo sapiens GN=GFM2 PE=4 SV=1 - [A0A024RAJ7_HUMAN]	1.23	2	1	1	2	2.003	2	52.240	4.240	732	81.149
A0A024R3E0	Interleukin 18 (Interferon-gamma-inducing factor), isoform CRA_a OS=Homo sapiens GN=IL18 PE=4 SV=1 - [A0A024R3E0_HUMAN]	8.47	4	2	2	2	0.900	2	15.704	4.237	189	21.882
Q86WV6	Stimulator of interferon genes protein OS=Homo sapiens GN=TMEM173 PE=1 SV=1 - [STING_HUMAN]	8.44	3	3	3	3	1.000	3	0.000	4.232	379	42.166
E9AQZ1	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0160 PE=3 SV=1 - [E9AQZ1_LEIMU]	0.64	1	1	1	2	0.933	1		4.231	1100	114.852
B7ZLE8	NAIP protein OS=Homo sapiens GN=NAIP PE=2 SV=1 - [B7ZLE8_HUMAN]	2.52	6	3	3	3	1.133	3	5.657	4.228	1347	153.013

Q86YR7	Probable guanine nucleotide exchange factor MCF2L2 OS=Homo sapiens GN=MCF2L2 PE=2 SV=3 - [MF2L2_HUMAN]	1.71	1	2	2	2	4.931	2	629.351	4.223	1114	126.913
D6W625	Chromatin assembly factor 1, subunit A (P150), isoform CRA_a OS=Homo sapiens GN=CHAF1A PE=4 SV=1 - [D6W625_HUMAN]	1.78	2	2	2	2	0.971	2	17.477	4.219	956	106.872
Q8NC96	Adaptin ear-binding coat-associated protein 1 OS=Homo sapiens GN=NECAP1 PE=1 SV=2 - [NECP1_HUMAN]	8.73	3	2	2	2	1.101	2	33.761	4.218	275	29.719
I3L413	G1/S-specific cyclin-E1 (Fragment) OS=Homo sapiens GN=CCNE1 PE=1 SV=1 - [I3L413_HUMAN]	7.07	4	1	2	2	0.855	1		4.216	283	32.352
E9B4J2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0240 PE=4 SV=1 - [E9B4J2_LEIMU]	0.9	7	1	2	2				4.214	1336	148.101
Q7Z7C8	Transcription initiation factor TFIID subunit 8 OS=Homo sapiens GN=TAF8 PE=1 SV=1 - [TAF8_HUMAN]	9.35	4	2	2	2	0.901	2	15.580	4.209	310	34.241
E9B354	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2750 PE=4 SV=1 - [E9B354_LEIMU]	0.72	1	1	1	2	0.705	2	57.464	4.209	1524	165.415
B4DNT5	cDNA FLJ60316, highly similar to Apolipoprotein-L1 OS=Homo sapiens PE=2 SV=1 - [B4DNT5_HUMAN]	5.05	34	1	2	2	0.811	1		4.208	277	30.791
E9AXD1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0540 PE=4 SV=1 - [E9AXD1_LEIMU]	2.37	1	1	1	2	0.982	2	2.662	4.205	295	32.409
U4Q365	Mediator complex subunit 27 OS=Homo sapiens GN=MED27 PE=2 SV=1 - [U4Q365_HUMAN]	6.25	3	1	1	2	1.000	2	0.000	4.205	160	17.789
O75064	DENN domain-containing protein 4B OS=Homo sapiens GN=DENND4B PE=1 SV=4 - [DEN4B_HUMAN]	1.74	3	3	3	4	1.000	3	0.000	4.204	1496	163.743
E9PLF1	Glutathione S-transferase Mu 2 (Fragment) OS=Homo sapiens GN=GSTM2 PE=1 SV=2 - [E9PLF1_HUMAN]	14.29	9	2	3	4	0.848	3	19.725	4.200	147	17.358
E9AT88	Putative ATP synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3100 PE=4 SV=1 - [E9AT88_LEIMU]	3.7	1	1	1	2	1.483	2	32.207	4.196	216	25.242
E9AR16	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0470 PE=4 SV=1 - [E9AR16_LEIMU]	0.56	1	1	1	2	1.000	2	0.000	4.195	3547	379.580
M0QXT2	Deoxyhypusine synthase (Fragment) OS=Homo sapiens GN=DHPS PE=4 SV=1 - [M0QXT2_HUMAN]	25.93	7	1	1	2	0.764	2	44.194	4.193	27	2.930
Q9ULW3	Activator of basal transcription 1 OS=Homo sapiens GN=ABT1 PE=1 SV=1 - [ABT1_HUMAN]	5.51	1	2	2	2	1.864	2	116.000	4.190	272	31.060
D6RJA0	Histone-lysine N-methyltransferase SETD7 OS=Homo sapiens GN=SETD7 PE=1 SV=1 - [D6RJA0_HUMAN]	2.49	2	1	1	2	1.000	1		4.190	362	40.102
B4DYP7	cDNA FLJ55435, highly similar to Gamma-tubulin complex component 3 OS=Homo sapiens PE=2 SV=1 - [B4DYP7_HUMAN]	1.9	4	2	2	2	0.784	2	37.371	4.188	897	102.508
Q9UJX2	Cell division cycle protein 23 homolog OS=Homo sapiens GN=CDC23 PE=1 SV=3 - [CDC23_HUMAN]	2.68	1	2	2	2	1.075	2	10.698	4.183	597	68.790
Q9UKL6	Phosphatidylcholine transfer protein OS=Homo sapiens GN=PCTP PE=1 SV=1 - [PPCT_HUMAN]	3.27	1	1	1	2	1.196	2	16.265	4.181	214	24.827
E9AWE0	T-complex protein 1 subunit gamma OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1220 PE=3 SV=1 - [E9AWE0_LEIMU]	5.44	1	3	3	3	1.000	3	14.962	4.179	551	60.192
Q70W25	GP63 OS=Leishmania aethiopica GN=mspC PE=4 SV=1 - [Q70W25_9TRYP]	4.72	2	1	2	2				4.176	657	70.150
O94919	Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2 - [ENDD1_HUMAN]	2.8	1	1	1	1	1.206	1		4.172	500	54.981
Q9Y5T4	DnaJ homolog subfamily C member 15 OS=Homo sapiens GN=DNAJC15 PE=1 SV=2 - [DJC15_HUMAN]	6.67	1	1	1	2	1.000	2	0.000	4.171	150	16.373
Q9UKX3	Myosin-13 OS=Homo sapiens GN=MYH13 PE=1 SV=2 - [MYH13_HUMAN]	1.81	19	1	4	4	0.963	1		4.171	1938	223.465
A7E2Y1	Myosin-7B OS=Homo sapiens GN=MYH7B PE=1 SV=3 - [MYH7B_HUMAN]	1.34	7	1	3	3	1.000	1		4.171	1941	221.251
E9AKE2	Putative ATP-dependent RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0360 PE=3 SV=1 - [E9AKE2_LEIMU]	2.42	1	1	2	2	1.594	1		4.170	621	65.925
B4E336	cDNA FLJ53287, highly similar to CD97 antigen OS=Homo sapiens PE=2 SV=1 - [B4E336_HUMAN]	2.29	12	2	2	2	1.119	2	8.396	4.169	655	72.248
Q5H9P3	Putative uncharacterized protein DKFZp779M164 (Fragment) OS=Homo sapiens GN=DKFZp779M164 PE=4 SV=1 - [Q5H9P3_HUMAN]	1.91	5	2	2	2	0.848	2	67.556	4.167	1154	134.493
B3KQT0	cDNA PSEC0144 fis, clone PLACE1006610, highly similar to Gamma-secretase subunit APH-1A OS=Homo sapiens PE=2 SV=1 - [B3KQT0_HUMAN]	5.67	2	1	1	1	0.952	1		4.157	247	26.751
F2Z356	General transcription factor 3C polypeptide 4 OS=Homo sapiens GN=GTF3C4 PE=1 SV=1 - [F2Z356_HUMAN]	4.7	3	1	1	2	0.673	2	92.343	4.156	149	15.491
Q5FWF5	N-acetyltransferase ESCO1 OS=Homo sapiens GN=ESCO1 PE=1 SV=3 - [ESCO1_HUMAN]	0.95	1	1	1	2	1.008	2	2.427	4.156	840	94.923
B7Z756	cDNA FLJ56256, highly similar to Choline/ethanolamine kinase OS=Homo sapiens PE=2 SV=1 - [B7Z756_HUMAN]	6.2	2	1	1	1	0.866	1		4.148	274	32.087
K7EQA8	Histone-arginine methyltransferase CARM1 (Fragment) OS=Homo sapiens GN=CARM1 PE=1 SV=1 - [K7EQA8_HUMAN]	4.08	2	2	2	2	0.948	2	1.165	4.147	343	38.393
B4DSG1	cDNA FLJ51294, highly similar to JmjC domain-containing histone demethylation protein 1A (EC 1.14.11.-) OS=Homo sapiens PE=2 SV=1 - [B4DSG1_HUMAN]	3.33	3	1	1	1	1.000	1		4.147	420	47.019
Q15463	Cell surface glycoprotein (Fragment) OS=Homo sapiens GN=P3.58 PE=2 SV=1 - [Q15463_HUMAN]	5.07	7	1	1	1	0.296	1		4.147	276	30.189
D3DR37	Centrosomal protein 55kDa, isoform CRA_a OS=Homo sapiens GN=CEP55 PE=4 SV=1 - [D3DR37_HUMAN]	5.17	2	2	3	3	1.072	2	10.355	4.146	464	54.091
Q9H5Q4	Dimethyladenosine transferase 2, mitochondrial OS=Homo sapiens GN=TFB2M PE=1 SV=1 - [TFB2M_HUMAN]	3.79	3	2	2	2	0.631	2	35.619	4.145	396	45.320
Q9NVF7	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1 - [FBX28_HUMAN]	2.17	1	1	1	2	1.043	2	6.236	4.143	368	41.123
H3BUY2	Poly [ADP-ribose] polymerase 6 (Fragment) OS=Homo sapiens GN=PARP6 PE=4 SV=1 - [H3BUY2_HUMAN]	15.07	11	1	1	2	0.964	2	5.777	4.141	73	8.296
P10109	Adrenodoxin, mitochondrial OS=Homo sapiens GN=FDX1 PE=1 SV=1 - [ADX_HUMAN]	8.15	1	2	2	2	1.001	2	25.124	4.141	184	19.381
H7C519	5'-nucleotidase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=NT5DC2 PE=1 SV=1 - [H7C519_HUMAN]	5.15	2	1	1	2	1.000	2	0.000	4.139	194	23.358
Q4KWH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1 PE=1 SV=1 - [PLCH1_HUMAN]	0.47	1	1	1	3	0.900	2	15.740	4.138	1693	189.104
E9AV89	Putative 60S ribosomal protein L9 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1050 PE=4 SV=1 - [E9AV89_LEIMU]	9.47	1	1	2	3	1.000	1		4.136	190	21.514
E9AM77	Transcription factor-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0020 PE=4 SV=1 - [E9AM77_LEIMU]	1.53	1	2	2	3	1.000	3	0.000	4.136	1045	114.871
E9B5R9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0310 PE=4 SV=1 - [E9B5R9_LEIMU]	1.87	1	1	1	2	0.775	2	39.195	4.131	427	46.491
B3KW23	cDNA FLJ41961 fis, clone PUAEN2004083, highly similar to Nucleoporin p58/p45 OS=Homo sapiens PE=2 SV=1 - [B3KW23_HUMAN]	4.17	5	3	3	3	1.055	3	7.932	4.130	576	58.831
C6KG45	Mutant methyl CpG binding protein 2 transcript variant 1 OS=Homo sapiens GN=MECP2 PE=2 SV=1 - [C6KG45_HUMAN]	4.94	18	2	2	3	1.000	3	0.000	4.130	486	52.375
Q9H0E2	Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=1 SV=1 - [TOLIP_HUMAN]	6.2	6	2	2	2	1.019	2	17.858	4.130	274	30.262
B1AA17	Gastric cancer hepatocellular carcinoma suppressor 1 variant OS=Homo sapiens GN=HCCS1 PE=2 SV=1 - [B1AA17_HUMAN]	2.99	9	2	2	2	0.914	2	13.366	4.130	670	76.346
A0A024RAB6	Heparan sulfate proteoglycan 2 (Perlecan), isoform CRA_b OS=Homo sapiens GN=HSPG2 PE=4 SV=1 - [A0A024RAB6_HUMAN]	0.44	3	2	2	2	1.062	2	8.905	4.128	4346	463.723
D6RHU3	Caspase-6 subunit p18 (Fragment) OS=Homo sapiens GN=CASP6 PE=1 SV=1 - [D6RHU3_HUMAN]	4.9	3	1	1	2	1.000	2	0.000	4.127	143	16.705
B3KSH0	cDNA FLJ36190 fis, clone TESTI2027271, highly similar to N6-adenosine-methyltransferase 70 kDa subunit (EC 2.1.1.62) OS=Homo sapiens PE=2 SV=1 - [B3KSH0_HU	3.53	3	2	2	2	0.949	2	7.707	4.127	425	47.685
O00488	Zinc finger protein 593 OS=Homo sapiens GN=ZNF593 PE=1 SV=2 - [ZN593_HUMAN]	10.45	1	1	1	1	2.120	1		4.127	134	15.190
I3L1H3	Lipopolysaccharide-induced tumor necrosis factor-alpha factor OS=Homo sapiens GN=LITAF PE=4 SV=1 - [I3L1H3_HUMAN]	10.29	2	1	1	2	1.129	2	6.634	4.127	68	7.367
I3L0W4	Diamine acetyltransferase 2 OS=Homo sapiens GN=SAT2 PE=1 SV=1 - [I3L0W4_HUMAN]	11.76	4	2	2	2	1.252	2	17.885	4.124	136	15.047
I3L531	Cytosolic Fe-S cluster assembly factor NUBP1 (Fragment) OS=Homo sapiens GN=NUBP1 PE=1 SV=1 - [I3L531_HUMAN]	10.71	2	2	2	5	0.818	2	30.459	4.123	168	17.859
E9B713	Proteasome subunit alpha type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4850 PE=3 SV=1 - [E9B713_LEIMU]	4	1	1	1	2	1.000	2	0.000	4.120	250	27.248
Q59F44	Cytochrome b-5 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59F44_HUMAN]	25.76	2	2	2	2	1.000	2	0.000	4.116	132	14.563
E9ANQ5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_1160 PE=4 SV=1 - [E9ANQ5_LEIMU]	1.03	1	1	1	2	1.090	2	12.852	4.115	1164	123.322
Q9UG01	Intraflagellar transport protein 172 homolog OS=Homo sapiens GN=IFT172 PE=1 SV=2 - [IF172_HUMAN]	0.91	3	2	2	2	0.799	1		4.112	1749	197.451
A0A024R973	Chromosome 1 open reading frame 27, isoform CRA_b OS=Homo sapiens GN=C1orf27 PE=4 SV=1 - [A0A024R973_HUMAN]	11.02	2	4	4	4	1.053	4	7.702	4.112	354	39.763
P04921	Glycophorin-C OS=Homo sapiens GN=GYPC PE=1 SV=1 - [GLPC_HUMAN]	27.34	11	2	2	2	1.020	1		4.110	128	13.802
Q06330	Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 - [SUH_HUMAN]	6.4	19	3	3	3	1.170	3	2.158	4.108	500	55.602
E9AR86	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_1140 PE=4 SV=1 - [E9AR86_LEIMU]	0.5	1	1	1	2	0.868	1		4.101	1394	148.970
B2RA72	cDNA, FLJ94734, Homo sapiens CHMP1.5 protein (CHMP1.5), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RA72_HUMAN]	8.16	2	2	2	2	0.921	2	16.910	4.097	196	21.763
R4GNB2	DENN domain-containing protein 4C OS=Homo sapiens GN=DENND4C PE=1 SV=1 - [R4GNB2_HUMAN]	0.68	2	1	1	2	1.000	1		4.094	1909	212.576
H9E7C9	NADH-ubiquinone oxidoreductase chain 2 OS=Homo sapiens GN=ND2 PE=3 SV=1 - [H9E7C9_HUMAN]	2.02	7	1	1	2	1.000	2	0.000	4.093	347	38.982
P16278	Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2 - [BGAL_HUMAN]	3.55	7	2	2	4	1.210	4	22.603	4.092	677	76.027
P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	4.33	3	2	2	2	0.800	2	34.014	4.092	462	51.643
A0A024RBT0	WD repeat domain 66, isoform CRA_a OS=Homo sapiens GN=WDR66 PE=4 SV=1 - [A0A024RBT0_HUMAN]	1.65	2	2	2	2	0.738	2	1.559	4.087	1154	130.514
B2R9D9	cDNA, FLJ94347 OS=Homo sapiens PE=2 SV=1 - [B2R9D9_HUMAN]	1.98	2	1	1	2	0.982	2	1.268	4.084	354	38.534
Q96GX5	Serine/threonine-protein kinase greatwall OS=Homo sapiens GN=MASTL PE=1 SV=1 - [GWL_HUMAN]	3.75	13	3	4	4	1.000	3	36.340	4.081	879	97.257
P25054	Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2 - [APC_HUMAN]	0.81	3	2	2	2	1.000	1		4.081	2843	311.455
B2RAR2	cDNA, FLJ95064, highly similar to Homo sapiens nin one binding protein (NOB1P), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAR2_HUMAN]	3.88	2	2	2	2	1.597	2	38.184	4.081	412	46.616
Q96QU6	1-aminocyclopropane-1-carboxylate synthase-like protein 1 OS=Homo sapiens GN=ACCS PE=2 SV=1 - [1A1L1_HUMAN]	3.79	1	1	1	3	1.000	3	0.000	4.071	501	57.287
E9AZ69	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1660 PE=4 SV=1 - [E9AZ69_LEIMU]	0.46	1	1	1	2	0.839	2	26.395	4.071	1294	143.424
A0A087WXC4	Tenascin-N OS=Homo sapiens GN=TNN PE=4 SV=1 - [A0A087WXC4_HUMAN]	1.34	5	2	2	2	0.223	2	641.786	4.068	1122	124.442
P48553	Trafficking protein particle complex subunit 10 OS=Homo sapiens GN=TRAPPC10 PE=1 SV=2 - [TPC10_HUMAN]	1.75	2	3	3	3	1.000	3	18.237	4.067	1259	142.098
B7Z854	cDNA FLJ61649, highly similar to Homo sapiens estrogen receptor binding protein (ERBP), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z854_HUMAN]	2.5	3	1	1	1	1.088	1		4.062	601	66.121
Q96N46	Tetratricopeptide repeat protein 14 OS=Homo sapiens GN=TTC14 PE=1 SV=1 - [TTC14_HUMAN]	1.95	1	1	2	2	1.000	1		4.053	770	88.265
Q59GQ7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a3 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GQ7_HUMAN]	1.71	4	2	2	3	0.904	3	15.103	4.052	992	111.896
B3KWF6	cDNA FLJ42989 fis, clone BRTHA2009803, highly similar to Centaurin-alpha 1 OS=Homo sapiens PE=2 SV=1 - [B3KWF6_HUMAN]	4	8	1	1	2	1.032	2	19.345	4.052	200	23.212
Q9NPD3	Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3 - [EXOS4_HUMAN]	6.53	2	2	2	2	0.838	2	26.639	4.048	245	26.366
A0A087X0R7	Protein SENP3-EIF4A1 (Fragment) OS=Homo sapiens GN=SENP3-EIF4A1 PE=4 SV=1 - [A0A087X0R7_HUMAN]	4.26	6	2	2	2	0.717	2	52.442	4.048	540	61.239
E9AJW9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_03_0850 PE=4 SV=1 - [E9AJW9_LEIMU]	0.31	1	1	1	2	0.943	2	21.593	4.045	2233	236.238
C9JGT3	cGMP-specific 3',5'-cyclic phosphodiesterase (Fragment) OS=Homo sapiens GN=PDE5A PE=4 SV=1 - [C9JGT3_HUMAN]	3.13	4	1	1	2	1.000	2	0.000	4.044	224	25.103
B7Z871	cDNA FLJ50930, highly similar to Lipoma-preferred partner OS=Homo sapiens PE=2 SV=1 - [B7Z871_HUMAN]	5.12	5	2	2	2	0.991	2	7.013	4.039	449	48.485
K7EQG1	Glutaminyl-peptide cyclotransferase-like protein (Fragment) OS=Homo sapiens GN=QPCTL PE=1 SV=1 - [K7EQG1_HUMAN]	16.53	2	2	2	2	1.181	2	27.729	4.035	121	13.971
E9AJM9	Putative mitochondrial carrier protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0670 PE=3 SV=1 - [E9AJM9_LEIMU]	2.88	1	1	1	2	1.609	1		4.030	313	34.363
B4E0E6	cDNA FLJ53398, highly similar to Homo sapiens denticleless homolog (DTL), mRNA OS=Homo sapiens PE=2 SV=1 - [B4E0E6_HUMAN]	1.02	3	1	1	2	1.076	2	0.600	4.028	688	74.964
Q6PGP6	HELZ protein (Fragment) OS=Homo sapiens GN=HELZ PE=2 SV=1 - [Q6PGP6_HUMAN]	6.39	7	2	2	3	1.000	3	0.000	4.028	454	51.597
B4E394	cDNA FLJ51483, highly similar to Multiple inositol polyphosphate phosphatase 1 (EC 3.1.3.62) OS=Homo sapiens PE=2 SV=1 - [B4E394_HUMAN]	5.2	3	2	2	2	0.790	2	47.477	4.027	346	39.824
F8VSL3	Nuclear transcription factor Y subunit beta (Fragment) OS=Homo sapiens GN=NFYB PE=1 SV=1 - [F8VSL3_HUMAN]	6.11	2	1	1	2	0.878	2	1.695	4.024	131	14.539
P58004	Sestrin-2 OS=Homo sapiens GN=SESN2 PE=1 SV=1 - [SESN2_HUMAN]	2.5	1	1	1	3				4.017	480	54.459
E9ATV0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5160 PE=4 SV=1 - [E9ATV0_LEIMU]	2.12	1	1	1	2	1.101	2	14.363	4.014	565	65.289
A0A087WUU9	Zinc finger protein 36, C3H1 type-like 2 OS=Homo sapiens GN=ZFP36L2 PE=4 SV=1 - [A0A087WUU9_HUMAN]	2.24	2	1	1	2	0.950	1		4.007	492	51.016
B4DNS2	cDNA FLJ51602, highly similar to Interferon-induced guanylate-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DNS2_HUMAN]	4.76	4	2	2	2	1.107	2	10.340	4.000	357	41.244
Q2M3G0	ATP-binding cassette sub-family B member 5 OS=Homo sapiens GN=ABCB5 PE=1 SV=4 - [ABCB5_HUMAN]	1.59	2	2	2	2	1.011	2	1.616	3.996	1257	138.553
C9JW94	Kinetochore protein Spc25 (Fragment) OS=Homo sapiens GN=SPC25 PE=1 SV=1 - [C9JW94_HUMAN]	10.43	2	1	1	1	1.074	1		3.996	115	13.634
B3KSK3	cDNA FLJ36473 fis, clone THYMU2016840, highly similar to Death-associated protein kinase 3 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B3KSK3_HUMAN]	3.66	3	1	1	2	0.687	2	45.962	3.991	191	22.233
H0Y7V4	Dynein heavy chain 8, axonemal OS=Homo sapiens GN=DNAH8 PE=1 SV=1 - [H0Y7V4_HUMAN]	0.36	3	2	2	2	1.741	2	62.731	3.987	4188	478.566
Q6ZT12	E3 ubiquitin-protein ligase UBR3 OS=Homo sapiens GN=UBR3 PE=2 SV=2 - [UBR3_HUMAN]	0.85	1	1	1	1	1.000	1		3.984	1888	212.296
Q4G0X9	Coiled-coil domain-containing protein 40 OS=Homo sapiens GN=CCDC40 PE=2 SV=2 - [CCD40_HUMAN]	1.14	3	1	2	3	1.000	1		3.984	1142	130.033
E9ARJ8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0600 PE=4 SV=1 - [E9ARJ8_LEIMU]	2.36	1	1	1	1	1.000	1		3.984	636	67.982
A0A075B6K9	Ig lambda-2 chain C regions (Fragment) OS=Homo sapiens GN=IGLC2 PE=4 SV=1 - [A0A075B6K9_HUMAN]	16.04	34	2	2	2	1.388	2	51.649	3.983	106	11.340
E9AM02	Putative lipophosphoglycan biosynthetic protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0760 PE=3 SV=1 - [E9AM02_LEIMU]	2.98	1	2	2	2	1.000	2	0.000	3.981	771	86.764
E9B193	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3190 PE=3 SV=1 - [E9B193_LEIMU]	3.69	1	2	2	2	1.023	2	3.383	3.980	434	45.736
J3KN23	Protein lin-7 homolog A OS=Homo sapiens GN=LIN7A PE=4 SV=1 - [J3KN23_HUMAN]	6.93	6	1	1	2	0.659	2	68.200	3.980	101	11.310
Q5VUG0	Scm-like with four MBT domains protein 2 OS=Homo sapiens GN=SFMBT2 PE=1 SV=1 - [SMBT2_HUMAN]	1.45	1	1	1	1	1.038	1		3.977	894	100.498
O14880	Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1 - [MGST3_HUMAN]	5.26	3	1	1	3	1.064	3	1.430	3.975	152	16.506
B4DEM1	cDNA FLJ57952, highly similar to CMP-sialic acid transporter OS=Homo sapiens PE=2 SV=1 - [B4DEM1_HUMAN]	6.9	2	1	1	2	1.000	1		3.966	203	22.094
Q9UBW8	COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 - [CSN7A_HUMAN]	3.27	1	1	1	2	1.000	2	0.000	3.952	275	30.258
A8K901	cDNA FLJ77190, highly similar to Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K90	0.89	4	1	1	3	1.000	3	0.000	3.950	1013	117.157
E9PP78	FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=1 SV=1 - [E9PP78_HUMAN]	5.41	2	1	1	2	1.021	2	3.152	3.949	185	20.293
Q8NB78	Lysine-specific histone demethylase 1B OS=Homo sapiens GN=KDM1B PE=1 SV=3 - [KDM1B_HUMAN]	1.82	1	1	1	2	1.000	1		3.942	822	92.039
B3KNV2	cDNA FLJ30524 fis, clone BRAWH2000926, highly similar to Peptide chain release factor 1, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B3KNV2_HUMAN]	1.57	2	1	1	2	1.000	2	0.000	3.939	445	52.225
Q9UGR2	Zinc finger CCCH domain-containing protein 7B OS=Homo sapiens GN=ZC3H7B PE=1 SV=1 - [Z3H7B_HUMAN]	1.51	1	2	2	2	0.915	2	13.153	3.934	993	111.506
E9B634	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1560 PE=4 SV=1 - [E9B634_LEIMU]	0.49	1	1	1	2	1.000	2	0.000	3.927	1843	198.922
D2DGW5	Alpha-dystrobrevin (Fragment) OS=Homo sapiens GN=DTNA PE=2 SV=1 - [D2DGW5_HUMAN]	3.17	3	1	1	2	2.984	2	473.588	3.919	252	28.139
B7Z6I3	DNA ligase OS=Homo sapiens PE=2 SV=1 - [B7Z6I3_HUMAN]	2.57	4	2	2	2	0.956	2	6.602	3.918	738	82.270
C9JLG5	Interferon-related developmental regulator 1 (Fragment) OS=Homo sapiens GN=IFRD1 PE=1 SV=1 - [C9JLG5_HUMAN]	38.71	5	1	1	1	1.000	1		3.916	62	6.186
A1L471	ATP-binding cassette, sub-family B (MDR/TAP), member 1 OS=Homo sapiens GN=ABCB1 PE=2 SV=1 - [A1L471_HUMAN]	1.09	3	2	2	2	1.360	2	19.765	3.913	1280	141.400
Q6ZMG9	Ceramide synthase 6 OS=Homo sapiens GN=CERS6 PE=1 SV=1 - [CERS6_HUMAN]	2.6	1	1	1	2	1.000	2	0.000	3.909	384	44.861
E9AU34	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5990 PE=4 SV=1 - [E9AU34_LEIMU]	1.41	1	1	1	2	1.000	2	0.000	3.909	639	71.169
B7Z5R3	Src family associated phosphoprotein 2, isoform CRA_c OS=Homo sapiens GN=SCAP2 PE=2 SV=1 - [B7Z5R3_HUMAN]	4.28	3	1	1	2	0.999	2	12.955	3.898	187	21.635
Q2TAC2	Coiled-coil domain-containing protein 57 OS=Homo sapiens GN=CCDC57 PE=2 SV=2 - [CCD57_HUMAN]	1.31	6	2	2	2	1.006	2	0.825	3.898	916	103.104
B4E3D6	Myeloid differentiation primary response protein MyD88 OS=Homo sapiens PE=2 SV=1 - [B4E3D6_HUMAN]	10.18	4	2	2	3	1.000	3	0.000	3.896	285	31.962
B3KNP0	cDNA FLJ30074 fis, clone BGGI11000123, highly similar to Homo sapiens formin binding protein 4 (FNBP4), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KNP	3.56	3	2	2	2	1.000	2	0.000	3.895	928	99.796
B2RAK1	cDNA, FLJ94965, highly similar to Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAK1_HUMAN]	3.12	2	2	2	2	0.903	2	15.166	3.894	1025	117.270
P82663	28S ribosomal protein S25, mitochondrial OS=Homo sapiens GN=MRPS25 PE=1 SV=1 - [RT25_HUMAN]	16.18	2	2	2	2	1.000	2	0.000	3.888	173	20.103
Q5THK1	Protein PRR14L OS=Homo sapiens GN=PRR14L PE=1 SV=1 - [PR14L_HUMAN]	1.16	1	2	3	3	1.205	2	28.126	3.882	2151	237.150
Q14728	Major facilitator superfamily domain-containing protein 10 OS=Homo sapiens GN=MFSD10 PE=2 SV=1 - [MFS10_HUMAN]	3.96	4	2	2	2	0.980	2	9.098	3.869	455	48.308
H9KVB6	Ubiquitin carboxyl-terminal hydrolase 16 (Fragment) OS=Homo sapiens GN=USP16 PE=4 SV=1 - [H9KVB6_HUMAN]	14.95	2	1	1	1	1.000	1		3.865	107	12.172
E9ASQ7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1380 PE=4 SV=1 - [E9ASQ7_LEIMU]	2.41	1	2	2	2	1.038	2	1.788	3.862	622	68.406
Q9Y3E7	Charged multivesicular body protein 3 OS=Homo sapiens GN=CHMP3 PE=1 SV=3 - [CHMP3_HUMAN]	6.76	1	2	2	3	1.097	3	4.913	3.858	222	25.057
B7ZKR8	USP48 protein OS=Homo sapiens GN=USP48 PE=2 SV=1 - [B7ZKR8_HUMAN]	0.71	3	1	1	2	0.729	2	49.603	3.857	983	112.915
Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN]	1.47	1	1	1	1	1.000	1		3.856	2850	282.228
D3VVJ5	Ataxin 3 variant e (Fragment) OS=Homo sapiens GN=ATXN3 PE=2 SV=1 - [D3VVJ5_HUMAN]	8.62	1	1	1	1	1.000	1		3.849	290	33.423
Q9BYC8	39S ribosomal protein L32, mitochondrial OS=Homo sapiens GN=MRPL32 PE=1 SV=1 - [RM32_HUMAN]	6.91	1	1	1	1	1.079	1		3.846	188	21.391
M4VP52	Apolipoprotein B editing enzyme catalytic polypeptide-like 3C OS=Homo sapiens GN=APOBEC3C PE=2 SV=1 - [M4VP52_HUMAN]	6.84	3	1	1	2	0.943	2	2.076	3.845	190	22.781
O75061	Putative tyrosine-protein phosphatase auxilin OS=Homo sapiens GN=DNAJC6 PE=1 SV=3 - [AUXI_HUMAN]	1.2	1	1	1	1	1.000	1		3.832	913	99.933
Q6FG43	FLOT2 protein OS=Homo sapiens GN=FLOT2 PE=2 SV=1 - [Q6FG43_HUMAN]	2.9	5	1	1	1	1.004	1		3.830	379	41.659
H3BT44	Protein spinster homolog 1 (Fragment) OS=Homo sapiens GN=SPNS1 PE=1 SV=1 - [H3BT44_HUMAN]	7.87	6	1	1	1	1.144	1		3.830	178	18.956
B4DWT0	cDNA FLJ60187 OS=Homo sapiens PE=2 SV=1 - [B4DWT0_HUMAN]	5.73	4	1	1	2	1.000	2	0.000	3.810	157	15.750
P43251	Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2 - [BTD_HUMAN]	2.21	1	1	1	1	0.998	1		3.807	543	61.093
Q7Z7K0	COX assembly mitochondrial protein homolog OS=Homo sapiens GN=CMC1 PE=1 SV=1 - [COXM1_HUMAN]	16.04	3	2	2	2	1.223	2	0.991	3.802	106	12.481
H0YFP7	Ethanolamine kinase 1 (Fragment) OS=Homo sapiens GN=ETNK1 PE=4 SV=1 - [H0YFP7_HUMAN]	14.63	5	1	1	1	1.058	1		3.801	82	8.994
Q99676	Zinc finger protein 184 OS=Homo sapiens GN=ZNF184 PE=1 SV=4 - [ZN184_HUMAN]	5.19	119	1	3	4	1.155	1		3.796	751	86.119
F8WBK6	Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=4 SV=1 - [F8WBK6_HUMAN]	5.22	4	1	1	2	1.328	2	3.580	3.782	134	15.619
Q96BZ8	Leukocyte receptor cluster member 1 OS=Homo sapiens GN=LENG1 PE=1 SV=1 - [LENG1_HUMAN]	6.06	1	1	1	1	1.000	1		3.775	264	30.511
Q9UHF1	Epidermal growth factor-like protein 7 OS=Homo sapiens GN=EGFL7 PE=1 SV=3 - [EGFL7_HUMAN]	5.13	1	1	1	1	1.000	1		3.769	273	29.598
B4E184	cDNA FLJ53267, highly similar to Optineurin OS=Homo sapiens PE=2 SV=1 - [B4E184_HUMAN]	1.92	3	1	1	3	1.000	3	0.000	3.768	520	59.576
I3L4N6	Solute carrier family 12 member 4 OS=Homo sapiens GN=SLC12A4 PE=1 SV=1 - [I3L4N6_HUMAN]	2.22	3	2	2	2	1.159	2	13.069	3.766	1037	114.979
B2R841	Serine/threonine-protein kinase PLK OS=Homo sapiens PE=2 SV=1 - [B2R841_HUMAN]	4.48	7	2	2	2	0.950	2	7.651	3.752	603	68.222
Q5TAX3	Terminal uridylyltransferase 4 OS=Homo sapiens GN=ZCCHC11 PE=1 SV=3 - [TUT4_HUMAN]	1.82	3	3	3	3	1.025	2	3.665	3.749	1644	185.048
B4DVK6	cDNA FLJ55564, highly similar to Probable E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens PE=2 SV=1 - [B4DVK6_HUMAN]	2.2	2	1	1	1	1.075	1		3.747	727	81.646
E9AJK7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0450 PE=4 SV=1 - [E9AJK7_LEIMU]	2.89	1	1	1	2	1.000	2	0.000	3.746	277	29.936
A0JLR2	NFX1 protein (Fragment) OS=Homo sapiens GN=NFX1 PE=2 SV=1 - [A0JLR2_HUMAN]	1.76	2	1	1	1	1.185	1		3.737	681	75.148
B4DGW0	E3 SUMO-protein ligase PIAS2 OS=Homo sapiens GN=PIAS2 PE=1 SV=1 - [B4DGW0_HUMAN]	5.32	9	1	1	1	1.250	1		3.737	282	31.219
Q9H9F9	Actin-related protein 5 OS=Homo sapiens GN=ACTR5 PE=1 SV=2 - [ARP5_HUMAN]	1.48	1	1	1	2	1.000	2	0.000	3.732	607	68.254
Q59H82	PR-domain zinc finger protein 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H82_HUMAN]	0.89	8	2	2	2	0.982	2	16.875	3.728	1576	172.490
M0QYV5	ATP-dependent Clp protease proteolytic subunit (Fragment) OS=Homo sapiens GN=CLPP PE=1 SV=1 - [M0QYV5_HUMAN]	9.38	3	1	1	1	1.844	1		3.726	160	16.980
E9B5Q8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0200 PE=4 SV=1 - [E9B5Q8_LEIMU]	0.71	3	1	2	2	1.000	1		3.720	2123	239.784
F8VPC8	BTB/POZ domain-containing protein 6 (Fragment) OS=Homo sapiens GN=BTBD6 PE=4 SV=1 - [F8VPC8_HUMAN]	1.72	2	1	1	2	0.742	2	13.137	3.719	407	44.933
H0YM76	WD repeat-containing protein 61 OS=Homo sapiens GN=WDR61 PE=1 SV=1 - [H0YM76_HUMAN]	33.33	5	1	1	1	1.000	1		3.714	48	5.479
Q5T670	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=MCM10 PE=1 SV=1 - [Q5T670_HUMAN]	1.05	2	1	1	2	0.932	2	10.446	3.714	855	96.062
P0C0L4	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2 - [CO4A_HUMAN]	0.86	7	2	2	2	1.049	2	7.095	3.703	1744	192.664
P15309	Prostatic acid phosphatase OS=Homo sapiens GN=ACPP PE=1 SV=3 - [PPAP_HUMAN]	4.15	3	2	2	2	0.572	2	71.190	3.701	386	44.537
B3KRG2	cDNA FLJ34181 fis, clone FCBBF3016667, highly similar to TFIIH basal transcription factor complexhelicase XPB subunit (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [E	1.25	6	1	1	1	1.441	1		3.699	718	81.960
E9ARX0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0190 PE=4 SV=1 - [E9ARX0_LEIMU]	7.98	1	1	1	1	1.000	1		3.689	163	18.454
E9AP92	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0680 PE=4 SV=1 - [E9AP92_LEIMU]	2.83	1	2	2	2	1.218	2	25.294	3.688	565	60.559
H7BXZ6	Mitochondrial Rho GTPase OS=Homo sapiens GN=TMEM91 PE=3 SV=2 - [H7BXZ6_HUMAN]	2.35	2	1	1	1	0.530	1		3.686	597	68.406
B4E0V7	cDNA FLJ51709, highly similar to Myotubularin-related protein 9 OS=Homo sapiens PE=2 SV=1 - [B4E0V7_HUMAN]	2.64	3	1	1	1	1.851	1		3.686	530	61.177
Q05CU9	MNDA protein (Fragment) OS=Homo sapiens GN=MNDA PE=2 SV=1 - [Q05CU9_HUMAN]	5.16	3	1	1	1	1.015	1		3.685	310	34.960
B5MD17	Chromobox protein homolog 1 (Fragment) OS=Homo sapiens GN=CBX1 PE=1 SV=1 - [B5MD17_HUMAN]	6.55	3	1	1	1	0.943	1		3.677	168	19.314
K7EM75	Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=1 - [K7EM75_HUMAN]	17.72	5	1	1	2	1.000	2	0.000	3.677	79	8.924
E9AVH3	Putative ATP synthase F1 subunit gamma protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1770 PE=4 SV=1 - [E9AVH3_LEIMU]	3.96	1	1	1	1	1.000	1		3.669	303	34.386
F8W8T1	Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=1 - [F8W8T1_HUMAN]	1.88	3	1	1	1	0.987	1		3.658	639	73.290
Q969Z3	Mitochondrial amidoxime reducing component 2 OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MARC2_HUMAN]	7.16	3	2	2	2	1.000	2	0.000	3.648	335	37.999
A0A087X208	Agrin OS=Homo sapiens GN=AGRN PE=4 SV=1 - [A0A087X208_HUMAN]	1.66	2	3	3	3	1.000	3	28.639	3.638	1930	202.162
M0QXH0	Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 - [M0QXH0_HUMAN]	10.94	3	1	1	2	0.937	2	11.192	3.622	64	7.023
A6NDU8	UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 - [CE051_HUMAN]	3.4	1	1	1	1	1.000	1		3.616	294	33.599
F8W1I9	Acyl-CoA dehydrogenase family member 10 OS=Homo sapiens GN=ACAD10 PE=4 SV=1 - [F8W1I9_HUMAN]	1.69	2	1	1	2	1.000	2	0.000	3.615	710	80.413
B4DX97	cDNA FLJ56263 OS=Homo sapiens PE=2 SV=1 - [B4DX97_HUMAN]	2.92	1	1	1	1	1.000	1		3.613	480	54.264
C9J384	Protein CMSS1 (Fragment) OS=Homo sapiens GN=CMSS1 PE=1 SV=1 - [C9J384_HUMAN]	7.56	4	1	2	2	1.301	1		3.611	225	26.211
D6CHE9	Proteinase 3 OS=Homo sapiens GN=PRTN3 PE=2 SV=1 - [D6CHE9_HUMAN]	5.58	3	1	1	1	0.503	1		3.610	215	23.610
P41162	ETS translocation variant 3 OS=Homo sapiens GN=ETV3 PE=1 SV=2 - [ETV3_HUMAN]	2.93	1	1	1	1	0.721	1		3.604	512	56.966
Q9BVR6	TUBGCP4 protein OS=Homo sapiens GN=TUBGCP4 PE=2 SV=1 - [Q9BVR6_HUMAN]	3.51	3	1	1	1	0.589	1		3.594	342	38.670

E9ASN4	Short chain 3-hydroxyacyl-CoA dehydrogenase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1140 PE=4 SV=1 - [E9ASN4_LEIMU]	4.26	1	1	1	1	2.946	1		3.591	305	33.106
A0A024R307	Three prime repair exonuclease 1, isoform CRA_d OS=Homo sapiens GN=TREX1 PE=4 SV=1 - [A0A024R307_HUMAN]	1.44	2	1	1	2	1.052	2	5.180	3.589	764	82.951
F5H1I4	DNA helicase B OS=Homo sapiens GN=HELB PE=1 SV=1 - [F5H1I4_HUMAN]	1.54	2	1	1	1	1.000	1		3.584	846	96.347
H7BZL0	MKI67 FHA domain-interacting nucleolar phosphoprotein (Fragment) OS=Homo sapiens GN=NIFK PE=1 SV=1 - [H7BZL0_HUMAN]	12.75	2	1	1	1	1.080	1		3.577	102	11.734
K7ESL1	Thioredoxin-like protein 4A OS=Homo sapiens GN=TXNL4A PE=1 SV=1 - [K7ESL1_HUMAN]	9.86	2	1	1	2	0.967	2	3.788	3.576	71	8.457
O95365	Zinc finger and BTB domain-containing protein 7A OS=Homo sapiens GN=ZBTB7A PE=1 SV=1 - [ZBT7A_HUMAN]	3.25	1	1	1	1	0.980	1		3.572	584	61.401
E9PQD0	Probable RNA-binding protein EIF1AD OS=Homo sapiens GN=EIF1AD PE=1 SV=1 - [E9PQD0_HUMAN]	25	5	1	1	1	2.666	1		3.570	64	7.327
Q8N523	Tuftelin-interacting protein 11 OS=Homo sapiens GN=TFIP11 PE=2 SV=1 - [Q8N523_HUMAN]	2.63	5	2	2	2	1.000	2	0.000	3.566	837	96.732
B4DXP6	Radical fringe homolog (Drosophila), isoform CRA_b OS=Homo sapiens GN=RFNG PE=2 SV=1 - [B4DXP6_HUMAN]	9.27	4	1	1	1	1.000	1		3.565	205	22.780
B4E3T6	cDNA FLJ56405, highly similar to Epidermal growth factor receptor kinase substrate 8 OS=Homo sapiens PE=2 SV=1 - [B4E3T6_HUMAN]	2.17	2	1	1	1	1.011	1		3.558	691	77.040
S4R3U9	ER membrane protein complex subunit 3 (Fragment) OS=Homo sapiens GN=EMC3 PE=1 SV=1 - [S4R3U9_HUMAN]	17.95	2	1	1	1	1.947	1		3.553	78	9.098
P56181	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial OS=Homo sapiens GN=NDUFV3 PE=1 SV=2 - [NDUV3_HUMAN]	14.81	1	1	1	1	1.000	1		3.549	108	11.933
E9B0L7	Putative adenosine kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_0880 PE=4 SV=1 - [E9B0L7_LEIMU]	3.77	1	1	1	1	1.000	1		3.543	345	37.195
A8K9X0	cDNA FLJ76634, highly similar to Homo sapiens Yip1 domain family, member 6 (YIPF6), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9X0_HUMAN]	5.08	2	1	1	1	0.943	1		3.539	236	26.209
O60486	Plexin-C1 OS=Homo sapiens GN=PLXNC1 PE=1 SV=1 - [PLXC1_HUMAN]	0.7	1	1	1	1	1.000	1		3.531	1568	175.630
E9B4C0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2800 PE=4 SV=1 - [E9B4C0_LEIMU]	9.21	1	1	1	1	1.000	1		3.519	152	17.360
Q6ZSR9	Uncharacterized protein FLJ45252 OS=Homo sapiens PE=1 SV=2 - [YJ005_HUMAN]	3.38	1	1	1	1	0.579	1		3.515	355	37.953
H7C4P4	U2 snRNP-associated SURP motif-containing protein (Fragment) OS=Homo sapiens GN=U2SURP PE=1 SV=1 - [H7C4P4_HUMAN]	13.83	1	1	1	2	0.969	2	4.598	3.513	94	10.816
C9JBL1	Signal peptidase complex subunit 1 OS=Homo sapiens GN=SPCS1 PE=1 SV=1 - [C9JBL1_HUMAN]	15	3	1	1	1	0.777	1		3.510	80	9.269
Q5UW39	L2 OS=Homo sapiens PE=2 SV=1 - [Q5UW39_HUMAN]	2.64	2	1	1	1	1.000	1		3.502	644	73.648
C9J494	Probable E3 ubiquitin-protein ligase makorin-2 OS=Homo sapiens GN=MKRN2 PE=1 SV=1 - [C9J494_HUMAN]	3.86	2	2	2	2	1.142	2	19.940	3.502	414	46.650
F8W8H5	Ras-related protein Rab-24 OS=Homo sapiens GN=RAB24 PE=1 SV=1 - [F8W8H5_HUMAN]	6.32	2	1	1	1	1.724	1		3.484	174	19.659
B4DSB0	Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN PE=1 SV=1 - [B4DSB0_HUMAN]	2.8	2	1	1	1	0.666	1		3.481	464	52.956
Q8WXD5	Gem-associated protein 6 OS=Homo sapiens GN=GEMIN6 PE=1 SV=1 - [GEMI6_HUMAN]	7.78	1	1	1	1	0.961	1		3.481	167	18.812
Q9BSN4	SCD5 protein OS=Homo sapiens GN=SCD5 PE=2 SV=1 - [Q9BSN4_HUMAN]	13.64	2	1	1	1	1.000	1		3.479	132	14.260
A8MXV4	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial OS=Homo sapiens GN=NUDT19 PE=1 SV=1 - [NUD19_HUMAN]	3.73	1	1	1	1	1.000	1		3.470	375	42.207
B4DEH0	Mitochondrial ribosomal protein L10, isoform CRA_d OS=Homo sapiens GN=MRPL10 PE=2 SV=1 - [B4DEH0_HUMAN]	4.5	2	1	1	1	1.000	1		3.460	222	25.123
E9ALD8	40S ribosomal protein S19-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2860 PE=4 SV=1 - [E9ALD8_LEIMU]	8.07	2	1	1	1	1.100	1		3.457	161	18.142
C9J840	Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=3 - [C9J840_HUMAN]	1.82	15	1	1	2	1.000	2	0.000	3.450	987	113.492
B4DN75	cDNA FLJ60724, highly similar to Cartilage oligomeric matrix protein OS=Homo sapiens PE=2 SV=1 - [B4DN75_HUMAN]	1.75	6	1	1	1	1.255	1		3.449	684	75.054
B3KXE7	cDNA FLJ45304 fis, clone BRHIP3003984, highly similar to IkappaB kinase complex-associated protein OS=Homo sapiens PE=2 SV=1 - [B3KXE7_HUMAN]	1.02	7	1	1	1	0.760	1		3.440	983	111.444
Q9UJK0	Ribosome biogenesis protein TSR3 homolog OS=Homo sapiens GN=TSR3 PE=1 SV=1 - [TSR3_HUMAN]	5.13	1	1	1	1	1.000	1		3.417	312	33.575
E9B1V0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1500 PE=4 SV=1 - [E9B1V0_LEIMU]	1.31	1	1	1	1	1.000	1		3.414	1148	120.143
E9ASE2	Eukaryotic translation initiation factor 3 subunit L OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0250 PE=3 SV=1 - [E9ASE2_LEIMU]	1.84	1	1	1	1	0.984	1		3.407	544	62.670
Q8NCN4	E3 ubiquitin-protein ligase RNF169 OS=Homo sapiens GN=RNF169 PE=1 SV=2 - [RN169_HUMAN]	2.68	2	2	2	2	0.876	2	19.764	3.400	708	77.147
Q9NRZ7	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma OS=Homo sapiens GN=AGPAT3 PE=1 SV=1 - [PLCC_HUMAN]	2.66	1	1	1	1	0.744	1		3.396	376	43.353
B2RC45	cDNA, FLJ95846, highly similar to Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 10 (SERPINB10), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R	3.78	3	1	1	1	1.000	1		3.394	397	45.287
O95243	Methyl-CpG-binding domain protein 4 OS=Homo sapiens GN=MBD4 PE=1 SV=1 - [MBD4_HUMAN]	1.9	1	1	1	1	1.000	1		3.391	580	66.009
C9JVC3	Zinc finger protein 717 OS=Homo sapiens GN=ZNF717 PE=4 SV=1 - [C9JVC3_HUMAN]	9.95	73	0	2	2				3.382	864	100.447
Q96F46	Interleukin-17 receptor A OS=Homo sapiens GN=IL17RA PE=1 SV=2 - [I17RA_HUMAN]	1.39	1	1	1	1	1.000	1		3.381	866	96.061
B4E2E1	cDNA FLJ54322, highly similar to Protein transport protein Sec24B OS=Homo sapiens PE=2 SV=1 - [B4E2E1_HUMAN]	2.08	3	2	2	2	1.035	2	5.071	3.379	867	96.115
E9B0P1	Importin subunit alpha OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1120 PE=3 SV=1 - [E9B0P1_LEIMU]	2.23	1	1	1	1	1.487	1		3.379	539	58.009
Q59GT1	Conserved helix-loop-helix ubiquitous kinase variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GT1_HUMAN]	1.65	3	1	1	1	0.897	1		3.379	726	82.391
H7C0K6	Kinesin-like protein KIF1A (Fragment) OS=Homo sapiens GN=KIF1A PE=3 SV=1 - [H7C0K6_HUMAN]	5.73	12	1	1	1	1.000	1		3.377	227	24.852
J3KSG3	ADP-ribosylation factor-binding protein GGA3 (Fragment) OS=Homo sapiens GN=GGA3 PE=1 SV=1 - [J3KSG3_HUMAN]	8.82	6	1	1	1	1.137	1		3.375	136	15.692
Q96F63	Coiled-coil domain-containing protein 97 OS=Homo sapiens GN=CCDC97 PE=1 SV=1 - [CCD97_HUMAN]	2.92	2	1	1	1	0.906	1		3.370	343	38.923
K7EPF7	PHD finger protein 12 (Fragment) OS=Homo sapiens GN=PHF12 PE=1 SV=1 - [K7EPF7_HUMAN]	4.76	7	1	1	1	1.000	1		3.370	273	28.376
O60927	Protein phosphatase 1 regulatory subunit 11 OS=Homo sapiens GN=PPP1R11 PE=1 SV=1 - [PP1RB_HUMAN]	12.7	1	1	1	1	0.224	1		3.369	126	13.944
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens GN=ADI1 PE=1 SV=1 - [MTND_HUMAN]	16.76	1	2	2	3	1.000	3	0.000	3.361	179	21.485
Q96KN9	Gap junction delta-4 protein OS=Homo sapiens GN=GJD4 PE=2 SV=1 - [CXD4_HUMAN]	1.89	1	1	1	2	0.967	2	4.995	3.359	370	40.115
A8K2R3	cDNA FLJ75083, highly similar to Homo sapiens amine oxidase (flavin containing) domain 2 (AOF2),mRNA OS=Homo sapiens PE=2 SV=1 - [A8K2R3_HUMAN]	4.38	3	3	3	3	0.927	3	31.411	3.359	730	81.119
A0A087WZX3	WD repeat and FYVE domain-containing protein 2 OS=Homo sapiens GN=WDFY2 PE=4 SV=1 - [A0A087WZX3_HUMAN]	17.74	2	1	1	1	1.066	1		3.351	62	6.816
Q8N7E6	cDNA FLJ25727 fis, clone TST05479 OS=Homo sapiens PE=2 SV=1 - [Q8N7E6_HUMAN]	4.48	3	1	1	1	1.158	1		3.350	268	31.119
F5H169	26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 - [F5H169_HUMAN]	23.44	5	3	3	3	1.110	3	20.571	3.350	128	14.308
A0A087WW00	Ubiquitin-conjugating enzyme E2 D1 OS=Homo sapiens GN=UBE2D1 PE=4 SV=1 - [A0A087WW00_HUMAN]	10.09	5	1	1	1	0.312	1		3.350	109	12.413
Q8IXW5	Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2 OS=Homo sapiens GN=RPAP2 PE=1 SV=1 - [RPAP2_HUMAN]	3.43	1	2	2	2	1.000	1		3.349	612	69.466
Q8IVG5	Sterile alpha motif domain-containing protein 9-like OS=Homo sapiens GN=SAMD9L PE=1 SV=2 - [SAM9L_HUMAN]	1.26	3	1	2	2	1.000	1		3.342	1584	184.415
H0YNN4	Complex I intermediate-associated protein 30, mitochondrial (Fragment) OS=Homo sapiens GN=NDUFAF1 PE=1 SV=1 - [H0YNN4_HUMAN]	5.76	4	1	1	1	0.991	1		3.341	191	21.543
Q12981	Vesicle transport protein SEC20 OS=Homo sapiens GN=BNIP1 PE=1 SV=3 - [SEC20_HUMAN]	7.89	1	2	2	2	0.925	2	19.763	3.333	228	26.116
B7Z9U0	CCR4-NOT transcription complex subunit 8 OS=Homo sapiens GN=CNOT8 PE=1 SV=1 - [B7Z9U0_HUMAN]	8.59	3	1	1	1	1.000	1		3.332	128	14.646
Q5SVL2	Caspase-7 (Fragment) OS=Homo sapiens GN=CASP7 PE=1 SV=1 - [Q5SVL2_HUMAN]	10.36	3	1	1	1				3.326	222	24.774
B4DMR6	cDNA FLJ58915 OS=Homo sapiens PE=2 SV=1 - [B4DMR6_HUMAN]	4	4	1	1	1	1.000	1		3.326	350	38.925
E9AS63	Proteasome regulatory non-ATP-ase subunit,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1120 PE=4 SV=1 - [E9AS63_LEIMU]	4.13	1	1	1	1	1.000	1		3.316	412	46.477
E9AKC3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0190 PE=4 SV=1 - [E9AKC3_LEIMU]	3.77	1	1	1	1	0.988	1		3.313	371	39.346
Q9P1J8	PRO1289 OS=Homo sapiens PE=2 SV=1 - [Q9P1J8_HUMAN]	6.29	4	1	1	1	1.000	1		3.312	175	20.389
A0A024R143	Tripartite motif-containing 14, isoform CRA_c OS=Homo sapiens GN=TRIM14 PE=4 SV=1 - [A0A024R143_HUMAN]	5.44	4	2	2	2	0.843	1		3.311	349	39.649
E9B6P1	Putative iron-sulfur cluster assembly protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3620 PE=4 SV=1 - [E9B6P1_LEIMU]	8.7	1	1	1	1	1.000	1		3.310	161	17.359
H3BQG3	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=1 - [H3BQG3_HUMAN]	2.65	5	1	1	1	1.425	1		3.305	491	54.756
C9J9F0	Tripartite motif-containing protein 59 (Fragment) OS=Homo sapiens GN=TRIM59 PE=4 SV=1 - [C9J9F0_HUMAN]	15.32	9	1	1	1	0.873	1		3.303	111	12.946
H0YJ17	Neuroguidin (Fragment) OS=Homo sapiens GN=NGDN PE=1 SV=1 - [H0YJ17_HUMAN]	4.18	2	1	1	1	0.901	1		3.299	263	30.039
H0YKF8	Small kinetochore-associated protein (Fragment) OS=Homo sapiens GN=KNSTRN PE=1 SV=1 - [H0YKF8_HUMAN]	10.48	6	1	1	1	2.594	1		3.298	124	13.328
A0A087WZA9	Transmembrane protein 120A (Fragment) OS=Homo sapiens GN=TMEM120A PE=4 SV=1 - [A0A087WZA9_HUMAN]	6.32	4	1	1	1	1.000	1		3.297	174	20.447
F5GWI4	Adenosine deaminase OS=Homo sapiens GN=ADA PE=1 SV=1 - [F5GWI4_HUMAN]	3.24	3	1	1	1	1.000	1		3.295	339	38.268
Q7LFL8	CXXC-type zinc finger protein 5 OS=Homo sapiens GN=CXXC5 PE=2 SV=1 - [CXXC5_HUMAN]	12.11	5	2	2	2	1.000	2	0.000	3.285	322	32.956
F5H8A0	tRNA 2'-phosphotransferase 1 (Fragment) OS=Homo sapiens GN=TRPT1 PE=1 SV=1 - [F5H8A0_HUMAN]	5.24	2	1	1	1	0.973	1		3.284	191	20.602
Q5T8C6	Cell division cycle protein 16 homolog OS=Homo sapiens GN=CDC16 PE=1 SV=1 - [Q5T8C6_HUMAN]	1.89	4	1	1	1	2.069	1		3.283	475	54.669
B2R5S9	cDNA, FLJ92604, highly similar to Homo sapiens paraneoplastic antigen MA3 (PNMA3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5S9_HUMAN]	2.59	2	1	1	1	0.979	1		3.271	463	52.309
E9AQD9	Putative glutaminyl-tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_1440 PE=3 SV=1 - [E9AQD9_LEIMU]	1.75	1	1	1	2	2.204	2	171.606	3.271	570	65.831
E9B5N2	Cell differentiation protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_4550 PE=4 SV=1 - [E9B5N2_LEIMU]	3.06	1	1	1	1	1.000	1		3.270	360	41.164
Q9BRS2	Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2 - [RIOK1_HUMAN]	1.58	1	1	1	1	1.000	1		3.267	568	65.542
A8MY26	Down syndrome critical region protein 3 OS=Homo sapiens GN=DSCR3 PE=2 SV=1 - [A8MY26_HUMAN]	6.98	4	1	1	1	1.000	1		3.257	172	19.138
E9AXM1	Putative GTP-binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1420 PE=4 SV=1 - [E9AXM1_LEIMU]	8.8	1	1	2	2	14.445	1		3.255	216	24.208
Q9NZE0	BM-016 OS=Homo sapiens PE=2 SV=1 - [Q9NZE0_HUMAN]	14.53	2	1	1	1	0.883	1		3.254	117	12.826
E5RHT1	Presenilin-2 CTF subunit (Fragment) OS=Homo sapiens GN=PSEN2 PE=1 SV=1 - [E5RHT1_HUMAN]	10.85	3	1	1	1	1.000	1		3.242	129	14.446
Q2VYF2	Phosphatidic acid-preferring phospholipase A1-like protein OS=Homo sapiens PE=2 SV=1 - [Q2VYF2_HUMAN]	5.26	5	1	1	1	1.000	1		3.242	209	22.659
B2RE68	cDNA, FLJ94243 OS=Homo sapiens PE=2 SV=1 - [B2RE68_HUMAN]	6.12	2	1	1	1	0.945	1		3.237	196	21.667
F8VW54	Tetraspanin-31 (Fragment) OS=Homo sapiens GN=TSPAN31 PE=4 SV=1 - [F8VW54_HUMAN]	13.95	5	1	1	1	1.000	1		3.236	86	9.894
P10153	Non-secretory ribonuclease OS=Homo sapiens GN=RNASE2 PE=1 SV=2 - [RNAS2_HUMAN]	9.32	1	1	1	1	1.053	1		3.236	161	18.342
E9B4G7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0010 PE=4 SV=1 - [E9B4G7_LEIMU]	3.27	1	1	1	1	1.784	1		3.233	306	33.474
M0R317	Striatin-4 (Fragment) OS=Homo sapiens GN=STRN4 PE=1 SV=1 - [M0R317_HUMAN]	5.05	8	1	1	1	0.885	1		3.229	198	20.980
A8K9D2	Mitochondrial ribosomal protein L18, isoform CRA_b OS=Homo sapiens GN=MRPL18 PE=2 SV=1 - [A8K9D2_HUMAN]	7.26	2	1	1	1	0.726	1		3.222	179	20.422
B3KRB8	DPH2 homolog (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=DPH2 PE=2 SV=1 - [B3KRB8_HUMAN]	3.15	2	1	1	1	0.725	1		3.219	413	43.967
Q14587	Zinc finger protein 268 OS=Homo sapiens GN=ZNF268 PE=1 SV=2 - [ZN268_HUMAN]	3.17	3	2	2	3	1.000	3	8.467	3.217	947	108.303
H7C504	Probable ATP-dependent RNA helicase DHX34 (Fragment) OS=Homo sapiens GN=DHX34 PE=1 SV=1 - [H7C504_HUMAN]	4.41	2	1	1	1	1.000	1		3.215	272	30.308
H0YL91	Activating signal cointegrator 1 OS=Homo sapiens GN=TRIP4 PE=1 SV=1 - [H0YL91_HUMAN]	2.45	2	1	1	1	1.049	1		3.215	368	42.027
C9J3I2	E3 ubiquitin-protein ligase KCMF1 (Fragment) OS=Homo sapiens GN=KCMF1 PE=1 SV=1 - [C9J3I2_HUMAN]	6.04	2	1	1	1	1.000	1		3.213	149	16.285
E8NHL4	Brix domain containing-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0010 PE=4 SV=1 - [E8NHL4_LEIMU]	5.52	1	1	1	1	1.000	1		3.211	362	40.303
E9AN97	Histone H3 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0870 PE=4 SV=1 - [E9AN97_LEIMU]	7.69	1	1	1	1	39.079	1		3.210	130	14.677
Q14CB2	DOK1 protein OS=Homo sapiens GN=DOK1 PE=2 SV=1 - [Q14CB2_HUMAN]	4.49	6	1	1	2	1.071	2	11.435	3.202	267	28.665
Q96RF0	Sorting nexin-18 OS=Homo sapiens GN=SNX18 PE=1 SV=2 - [SNX18_HUMAN]	1.91	1	1	1	1	0.828	1		3.200	628	68.851
Q0P685	EYA3 protein OS=Homo sapiens GN=EYA3 PE=2 SV=1 - [Q0P685_HUMAN]	3.87	3	1	1	1	1.214	1		3.198	362	39.228
B9ZVT1	RNA-binding protein 12B OS=Homo sapiens GN=RBM12B PE=1 SV=2 - [B9ZVT1_HUMAN]	1.14	2	1	1	1	1.232	1		3.192	881	102.641
H3BNV7	Mitotic spindle-associated MMXD complex subunit MIP18 (Fragment) OS=Homo sapiens GN=FAM96B PE=1 SV=1 - [H3BNV7_HUMAN]	13.66	2	1	1	2	1.000	1		3.184	161	17.560
H7C2M7	Armadillo repeat-containing protein 10 (Fragment) OS=Homo sapiens GN=ARMC10 PE=1 SV=1 - [H7C2M7_HUMAN]	5.95	2	1	1	1	0.956	1		3.181	185	20.552
H0YAS9	ER membrane protein complex subunit 2 (Fragment) OS=Homo sapiens GN=EMC2 PE=1 SV=1 - [H0YAS9_HUMAN]	8.89	4	1	1	1	1.015	1		3.180	135	16.031
E9AYY4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0820 PE=4 SV=1 - [E9AYY4_LEIMU]	0.4	1	1	1	1	1.099	1		3.177	3289	347.318
B7Z7H3	cDNA FLJ57654, highly similar to Zinc finger protein 307 OS=Homo sapiens PE=2 SV=1 - [B7Z7H3_HUMAN]	3.85	3	1	1	1	1.000	1		3.172	390	44.070
Q8NAV1	Pre-mRNA-splicing factor 38A OS=Homo sapiens GN=PRPF38A PE=1 SV=1 - [PR38A_HUMAN]	7.05	1	2	2	2	1.053	2	7.639	3.169	312	37.453
Q0IIN7	Nuclear receptor coactivator 3 OS=Homo sapiens GN=NCOA3 PE=2 SV=1 - [Q0IIN7_HUMAN]	0.7	5	1	1	1	0.320	1		3.165	1419	154.666
I3L305	Syntaxin-8 (Fragment) OS=Homo sapiens GN=STX8 PE=1 SV=2 - [I3L305_HUMAN]	8.93	2	1	1	1	0.909	1		3.164	112	12.884
Q2T9J0	Peroxisomal leader peptide-processing protease OS=Homo sapiens GN=TYSND1 PE=1 SV=3 - [TYSD1_HUMAN]	1.77	1	1	1	1	1.000	1		3.162	566	59.271
C9JK89	SH2B adapter protein 2 (Fragment) OS=Homo sapiens GN=SH2B2 PE=4 SV=3 - [C9JK89_HUMAN]	4.94	2	1	1	1	0.923	1		3.162	243	26.502
C9JZB0	Inositol polyphosphate 5-phosphatase K (Fragment) OS=Homo sapiens GN=INPP5K PE=4 SV=1 - [C9JZB0_HUMAN]	4.37	4	1	1	1	1.013	1		3.160	229	26.707
Q9NWK9	Box C/D snoRNA protein 1 OS=Homo sapiens GN=ZNHIT6 PE=1 SV=1 - [BCD1_HUMAN]	2.13	1	1	1	1	1.000	1		3.159	470	53.884
A0PJL1	EFR3A protein (Fragment) OS=Homo sapiens GN=EFR3A PE=2 SV=1 - [A0PJL1_HUMAN]	6.03	5	1	1	1	1.000	1		3.147	199	22.633
Q9H9T3	Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=1 SV=2 - [ELP3_HUMAN]	6.4	10	3	3	3	0.895	2	3.261	3.142	547	62.219
C9JPX5	MLN64 N-terminal domain homolog (Fragment) OS=Homo sapiens GN=STARD3NL PE=1 SV=1 - [C9JPX5_HUMAN]	5.34	3	1	1	1	1.184	1		3.141	206	23.490
E9AW40	Putative NADP-dependent alcohol dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0360 PE=3 SV=1 - [E9AW40_LEIMU]	3.41	1	1	1	1	3.441	1		3.134	352	38.458
B7Z4K4	Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens GN=FTSJ1 PE=1 SV=1 - [B7Z4K4_HUMAN]	5.73	3	1	1	1	0.436	1		3.133	192	21.217
Q7Z5G4	Golgin subfamily A member 7 OS=Homo sapiens GN=GOLGA7 PE=1 SV=2 - [GOGA7_HUMAN]	5.84	3	1	1	1	0.818	1		3.128	137	15.814
S4R3P6	MAP3K12-binding inhibitory protein 1 (Fragment) OS=Homo sapiens GN=MBIP PE=1 SV=1 - [S4R3P6_HUMAN]	4.5	7	1	1	1	1.000	1		3.120	222	25.268
B7Z2R9	cDNA FLJ52540, highly similar to Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens PE=2 SV=1 - [B7Z2R9_HUMAN]	3	3	1	1	1	0.878	1		3.118	300	32.959
B7Z8H0	cDNA FLJ61742, highly similar to Origin recognition complex subunit 1 OS=Homo sapiens PE=2 SV=1 - [B7Z8H0_HUMAN]	1.29	4	1	1	1				3.116	856	96.689
Q9NQG6	Mitochondrial dynamics protein MID51 OS=Homo sapiens GN=MIEF1 PE=1 SV=1 - [MID51_HUMAN]	2.16	3	1	1	1	1.273	1		3.113	463	51.261
Q6GYQ0	Ral GTPase-activating protein subunit alpha-1 OS=Homo sapiens GN=RALGAPA1 PE=1 SV=1 - [RGPA1_HUMAN]	0.59	1	1	1	1	1.000	1		3.113	2036	229.686
Q96M27	Protein PRRC1 OS=Homo sapiens GN=PRRC1 PE=1 SV=1 - [PRRC1_HUMAN]	3.6	1	2	2	2	1.003	2	9.091	3.101	445	46.672
B1ALM7	Transmembrane protein 9 (Fragment) OS=Homo sapiens GN=TMEM9 PE=4 SV=1 - [B1ALM7_HUMAN]	13.77	8	1	1	1	1.000	1		3.098	138	15.548
M0R050	Exosome complex component RRP46 OS=Homo sapiens GN=EXOSC5 PE=1 SV=1 - [M0R050_HUMAN]	7.11	3	1	1	1	1.000	1		3.097	197	21.243
Q3B768	KIAA0406 protein (Fragment) OS=Homo sapiens GN=KIAA0406 PE=2 SV=1 - [Q3B768_HUMAN]	1.62	2	1	1	1	0.856	1		3.095	803	90.259
B7Z5P7	Leupaxin OS=Homo sapiens GN=LPXN PE=1 SV=1 - [B7Z5P7_HUMAN]	7.38	2	2	2	2	0.608	2	81.494	3.094	366	41.615
M0R391	Pleckstrin homology domain-containing family G member 2 (Fragment) OS=Homo sapiens GN=PLEKHG2 PE=4 SV=3 - [M0R391_HUMAN]	28.57	6	1	1	1	1.000	1		3.086	49	4.806
B4DIZ6	cDNA FLJ57941, highly similar to Nucleoside diphosphate-linked moiety X motif16 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DIZ6_HUMAN]	5.37	2	1	1	1	0.870	1		3.082	149	16.275
O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4 - [H2AY_HUMAN]	5.91	1	1	1	1	1.000	1		3.081	372	39.592
Q9UHA2	SS18-like protein 2 OS=Homo sapiens GN=SS18L2 PE=2 SV=1 - [S18L2_HUMAN]	15.58	1	1	1	1	0.704	1		3.081	77	8.829
Q53EU6	Glycerol-3-phosphate acyltransferase 3 OS=Homo sapiens GN=AGPAT9 PE=1 SV=2 - [GPAT3_HUMAN]	2.76	1	1	1	1	1.000	1		3.079	434	48.673
G3V3M5	Protein numb homolog (Fragment) OS=Homo sapiens GN=NUMB PE=4 SV=3 - [G3V3M5_HUMAN]	15.63	12	2	2	2	1.233	2	16.033	3.079	224	24.959
Q3B874	STRN protein (Fragment) OS=Homo sapiens GN=STRN PE=2 SV=1 - [Q3B874_HUMAN]	1.32	2	1	1	1	1.426	1		3.079	755	84.215
A8K0D0	cDNA FLJ76696 OS=Homo sapiens PE=2 SV=1 - [A8K0D0_HUMAN]	3.95	2	1	1	1	1.000	1		3.072	253	27.638
M0QXH7	Neuropathy target esterase (Fragment) OS=Homo sapiens GN=PNPLA6 PE=4 SV=1 - [M0QXH7_HUMAN]	13.55	2	1	1	1	1.000	1		3.072	155	17.076
Q5T911	Mediator of RNA polymerase II transcription subunit 4 (Fragment) OS=Homo sapiens GN=MED4 PE=1 SV=1 - [Q5T911_HUMAN]	3.78	3	1	1	1	0.891	1		3.068	238	27.060
B5MC35	Protein CFAP36 OS=Homo sapiens GN=CFAP36 PE=1 SV=1 - [B5MC35_HUMAN]	5.05	4	1	1	1	0.791	1		3.068	218	24.955
Q6PL24	Protein TMED8 OS=Homo sapiens GN=TMED8 PE=1 SV=1 - [TMED8_HUMAN]	3.69	1	1	1	1	1.000	1		3.067	325	35.718
Q2V8N0	HCV p7-transregulated protein 3 transcript variant 1 OS=Homo sapiens PE=2 SV=1 - [Q2V8N0_HUMAN]	8.73	3	1	1	1	1.000	1		3.065	126	14.156
K7ER15	Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=HDHD2 PE=1 SV=1 - [K7ER15_HUMAN]	4.41	2	1	1	2	1.656	2	91.959	3.060	204	22.476
B4DGH0	cDNA FLJ60107, highly similar to DNA replication complex GINS protein PSF1 OS=Homo sapiens PE=2 SV=1 - [B4DGH0_HUMAN]	9.09	2	1	1	1	1.000	1		3.047	165	18.934
H3BSW0	Leucine-rich repeat-containing protein 57 (Fragment) OS=Homo sapiens GN=LRRC57 PE=1 SV=1 - [H3BSW0_HUMAN]	5.41	2	1	1	1	1.309	1		3.037	148	16.314
A4D1E9	GTP-binding protein 10 OS=Homo sapiens GN=GTPBP10 PE=1 SV=1 - [GTPBA_HUMAN]	3.88	1	1	1	1	1.000	1		3.037	387	42.906
O14657	Torsin-1B OS=Homo sapiens GN=TOR1B PE=1 SV=2 - [TOR1B_HUMAN]	3.27	1	1	1	1	3.930	1		3.036	336	37.955
E9AX52	Transketolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_2060 PE=3 SV=1 - [E9AX52_LEIMU]	1.49	1	1	1	1	10.907	1		3.031	671	71.812
D6RA00	Enolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1 - [D6RA00_HUMAN]	6.94	4	1	1	1	1.000	1		3.031	173	19.175
F8WDR2	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial OS=Homo sapiens GN=TRMT61B PE=4 SV=1 - [F8WDR2_HUMAN]	3.01	2	1	1	1	1.000	1		3.028	366	40.374
Q969M1	Mitochondrial import receptor subunit TOM40B OS=Homo sapiens GN=TOMM40L PE=2 SV=1 - [TM40L_HUMAN]	5.19	1	1	1	1	1.174	1		3.026	308	33.895
H0YLW8	Proline-serine-threonine phosphatase-interacting protein 1 (Fragment) OS=Homo sapiens GN=PSTPIP1 PE=4 SV=3 - [H0YLW8_HUMAN]	5.26	6	1	1	1	1.000	1		3.024	209	24.698
E9AKF4	Monocarboxylate transporter-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0480 PE=4 SV=1 - [E9AKF4_LEIMU]	3.66	1	1	1	1	1.000	1		3.020	573	61.676
E9AQE0	Proliferating cell nuclear antigen OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_1450 PE=3 SV=1 - [E9AQE0_LEIMU]	4.1	1	1	1	1	0.971	1		3.019	293	32.422
K7EQR1	Ubinuclein-1 (Fragment) OS=Homo sapiens GN=UBN1 PE=4 SV=1 - [K7EQR1_HUMAN]	11.73	2	1	1	1	1.000	1		3.015	179	20.418
G3XAN4	Translocating chain-associated membrane protein 1 OS=Homo sapiens GN=TRAM1 PE=1 SV=1 - [G3XAN4_HUMAN]	3.82	4	1	1	1	0.872	1		3.014	288	33.414
Q6ZNS7	CDNA FLJ27229 fis, clone SYN05701 OS=Homo sapiens PE=2 SV=1 - [Q6ZNS7_HUMAN]	6.19	5	1	1	1	0.836	1		3.009	194	20.772
Q6UXE8	Butyrophilin-like protein 3 OS=Homo sapiens GN=BTNL3 PE=2 SV=2 - [BTNL3_HUMAN]	1.5	1	1	1	1	0.995	1		3.004	466	52.217
E9ANP9	Pretranslocation protein, alpha subunit,putative (Sec61-like (Pretranslocation process) protein,putative) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=L	1.65	1	1	1	1	11.136	1		3.004	486	53.953
F5H2F2	Branched-chain-amino-acid aminotransferase, cytosolic (Fragment) OS=Homo sapiens GN=BCAT1 PE=1 SV=1 - [F5H2F2_HUMAN]	7.64	2	1	1	1	1.081	1		2.999	144	16.509
B4DLQ4	cDNA FLJ61312, highly similar to Serologically defined colon cancer antigen 8 OS=Homo sapiens PE=2 SV=1 - [B4DLQ4_HUMAN]	1.71	4	1	1	1	1.108	1		2.994	525	61.626
B4DZ36	cDNA FLJ58441, highly similar to Attractin OS=Homo sapiens PE=2 SV=1 - [B4DZ36_HUMAN]	1.04	2	1	1	1	1.000	1		2.992	1156	129.748
Q68DS3	Putative uncharacterized protein DKFZp686H17246 (Fragment) OS=Homo sapiens GN=DKFZp686H17246 PE=2 SV=1 - [Q68DS3_HUMAN]	9.02	4	1	1	1	0.879	1		2.992	133	14.699
E9AKM9	Histone H4 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0010 PE=3 SV=1 - [E9AKM9_LEIMU]	10	3	1	1	1	3.139	1		2.990	100	11.265
H7C2F7	Trafficking protein particle complex subunit 12 (Fragment) OS=Homo sapiens GN=TRAPPC12 PE=1 SV=1 - [H7C2F7_HUMAN]	5.86	5	1	1	1	1.210	1		2.988	222	23.149
E8NHG4	WGS CADB00000000 data, contig 21 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_22_1690a_1 PE=4 SV=1 - [E8NHG4_LEIMU]	3.15	1	1	1	1	1.000	1		2.980	1428	146.190
B2RBI0	cDNA, FLJ95518 OS=Homo sapiens PE=2 SV=1 - [B2RBI0_HUMAN]	2.91	4	1	2	3	0.780	1		2.978	515	59.431
R4GMU8	Ragulator complex protein LAMTOR5 OS=Homo sapiens GN=LAMTOR5 PE=1 SV=1 - [R4GMU8_HUMAN]	12.66	3	1	1	1	0.912	1		2.976	79	8.210
E9ATC5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3460 PE=4 SV=1 - [E9ATC5_LEIMU]	5	1	1	1	1	1.142	1		2.975	200	23.139
O75446	Histone deacetylase complex subunit SAP30 OS=Homo sapiens GN=SAP30 PE=1 SV=1 - [SAP30_HUMAN]	8.18	1	2	2	2	1.143	2	13.395	2.974	220	23.292
E9B156	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2830 PE=4 SV=1 - [E9B156_LEIMU]	0.88	1	1	1	1	4.875	1		2.967	798	91.948
M0QXT0	Upstream stimulatory factor 2 (Fragment) OS=Homo sapiens GN=USF2 PE=4 SV=2 - [M0QXT0_HUMAN]	6.32	2	1	1	1	1.210	1		2.964	253	28.131
Q9Y3D3	28S ribosomal protein S16, mitochondrial OS=Homo sapiens GN=MRPS16 PE=1 SV=1 - [RT16_HUMAN]	10.95	2	2	2	2	0.875	2	15.285	2.961	137	15.335
Q13472	DNA topoisomerase 3-alpha OS=Homo sapiens GN=TOP3A PE=1 SV=1 - [TOP3A_HUMAN]	1.1	1	1	1	1	1.000	1		2.959	1001	112.300
Q96QE3	ATPase family AAA domain-containing protein 5 OS=Homo sapiens GN=ATAD5 PE=1 SV=4 - [ATAD5_HUMAN]	0.49	1	1	1	1	0.968	1		2.958	1844	207.441
C9JHF5	Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=1 SV=1 - [C9JHF5_HUMAN]	5.8	3	1	1	1	0.961	1		2.956	138	15.617
B4DWB3	cDNA FLJ61432, highly similar to Transient receptor potential cation channel subfamily M member 2 (EC 3.6.1.13) OS=Homo sapiens PE=2 SV=1 - [B4DWB3_HUMAN]	2.63	5	1	1	1	1.037	1		2.955	457	52.632
Q5JS34	Proline and serine-rich protein 1 (Fragment) OS=Homo sapiens GN=PROSER1 PE=4 SV=1 - [Q5JS34_HUMAN]	6.37	3	1	1	1	1.000	1		2.951	157	17.487
E9AM28	Cofilin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0510 PE=4 SV=1 - [E9AM28_LEIMU]	7.19	1	1	1	1	10.427	1		2.945	139	15.679
C9JRT8	Uncharacterized protein OS=Homo sapiens GN=ADCY5 PE=4 SV=1 - [C9JRT8_HUMAN]	4.47	5	1	1	1	1.000	1		2.943	492	55.427
D3VVN1	Ataxin 3 variant ref (Fragment) OS=Homo sapiens GN=ATXN3 PE=2 SV=1 - [D3VVN1_HUMAN]	7.29	1	1	1	1	1.000	1		2.939	343	39.656
B2RCF3	Glycylpeptide N-tetradecanoyltransferase OS=Homo sapiens PE=2 SV=1 - [B2RCF3_HUMAN]	2.21	3	1	1	1	1.000	1		2.932	498	56.872
C9JM54	Chromobox protein homolog 8 (Fragment) OS=Homo sapiens GN=CBX8 PE=1 SV=2 - [C9JM54_HUMAN]	7.43	3	1	1	1	0.831	1		2.931	175	20.494
E9B5M9	Proteasome subunit beta type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_4340 PE=3 SV=1 - [E9B5M9_LEIMU]	3.64	1	1	1	1	1.432	1		2.931	220	24.632
K7ELQ4	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [K7ELQ4_HUMAN]	2.16	3	1	1	1	1.322	1		2.928	463	49.920
A8K4Q6	cDNA FLJ77930, highly similar to Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 1, transcript variant 2, mRNA OS=Homo sapiens PE=	1.36	2	1	1	1	1.000	1		2.924	736	81.805
Q8IY33	MICAL-like protein 2 OS=Homo sapiens GN=MICALL2 PE=1 SV=1 - [MILK2_HUMAN]	1.33	1	1	1	1	1.392	1		2.921	904	97.442
E9AZH2	Proteasome subunit beta type OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_0110 PE=3 SV=1 - [E9AZH2_LEIMU]	4.39	1	1	1	1	0.745	1		2.921	205	22.507

B5MCZ4	Kelch repeat and BTB domain-containing protein 12 OS=Homo sapiens GN=KBTBD12 PE=4 SV=1 - [B5MCZ4_HUMAN]	5.22	3	1	1	1	1.000	1		2.920	230	26.014
F8W681	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase OS=Homo sapiens GN=DPAGT1 PE=4 SV=1 - [F8W681_HUMAN]	14.04	5	1	1	1	1.167	1		2.920	57	6.405
B4DJC2	cDNA FLJ51665, highly similar to Homo sapiens plasma glutamate carboxypeptidase (PGCP), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DJC2_HUMAN]	2.3	3	1	1	1	0.851	1		2.917	391	42.986
A0A024RB67	Exportin, tRNA (Nuclear export receptor for tRNAs), isoform CRA_a OS=Homo sapiens GN=XPOT PE=4 SV=1 - [A0A024RB67_HUMAN]	1.46	3	1	1	1	1.088	1		2.917	617	70.583
E9AMB1	Putative mitochondrial associated ribonuclease OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0320 PE=4 SV=1 - [E9AMB1_LEIMU]	5.86	1	1	1	1	1.000	1		2.916	222	24.535
S4R2Z4	Protein UXT OS=Homo sapiens GN=UXT PE=1 SV=1 - [S4R2Z4_HUMAN]	8.08	2	1	1	1	0.517	1		2.916	99	11.586
E9B469	Putative udp-glc 4'-epimerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2300 PE=3 SV=1 - [E9B469_LEIMU]	2.3	1	1	1	1	1.202	1		2.914	391	43.459
R4GNA5	ATP-dependent zinc metalloprotease YME1L1 (Fragment) OS=Homo sapiens GN=YME1L1 PE=1 SV=1 - [R4GNA5_HUMAN]	10.7	8	2	2	2	1.000	2	0.000	2.908	243	26.672
Q05DU0	RBMX2 protein (Fragment) OS=Homo sapiens GN=RBMX2 PE=2 SV=1 - [Q05DU0_HUMAN]	6.13	5	1	1	1	2.124	1		2.907	163	18.544
G3V1X5	Proteinase-activated receptor 4 OS=Homo sapiens GN=F2RL3 PE=4 SV=1 - [G3V1X5_HUMAN]	12.5	6	1	1	1	0.822	1		2.903	56	6.344
D6R917	Glucosamine-6-phosphate isomerase 1 (Fragment) OS=Homo sapiens GN=GNPDA1 PE=1 SV=1 - [D6R917_HUMAN]	7.25	8	1	1	1	0.944	1		2.900	138	15.901
E9PH99	Zinc finger protein 451 OS=Homo sapiens GN=ZNF451 PE=1 SV=1 - [E9PH99_HUMAN]	1.06	3	1	1	1	1.000	1		2.899	1041	119.250
Q9P0T4	Zinc finger protein 581 OS=Homo sapiens GN=ZNF581 PE=2 SV=1 - [ZN581_HUMAN]	5.08	1	1	1	1	1.000	1		2.899	197	21.996
E9AT43	Dihydrolipoamide acetyltransferase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2660 PE=3 SV=1 - [E9AT43_LEIMU]	1.93	1	1	1	1	11.775	1		2.898	466	48.744
B3KPF3	cDNA FLJ31722 fis, clone NT2RI2006679, highly similar to Homo sapiens follistatin-like 4 (FSTL4), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KPF3_HUMAN]	2.65	1	1	1	1	1.728	1		2.897	491	54.297
Q8TER9	FLJ00124 protein (Fragment) OS=Homo sapiens GN=FLJ00124 PE=2 SV=1 - [Q8TER9_HUMAN]	5.93	3	1	1	1	0.979	1		2.894	118	13.699
Q96I51	Williams-Beuren syndrome chromosomal region 16 protein OS=Homo sapiens GN=WBSCR16 PE=1 SV=2 - [WBS16_HUMAN]	3.88	1	1	1	1	1.000	1		2.890	464	49.965
Q8TEQ8	GPI ethanolamine phosphate transferase 3 OS=Homo sapiens GN=PIGO PE=1 SV=3 - [PIGO_HUMAN]	1.01	1	1	1	1				2.888	1089	118.623
E9AP91	Putative lectin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0670 PE=4 SV=1 - [E9AP91_LEIMU]	2.46	1	1	1	1	1.000	1		2.883	447	51.057
Q29RX5	GAS7 protein (Fragment) OS=Homo sapiens GN=GAS7 PE=2 SV=1 - [Q29RX5_HUMAN]	8.85	6	1	1	1	1.000	1		2.882	113	13.452
Q96L91	E1A-binding protein p400 OS=Homo sapiens GN=EP400 PE=1 SV=4 - [EP400_HUMAN]	0.76	2	2	2	2	1.000	2	0.000	2.878	3159	343.276
Q9H9L3	Interferon-stimulated 20 kDa exonuclease-like 2 OS=Homo sapiens GN=ISG20L2 PE=1 SV=1 - [I20L2_HUMAN]	3.97	1	1	1	1	0.989	1		2.878	353	39.130
B2RBJ8	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial OS=Homo sapiens GN=QRSL1 PE=2 SV=1 - [B2RBJ8_HUMAN]	2.08	2	1	1	1	1.117	1		2.874	528	57.396
A0A075XDK3	NADH dehydrogenase subunit 3 (Fragment) OS=Homo sapiens GN=ND3 PE=4 SV=1 - [A0A075XDK3_HUMAN]	28.3	226	1	1	1	1.240	1		2.871	53	6.081
E9AQ66	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0680 PE=4 SV=1 - [E9AQ66_LEIMU]	5.45	1	1	1	1	1.000	1		2.869	202	24.174
E9AWR7	Malic enzyme OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0761 PE=3 SV=1 - [E9AWR7_LEIMU]	3.15	1	2	2	2	1.178	2	24.614	2.869	571	62.523
Q8TC59	Piwi-like protein 2 OS=Homo sapiens GN=PIWIL2 PE=1 SV=1 - [PIWL2_HUMAN]	0.92	1	1	1	1	1.152	1		2.866	973	109.778
E9AL62	Putative 60S ribosomal protein L7a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0500 PE=4 SV=1 - [E9AL62_LEIMU]	7.2	2	1	1	1	1.000	1		2.866	264	29.743
H7C835	F-box and leucine-rich repeat protein 17 OS=Homo sapiens GN=FBXL17 PE=2 SV=1 - [H7C835_HUMAN]	4.54	2	1	1	1	1.000	1		2.863	463	51.522
V9GYL3	Solute carrier family 12 member 5 OS=Homo sapiens GN=SLC12A5 PE=4 SV=1 - [V9GYL3_HUMAN]	10.81	12	1	1	1	1.000	1		2.862	111	11.944
A0A087WUD2	Enhancer of filamentation 1 OS=Homo sapiens GN=NEDD9 PE=4 SV=1 - [A0A087WUD2_HUMAN]	2.04	3	1	1	1	1.000	1		2.862	685	76.508
C9J7Z4	tRNA-splicing endonuclease subunit Sen2 (Fragment) OS=Homo sapiens GN=TSEN2 PE=4 SV=1 - [C9J7Z4_HUMAN]	2.38	4	1	1	1	1.002	1		2.861	378	43.147
B3KQF7	cDNA FLJ90383 fis, clone NT2RP2005163 OS=Homo sapiens PE=2 SV=1 - [B3KQF7_HUMAN]	3.29	4	1	1	1	0.586	1		2.861	486	53.515
E9PG22	Centrosomal protein of 97 kDa OS=Homo sapiens GN=CEP97 PE=1 SV=1 - [E9PG22_HUMAN]	1.24	2	1	1	1	0.810	1		2.860	806	90.254
B7Z4Q6	Oxysterol-binding protein OS=Homo sapiens PE=2 SV=1 - [B7Z4Q6_HUMAN]	3.51	4	1	2	2				2.858	655	73.828
B4E1W3	cDNA FLJ51732, highly similar to Peroxisomal NADH pyrophosphatase NUDT12 (EC 3.6.1.22) OS=Homo sapiens PE=2 SV=1 - [B4E1W3_HUMAN]	2.03	3	1	1	1	2.016	1		2.858	444	50.048
B4DK77	Optic atrophy 3 protein OS=Homo sapiens GN=OPA3 PE=1 SV=1 - [B4DK77_HUMAN]	6.35	2	1	1	1	1.250	1		2.856	126	13.853
A0A087WX71	ESF1 homolog OS=Homo sapiens GN=ESF1 PE=4 SV=1 - [A0A087WX71_HUMAN]	2.41	4	1	1	1	1.000	1		2.854	456	52.340
B3KYB1	cDNA FLJ16760 fis, clone BRACE3050764, highly similar to Cell division protein kinase 10 (EC 2.7.11.22) OS=Homo sapiens PE=2 SV=1 - [B3KYB1_HUMAN]	3.51	3	1	1	1	1.000	1		2.850	313	35.631
B1AH87	Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=1 SV=1 - [B1AH87_HUMAN]	7.48	4	1	1	1	1.058	1		2.849	107	11.888
E9AS19	Putative U3 snoRNA-associated protein UTP11 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0670 PE=4 SV=1 - [E9AS19_LEIMU]	5.54	1	1	1	1				2.847	361	41.769
B3KQ93	cDNA FLJ33155 fis, clone UTERU2000349, highly similar to Zinc finger protein 334 OS=Homo sapiens PE=2 SV=1 - [B3KQ93_HUMAN]	4.67	33	0	2	2				2.843	642	74.945
Q9BXB4	Oxysterol-binding protein-related protein 11 OS=Homo sapiens GN=OSBPL11 PE=1 SV=2 - [OSB11_HUMAN]	3.48	1	2	2	3	0.850	2	24.425	2.842	747	83.591
D0W033	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [D0W033_HUMAN]	8.79	1	1	1	2	1.000	2	0.000	2.841	273	31.573
C9K058	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Homo sapiens GN=PPIL3 PE=1 SV=1 - [C9K058_HUMAN]	17.5	4	1	1	1	0.415	1		2.841	80	9.028
E9AL95	Flavoprotein subunit-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0800 PE=4 SV=1 - [E9AL95_LEIMU]	2.98	1	1	1	1	1.000	1		2.840	672	71.001
E9B159	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2850 PE=4 SV=1 - [E9B159_LEIMU]	7.83	1	1	1	1	1.000	1		2.839	115	13.057
E9AN77	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0670 PE=4 SV=1 - [E9AN77_LEIMU]	5.25	1	1	1	2	1.000	1		2.838	324	36.379
K7EPS7	Neuralized-like protein 4 (Fragment) OS=Homo sapiens GN=NEURL4 PE=1 SV=1 - [K7EPS7_HUMAN]	4.42	6	1	1	1	1.000	1		2.834	249	27.435
B1AL69	Hsp90 co-chaperone Cdc37-like 1 OS=Homo sapiens GN=CDC37L1 PE=1 SV=1 - [B1AL69_HUMAN]	2.92	2	1	1	1	1.200	1		2.833	308	35.557
E9AL33	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0230 PE=4 SV=1 - [E9AL33_LEIMU]	12.61	1	1	1	1	1.000	1		2.830	119	12.843
F8VNV1	La-related protein 4 (Fragment) OS=Homo sapiens GN=LARP4 PE=4 SV=3 - [F8VNV1_HUMAN]	7.76	5	1	1	1	1.039	1		2.825	116	12.316
C9JZJ1	Serine/threonine-protein kinase 17B (Fragment) OS=Homo sapiens GN=STK17B PE=1 SV=1 - [C9JZJ1_HUMAN]	13.43	5	1	1	1	1.000	1		2.821	67	7.757
O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2 - [PAPS2_HUMAN]	1.3	2	1	1	1	2.538	1		2.820	614	69.457
D3VVT1	Ataxin 3 variant h (Fragment) OS=Homo sapiens GN=ATXN3 PE=2 SV=1 - [D3VVT1_HUMAN]	7.28	1	1	1	1	1.000	1		2.818	261	30.539
G3V4G8	Uncharacterized protein C14orf28 OS=Homo sapiens GN=C14orf28 PE=4 SV=1 - [G3V4G8_HUMAN]	3.93	3	1	1	1	1.000	1		2.817	280	32.930
Q9UDX5	Mitochondrial fission process protein 1 OS=Homo sapiens GN=MTFP1 PE=1 SV=1 - [MTFP1_HUMAN]	6.63	2	1	1	1	0.936	1		2.816	166	17.999
Q13546	Receptor-interacting serine/threonine-protein kinase 1 OS=Homo sapiens GN=RIPK1 PE=1 SV=3 - [RIPK1_HUMAN]	1.49	1	1	1	1	0.815	1		2.816	671	75.883
A8KAQ3	cDNA FLJ76489, highly similar to Homo sapiens sortilin 1 (SORT1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8KAQ3_HUMAN]	1.32	2	1	1	1	1.000	1		2.816	831	91.978
Q8NEF9	Serum response factor-binding protein 1 OS=Homo sapiens GN=SRFBP1 PE=1 SV=1 - [SRFB1_HUMAN]	2.1	1	1	1	1	0.849	1		2.815	429	48.604
E9B2T4	Mannose-6-phosphate isomerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_1580 PE=3 SV=1 - [E9B2T4_LEIMU]	2.14	1	1	1	1	1.426	1		2.813	421	46.512
E9AKY3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_1040 PE=4 SV=1 - [E9AKY3_LEIMU]	2.08	1	1	1	1	1.282	1		2.813	722	79.058
E7EU96	Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1 - [E7EU96_HUMAN]	6.75	9	2	2	2	1.242	2	33.026	2.813	385	45.282
C9JAU5	Protein FAM107A (Fragment) OS=Homo sapiens GN=FAM107A PE=4 SV=1 - [C9JAU5_HUMAN]	6.67	5	1	1	1	1.130	1		2.811	105	12.750
Q96L35	EPH receptor B4, isoform CRA_b OS=Homo sapiens GN=EPHB4 PE=1 SV=1 - [Q96L35_HUMAN]	1.71	30	1	2	2	1.450	1		2.811	935	102.493
Q9BW61	DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1 - [DDA1_HUMAN]	8.82	1	1	1	1	0.757	1		2.807	102	11.828
Q9H1C7	Cysteine-rich and transmembrane domain-containing protein 1 OS=Homo sapiens GN=CYSTM1 PE=1 SV=1 - [CYTM1_HUMAN]	10.31	1	1	1	1	0.759	1		2.806	97	10.624
Q86WC4	Osteopetrosis-associated transmembrane protein 1 OS=Homo sapiens GN=OSTM1 PE=1 SV=1 - [OSTM1_HUMAN]	2.1	1	1	1	1	1.135	1		2.805	334	37.233
A0A024QZZ1	Butyrophilin, subfamily 3, member A2, isoform CRA_a OS=Homo sapiens GN=BTN3A2 PE=4 SV=1 - [A0A024QZZ1_HUMAN]	2.99	3	1	1	1	1.598	1		2.803	334	36.439
C9JPH1	Golgi apparatus membrane protein TVP23 homolog OS=Homo sapiens GN=FAM18B2 PE=3 SV=2 - [C9JPH1_HUMAN]	7.27	9	1	1	2	1.132	2	18.483	2.799	110	12.626
F8VPW7	2'-5'-oligoadenylate synthase 1 (Fragment) OS=Homo sapiens GN=OAS1 PE=4 SV=1 - [F8VPW7_HUMAN]	12.05	8	1	1	1	0.991	1		2.798	83	9.626
E5RFF3	Zinc finger transcription factor Trps1 OS=Homo sapiens GN=TRPS1 PE=1 SV=1 - [E5RFF3_HUMAN]	3.96	6	2	3	3	1.000	2	0.000	2.797	1035	114.470
G3V583	Protein FAM177A1 (Fragment) OS=Homo sapiens GN=FAM177A1 PE=1 SV=1 - [G3V583_HUMAN]	7.86	2	2	2	2	1.000	1		2.794	140	16.312
Q16254	Transcription factor E2F4 OS=Homo sapiens GN=E2F4 PE=1 SV=2 - [E2F4_HUMAN]	1.94	1	1	1	1	0.619	1		2.792	413	43.933
B3KUV8	cDNA FLJ40730 fis, clone TKIDN2000464, highly similar to N-acetylgalactosamine kinase (EC 2.7.1.157) OS=Homo sapiens PE=2 SV=1 - [B3KUV8_HUMAN]	4.35	4	1	1	1	0.885	1		2.787	207	22.390
A8K1E4	cDNA FLJ77411, highly similar to Homo sapiens gamma-tubulin complex component GCP5 (GCP5) mRNA OS=Homo sapiens PE=2 SV=1 - [A8K1E4_HUMAN]	1.76	3	1	1	1	1.000	1		2.787	1024	118.274
B3KTA8	cDNA FLJ37971 fis, clone CTONG2009958, highly similar to CERULOPLASMIN (EC 1.16.3.1) OS=Homo sapiens PE=2 SV=1 - [B3KTA8_HUMAN]	1.8	7	1	1	1	1.000	1		2.784	778	88.989
Q96BZ9	TBC1 domain family member 20 OS=Homo sapiens GN=TBC1D20 PE=1 SV=1 - [TBC20_HUMAN]	2.48	1	1	1	1	0.888	1		2.784	403	45.826
Q9Y4B4	Helicase ARIP4 OS=Homo sapiens GN=RAD54L2 PE=1 SV=4 - [ARIP4_HUMAN]	0.61	1	1	1	1	1.119	1		2.769	1467	162.667
G3V1T9	RNA binding motif protein 7, isoform CRA_a OS=Homo sapiens GN=RBM7 PE=1 SV=1 - [G3V1T9_HUMAN]	6.85	8	1	1	1	0.761	1		2.767	146	17.213
Q59F18	Smoothelin isoform b variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59F18_HUMAN]	1.69	9	1	1	1	1.000	1		2.767	534	55.775
E9AZ67	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1640 PE=4 SV=1 - [E9AZ67_LEIMU]	1.11	1	1	1	1	1.000	1		2.766	900	100.636
B3KQ74	cDNA FLJ33011 fis, clone THYMU1000359, highly similar to Rho-GTPase-activating protein 9 OS=Homo sapiens PE=2 SV=1 - [B3KQ74_HUMAN]	2.14	5	1	1	1	0.643	1		2.766	420	47.075
E9ARH0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0330 PE=4 SV=1 - [E9ARH0_LEIMU]	6.97	1	1	1	1	1.000	1		2.766	244	27.448
Q6QNY5	UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase OS=Homo sapiens GN=GNE PE=2 SV=1 - [Q6QNY5_HUMAN]	2.49	4	2	2	2	1.038	2	5.473	2.765	722	79.323
H0YAI9	Ribosome biogenesis protein NSA2 homolog (Fragment) OS=Homo sapiens GN=NSA2 PE=4 SV=1 - [H0YAI9_HUMAN]	9.18	2	1	1	1	1.683	1		2.763	98	11.528
E9B484	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2450 PE=4 SV=1 - [E9B484_LEIMU]	0.49	1	1	1	1	0.735	1		2.763	1625	168.999
Q96AG3	Solute carrier family 25 member 46 OS=Homo sapiens GN=SLC25A46 PE=1 SV=1 - [S2546_HUMAN]	2.63	1	1	1	1	0.965	1		2.754	418	46.145
H7C0D5	Protein YIPF4 (Fragment) OS=Homo sapiens GN=YIPF4 PE=1 SV=1 - [H7C0D5_HUMAN]	15.52	2	1	1	1	1.230	1		2.751	58	6.443
E9AMK2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0010 PE=4 SV=1 - [E9AMK2_LEIMU]	7.48	1	1	1	1	1.297	1		2.751	107	12.348
O95685	Protein phosphatase 1 regulatory subunit 3D OS=Homo sapiens GN=PPP1R3D PE=1 SV=1 - [PPR3D_HUMAN]	10.03	2	2	2	2	1.119	1		2.750	299	32.538
E9AMP7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0460 PE=4 SV=1 - [E9AMP7_LEIMU]	0.41	1	1	1	1	1.000	1		2.747	2916	304.317
O95864	Fatty acid desaturase 2 OS=Homo sapiens GN=FADS2 PE=1 SV=1 - [FADS2_HUMAN]	3.38	1	1	1	1	1.000	1		2.743	444	52.226
E9AMC7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0480 PE=4 SV=1 - [E9AMC7_LEIMU]	5.43	1	1	1	1	1.000	1		2.742	276	29.946
Q658M9	Putative uncharacterized protein DKFZp666K145 (Fragment) OS=Homo sapiens GN=DKFZp666K145 PE=2 SV=1 - [Q658M9_HUMAN]	4.44	3	1	1	1	1.000	1		2.742	338	38.845
C9JUJ0	CGG triplet repeat-binding protein 1 (Fragment) OS=Homo sapiens GN=CGGBP1 PE=1 SV=1 - [C9JUJ0_HUMAN]	8.49	2	1	1	1	1.000	1		2.740	106	11.932
A0A087WXP0	Azurocidin OS=Homo sapiens GN=AZU1 PE=4 SV=1 - [A0A087WXP0_HUMAN]	6.67	3	1	1	1	2.001	1		2.740	150	16.413
B4DDK6	Putative mitochondrial import inner membrane translocase subunit Tim23B OS=Homo sapiens GN=TIMM23B PE=2 SV=1 - [B4DDK6_HUMAN]	14.29	7	1	1	1	1.000	1		2.739	140	14.590
E9AY48	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0690 PE=4 SV=1 - [E9AY48_LEIMU]	5.6	1	1	1	1	1.000	1		2.738	250	27.979
A0A087WWW9	B-cell lymphoma/leukemia 10 OS=Homo sapiens GN=BCL10 PE=4 SV=1 - [A0A087WWW9_HUMAN]	5.77	3	1	1	1	1.068	1		2.733	156	18.062
B2RA52	cDNA, FLJ94700, highly similar to Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RA52_HUMAN]	1.85	2	1	1	1	1.034	1		2.731	596	67.695
E9AVE5	Choline dehydrogenase, like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1563 PE=4 SV=1 - [E9AVE5_LEIMU]	2.24	1	1	1	1	1.000	1		2.730	535	58.672
Q9HAY2	Melanoma-associated antigen F1 OS=Homo sapiens GN=MAGEF1 PE=1 SV=2 - [MAGF1_HUMAN]	2.28	1	1	1	1	1.079	1		2.729	307	35.200
E9AT34	Membrane-bound acid phosphatase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2570 PE=4 SV=1 - [E9AT34_LEIMU]	1.74	1	1	1	1	1.000	1		2.728	516	57.419
Q8TDH9	Biogenesis of lysosome-related organelles complex 1 subunit 5 OS=Homo sapiens GN=BLOC1S5 PE=1 SV=1 - [BL1S5_HUMAN]	4.28	1	1	1	1	1.000	1		2.726	187	21.596
Q96EB1	Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 - [ELP4_HUMAN]	5.66	3	2	2	2	1.009	2	1.328	2.724	424	46.558
Q9BUE6	Iron-sulfur cluster assembly 1 homolog, mitochondrial OS=Homo sapiens GN=ISCA1 PE=2 SV=1 - [ISCA1_HUMAN]	11.63	1	1	1	1	1.000	1		2.721	129	14.170
Q2VPK5	Cytoplasmic tRNA 2-thiolation protein 2 OS=Homo sapiens GN=CTU2 PE=1 SV=1 - [CTU2_HUMAN]	2.14	2	1	1	1	0.902	1		2.720	515	56.071
E9AQK4	Putative 60S ribosomal protein L21 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0460 PE=4 SV=1 - [E9AQK4_LEIMU]	6.92	1	1	1	1	1.453	1		2.719	159	17.984
B5MDS5	Adenomatous polyposis coli protein 2 (Fragment) OS=Homo sapiens GN=APC2 PE=4 SV=3 - [B5MDS5_HUMAN]	1.09	2	1	1	1	0.692	1		2.718	731	80.582
B3KRK7	cDNA FLJ34488 fis, clone HLUNG2004388, highly similar to BCL-2 HOMOLOGOUS ANTAGONIST/KILLER OS=Homo sapiens PE=2 SV=1 - [B3KRK7_HUMAN]	7.8	7	1	1	1	1.266	1		2.717	141	15.871
Q70CQ2	Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens GN=USP34 PE=1 SV=2 - [UBP34_HUMAN]	0.51	3	2	2	2	1.000	2	0.000	2.716	3546	403.973
E9AZS4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1070 PE=4 SV=1 - [E9AZS4_LEIMU]	0.58	1	1	1	1	1.371	1		2.715	1548	164.595
Q5TC84	Opioid growth factor receptor-like protein 1 OS=Homo sapiens GN=OGFRL1 PE=2 SV=1 - [OGRL1_HUMAN]	4.66	1	1	1	1	0.741	1		2.712	451	51.220
A0A024RAL3	Zinc finger, FYVE domain containing 16, isoform CRA_a OS=Homo sapiens GN=ZFYVE16 PE=4 SV=1 - [A0A024RAL3_HUMAN]	0.52	2	1	1	1	1.044	1		2.710	1539	168.743
A0A087WW78	Golgi pH regulator B (Fragment) OS=Homo sapiens GN=GPR89B PE=4 SV=1 - [A0A087WW78_HUMAN]	12.9	12	1	1	1	1.018	1		2.706	93	10.724
E9AXB8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0410 PE=4 SV=1 - [E9AXB8_LEIMU]	4.41	1	1	1	1	1.000	1		2.706	295	32.915
P14174	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 - [MIF_HUMAN]	7.83	1	1	1	1	1.000	1		2.706	115	12.468
F6S7Q7	Threonine--tRNA ligase, mitochondrial OS=Homo sapiens GN=TARS2 PE=4 SV=1 - [F6S7Q7_HUMAN]	2.03	4	1	1	1	0.971	1		2.705	443	49.831
Q59G34	alpha-1,2-Mannosidase (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G34_HUMAN]	2.49	2	1	1	1	1.000	1		2.704	482	54.507
A8K4Z6	cDNA FLJ76180 OS=Homo sapiens PE=2 SV=1 - [A8K4Z6_HUMAN]	1.45	2	1	1	1	1.238	1		2.702	619	70.478
Q96BK5	PIN2/TERF1-interacting telomerase inhibitor 1 OS=Homo sapiens GN=PINX1 PE=1 SV=2 - [PINX1_HUMAN]	4.88	1	1	1	1	0.777	1		2.701	328	37.012
Q5SZE3	Ceramide synthase 2 (Fragment) OS=Homo sapiens GN=CERS2 PE=1 SV=1 - [Q5SZE3_HUMAN]	4.69	7	1	1	1	0.784	1		2.695	192	23.238
H0Y6Y2	Caspase-9 subunit p35 (Fragment) OS=Homo sapiens GN=CASP9 PE=3 SV=1 - [H0Y6Y2_HUMAN]	4.55	8	1	1	1	2.587	1		2.695	198	21.907
O75600	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial OS=Homo sapiens GN=GCAT PE=1 SV=1 - [KBL_HUMAN]	3.34	1	1	1	1	0.923	1		2.694	419	45.256
B4DQG8	cDNA FLJ54124, highly similar to DNA methyltransferase 1-associated protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DQG8_HUMAN]	5.25	5	2	2	2	0.835	2	27.129	2.694	457	51.829
D6R9V2	Histone-lysine N-methyltransferase NSD2 (Fragment) OS=Homo sapiens GN=WHSC1 PE=1 SV=1 - [D6R9V2_HUMAN]	2.04	3	1	1	1	0.981	1		2.693	392	43.184
E9AQ69	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0710 PE=4 SV=1 - [E9AQ69_LEIMU]	0.3	1	1	1	1	1.136	1		2.692	3366	361.649
E9ANX3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0450 PE=4 SV=1 - [E9ANX3_LEIMU]	0.82	1	1	1	1	1.138	1		2.691	1091	116.480
A8MZH0	Leukocyte immunoglobulin-like receptor subfamily A member 2 OS=Homo sapiens GN=LILRA2 PE=4 SV=2 - [A8MZH0_HUMAN]	2.86	2	1	1	1	1.000	1		2.690	454	49.925
Q9UMT9	Sulfotransferase (Fragment) OS=Homo sapiens GN=STP1 PE=3 SV=1 - [Q9UMT9_HUMAN]	19.05	11	1	1	1	0.882	1		2.690	42	4.791
Q96G74	OTU domain-containing protein 5 OS=Homo sapiens GN=OTUD5 PE=1 SV=1 - [OTUD5_HUMAN]	3.5	1	1	1	1	1.000	1		2.689	571	60.588
Q14320	Protein FAM50A OS=Homo sapiens GN=FAM50A PE=1 SV=2 - [FA50A_HUMAN]	2.06	1	1	1	1	1.000	1		2.687	339	40.216
Q6FI30	Nuclear factor 1 OS=Homo sapiens GN=NFIC PE=2 SV=1 - [Q6FI30_HUMAN]	2.2	3	1	1	1	1.363	1		2.687	499	54.620
B4DS21	cDNA FLJ57856, highly similar to TATA box-binding protein-associated factor RNA polymerase I subunit A OS=Homo sapiens PE=2 SV=1 - [B4DS21_HUMAN]	4.5	3	1	1	1	1.212	1		2.686	311	36.122
Q8N878	FERM domain-containing protein 1 OS=Homo sapiens GN=FRMD1 PE=2 SV=2 - [FRMD1_HUMAN]	6.19	9	2	2	2	0.918	2	12.793	2.685	549	62.483
B3KW96	cDNA FLJ42619 fis, clone BRACE3015027, highly similar to Homo sapiens DAB2 interacting protein (DAB2IP), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=	1.27	3	1	1	1	1.174	1		2.684	551	58.854
Q8IUW5	RELT-like protein 1 OS=Homo sapiens GN=RELL1 PE=1 SV=1 - [RELL1_HUMAN]	7.75	1	1	1	1	1.000	1		2.679	271	29.322
B4DN94	cDNA FLJ58848, highly similar to Homo sapiens transcription factor IIB OS=Homo sapiens PE=2 SV=1 - [B4DN94_HUMAN]	5.2	2	1	1	1	1.000	1		2.679	173	20.185
E9B668	Ribosomal protein L15 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1910 PE=3 SV=1 - [E9B668_LEIMU]	4.5	2	1	1	1	1.000	1		2.678	200	24.014
E9AS25	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0730 PE=4 SV=1 - [E9AS25_LEIMU]	2.34	1	1	1	1	1.258	1		2.676	385	43.817
E9AMV9	Putative eukaryotic translation initiation factor 2 subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_1070 PE=4 SV=1 - [E9AMV9_LEIMU]	2.92	1	1	1	1	3.127	1		2.669	479	52.515
B4DMP5	cDNA FLJ60050, highly similar to Vacuolar protein sorting protein 72 homolog OS=Homo sapiens PE=2 SV=1 - [B4DMP5_HUMAN]	4.66	2	1	1	1	0.702	1		2.668	236	26.712
Q8N954	G patch domain-containing protein 11 OS=Homo sapiens GN=GPATCH11 PE=1 SV=3 - [GPT11_HUMAN]	3.47	1	1	1	1	0.813	1		2.668	259	30.180
Q6XLA1	Protein CASC2, isoform 3 OS=Homo sapiens GN=CASC2 PE=2 SV=1 - [CSC2A_HUMAN]	13.73	1	1	1	1	1.000	1		2.665	102	11.894
B9W0P3	Ataxin 3 (Fragment) OS=Homo sapiens GN=ATXN3 PE=4 SV=1 - [B9W0P3_HUMAN]	58.54	6	1	1	3	1.000	2	0.000	2.664	41	5.025
E9B5Z2	Oligosaccharyl transferase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1130 PE=4 SV=1 - [E9B5Z2_LEIMU]	1.39	1	1	1	1	1.000	1		2.664	863	96.231
B3KQ34	cDNA FLJ32716 fis, clone TESTI2000808, highly similar to Contactin-4 OS=Homo sapiens PE=2 SV=1 - [B3KQ34_HUMAN]	1	3	1	1	1	2.820	1		2.664	698	76.547
Q9NYQ8	Protocadherin Fat 2 OS=Homo sapiens GN=FAT2 PE=1 SV=2 - [FAT2_HUMAN]	0.46	1	1	1	1	1.000	1		2.661	4349	479.018
A8K4M5	cDNA FLJ76043, highly similar to Homo sapiens cyclin T1 (CCNT1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4M5_HUMAN]	1.24	2	1	1	1	0.769	1		2.661	726	80.535
Q15031	Probable leucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=LARS2 PE=1 SV=2 - [SYLM_HUMAN]	3.21	3	3	3	3	1.065	3	4.943	2.659	903	101.911
A8K646	cDNA FLJ75699, highly similar to Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K646_HUMAN]	7.01	2	1	1	1	1.077	1		2.658	214	23.700
E9AKG5	Putative ATP-dependent RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0590 PE=3 SV=1 - [E9AKG5_LEIMU]	0.7	1	1	1	1	0.900	1		2.656	995	105.208
Q92995	Ubiquitin carboxyl-terminal hydrolase 13 OS=Homo sapiens GN=USP13 PE=1 SV=2 - [UBP13_HUMAN]	1.04	1	1	1	1	1.911	1		2.654	863	97.265
Q8WWF5	Zinc/RING finger protein 4 OS=Homo sapiens GN=ZNRF4 PE=2 SV=3 - [ZNRF4_HUMAN]	1.4	1	1	1	1	2.685	1		2.653	429	46.928
Q9H6B7	cDNA: FLJ22410 fis, clone HRC08422 OS=Homo sapiens PE=2 SV=1 - [Q9H6B7_HUMAN]	3.85	5	1	1	1	1.000	1		2.650	286	31.553
B8ZZS4	Ankyrin repeat and zinc finger domain-containing protein 1 OS=Homo sapiens GN=ANKZF1 PE=1 SV=1 - [B8ZZS4_HUMAN]	4.84	4	3	3	3	1.000	3	0.000	2.645	516	57.538
Q96CJ1	ELL-associated factor 2 OS=Homo sapiens GN=EAF2 PE=1 SV=1 - [EAF2_HUMAN]	6.15	3	1	2	2	0.683	1		2.645	260	28.774
U3KPR5	Transcription factor jun-D (Fragment) OS=Homo sapiens GN=JUND PE=1 SV=2 - [U3KPR5_HUMAN]	4.22	6	1	1	1	1.126	1		2.644	166	17.823
E9APW5	Putative poly(A) polymerase (Putative polynucleotide adenylyltransferase) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1180 PE=4 SV=1 -	1.42	1	1	1	1	0.639	1		2.643	706	76.795
C9JJV1	Protein TSSC4 (Fragment) OS=Homo sapiens GN=TSSC4 PE=1 SV=3 - [C9JJV1_HUMAN]	4.81	3	1	1	1	0.737	1		2.642	208	21.952
A0A087WZV3	Voltage-dependent L-type calcium channel subunit alpha-1C OS=Homo sapiens GN=CACNA1C PE=4 SV=1 - [A0A087WZV3_HUMAN]	1.09	11	1	1	1	1.255	1		2.641	829	91.440
C9JUH3	Malcavernin OS=Homo sapiens GN=CCM2 PE=1 SV=1 - [C9JUH3_HUMAN]	3.17	2	1	1	1	0.928	1		2.641	347	38.795
E9AYW6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0650 PE=4 SV=1 - [E9AYW6_LEIMU]	5.99	1	1	1	1	0.811	1		2.638	167	19.645
Q05C66	CABIN1 protein (Fragment) OS=Homo sapiens GN=CABIN1 PE=2 SV=1 - [Q05C66_HUMAN]	2.21	4	1	1	1	0.579	1		2.636	407	45.627
A6NGG8	Uncharacterized protein C2orf71 OS=Homo sapiens GN=C2orf71 PE=1 SV=1 - [CB071_HUMAN]	0.62	1	1	1	1	0.812	1		2.635	1288	139.569
Q53G34	Mitochondrial carrier homolog 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53G34_HUMAN]	6.93	2	1	1	1	1.000	1		2.634	303	33.287
Q19RM2	PS1TP5-transactivated protein 1 OS=Homo sapiens PE=2 SV=1 - [Q19RM2_HUMAN]	11.54	1	1	1	1	0.830	1		2.634	78	8.402
B4DP61	Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1 - [B4DP61_HUMAN]	8.37	13	2	2	2	0.978	2	3.234	2.634	227	24.365
B4DEL7	cDNA FLJ57719, highly similar to Gamma-aminobutyric-acid receptor beta-1 subunit OS=Homo sapiens PE=2 SV=1 - [B4DEL7_HUMAN]	3.96	2	1	1	1	1.000	1		2.634	404	46.366
E9ART7	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1530 PE=3 SV=1 - [E9ART7_LEIMU]	0.97	1	1	1	2	1.000	2	0.000	2.633	1240	134.032
B4E183	cDNA FLJ58663, moderately similar to P2Y purinoceptor 12 OS=Homo sapiens PE=2 SV=1 - [B4E183_HUMAN]	5.71	5	1	2	2				2.632	245	28.097
E9AQK6	Putative fucose kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0480 PE=3 SV=1 - [E9AQK6_LEIMU]	0.75	1	1	1	1	1.174	1		2.629	1201	127.565
Q9Y2P8	RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens GN=RCL1 PE=1 SV=3 - [RCL1_HUMAN]	4.02	1	1	1	1				2.629	373	40.817
Q9BTT4	Mediator of RNA polymerase II transcription subunit 10 OS=Homo sapiens GN=MED10 PE=1 SV=1 - [MED10_HUMAN]	7.41	1	1	1	1	0.689	1		2.627	135	15.678
H0YN34	Spatacsin OS=Homo sapiens GN=SPG11 PE=4 SV=1 - [H0YN34_HUMAN]	1.16	4	1	1	1	1.820	1		2.625	779	87.195
C9JFL1	Nuclear envelope pore membrane protein POM 121C (Fragment) OS=Homo sapiens GN=POM121C PE=4 SV=1 - [C9JFL1_HUMAN]	10.28	6	1	1	1	1.000	1		2.625	107	11.310
B3KT25	cDNA FLJ37504 fis, clone BRAWH2017103, highly similar to ATPase WRNIP1 OS=Homo sapiens PE=2 SV=1 - [B3KT25_HUMAN]	2.93	2	2	2	2	1.000	2	0.000	2.625	614	66.633
E9ARP6	Putative phosphodiesterase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1090 PE=4 SV=1 - [E9ARP6_LEIMU]	1.58	1	1	1	1	0.839	1		2.623	631	70.651
B7Z8T5	cDNA FLJ53003, highly similar to Presenilin-1 (EC 3.4.23.-) OS=Homo sapiens PE=2 SV=1 - [B7Z8T5_HUMAN]	3.03	4	1	1	1	0.974	1		2.623	264	29.526
B4DWC8	cDNA FLJ58838, highly similar to Homo sapiens radical S-adenosyl methionine and flavodoxin domains 1 (RSAFD1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DWC8_	2.93	8	1	1	1	0.878	1		2.620	273	31.269
E9B267	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2690 PE=4 SV=1 - [E9B267_LEIMU]	2.13	1	1	2	2	1.000	1		2.619	1316	143.536
E9AZ13	Mitochondrial RNA binding protein 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1110 PE=4 SV=1 - [E9AZ13_LEIMU]	4.27	1	1	1	1	1.379	1		2.619	234	26.598
E9B0V4	Putative splicing factor 3a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1830 PE=4 SV=1 - [E9B0V4_LEIMU]	2.25	1	1	1	1	1.000	1		2.619	621	69.389
Q4G1C1	ATP8A1 protein OS=Homo sapiens GN=ATP8A1 PE=1 SV=1 - [Q4G1C1_HUMAN]	18.18	4	1	1	1	1.443	1		2.616	55	6.453
X6REY2	Protein Simiate (Fragment) OS=Homo sapiens GN=FAM206A PE=4 SV=1 - [X6REY2_HUMAN]	7.75	2	1	1	1	0.784	1		2.616	129	14.248
H7C2P6	LisH domain-containing protein ARMC9 (Fragment) OS=Homo sapiens GN=ARMC9 PE=4 SV=1 - [H7C2P6_HUMAN]	17.81	1	1	1	1	1.124	1		2.616	73	8.145
E9ARU2	Nonspecific nucleoside hydrolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1580 PE=4 SV=1 - [E9ARU2_LEIMU]	2.87	1	1	1	1	1.000	1		2.615	314	34.169
B7Z2G7	cDNA FLJ61607, weakly similar to Glioma tumor suppressor candidate region gene 1 protein OS=Homo sapiens PE=2 SV=1 - [B7Z2G7_HUMAN]	2.29	2	1	1	1	1.000	1		2.614	830	87.883

P60673	Profilin-3 OS=Homo sapiens GN=PFN3 PE=2 SV=1 - [PROF3_HUMAN]	6.57	1	1	1	1	0.799	1		2.613	137	14.587
E9PLG8	Glycosylphosphatidylinositol anchor attachment 1 protein (Fragment) OS=Homo sapiens GN=GPAA1 PE=1 SV=1 - [E9PLG8_HUMAN]	13.58	5	1	1	1	1.065	1		2.611	81	9.157
D3DPU8	Collagen, type IX, alpha 2, isoform CRA_a OS=Homo sapiens GN=COL9A2 PE=4 SV=1 - [D3DPU8_HUMAN]	1.51	2	1	1	1	1.024	1		2.610	595	56.325
B8ZZV5	39S ribosomal protein L30, mitochondrial OS=Homo sapiens GN=MRPL30 PE=1 SV=1 - [B8ZZV5_HUMAN]	9.9	2	1	1	1	1.029	1		2.610	101	11.927
A0A087X0S7	Leucine-rich repeat-containing protein 41 OS=Homo sapiens GN=LRRC41 PE=4 SV=1 - [A0A087X0S7_HUMAN]	1.73	5	1	1	1	0.963	1		2.609	521	56.365
O95251	Histone acetyltransferase KAT7 OS=Homo sapiens GN=KAT7 PE=1 SV=1 - [KAT7_HUMAN]	1.8	1	1	1	2	1.000	2	0.000	2.608	611	70.598
E9AJL4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0520 PE=4 SV=1 - [E9AJL4_LEIMU]	0.43	1	1	1	1	0.866	1		2.608	2092	217.021
E9B2U9	Putative coatomer epsilon subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_1730 PE=4 SV=1 - [E9B2U9_LEIMU]	2.17	1	1	1	1	3.343	1		2.607	323	34.969
H0YKE7	Calcineurin B homologous protein 1 OS=Homo sapiens GN=CHP1 PE=1 SV=1 - [H0YKE7_HUMAN]	8.94	5	1	1	1	0.300	1		2.606	123	14.261
H0YML0	DTW domain-containing protein 1 (Fragment) OS=Homo sapiens GN=DTWD1 PE=1 SV=1 - [H0YML0_HUMAN]	5.26	4	1	1	1	1.000	1		2.605	152	17.095
E9B233	Putative 3,2-trans-enoyl-CoA isomerase, mitochondrial OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2330 PE=3 SV=1 - [E9B233_LEIMU]	2.06	2	1	1	1	0.952	1		2.603	339	38.337
E9B082	Putative leucine-rich repeat protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2580 PE=4 SV=1 - [E9B082_LEIMU]	2.15	1	2	2	2	1.203	2	31.826	2.602	885	96.175
G3V504	E3 ubiquitin-protein ligase RNF34 (Fragment) OS=Homo sapiens GN=RNF34 PE=4 SV=1 - [G3V504_HUMAN]	4.29	3	1	1	1	0.882	1		2.600	163	18.116
E9PNW8	Fatty acyl-CoA reductase 1 (Fragment) OS=Homo sapiens GN=FAR1 PE=1 SV=1 - [E9PNW8_HUMAN]	2.39	4	1	1	1	1.000	1		2.599	335	37.458
Q9BX82	Zinc finger protein 471 OS=Homo sapiens GN=ZNF471 PE=2 SV=1 - [ZN471_HUMAN]	10.22	172	0	3	4				2.596	626	72.961
E9ASM6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1060 PE=4 SV=1 - [E9ASM6_LEIMU]	1.1	1	1	1	1	0.627	1		2.596	1003	111.367
A4D251	HCG2000720 OS=Homo sapiens GN=LOC401437 PE=4 SV=1 - [A4D251_HUMAN]	8.49	1	1	1	1	0.898	1		2.595	106	11.432
B4DPB6	cDNA FLJ56537, highly similar to Coiled-coil domain-containing protein 22 OS=Homo sapiens PE=2 SV=1 - [B4DPB6_HUMAN]	4.83	4	3	3	3	1.048	3	9.550	2.594	580	65.116
H7C2N6	Cyclic AMP-dependent transcription factor ATF-2 (Fragment) OS=Homo sapiens GN=ATF2 PE=1 SV=1 - [H7C2N6_HUMAN]	3.4	10	1	1	1	1.281	1		2.594	265	30.069
E9B308	Membrane associated protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2270 PE=4 SV=1 - [E9B308_LEIMU]	12.9	1	1	1	1	1.000	1		2.593	1465	163.768
J3QQH9	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [J3QQH9_HUMAN]	23.93	5	2	2	2	1.028	2	4.102	2.591	117	13.120
E9AVV5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_1230 PE=4 SV=1 - [E9AVV5_LEIMU]	1.2	1	1	1	1	1.150	1		2.591	919	101.737
O95714	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 - [HERC2_HUMAN]	0.43	1	2	2	2	0.990	2	1.463	2.589	4834	526.895
H7C317	N-acylglucosamine 2-epimerase (Fragment) OS=Homo sapiens GN=RENBP PE=4 SV=1 - [H7C317_HUMAN]	4.8	3	1	1	1	1.010	1		2.589	125	14.149
B9EG80	DMRTA2 protein OS=Homo sapiens GN=DMRTA2 PE=2 SV=1 - [B9EG80_HUMAN]	1.86	3	1	1	1	1.000	1		2.584	538	53.005
H0YEB8	RNA-binding protein 40 (Fragment) OS=Homo sapiens GN=RNPC3 PE=4 SV=1 - [H0YEB8_HUMAN]	5.49	2	1	1	1	1.000	1		2.582	182	21.320
E9AUJ5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_0510 PE=4 SV=1 - [E9AUJ5_LEIMU]	2.33	1	1	1	1	0.742	1		2.582	429	50.402
L0R819	Alternative protein ASNSD1 OS=Homo sapiens GN=ASNSD1 PE=4 SV=1 - [L0R819_HUMAN]	8.33	2	1	1	1	0.882	1		2.580	96	11.243
J3QRZ6	Homeobox protein MOX-1 (Fragment) OS=Homo sapiens GN=MEOX1 PE=4 SV=3 - [J3QRZ6_HUMAN]	7.32	6	2	2	2	1.018	2	13.668	2.580	205	23.380
Q9BYN8	28S ribosomal protein S26, mitochondrial OS=Homo sapiens GN=MRPS26 PE=1 SV=1 - [RT26_HUMAN]	9.76	1	2	2	2	1.559	2	73.702	2.578	205	24.197
B4DKV5	cDNA FLJ55614 OS=Homo sapiens PE=2 SV=1 - [B4DKV5_HUMAN]	1.67	5	1	1	1	1.000	1		2.577	718	81.407
Q96CM4	Nucleoredoxin-like protein 1 OS=Homo sapiens GN=NXNL1 PE=2 SV=1 - [NXNL1_HUMAN]	3.77	2	1	1	1	0.817	1		2.577	212	23.928
Q9H2F5	Enhancer of polycomb homolog 1 OS=Homo sapiens GN=EPC1 PE=1 SV=1 - [EPC1_HUMAN]	2.15	1	1	1	1	1.000	1		2.576	836	93.405
B7Z954	cDNA FLJ61560, highly similar to Tight junction protein ZO-2 OS=Homo sapiens PE=2 SV=1 - [B7Z954_HUMAN]	0.99	3	1	1	1	1.074	1		2.575	1108	124.801
Q53GY5	DiGeorge syndrome critical region gene 8 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GY5_HUMAN]	1.4	2	1	1	1	1.024	1		2.574	570	64.447
B2R728	cDNA, FLJ93255, highly similar to Homo sapiens solute carrier family 7 (cationic amino acidtransporter, y+ system), member 1 (SLC7A1), mRNA OS=Homo sapiens PE=	1.59	2	1	1	1	0.868	1		2.574	629	67.606
O95363	Phenylalanine--tRNA ligase, mitochondrial OS=Homo sapiens GN=FARS2 PE=1 SV=1 - [SYFM_HUMAN]	4.88	2	2	2	2	1.120	2	16.951	2.571	451	52.324
B4DG83	cDNA FLJ50136, highly similar to Induced myeloid leukemia cell differentiation protein Mcl-1 OS=Homo sapiens PE=2 SV=1 - [B4DG83_HUMAN]	2.92	4	1	1	1	1.000	1		2.571	240	26.404
B4DFU8	cDNA FLJ54647, highly similar to Liprin-beta-1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DFU8_HUMAN]	2.15	4	1	1	1	1.011	1		2.570	744	84.005
K7ELV9	Kynurenine formamidase OS=Homo sapiens GN=AFMID PE=4 SV=1 - [K7ELV9_HUMAN]	21.62	10	1	1	1	1.035	1		2.568	37	4.276
Q9NSV4	Protein diaphanous homolog 3 OS=Homo sapiens GN=DIAPH3 PE=1 SV=4 - [DIAP3_HUMAN]	0.75	1	1	1	1	1.000	1		2.568	1193	136.839
B4DTW0	cDNA FLJ58941, moderately similar to Arginine/serine-rich coiled coil protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DTW0_HUMAN]	4.73	4	1	1	1	1.341	1		2.568	169	19.708
F5H4R1	Mitogen-activated protein kinase kinase kinase 4 OS=Homo sapiens GN=MAP3K4 PE=1 SV=1 - [F5H4R1_HUMAN]	0.83	7	1	2	2	1.000	1		2.568	1442	162.912
Q96PG1	Putative membrane-spanning 4-domains subfamily A member 4E OS=Homo sapiens GN=MS4A4E PE=2 SV=2 - [M4A4E_HUMAN]	12.12	1	1	1	1	1.000	1		2.566	132	15.199
E9PRL8	7-dehydrocholesterol reductase (Fragment) OS=Homo sapiens GN=DHCR7 PE=1 SV=1 - [E9PRL8_HUMAN]	9.89	10	1	1	1	1.000	1		2.565	91	10.059
B4E1R1	cDNA FLJ52389, highly similar to Alcohol dehydrogenase 1B (EC 1.1.1.1) OS=Homo sapiens PE=2 SV=1 - [B4E1R1_HUMAN]	9.64	8	1	1	1	1.000	1		2.562	166	17.910
Q8N4V1	Membrane magnesium transporter 1 OS=Homo sapiens GN=MMGT1 PE=1 SV=1 - [MMGT1_HUMAN]	6.87	1	1	1	1	1.258	1		2.561	131	14.677
J3KNV5	Integrator complex subunit 8 OS=Homo sapiens GN=INTS8 PE=1 SV=1 - [J3KNV5_HUMAN]	1.06	4	1	1	1	1.000	1		2.561	758	85.674
E9B0Z8	Conserved zinc-finger protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2250 PE=4 SV=1 - [E9B0Z8_LEIMU]	2.16	1	1	1	1	1.000	1		2.560	371	41.888
E9AVS2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0900 PE=4 SV=1 - [E9AVS2_LEIMU]	0.86	1	1	1	1	1.009	1		2.556	925	99.720
Q70WD9	Maab3 protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q70WD9_HUMAN]	3.89	8	1	1	1	0.961	1		2.554	283	30.450
Q8IVT5	Kinase suppressor of Ras 1 OS=Homo sapiens GN=KSR1 PE=1 SV=3 - [KSR1_HUMAN]	1.84	5	1	2	2	1.000	1		2.553	923	102.096
E9AY90	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1110 PE=4 SV=1 - [E9AY90_LEIMU]	0.31	1	1	1	1	0.838	1		2.552	4172	445.292
E9API7	Mitochondrial DNA polymerase I protein D,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1630 PE=4 SV=1 - [E9API7_LEIMU]	0.51	1	1	1	1	1.000	1		2.551	1579	177.207
C9J9X2	Kinesin-like protein KIF3A (Fragment) OS=Homo sapiens GN=KIF3A PE=1 SV=1 - [C9J9X2_HUMAN]	6.51	9	1	1	1	1.000	1		2.551	169	19.072
C9J5J4	Protein lin-9 homolog OS=Homo sapiens GN=LIN9 PE=1 SV=1 - [C9J5J4_HUMAN]	2.25	5	1	1	1	0.690	1		2.550	489	55.898
B7Z2B7	cDNA FLJ60493 OS=Homo sapiens PE=2 SV=1 - [B7Z2B7_HUMAN]	7.96	5	1	2	2	1.000	1		2.549	201	22.122
E9AWE4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1260 PE=4 SV=1 - [E9AWE4_LEIMU]	0.52	1	1	1	1	1.038	1		2.549	1526	166.198
Q8TDQ1	CMRF35-like molecule 1 OS=Homo sapiens GN=CD300LF PE=1 SV=3 - [CLM1_HUMAN]	3.1	3	1	1	1	0.681	1		2.545	290	32.314
Q9NQG1	Protein MANBAL OS=Homo sapiens GN=MANBAL PE=1 SV=1 - [MANBL_HUMAN]	14.12	1	1	1	1	1.516	1		2.545	85	9.461
Q6IQ49	Protein SDE2 homolog OS=Homo sapiens GN=SDE2 PE=1 SV=1 - [SDE2_HUMAN]	2.88	1	2	2	2	1.075	2	26.914	2.544	451	49.711
E9ART0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1460 PE=4 SV=1 - [E9ART0_LEIMU]	0.99	1	1	1	1	1.025	1		2.542	906	97.210
H0YEW4	ATP synthase mitochondrial F1 complex assembly factor 1 (Fragment) OS=Homo sapiens GN=ATPAF1 PE=1 SV=1 - [H0YEW4_HUMAN]	6.32	4	1	1	1	1.063	1		2.541	174	19.898
C9JFU6	UDP-glucuronic acid decarboxylase 1 (Fragment) OS=Homo sapiens GN=UXS1 PE=4 SV=1 - [C9JFU6_HUMAN]	5.79	8	1	1	1	4.313	1		2.540	121	13.537
B7ZB72	cDNA, FLJ79436, highly similar to Homo sapiens prune homolog (PRUNE), mRNA OS=Homo sapiens PE=2 SV=1 - [B7ZB72_HUMAN]	7.69	3	1	1	1	1.000	1		2.539	169	18.525
V9GYD1	RAS protein activator-like-3 (Fragment) OS=Homo sapiens GN=RASAL3 PE=4 SV=1 - [V9GYD1_HUMAN]	4.39	3	1	1	1	1.036	1		2.536	228	25.792
E9B662	Putative COP-coated vesicle membrane protein gp25L (Putative er--golgi transport protein gp25l) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_	3.7	1	1	1	1	3.133	1		2.536	216	24.546
B4DSU2	cDNA FLJ50854, highly similar to Homo sapiens solute carrier family 30 (zinc transporter), member 9 (SLC30A9), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DSU2_HUI	2.27	4	1	1	1	1.002	1		2.535	397	44.482
Q9H8R7	cDNA FLJ13292 fis, clone OVARC1001180, weakly similar to UBIQUITIN-LIKE PROTEIN DSK2 OS=Homo sapiens PE=2 SV=1 - [Q9H8R7_HUMAN]	3.5	4	1	1	1	1.367	1		2.534	314	33.993
H7C3J3	THUMP domain-containing protein 3 (Fragment) OS=Homo sapiens GN=THUMPD3 PE=1 SV=1 - [H7C3J3_HUMAN]	7.06	3	2	2	2	0.966	2	5.184	2.534	269	30.326
H0YGX8	Conserved oligomeric Golgi complex subunit 6 (Fragment) OS=Homo sapiens GN=COG6 PE=4 SV=1 - [H0YGX8_HUMAN]	6.72	4	1	1	1	1.039	1		2.531	134	15.287
B4DSW6	cDNA FLJ58422, highly similar to HIRA protein OS=Homo sapiens PE=2 SV=1 - [B4DSW6_HUMAN]	1.24	3	1	1	1	1.000	1		2.531	806	88.088
E9APZ5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1470 PE=4 SV=1 - [E9APZ5_LEIMU]	2.27	1	1	1	1	1.012	1		2.531	484	56.329
A6NP16	Angiomotin OS=Homo sapiens GN=AMOT PE=1 SV=1 - [A6NP16_HUMAN]	4.86	6	2	2	2	1.125	1		2.531	597	68.350
E9AYI0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_2000 PE=4 SV=1 - [E9AYI0_LEIMU]	2.87	1	1	1	2	3.920	1		2.530	348	39.304
H0YEM7	Autophagy-related protein 13 (Fragment) OS=Homo sapiens GN=ATG13 PE=4 SV=1 - [H0YEM7_HUMAN]	11.92	6	1	1	1				2.529	193	20.571
C9JWE1	Serpin I2 (Fragment) OS=Homo sapiens GN=SERPINI2 PE=4 SV=1 - [C9JWE1_HUMAN]	8.28	3	1	1	1	1.000	1		2.529	157	17.881
Q96T59	CMT1A duplicated region transcript 15 protein OS=Homo sapiens GN=CDRT15 PE=2 SV=1 - [CDRTF_HUMAN]	7.45	2	1	1	1	1.000	1		2.529	188	20.638
G3V1P3	Loss of heterozygosity 12 chromosomal region 1 protein OS=Homo sapiens GN=LOH12CR1 PE=1 SV=1 - [G3V1P3_HUMAN]	3.95	2	1	1	1	1.442	1		2.528	177	20.235
E9AVK9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0260 PE=4 SV=1 - [E9AVK9_LEIMU]	3.9	1	1	1	1	1.000	1		2.527	282	30.742
C9J3C0	Cysteine protease ATG4B (Fragment) OS=Homo sapiens GN=ATG4B PE=1 SV=1 - [C9J3C0_HUMAN]	11.56	8	1	1	1				2.527	147	16.607
A7E2U9	SLC12A6 protein (Fragment) OS=Homo sapiens GN=SLC12A6 PE=2 SV=1 - [A7E2U9_HUMAN]	6.02	6	1	1	1	1.000	1		2.526	133	15.049
B3KP18	cDNA FLJ30946 fis, clone FEBRA2007622, highly similar to RAD50-interacting protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KP18_HUMAN]	1.52	2	1	1	1	1.000	1		2.526	792	90.540
A0A087WUE0	Dehydrogenase/reductase SDR family member 12 (Fragment) OS=Homo sapiens GN=DHRS12 PE=4 SV=1 - [A0A087WUE0_HUMAN]	9	2	1	1	1	1.136	1		2.525	100	10.779
H7C0U4	EF-hand domain-containing family member B (Fragment) OS=Homo sapiens GN=EFHB PE=4 SV=3 - [H7C0U4_HUMAN]	3.07	3	1	1	1	1.000	1		2.525	261	29.721
Q99942	E3 ubiquitin-protein ligase RNF5 OS=Homo sapiens GN=RNF5 PE=1 SV=1 - [RNF5_HUMAN]	3.89	2	1	1	1	1.532	1		2.525	180	19.869
Q6PIR0	CENPC1 protein OS=Homo sapiens GN=CENPC1 PE=1 SV=1 - [Q6PIR0_HUMAN]	5.54	3	2	2	2	1.000	2	0.000	2.525	542	61.506
A8K4B4	cDNA FLJ78441, highly similar to Homo sapiens nucleolar and spindle associated protein 1 (NUSAP1),mRNA OS=Homo sapiens PE=2 SV=1 - [A8K4B4_HUMAN]	6.58	2	2	2	2	0.989	2	1.614	2.524	441	49.409
B4E1G8	cDNA FLJ52827, highly similar to Zinc finger protein 410 OS=Homo sapiens PE=2 SV=1 - [B4E1G8_HUMAN]	5.04	6	1	1	1	0.778	1		2.523	278	30.562
B4DNA9	cDNA FLJ60024, highly similar to Cytochrome P450 4F12 (EC 1.14.14.1) OS=Homo sapiens PE=2 SV=1 - [B4DNA9_HUMAN]	4.19	1	1	1	1	0.969	1		2.522	191	22.437
E9PL47	Phosphatidylinositol 4-kinase beta (Fragment) OS=Homo sapiens GN=PI4KB PE=1 SV=1 - [E9PL47_HUMAN]	7.37	3	1	1	1	1.085	1		2.520	95	10.819
H3BUC0	Kinesin-like protein KIFC3 (Fragment) OS=Homo sapiens GN=KIFC3 PE=3 SV=1 - [H3BUC0_HUMAN]	6.63	10	1	1	1	1.082	1		2.520	196	20.277
P50479	PDZ and LIM domain protein 4 OS=Homo sapiens GN=PDLIM4 PE=1 SV=2 - [PDLI4_HUMAN]	3.33	1	1	1	2	0.989	2	16.278	2.519	330	35.376
Q8WZ25	Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1 - [Q8WZ25_HUMAN]	12.26	1	1	1	1	1.000	1		2.518	106	11.274
Q05D07	SPA17 protein (Fragment) OS=Homo sapiens GN=SPA17 PE=2 SV=1 - [Q05D07_HUMAN]	6.12	2	1	1	1	1.000	1		2.518	147	17.006
B3KVW3	Lysophospholipase-like 1, isoform CRA_a OS=Homo sapiens GN=LYPLAL1 PE=2 SV=1 - [B3KVW3_HUMAN]	6.19	2	1	1	1	0.930	1		2.517	113	12.643
J3KSS8	Multidrug and toxin extrusion protein 1 OS=Homo sapiens GN=SLC47A1 PE=4 SV=1 - [J3KSS8_HUMAN]	4.75	1	1	1	1	1.000	1		2.516	316	34.278
G3V132	Interactor protein for cytohesin exchange factors 1 OS=Homo sapiens GN=IPCEF1 PE=4 SV=1 - [G3V132_HUMAN]	2.2	3	1	1	1	1.000	1		2.514	409	45.816
J3QQP1	Zinc transporter ZIP11 (Fragment) OS=Homo sapiens GN=SLC39A11 PE=4 SV=1 - [J3QQP1_HUMAN]	25	6	1	1	1	1.000	1		2.513	68	7.155
Q9Y3S8	Putative uncharacterized protein DKFZp564M1416 (Fragment) OS=Homo sapiens GN=DKFZp564M1416 PE=2 SV=1 - [Q9Y3S8_HUMAN]	4.97	10	1	1	1	0.959	1		2.513	181	21.870
Q96DE5	Anaphase-promoting complex subunit 16 OS=Homo sapiens GN=ANAPC16 PE=1 SV=1 - [APC16_HUMAN]	10.91	1	1	1	1	1.000	1		2.511	110	11.660
B3KRE9	POU domain protein OS=Homo sapiens PE=2 SV=1 - [B3KRE9_HUMAN]	3.51	4	2	2	2	0.717	2	52.377	2.511	741	76.648
Q6ZQY7	Putative uncharacterized protein FLJ46792 OS=Homo sapiens PE=2 SV=1 - [YO026_HUMAN]	11.9	1	1	1	1	1.000	1		2.510	126	14.335
E9PIQ6	DNA polymerase alpha subunit B (Fragment) OS=Homo sapiens GN=POLA2 PE=1 SV=1 - [E9PIQ6_HUMAN]	7.53	2	1	1	1	0.640	1		2.510	146	15.885
G3V4T3	Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=4 SV=1 - [G3V4T3_HUMAN]	1.8	2	1	2	2	1.000	1		2.509	1113	129.591
Q9H705	CDNA: FLJ21611 fis, clone COL07344 OS=Homo sapiens PE=2 SV=1 - [Q9H705_HUMAN]	7.19	4	1	1	1	0.814	1		2.509	139	15.750
B4DSS3	cDNA FLJ55366, highly similar to Mitogen-activated protein kinase kinase kinase 3 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DSS3_HUMAN]	2.68	4	1	1	1	1.000	1		2.506	447	50.553
B1AJZ2	Vacuolar protein sorting 13 homolog D (S. cerevisiae) (Fragment) OS=Homo sapiens GN=VPS13D PE=4 SV=1 - [B1AJZ2_HUMAN]	0.75	3	1	1	1	1.000	1		2.505	2270	252.244
A0A087WZP0	Myb/SANT-like DNA-binding domain-containing protein 4 OS=Homo sapiens GN=MSANTD4 PE=4 SV=1 - [A0A087WZP0_HUMAN]	5.22	2	1	1	1	0.689	1		2.504	134	15.657
Q09LL4	CD40 (Fragment) OS=Homo sapiens PE=4 SV=1 - [Q09LL4_HUMAN]	7.69	5	1	1	1	1.067	1		2.504	117	13.149
K7EJ52	Phospholipid-transporting ATPase IK (Fragment) OS=Homo sapiens GN=ATP8B3 PE=4 SV=2 - [K7EJ52_HUMAN]	4.39	3	1	1	1	1.000	1		2.504	205	22.874
Q69YU5	Uncharacterized protein C12orf73 OS=Homo sapiens GN=C12orf73 PE=2 SV=2 - [CL073_HUMAN]	16.9	1	1	1	1	1.000	1		2.503	71	8.017
E5RJN3	Condensin-2 complex subunit H2 (Fragment) OS=Homo sapiens GN=NCAPH2 PE=1 SV=1 - [E5RJN3_HUMAN]	3.08	2	1	1	1	1.255	1		2.502	292	32.144
Q96JB3	Hypermethylated in cancer 2 protein OS=Homo sapiens GN=HIC2 PE=1 SV=2 - [HIC2_HUMAN]	1.63	1	1	1	1	1.000	1		2.501	615	66.114
E3P8H7	Pyrin/marenostrin variant del34-del78 OS=Homo sapiens GN=MEFV PE=2 SV=1 - [E3P8H7_HUMAN]	8.5	6	2	2	2	0.971	2	4.424	2.499	306	32.986
B4DW88	cDNA FLJ58633, highly similar to Leucine-rich repeat-containing protein 27 OS=Homo sapiens PE=2 SV=1 - [B4DW88_HUMAN]	1.63	3	1	1	1	1.051	1		2.497	368	42.259
F5GWN1	CD63 antigen OS=Homo sapiens GN=CD63 PE=4 SV=2 - [F5GWN1_HUMAN]	48.78	17	2	2	2	1.357	2	57.481	2.495	41	4.384
B2RE48	cDNA, FLJ96928, highly similar to Homo sapiens candidate tumor suppressor protein (LOC57107), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RE48_HUMAN]	8.77	4	2	2	2	1.940	1		2.494	399	44.129
B4E085	cDNA FLJ59132, highly similar to Caspase-2 (EC 3.4.22.-) OS=Homo sapiens PE=2 SV=1 - [B4E085_HUMAN]	6.93	4	1	1	1	0.827	1		2.494	202	22.546
E9AVQ4	5'a2rel-related protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0700 PE=4 SV=1 - [E9AVQ4_LEIMU]	0.88	1	1	1	1	1.156	1		2.494	1358	139.593
E9APH1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1470 PE=4 SV=1 - [E9APH1_LEIMU]	0.21	1	1	1	1	1.000	1		2.494	5610	591.733
E9B6V2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4220 PE=4 SV=1 - [E9B6V2_LEIMU]	4.55	1	1	1	1	1.000	1		2.493	593	61.818
E9PK85	Ras-related protein R-Ras2 (Fragment) OS=Homo sapiens GN=RRAS2 PE=1 SV=1 - [E9PK85_HUMAN]	7.23	2	1	1	1	1.000	1		2.493	166	19.557
E9AU44	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6090 PE=4 SV=1 - [E9AU44_LEIMU]	1.13	1	1	1	1	1.146	1		2.493	532	60.746
B4E0F7	cDNA FLJ61512 OS=Homo sapiens PE=2 SV=1 - [B4E0F7_HUMAN]	4.58	3	1	1	1	1.000	1		2.492	240	26.662
B4DH83	cDNA FLJ61115 OS=Homo sapiens PE=2 SV=1 - [B4DH83_HUMAN]	2.31	1	1	1	1	1.399	1		2.492	303	34.575
Q59GA8	WD repeat-containing protein 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GA8_HUMAN]	2.15	3	1	1	1	1.000	1		2.492	466	53.074
E9AP86	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0620 PE=4 SV=1 - [E9AP86_LEIMU]	1.65	1	1	1	2	0.979	2	3.143	2.491	423	44.077
Q86UK0	ATP-binding cassette sub-family A member 12 OS=Homo sapiens GN=ABCA12 PE=1 SV=3 - [ABCAC_HUMAN]	0.27	1	1	1	3	0.981	3	11.178	2.491	2595	293.049
E9AR70	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0980 PE=4 SV=1 - [E9AR70_LEIMU]	1.21	1	1	1	1	1.000	1		2.491	741	82.901
A0A024R2D7	Transcriptional adaptor 3 (NGG1 homolog, yeast)-like, isoform CRA_a OS=Homo sapiens GN=TADA3L PE=4 SV=1 - [A0A024R2D7_HUMAN]	3.25	3	1	1	1				2.490	369	41.367
E9B3X5	Putative mitogen activated protein kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1380 PE=4 SV=1 - [E9B3X5_LEIMU]	1.72	1	1	1	1	3.059	1		2.489	408	46.646
D6REL5	BRCA1-A complex subunit Abraxas OS=Homo sapiens GN=FAM175A PE=1 SV=1 - [D6REL5_HUMAN]	2.78	2	1	1	1				2.487	360	41.552
I6L994	RIOK3 protein OS=Homo sapiens GN=RIOK3 PE=2 SV=1 - [I6L994_HUMAN]	1.89	3	1	1	1	1.000	1		2.487	424	48.380
M0R3G1	Protein LOC101928524 (Fragment) OS=Homo sapiens GN=LOC101928524 PE=4 SV=1 - [M0R3G1_HUMAN]	5.91	3	1	1	1	1.000	1		2.487	203	23.227
E9B0Q4	Putative Pyridoxal kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1250 PE=4 SV=1 - [E9B0Q4_LEIMU]	6.95	1	2	2	2	0.900	2	15.680	2.487	302	33.117
H0Y746	MMS19 nucleotide excision repair protein homolog (Fragment) OS=Homo sapiens GN=MMS19 PE=1 SV=1 - [H0Y746_HUMAN]	1.84	2	1	1	1	1.267	1		2.486	598	65.374
Q1ED39	Lysine-rich nucleolar protein 1 OS=Homo sapiens GN=KNOP1 PE=1 SV=1 - [KNOP1_HUMAN]	2.62	1	1	1	1	1.194	1		2.485	458	51.557
H0Y750	Renin receptor (Fragment) OS=Homo sapiens GN=ATP6AP2 PE=4 SV=1 - [H0Y750_HUMAN]	3.7	6	1	1	1	0.504	1		2.485	243	26.615
A1L188	Uncharacterized protein C17orf89 OS=Homo sapiens GN=C17orf89 PE=2 SV=1 - [CQ089_HUMAN]	14.86	1	1	1	1	1.000	1		2.485	74	7.751
Q96J77	Tumor protein D55 OS=Homo sapiens GN=TPD52L3 PE=1 SV=2 - [TPD55_HUMAN]	4.29	1	1	1	1	0.997	1		2.485	140	15.493
B3KR89	cDNA FLJ33864 fis, clone CTONG2006412, highly similar to Mus musculus widely-interspaced zinc finger motifs (Wiz), transcript variant 1, mRNA OS=Homo sapiens PE	1.89	5	1	1	1	0.971	1		2.484	583	62.844
B0QY86	MICAL-like protein 1 (Fragment) OS=Homo sapiens GN=MICALL1 PE=1 SV=1 - [B0QY86_HUMAN]	5.71	2	1	1	1	0.965	1		2.484	210	22.135
Q8N8Q8	Mitochondrial inner membrane protein COX18 OS=Homo sapiens GN=COX18 PE=2 SV=1 - [COX18_HUMAN]	2.7	2	1	1	1	0.737	1		2.483	333	37.039
A0A087WUW9	ADP-ribosylation factor-like protein 15 OS=Homo sapiens GN=ARL15 PE=4 SV=1 - [A0A087WUW9_HUMAN]	4.41	3	1	1	1	0.487	1		2.482	204	22.862
B9TX22	Mediator complex subunit MED16 variant MED16_i29 OS=Homo sapiens GN=MED16 PE=2 SV=1 - [B9TX22_HUMAN]	8.94	20	1	1	1	1.824	1		2.482	123	14.004
C3UMV4	EWSR1/NFATC2 fusion protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [C3UMV4_HUMAN]	2.87	6	1	1	1	1.162	1		2.482	314	33.935
E9AW29	Putative argininosuccinate synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0260 PE=3 SV=1 - [E9AW29_LEIMU]	1.91	1	1	1	1	1.000	1		2.481	419	46.504
Q53S33	BolA-like protein 3 OS=Homo sapiens GN=BOLA3 PE=1 SV=1 - [BOLA3_HUMAN]	6.54	1	1	1	1	1.113	1		2.481	107	12.106
A0A087WT55	mRNA-decapping enzyme 1A (Fragment) OS=Homo sapiens GN=DCP1A PE=4 SV=1 - [A0A087WT55_HUMAN]	5.77	4	1	1	1	1.000	1		2.481	260	29.038
E9AQ19	Putative 60S ribosomal protein L13a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0200 PE=3 SV=1 - [E9AQ19_LEIMU]	4.5	1	1	1	1	6.537	1		2.481	222	25.505
Q8N8W2	cDNA FLJ38769 fis, clone KIDNE2015556, highly similar to RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 OS=Homo sapiens PE=2 SV=1 - [Q	1.11	4	1	1	1	1.112	1		2.481	632	68.127
Q6ZRP2	cDNA FLJ46208 fis, clone TESTI4010979 OS=Homo sapiens PE=2 SV=1 - [Q6ZRP2_HUMAN]	5.76	1	1	1	1	1.000	1		2.479	139	15.361
F5H4Q7	Glutamate receptor-interacting protein 1 (Fragment) OS=Homo sapiens GN=GRIP1 PE=4 SV=1 - [F5H4Q7_HUMAN]	2.67	6	1	1	1				2.479	787	84.103
A8K5P7	cDNA FLJ75523, highly similar to Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K5P7_HUMAN]	1.44	3	1	1	1	1.000	1		2.478	905	101.350
B2R6F5	cDNA, FLJ92928, highly similar to Homo sapiens retinitis pigmentosa 2 (X-linked recessive) (RP2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6F5_HUMAN]	4.29	2	2	2	3	1.000	3	30.266	2.477	350	39.599
C9JG98	Probable ATP-dependent RNA helicase DHX58 (Fragment) OS=Homo sapiens GN=DHX58 PE=4 SV=1 - [C9JG98_HUMAN]	3.64	5	1	1	1	1.067	1		2.477	302	34.035
Q5VYY2	Lipase member M OS=Homo sapiens GN=LIPM PE=2 SV=2 - [LIPM_HUMAN]	1.65	1	1	1	1	1.981	1		2.476	423	48.201
E9AXQ7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1750 PE=4 SV=1 - [E9AXQ7_LEIMU]	14.08	1	1	1	1	0.342	1		2.476	142	16.726
G3V3J8	Phospholipase D4 (Fragment) OS=Homo sapiens GN=PLD4 PE=4 SV=1 - [G3V3J8_HUMAN]	4.28	5	1	1	1	0.974	1		2.476	257	28.185
B4DLI3	cDNA FLJ51237, moderately similar to Carcinoembryonic antigen-related cell adhesion molecule 8 OS=Homo sapiens PE=2 SV=1 - [B4DLI3_HUMAN]	7.42	2	1	1	1	1.000	1		2.475	256	27.833
A8K029	Angiogenic factor with G patch and FHA domains 1, isoform CRA_a OS=Homo sapiens GN=AGGF1 PE=2 SV=1 - [A8K029_HUMAN]	2.76	4	1	1	1	1.000	1		2.474	399	44.857
Q8N2Q6	cDNA FLJ90047 fis, clone HEMBA1002316, highly similar to GTP-binding protein 6 OS=Homo sapiens PE=2 SV=2 - [Q8N2Q6_HUMAN]	6.32	4	1	1	1	0.482	1		2.473	174	18.902
E9B2S1	Putative phosphatidylinositol 3-related kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_1460 PE=4 SV=1 - [E9B2S1_LEIMU]	0.37	1	1	1	1	1.000	1		2.472	3211	351.663
E5RGG3	Caspase recruitment domain-containing protein 8 (Fragment) OS=Homo sapiens GN=CARD8 PE=4 SV=1 - [E5RGG3_HUMAN]	25.64	9	1	1	1	1.000	1		2.472	39	4.363
Q16176	Lsk protein OS=Homo sapiens GN=lsk PE=2 SV=1 - [Q16176_HUMAN]	1.72	5	1	1	1	1.000	1		2.468	465	51.876
Q8WW92	TAT protein OS=Homo sapiens PE=2 SV=1 - [Q8WW92_HUMAN]	7.04	3	1	1	2	1.396	2	52.611	2.468	142	15.876
B4E205	cDNA FLJ61651, highly similar to Protein transport protein Sec24A OS=Homo sapiens PE=2 SV=1 - [B4E205_HUMAN]	1.05	2	1	1	1	1.437	1		2.468	857	96.212
P55201	Peregrin OS=Homo sapiens GN=BRPF1 PE=1 SV=2 - [BRPF1_HUMAN]	1.65	1	2	2	2	1.000	2	0.000	2.467	1214	137.412
E9AU57	Putative flagellum transition zone component OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6220 PE=4 SV=1 - [E9AU57_LEIMU]	0.47	1	1	1	1	1.196	1		2.467	1474	156.197
B3KT88	cDNA FLJ37862 fis, clone BRSSN2015707, highly similar to 80 kDa MCM3-ASSOCIATED PROTEIN OS=Homo sapiens PE=2 SV=1 - [B3KT88_HUMAN]	1.89	4	1	1	1				2.467	475	53.687
Q05C46	CASC5 protein (Fragment) OS=Homo sapiens GN=CASC5 PE=2 SV=1 - [Q05C46_HUMAN]	2.37	3	1	1	1	1.000	1		2.467	422	47.851
B4DK21	cDNA FLJ58726 OS=Homo sapiens PE=2 SV=1 - [B4DK21_HUMAN]	1.31	3	1	1	1	4.014	1		2.465	918	102.604
H7BZM4	Caspase-8 subunit p10 (Fragment) OS=Homo sapiens GN=CASP8 PE=4 SV=1 - [H7BZM4_HUMAN]	8.43	12	1	1	1	1.020	1		2.464	83	9.408
X6R3Q3	Terminal uridylyltransferase 7 OS=Homo sapiens GN=ZCCHC6 PE=1 SV=1 - [X6R3Q3_HUMAN]	1.15	3	1	1	1	1.000	1		2.463	784	90.049
Q53Q75	Putative uncharacterized protein C2orf5 (Fragment) OS=Homo sapiens GN=C2orf5 PE=4 SV=1 - [Q53Q75_HUMAN]	14.89	3	1	1	1	1.000	1		2.463	94	10.496
O43677	NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial OS=Homo sapiens GN=NDUFC1 PE=2 SV=1 - [NDUC1_HUMAN]	13.16	2	1	1	1	0.970	1		2.461	76	8.729
E9B548	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2570 PE=4 SV=1 - [E9B548_LEIMU]	2.51	1	1	1	1	0.657	1		2.461	557	63.626
B4E218	cDNA FLJ61052, highly similar to Homo sapiens myosin head domain containing 1 (MYOHD1), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [B4E218_HU	1.03	2	1	1	1	1.000	1		2.461	970	109.073
A2TKE4	Cellular titin isoform PEVK variant 2 (Fragment) OS=Homo sapiens GN=TTN PE=2 SV=1 - [A2TKE4_HUMAN]	1.61	1	1	1	1	1.000	1		2.460	373	41.426
O60583	Cyclin-T2 OS=Homo sapiens GN=CCNT2 PE=1 SV=2 - [CCNT2_HUMAN]	1.78	1	1	1	1	1.000	1		2.458	730	80.979
A0A087X1Q5	Suppressor of cytokine-signaling 7 OS=Homo sapiens GN=SOCS7 PE=4 SV=1 - [A0A087X1Q5_HUMAN]	2.93	2	1	1	1	1.000	1		2.457	547	59.528
C9JYQ9	60S ribosomal protein L22-like 1 OS=Homo sapiens GN=RPL22L1 PE=1 SV=1 - [C9JYQ9_HUMAN]	5.79	3	1	1	1	0.987	1		2.455	121	14.470
Q53GK5	Small nuclear RNA activating complex, polypeptide 2, 45kDa variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GK5_HUMAN]	7.49	1	1	1	2	1.000	2	0.000	2.455	334	35.489
Q5SXN9	Mitochondrial-processing peptidase subunit alpha (Fragment) OS=Homo sapiens GN=PMPCA PE=1 SV=1 - [Q5SXN9_HUMAN]	7.75	2	1	2	2	1.000	1		2.455	271	29.513
H3BRE1	Cytosolic Fe-S cluster assembly factor NUBP2 (Fragment) OS=Homo sapiens GN=NUBP2 PE=1 SV=1 - [H3BRE1_HUMAN]	4.17	7	1	1	1	1.047	1		2.455	144	15.825
B7Z2G2	cDNA FLJ56958, highly similar to Homo sapiens latrophilin 3 (LPHN3), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z2G2_HUMAN]	3.66	16	1	1	1	0.520	1		2.451	273	30.961
E9AQU6	DNA-directed RNA polymerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1350 PE=3 SV=1 - [E9AQU6_LEIMU]	0.94	1	1	1	1	1.614	1		2.451	1810	200.046
Q8WXG6	MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD PE=1 SV=2 - [MADD_HUMAN]	0.97	2	2	2	2	1.030	2	4.400	2.449	1647	183.188

B7Z3U5	cDNA FLJ52185, highly similar to mRNA decapping enzyme 2 (EC 3.-.-.-) OS=Homo sapiens PE=2 SV=1 - [B7Z3U5_HUMAN]	11.96	3	1	1	1	1.000	1		2.448	209	23.836
O14523	C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3 - [C2C2L_HUMAN]	1.13	1	1	1	1	0.761	1		2.447	706	76.134
B4DDM8	cDNA FLJ59176, highly similar to ADAM 9 (EC 3.4.24.-) (A disintegrinand metalloproteinase domain 9) OS=Homo sapiens PE=2 SV=1 - [B4DDM8_HUMAN]	4.41	2	1	1	1	1.000	1		2.446	204	22.540
E9AJY0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_03_0960 PE=4 SV=1 - [E9AJY0_LEIMU]	10.58	1	1	1	1	1.000	1		2.444	104	12.542
Q16344	Protein-tyrosine phosphatase (Fragment) OS=Homo sapiens GN=BPTP-3 PE=2 SV=3 - [Q16344_HUMAN]	8.79	1	1	1	1	1.000	1		2.444	91	10.559
A2IDA3	DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 - [A2IDA3_HUMAN]	5.98	2	1	1	1	1.866	1		2.444	251	27.278
V9GYH1	Pantothenate kinase 2, mitochondrial (Fragment) OS=Homo sapiens GN=PANK2 PE=4 SV=1 - [V9GYH1_HUMAN]	7.83	10	1	1	1	1.000	1		2.443	115	12.779
E9B4X3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1480 PE=4 SV=1 - [E9B4X3_LEIMU]	1.9	1	1	1	1	1.000	1		2.443	999	106.409
E9AY94	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1150 PE=4 SV=1 - [E9AY94_LEIMU]	0.89	1	1	1	1	0.888	1		2.441	787	83.543
E9AUW8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0030 PE=4 SV=1 - [E9AUW8_LEIMU]	3.9	1	1	1	1	1.000	1		2.441	231	26.294
E9B0M6	Putative p22 protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_0970 PE=4 SV=1 - [E9B0M6_LEIMU]	3.86	1	1	1	1	0.683	1		2.441	233	25.836
A0A087WVM7	Ribosomal RNA small subunit methyltransferase NEP1 (Fragment) OS=Homo sapiens GN=EMG1 PE=4 SV=1 - [A0A087WVM7_HUMAN]	4.7	6	1	1	1	1.027	1		2.441	149	16.632
A2RRE0	WD repeat-containing protein 7 OS=Homo sapiens GN=WDR7 PE=2 SV=1 - [A2RRE0_HUMAN]	1.1	2	1	1	1	1.145	1		2.439	815	89.287
F5H6F8	MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=4 SV=3 - [F5H6F8_HUMAN]	3.67	2	1	1	1	1.000	1		2.438	218	23.786
B3KP31	cDNA FLJ31047 fis, clone HSYRA2000424, highly similar to Carbohydrate kinase-like protein (EC 2.7.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KP31_HUMAN]	3.56	2	1	1	1	1.000	1		2.437	478	51.456
E9ALD1	Proteasome regulatory non-ATP-ase subunit,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_1120 PE=4 SV=1 - [E9ALD1_LEIMU]	3.19	1	1	1	1	1.000	1		2.437	345	36.465
E9AME2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0630 PE=4 SV=1 - [E9AME2_LEIMU]	0.28	1	1	1	1	0.787	1		2.437	2178	232.757
Q9NXG0	Centlein OS=Homo sapiens GN=CNTLN PE=2 SV=5 - [CNTLN_HUMAN]	0.64	1	1	1	1	0.898	1		2.436	1405	161.504
Q6GQQ9	OTU domain-containing protein 7B OS=Homo sapiens GN=OTUD7B PE=1 SV=1 - [OTU7B_HUMAN]	2.37	1	2	2	2	1.017	2	2.569	2.435	843	92.468
F8W8N5	Rho GTPase-activating protein 26 (Fragment) OS=Homo sapiens GN=ARHGAP26 PE=4 SV=1 - [F8W8N5_HUMAN]	4.22	2	1	1	1	1.268	1		2.434	166	19.464
E9AR02	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0330 PE=4 SV=1 - [E9AR02_LEIMU]	0.46	1	1	1	1	0.966	1		2.434	1733	185.633
Q9NUL7	Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=1 SV=2 - [DDX28_HUMAN]	1.67	1	1	1	1	1.000	1		2.433	540	59.545
H0YEQ6	COMM domain-containing protein 5 (Fragment) OS=Homo sapiens GN=COMMD5 PE=1 SV=1 - [H0YEQ6_HUMAN]	4.71	2	1	1	1	1.824	1		2.432	170	18.896
H0YGL7	RING finger protein 10 (Fragment) OS=Homo sapiens GN=RNF10 PE=4 SV=1 - [H0YGL7_HUMAN]	8.65	8	1	1	1	1.000	1		2.431	104	11.026
G3CIG0	MUC19 variant 12 OS=Homo sapiens GN=MUC19 PE=2 SV=1 - [G3CIG0_HUMAN]	0.38	1	1	1	1	1.000	1		2.428	8384	804.768
Q86UT6	NLR family member X1 OS=Homo sapiens GN=NLRX1 PE=1 SV=1 - [NLRX1_HUMAN]	1.13	1	1	1	1	0.996	1		2.428	975	107.548
D3DP30	Kelch-like 2, Mayven (Drosophila), isoform CRA_a OS=Homo sapiens GN=KLHL2 PE=4 SV=1 - [D3DP30_HUMAN]	2.59	5	1	1	1	0.872	1		2.425	425	47.117
Q92755	Transcription factor AP2 (Fragment) OS=Homo sapiens GN=TFAP2 PE=4 SV=1 - [Q92755_HUMAN]	13.95	15	1	1	1				2.425	43	4.784
Q9P2P1	Protein NYNRIN OS=Homo sapiens GN=NYNRIN PE=2 SV=3 - [NYNRI_HUMAN]	0.68	1	1	1	1				2.424	1898	208.235
E9ATA6	Putative 60S ribosomal protein L22 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3270 PE=4 SV=1 - [E9ATA6_LEIMU]	13.18	1	1	1	1	1.000	1		2.423	129	15.065
E9AXZ8	Putative 60S ribosomal protein L7 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0170 PE=3 SV=1 - [E9AXZ8_LEIMU]	3.17	2	1	1	1	0.957	1		2.423	252	28.882
A6N6J7	JARID1C protein OS=Homo sapiens GN=JARID1C PE=2 SV=1 - [A6N6J7_HUMAN]	0.83	2	1	1	1	1.000	1		2.423	1440	162.625
B4DWX0	cDNA FLJ57642, highly similar to Homo sapiens spire homolog 1 (SPIRE1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DWX0_HUMAN]	1.28	3	1	1	1	1.430	1		2.421	545	62.842
E9AQ96	Putative NAD/FAD dependent dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0970 PE=4 SV=1 - [E9AQ96_LEIMU]	1.75	1	1	1	1	1.000	1		2.421	400	43.078
E9ASR4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1440 PE=4 SV=1 - [E9ASR4_LEIMU]	0.14	1	1	1	1	1.000	1		2.420	5606	601.391
F8VZY9	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=1 - [F8VZY9_HUMAN]	6.65	3	1	1	1	1.000	1		2.420	391	43.747
B3KUI2	cDNA FLJ39965 fis, clone SPLEN2027157, highly similar to Homo sapiens tumor necrosis factor, alpha-induced protein 8 (TNFAIP8), mRNA OS=Homo sapiens PE=2 S\	4.04	3	1	1	1	1.220	1		2.419	198	23.015
E9AQ53	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0560 PE=4 SV=1 - [E9AQ53_LEIMU]	3.34	1	1	1	1				2.419	539	56.180
Q9UMS0	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Homo sapiens GN=NFU1 PE=1 SV=2 - [NFU1_HUMAN]	8.66	4	2	2	2	1.077	2	11.087	2.419	254	28.444
A0A087WTY7	Cytosolic beta-glucosidase OS=Homo sapiens GN=GBA3 PE=4 SV=1 - [A0A087WTY7_HUMAN]	1.5	3	1	1	1	0.597	1		2.418	468	53.499
Q16585	Beta-sarcoglycan OS=Homo sapiens GN=SGCB PE=1 SV=1 - [SGCB_HUMAN]	3.77	2	1	1	1	1.000	1		2.416	318	34.755
Q9BTA1	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BTA1_HUMAN]	2.71	4	1	1	1	0.845	1		2.416	258	28.808
Q8IVQ8	XPO4 protein (Fragment) OS=Homo sapiens GN=XPO4 PE=2 SV=1 - [Q8IVQ8_HUMAN]	1.29	4	1	1	1	1.000	1		2.415	1008	113.963
B7ZKQ9	SCARB1 protein OS=Homo sapiens GN=SCARB1 PE=1 SV=1 - [B7ZKQ9_HUMAN]	2.49	8	1	1	1	1.000	1		2.415	481	53.812
A4FVC4	FGD6 protein (Fragment) OS=Homo sapiens GN=FGD6 PE=2 SV=1 - [A4FVC4_HUMAN]	1.1	3	1	1	1	1.091	1		2.414	639	72.851
F8VTQ3	ATP-dependent 6-phosphofructokinase, muscle type (Fragment) OS=Homo sapiens GN=PFKM PE=1 SV=1 - [F8VTQ3_HUMAN]	19.46	1	1	1	1	1.000	1		2.414	149	15.979
H3BMU8	Group XV phospholipase A2 (Fragment) OS=Homo sapiens GN=PLA2G15 PE=4 SV=1 - [H3BMU8_HUMAN]	3.02	2	1	1	1	0.811	1		2.414	298	33.857
E9AQL0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0520 PE=4 SV=1 - [E9AQL0_LEIMU]	2.44	1	1	1	1	1.313	1		2.411	328	36.644
Q96AS3	HSH2D protein (Fragment) OS=Homo sapiens GN=HSH2D PE=2 SV=1 - [Q96AS3_HUMAN]	5.3	2	1	1	1	1.000	1		2.409	264	29.142
B7ZB05	cDNA, FLJ79369, highly similar to JmjC domain-containing histone demethylation protein 1B (EC 1.14.11.-) OS=Homo sapiens PE=2 SV=1 - [B7ZB05_HUMAN]	2.32	6	2	2	2	0.900	2	15.699	2.408	776	87.936
Q9BRT2	Ubiquinol-cytochrome-c reductase complex assembly factor 2 OS=Homo sapiens GN=UQCC2 PE=1 SV=1 - [UQCC2_HUMAN]	5.56	2	1	1	1	1.147	1		2.405	126	14.865
A6NNZ3	Zinc finger protein 419 OS=Homo sapiens GN=ZNF419 PE=4 SV=2 - [A6NNZ3_HUMAN]	1.58	3	1	1	1	0.881	1		2.404	442	50.693
Q6P1L8	39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 - [RM14_HUMAN]	4.14	1	1	1	1	0.799	1		2.404	145	15.937
B4DVV7	cDNA FLJ51339, highly similar to Methionyl-tRNA synthetase, mitochondrial (EC 6.1.1.10) OS=Homo sapiens PE=2 SV=1 - [B4DVV7_HUMAN]	1.92	2	1	1	1	0.922	1		2.403	520	58.442
Q96IX5	Up-regulated during skeletal muscle growth protein 5 OS=Homo sapiens GN=USMG5 PE=1 SV=1 - [USMG5_HUMAN]	10.34	1	1	1	1	1.287	1		2.402	58	6.453
E9AL68	Putative ras-related protein rab-14 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0560 PE=3 SV=1 - [E9AL68_LEIMU]	3.11	1	1	1	1	1.000	1		2.401	225	24.396
A2VCL5	FLOT1 protein (Fragment) OS=Homo sapiens GN=FLOT1 PE=2 SV=1 - [A2VCL5_HUMAN]	11.39	4	2	2	2	1.000	1		2.401	237	26.348
P11801	Serine/threonine-protein kinase H1 OS=Homo sapiens GN=PSKH1 PE=1 SV=4 - [KPSH1_HUMAN]	1.89	1	1	1	1	0.919	1		2.401	424	48.005
A0A087X1N2	CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=4 SV=1 - [A0A087X1N2_HUMAN]	1.5	3	2	2	2	1.112	2	7.517	2.400	998	114.086
K7ELJ0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens GN=NDUFA11 PE=4 SV=1 - [K7ELJ0_HUMAN]	37.14	6	1	1	1	0.836	1		2.399	35	3.942
Q9NR16	Scavenger receptor cysteine-rich type 1 protein M160 OS=Homo sapiens GN=CD163L1 PE=1 SV=2 - [C163B_HUMAN]	0.41	1	1	1	1	1.000	1		2.399	1453	159.135
A5D8T4	TNFRSF8 protein (Fragment) OS=Homo sapiens GN=TNFRSF8 PE=2 SV=1 - [A5D8T4_HUMAN]	6.95	2	1	1	1	1.000	1		2.398	187	20.402
H7C0G1	Transmembrane protein 245 (Fragment) OS=Homo sapiens GN=TMEM245 PE=1 SV=1 - [H7C0G1_HUMAN]	6.57	1	1	2	2	0.848	1		2.396	472	52.797
B4DDG3	cDNA FLJ51688, highly similar to Cleavage stimulation factor 50 kDa subunit OS=Homo sapiens PE=2 SV=1 - [B4DDG3_HUMAN]	3.35	2	1	1	1	1.000	1		2.395	418	46.807
B7Z8Y9	cDNA FLJ57775, highly similar to Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein, mRNA OS=Homo sapiens PE	9.48	2	1	1	1	1.000	1		2.395	211	22.776
H7BY35	Ryanodine receptor 2 OS=Homo sapiens GN=RYR2 PE=4 SV=2 - [H7BY35_HUMAN]	0.65	3	2	2	2	1.000	1		2.394	4950	562.250
H0YHV1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 (Fragment) OS=Homo sapiens GN=SMARCD1 PE=4 SV=1 - [H0YHV1	11.3	6	1	1	1	1.000	1		2.393	115	13.628
Q9NQE9	Histidine triad nucleotide-binding protein 3 OS=Homo sapiens GN=HINT3 PE=1 SV=1 - [HINT3_HUMAN]	5.49	1	1	1	1	1.000	1		2.393	182	20.348
E9B752	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_5260 PE=4 SV=1 - [E9B752_LEIMU]	8.24	1	1	1	1	1.000	1		2.393	85	9.734
P34820	Bone morphogenetic protein 8B OS=Homo sapiens GN=BMP8B PE=2 SV=2 - [BMP8B_HUMAN]	2.24	2	1	1	1	1.000	1		2.392	402	44.740
H7C213	Translation initiation factor IF-2, mitochondrial (Fragment) OS=Homo sapiens GN=MTIF2 PE=1 SV=2 - [H7C213_HUMAN]	5.98	4	2	2	2	1.000	2	0.000	2.392	301	33.548
E9AMB8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0390 PE=4 SV=1 - [E9AMB8_LEIMU]	0.45	1	1	1	1	1.000	1		2.392	1782	191.772
E9B042	Putative ribosomal protein S29 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2205 PE=4 SV=1 - [E9B042_LEIMU]	31.58	1	2	2	2	1.106	2	15.047	2.392	57	6.678
Q9NZ09	Ubiquitin-associated protein 1 OS=Homo sapiens GN=UBAP1 PE=1 SV=1 - [UBAP1_HUMAN]	1.79	1	1	1	1	1.167	1		2.390	502	55.048
B3KMG9	cDNA FLJ10954 fis, clone PLACE1000383, highly similar to Myotubularin-related protein 1 (EC 3.1.3.-) OS=Homo sapiens PE=2 SV=1 - [B3KMG9_HUMAN]	2.04	5	1	1	1	1.000	1		2.389	393	44.633
Q9BRT6	Protein LLP homolog OS=Homo sapiens GN=LLPH PE=2 SV=1 - [LLPH_HUMAN]	6.2	1	1	1	1	0.948	1		2.388	129	15.215
E9B4V9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1350 PE=4 SV=1 - [E9B4V9_LEIMU]	1.38	1	1	1	1	1.002	1		2.388	579	61.668
X6R4A7	Zinc finger CCHC domain-containing protein 7 OS=Homo sapiens GN=ZCCHC7 PE=4 SV=1 - [X6R4A7_HUMAN]	7.32	3	1	1	1	1.000	1		2.387	205	22.949
B3KM90	cDNA FLJ10529 fis, clone NT2RP2000965, highly similar to Targeting protein for Xklp2 OS=Homo sapiens PE=2 SV=1 - [B3KM90_HUMAN]	3.64	4	2	2	2	0.410	2	34.565	2.387	605	69.715
H0YJ98	Integrin alpha-7 (Fragment) OS=Homo sapiens GN=ITGA7 PE=4 SV=1 - [H0YJ98_HUMAN]	3.41	5	1	1	1				2.387	205	21.419
E5RHK0	Protein FAM92A1 OS=Homo sapiens GN=FAM92A1 PE=4 SV=1 - [E5RHK0_HUMAN]	8.33	7	1	1	1	1.000	1		2.386	132	15.654
Q8TEQ0	Sorting nexin-29 OS=Homo sapiens GN=SNX29 PE=1 SV=3 - [SNX29_HUMAN]	1.72	1	1	1	1	1.000	1		2.385	813	91.197
P62072	Mitochondrial import inner membrane translocase subunit Tim10 OS=Homo sapiens GN=TIMM10 PE=1 SV=1 - [TIM10_HUMAN]	8.89	1	1	1	1	1.048	1		2.385	90	10.326
H7C5D6	MutS protein homolog 5 (Fragment) OS=Homo sapiens GN=MSH5 PE=4 SV=1 - [H7C5D6_HUMAN]	4.4	10	1	1	1	0.723	1		2.384	159	18.097
H0YBY0	Double-stranded RNA-binding protein Staufen homolog 2 (Fragment) OS=Homo sapiens GN=STAU2 PE=1 SV=1 - [H0YBY0_HUMAN]	9.26	10	1	1	2	1.267	1		2.384	162	17.314
Q96DP5	Methionyl-tRNA formyltransferase, mitochondrial OS=Homo sapiens GN=MTFMT PE=1 SV=2 - [FMT_HUMAN]	2.57	1	1	1	1				2.384	389	43.804
E9AS14	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0620 PE=4 SV=1 - [E9AS14_LEIMU]	1.35	1	1	1	1	0.279	1		2.383	742	81.060
A0A087WWY2	Folate receptor beta OS=Homo sapiens GN=FOLR2 PE=4 SV=1 - [A0A087WWY2_HUMAN]	5.33	2	1	1	1	1.000	1		2.383	244	26.164
A0A024QZ48	Integrator complex subunit 2, isoform CRA_a OS=Homo sapiens GN=INTS2 PE=4 SV=1 - [A0A024QZ48_HUMAN]	0.75	4	1	1	1	0.262	1		2.383	1196	133.316
D6RAZ6	Transmembrane protein 192 (Fragment) OS=Homo sapiens GN=TMEM192 PE=1 SV=1 - [D6RAZ6_HUMAN]	14.29	2	1	1	1	1.000	1		2.383	84	9.537
E9B299	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2990 PE=4 SV=1 - [E9B299_LEIMU]	0.47	1	1	1	1	1.169	1		2.383	1911	212.935
E9ALX5	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0970 PE=3 SV=1 - [E9ALX5_LEIMU]	1.16	2	1	2	2	1.000	1		2.382	1730	199.355
B4E2S3	cDNA FLJ56561 OS=Homo sapiens PE=2 SV=1 - [B4E2S3_HUMAN]	2.15	10	1	2	2	1.221	1		2.378	792	86.651
H0YET5	EGF-containing fibulin-like extracellular matrix protein 2 (Fragment) OS=Homo sapiens GN=EFEMP2 PE=4 SV=1 - [H0YET5_HUMAN]	3.3	2	1	1	1	0.668	1		2.377	182	19.687
M0R0X9	Interferon regulatory factor 3 (Fragment) OS=Homo sapiens GN=IRF3 PE=4 SV=3 - [M0R0X9_HUMAN]	8.49	11	1	1	1	1.671	1		2.376	106	11.460
B7Z390	cDNA FLJ53336, highly similar to ADAM 15 (EC 3.4.24.-) (Adisintegrin and metalloproteinase domain 15) OS=Homo sapiens PE=2 SV=1 - [B7Z390_HUMAN]	0.87	3	1	1	1	2.397	1		2.375	809	87.252
E9AP76	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0520 PE=4 SV=1 - [E9AP76_LEIMU]	2.88	1	1	1	1	1.000	1		2.374	278	31.601
E9AVR2	NADH-cytochrome b5 reductase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0780 PE=3 SV=1 - [E9AVR2_LEIMU]	3.46	1	1	1	1	1.000	1		2.374	289	32.323
Q9Y5Z9	UbiA prenyltransferase domain-containing protein 1 OS=Homo sapiens GN=UBIAD1 PE=1 SV=1 - [UBIA1_HUMAN]	4.73	1	1	1	1	0.667	1		2.373	338	36.808
E7EWD6	Putative Polycomb group protein ASXL2 OS=Homo sapiens GN=ASXL2 PE=1 SV=1 - [E7EWD6_HUMAN]	0.57	3	1	1	1	1.000	1		2.373	1407	150.373
Q6ZNC4	Zinc finger protein 704 OS=Homo sapiens GN=ZNF704 PE=1 SV=1 - [ZN704_HUMAN]	7.28	2	2	2	2	1.000	2	0.000	2.372	412	45.247
A0A024R8I8	Chromosome 9 open reading frame 140, isoform CRA_a OS=Homo sapiens GN=C9orf140 PE=4 SV=1 - [A0A024R8I8_HUMAN]	6.09	2	2	2	2	0.870	2	20.860	2.372	394	42.541
H0YCZ6	Transcriptional enhancer factor TEF-1 (Fragment) OS=Homo sapiens GN=TEAD1 PE=4 SV=2 - [H0YCZ6_HUMAN]	4.4	1	1	1	1	0.947	1		2.371	159	16.668
K7EK04	Pleckstrin homology domain-containing family H member 3 (Fragment) OS=Homo sapiens GN=PLEKHH3 PE=1 SV=1 - [K7EK04_HUMAN]	3.88	1	1	1	1	5.958	1		2.368	206	22.714
U3LYB8	Heat shock protein 20 (Fragment) OS=Leishmania aethiopica GN=hsp20 PE=3 SV=1 - [U3LYB8_9TRYP]	10.48	2	1	1	1	1.000	1		2.368	105	11.977
Q96H79	Zinc finger CCCH-type antiviral protein 1-like OS=Homo sapiens GN=ZC3HAV1L PE=1 SV=2 - [ZCCHL_HUMAN]	5.67	1	2	2	2				2.368	300	32.940
Q8IVM8	Solute carrier family 22 member 9 OS=Homo sapiens GN=SLC22A9 PE=1 SV=1 - [S22A9_HUMAN]	1.27	1	1	1	1	0.793	1		2.366	553	62.128
Q8NB14	Ubiquitin carboxyl-terminal hydrolase 38 OS=Homo sapiens GN=USP38 PE=2 SV=2 - [UBP38_HUMAN]	0.96	1	1	1	1	1.000	1		2.364	1042	116.472
K7EPK8	Coiled-coil domain-containing protein 151 OS=Homo sapiens GN=CCDC151 PE=4 SV=1 - [K7EPK8_HUMAN]	1.98	6	1	1	1	2.051	1		2.364	404	47.363
Q7Z6M1	Rab9 effector protein with kelch motifs OS=Homo sapiens GN=RABEPK PE=1 SV=1 - [RABEK_HUMAN]	2.42	1	1	1	1	1.000	1		2.361	372	40.539
E9AXI6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1070 PE=4 SV=1 - [E9AXI6_LEIMU]	0.82	1	1	1	1	5.409	1		2.360	858	95.252
Q5T179	Cyclin-dependent kinases regulatory subunit OS=Homo sapiens GN=CKS1B PE=1 SV=1 - [Q5T179_HUMAN]	10.45	3	1	1	1	0.966	1		2.359	67	8.022
E9AQT8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1270 PE=4 SV=1 - [E9AQT8_LEIMU]	2.14	1	2	2	2	1.000	2	0.000	2.359	2149	230.093
E9ALT6	Putative RNA binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1360 PE=4 SV=1 - [E9ALT6_LEIMU]	3.16	1	1	1	1	1.000	1		2.358	665	71.644
O00391	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 - [QSOX1_HUMAN]	3.61	3	2	2	2	0.942	2	8.809	2.358	747	82.526
Q702N8	Xin actin-binding repeat-containing protein 1 OS=Homo sapiens GN=XIRP1 PE=1 SV=1 - [XIRP1_HUMAN]	0.98	1	1	1	1	1.000	1		2.357	1843	198.439
B2RAP8	cDNA, FLJ95042, highly similar to Homo sapiens p53-regulated apoptosis-inducing protein 1 (P53AIP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAP8_HUMAN]	10.19	1	1	1	1	1.507	1		2.357	108	11.291
E9AS59	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1080 PE=4 SV=1 - [E9AS59_LEIMU]	0.48	1	1	1	1	1.000	1		2.357	3775	400.561
Q5VVJ2	Histone H2A deubiquitinase MYSM1 OS=Homo sapiens GN=MYSM1 PE=1 SV=1 - [MYSM1_HUMAN]	1.21	1	1	1	1	1.000	1		2.357	828	94.972
Q5T8U9	UPF0586 protein C9orf41 OS=Homo sapiens GN=C9orf41 PE=1 SV=1 - [Q5T8U9_HUMAN]	5.23	4	1	1	1	0.560	1		2.356	153	17.597
Q9NYP9	Protein Mis18-alpha OS=Homo sapiens GN=MIS18A PE=1 SV=1 - [MS18A_HUMAN]	4.72	1	1	1	1	1.000	1		2.354	233	25.846
E9B1P5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_0980 PE=4 SV=1 - [E9B1P5_LEIMU]	1.17	1	1	1	1	1.155	1		2.353	770	83.774
Q99735	Microsomal glutathione S-transferase 2 OS=Homo sapiens GN=MGST2 PE=1 SV=1 - [MGST2_HUMAN]	9.52	1	1	1	1	1.314	1		2.351	147	16.610
A0A024R5P7	Chromosome 1 open reading frame 71, isoform CRA_c OS=Homo sapiens GN=C1orf71 PE=4 SV=1 - [A0A024R5P7_HUMAN]	1.46	3	1	1	1	0.739	1		2.351	616	67.473
G3V5E4	Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens GN=GNPNAT1 PE=1 SV=1 - [G3V5E4_HUMAN]	9.73	3	1	1	1	1.249	1		2.351	113	12.968
Q8TE92	cDNA FLJ23782 fis, clone HEP20947 OS=Homo sapiens PE=2 SV=1 - [Q8TE92_HUMAN]	1.89	5	1	1	1	1.021	1		2.350	424	47.663
B3KNP5	cDNA FLJ30100 fis, clone BNGH41000104, highly similar to Leucine-rich repeat serine/threonine-protein kinase 1 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B3KNF	2	1	1	1	1	1.000	1		2.350	501	55.441
E9B4V5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1310 PE=4 SV=1 - [E9B4V5_LEIMU]	2.15	1	1	1	1	1.000	1		2.350	1114	121.699
C9J6G3	Geranylgeranyl pyrophosphate synthase (Fragment) OS=Homo sapiens GN=GGPS1 PE=1 SV=1 - [C9J6G3_HUMAN]	3.04	3	1	1	1	1.626	1		2.350	230	26.615
O94933	SLIT and NTRK-like protein 3 OS=Homo sapiens GN=SLITRK3 PE=2 SV=2 - [SLIK3_HUMAN]	0.72	1	1	1	1	0.955	1		2.349	977	108.865
E9APD9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1150 PE=4 SV=1 - [E9APD9_LEIMU]	2.19	1	1	1	1	1.000	1		2.348	320	35.941
A6NMU3	Signal transducing adapter molecule 1 (Fragment) OS=Homo sapiens GN=STAM PE=1 SV=2 - [A6NMU3_HUMAN]	9.25	4	2	2	2	1.032	2	8.159	2.348	173	19.185
Q6PXP3	Solute carrier family 2, facilitated glucose transporter member 7 OS=Homo sapiens GN=SLC2A7 PE=2 SV=2 - [GTR7_HUMAN]	2.93	1	1	1	1	1.848	1		2.347	512	55.692
E9B1M5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_0740 PE=4 SV=1 - [E9B1M5_LEIMU]	3.63	1	1	1	1	1.000	1		2.345	331	36.591
K7ESB0	Centromere protein S (Fragment) OS=Homo sapiens GN=APITD1 PE=4 SV=1 - [K7ESB0_HUMAN]	13.16	4	1	1	1	1.953	1		2.344	76	8.885
A8K7S5	Katanin p60 ATPase-containing subunit A1 OS=Homo sapiens GN=KATNA1 PE=2 SV=1 - [A8K7S5_HUMAN]	1.83	2	1	1	1	3.037	1		2.344	491	55.941
Q9BXH1	Bcl-2-binding component 3 OS=Homo sapiens GN=BBC3 PE=1 SV=1 - [BBC3_HUMAN]	3.63	2	1	1	1	1.422	1		2.342	193	20.519
H0Y4S8	Dyslexia-associated protein KIAA0319-like protein (Fragment) OS=Homo sapiens GN=KIAA0319L PE=4 SV=1 - [H0Y4S8_HUMAN]	2.96	6	1	1	1	1.000	1		2.342	304	33.115
A8KAK5	cDNA FLJ77399, highly similar to Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa (CRSP2), mRNA OS=Homo sapiens PE=2 SV=1 -	2.27	6	2	3	3	0.994	2	0.884	2.342	1454	160.514
Q59EE6	Latent transforming growth factor beta binding protein 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EE6_HUMAN]	0.65	5	1	1	1	1.248	1		2.342	1700	181.691
B7ZW05	AKAP13 protein (Fragment) OS=Homo sapiens GN=AKAP13 PE=2 SV=1 - [B7ZW05_HUMAN]	1.29	4	1	1	1	2.199	1		2.340	1085	123.346
E9B0R4	Putative GTPase activating protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1350 PE=4 SV=1 - [E9B0R4_LEIMU]	1.48	1	1	1	1	1.150	1		2.340	607	65.502
E9B0S5	p1/s1 nuclease OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1510 PE=4 SV=1 - [E9B0S5_LEIMU]	2.22	1	1	1	1	1.000	1		2.340	316	35.186
D9DBT0	Mutant Allgrove syndrome protein (Fragment) OS=Homo sapiens GN=AAAS PE=4 SV=1 - [D9DBT0_HUMAN]	24.49	6	1	1	1	1.000	1		2.339	49	5.662
E9ASL3	Putative 40S ribosomal protein S18 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0930 PE=3 SV=1 - [E9ASL3_LEIMU]	6.54	1	1	1	1	4.216	1		2.339	153	17.357
F8VRX9	Protein asunder homolog (Fragment) OS=Homo sapiens GN=ASUN PE=1 SV=1 - [F8VRX9_HUMAN]	7.26	4	1	1	1				2.339	124	13.734
Q15527	Surfeit locus protein 2 OS=Homo sapiens GN=SURF2 PE=1 SV=3 - [SURF2_HUMAN]	4.69	1	1	1	1	1.000	1		2.338	256	29.629
Q53T81	Putative uncharacterized protein PAPOLG (Fragment) OS=Homo sapiens GN=PAPOLG PE=4 SV=1 - [Q53T81_HUMAN]	2.96	4	1	1	1	1.000	1		2.338	270	29.421
Q8IVL5	Prolyl 3-hydroxylase 2 OS=Homo sapiens GN=LEPREL1 PE=1 SV=1 - [P3H2_HUMAN]	2.12	1	1	1	1	1.000	1		2.337	708	80.933
A4FU39	KLHDC7A protein (Fragment) OS=Homo sapiens GN=KLHDC7A PE=2 SV=1 - [A4FU39_HUMAN]	1.72	3	1	1	1	0.585	1		2.335	583	64.033
Q9HB73	PNAS-104 OS=Homo sapiens PE=2 SV=1 - [Q9HB73_HUMAN]	28.33	2	1	1	1	1.000	1		2.335	60	7.077
A8K874	cDNA FLJ77588, highly similar to Homo sapiens MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae) (MAK10), mRNA OS=Homo sapiens PE=2 SV=	1.1	2	1	1	1	0.920	1		2.334	725	83.554
B7Z7B6	cDNA FLJ50270 OS=Homo sapiens PE=2 SV=1 - [B7Z7B6_HUMAN]	1.18	3	1	1	1	0.731	1		2.333	594	63.916
D6RAG0	DNA-directed RNA polymerase II subunit RPB11-b2 OS=Homo sapiens GN=POLR2J3 PE=4 SV=1 - [D6RAG0_HUMAN]	13.7	14	1	1	1	0.947	1		2.333	73	7.969
A0A087WYV8	Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=4 SV=1 - [A0A087WYV8_HUMAN]	1.55	2	2	2	2	1.000	1		2.331	2911	314.460
E9AYL8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_2370 PE=4 SV=1 - [E9AYL8_LEIMU]	1.31	1	2	2	2	0.746	1		2.331	3979	421.621
B4DP94	cDNA FLJ59828, highly similar to Regulator of G-protein signaling 19 OS=Homo sapiens PE=2 SV=1 - [B4DP94_HUMAN]	5.64	3	1	1	1	1.423	1		2.331	195	22.222
F2Z2F3	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [F2Z2F3_HUMAN]	6.29	6	1	1	1	1.093	1		2.330	143	15.635
E9ARN6	UTP-glucose-1-phosphate uridylyltransferase 2,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0990 PE=4 SV=1 - [E9ARN6_LEIMU]	2.23	1	1	1	2	1.761	2	101.083	2.330	494	54.410
B3KMU4	cDNA FLJ12640 fis, clone NT2RM4001940, highly similar to Timeless homolog OS=Homo sapiens PE=2 SV=1 - [B3KMU4_HUMAN]	2.7	3	1	1	1	1.000	1		2.328	481	54.483
K7EM84	UPF0711 protein C18orf21 (Fragment) OS=Homo sapiens GN=C18orf21 PE=1 SV=3 - [K7EM84_HUMAN]	10.11	4	1	1	1	0.906	1		2.327	89	9.590
E9AMG5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0910 PE=4 SV=1 - [E9AMG5_LEIMU]	0.43	1	1	1	1	1.197	1		2.327	2108	220.770
Q6NTF9	Rhomboid domain-containing protein 2 OS=Homo sapiens GN=RHBDD2 PE=2 SV=2 - [RHBD2_HUMAN]	2.47	1	1	1	1	0.962	1		2.326	364	39.177
Q66K64	DDB1- and CUL4-associated factor 15 OS=Homo sapiens GN=DCAF15 PE=1 SV=1 - [DCA15_HUMAN]	2	1	1	1	1	1.000	1		2.326	600	66.421
E9APC8	Subtilisin-like serine peptidase (Serine peptidase, clan sb, family s8-like protein) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1040 PE=4 S	0.57	1	1	1	1	1.000	1		2.326	1761	186.229
M4VSD8	Apolipoprotein B editing enzyme catalytic polypeptide-like 3G OS=Homo sapiens GN=APOBEC3G PE=2 SV=1 - [M4VSD8_HUMAN]	1.57	5	1	1	1	0.529	1		2.323	382	46.188
E9AMF6	Complete genome, chromosome 8 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0801 PE=4 SV=1 - [E9AMF6_LEIMU]	2.82	2	1	1	1				2.322	355	39.007
H7C5V1	THUMP domain-containing protein 2 (Fragment) OS=Homo sapiens GN=THUMPD2 PE=4 SV=1 - [H7C5V1_HUMAN]	2.75	3	1	1	2	0.516	1		2.322	291	34.107
B9EH02	FLJ44653 protein OS=Homo sapiens GN=FLJ44653 PE=2 SV=1 - [B9EH02_HUMAN]	8.06	1	1	1	1	0.830	1		2.321	124	12.685
E9AVE8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1568 PE=4 SV=1 - [E9AVE8_LEIMU]	7.53	1	1	1	1	0.726	1		2.321	146	15.403
G4XUV3	Hydroxypyruvate isomerase OS=Homo sapiens PE=2 SV=1 - [G4XUV3_HUMAN]	12.44	6	2	2	2	1.295	2	32.481	2.321	217	23.964
B4DWW6	cDNA FLJ53934, highly similar to Homo sapiens RNA pseudouridylate synthase domain containing 2 (RPUSD2), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DWW6_HU	1.72	3	1	1	1	1.000	1		2.320	524	59.182
B4DWX9	cDNA FLJ58293, highly similar to Monocarboxylate transporter 2 OS=Homo sapiens PE=2 SV=1 - [B4DWX9_HUMAN]	2.9	2	1	1	1	1.000	1		2.319	379	41.678
F5GX58	Cell division cycle-associated protein 3 OS=Homo sapiens GN=CDCA3 PE=1 SV=1 - [F5GX58_HUMAN]	9.34	5	1	1	1	1.000	1		2.318	182	19.457
Q8IYA2	Putative coiled-coil domain-containing protein 144C OS=Homo sapiens GN=CCDC144CP PE=5 SV=3 - [C144C_HUMAN]	1.21	8	1	2	2	0.864	1		2.317	1237	143.023
E9B4W3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1390 PE=4 SV=1 - [E9B4W3_LEIMU]	0.23	1	1	1	1	1.000	1		2.317	4795	520.575
Q8NFV4	Alpha/beta hydrolase domain-containing protein 11 OS=Homo sapiens GN=ABHD11 PE=2 SV=1 - [ABHDB_HUMAN]	5.71	6	2	2	2	0.918	2	12.683	2.316	315	34.668
Q9NYG2	Palmitoyltransferase ZDHHC3 OS=Homo sapiens GN=ZDHHC3 PE=1 SV=2 - [ZDHC3_HUMAN]	3.68	1	1	1	1	1.211	1		2.316	299	34.147
O95235	Kinesin-like protein KIF20A OS=Homo sapiens GN=KIF20A PE=1 SV=1 - [KI20A_HUMAN]	0.79	1	1	1	1	3.056	1		2.315	890	100.215
E9APX8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1310 PE=4 SV=1 - [E9APX8_LEIMU]	2.2	1	1	1	1	0.706	1		2.315	363	38.698
Q6NSJ2	Pleckstrin homology-like domain family B member 3 OS=Homo sapiens GN=PHLDB3 PE=2 SV=3 - [PHLB3_HUMAN]	1.09	1	1	1	1	0.686	1		2.315	640	71.867
E9ARY4	Intraflagellar transport protein component,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0320 PE=4 SV=1 - [E9ARY4_LEIMU]	1.79	1	1	1	1				2.314	672	73.340
B7ZW82	GTF2H2C protein OS=Homo sapiens GN=GTF2H2C PE=2 SV=1 - [B7ZW82_HUMAN]	5.92	10	2	2	2	0.916	2	2.691	2.314	338	37.571
P05161	Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5 - [ISG15_HUMAN]	4.24	1	1	1	1	1.004	1		2.313	165	17.876
B7Z553	cDNA FLJ51266, highly similar to Vitronectin OS=Homo sapiens PE=2 SV=1 - [B7Z553_HUMAN]	3.74	2	1	1	1	1.617	1		2.312	214	23.590
Q6IQ43	PTPN9 protein OS=Homo sapiens GN=PTPN9 PE=2 SV=1 - [Q6IQ43_HUMAN]	3.77	3	2	2	2	0.955	2	6.811	2.312	583	66.971
H0YGE5	DENN domain-containing protein 5B (Fragment) OS=Homo sapiens GN=DENND5B PE=4 SV=1 - [H0YGE5_HUMAN]	1.3	3	1	1	1	0.987	1		2.310	537	61.798
Q9NYL2	Mitogen-activated protein kinase kinase kinase MLT OS=Homo sapiens GN=ZAK PE=1 SV=3 - [MLTK_HUMAN]	2.88	1	1	2	3	1.000	1		2.309	800	91.098
A0A024RCC2	HCG1640777, isoform CRA_b (Fragment) OS=Homo sapiens GN=hCG_1640777 PE=4 SV=1 - [A0A024RCC2_HUMAN]	4.44	3	1	1	1	0.856	1		2.309	225	23.474

B4E1D8	cDNA FLJ51597, highly similar to C4b-binding protein alpha chain OS=Homo sapiens PE=2 SV=1 - [B4E1D8_HUMAN]	1.49	3	1	1	1	1.755	1		2.309	536	60.366
E9ASY9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2120 PE=4 SV=1 - [E9ASY9_LEIMU]	0.46	1	1	1	1	1.000	1		2.307	1525	158.864
B9EGR5	MGA protein OS=Homo sapiens GN=MGA PE=2 SV=1 - [B9EGR5_HUMAN]	0.32	2	1	1	1	2.689	1		2.307	2856	314.940
H0YKJ9	Tetraspanin-3 OS=Homo sapiens GN=TSPAN3 PE=4 SV=1 - [H0YKJ9_HUMAN]	4.27	3	1	1	1	1.000	1		2.305	164	18.337
Q8NGM0	Seven transmembrane helix receptor OS=Homo sapiens PE=4 SV=1 - [Q8NGM0_HUMAN]	2.99	3	1	1	1	2.055	1		2.305	301	33.557
E9ATS2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4890 PE=4 SV=1 - [E9ATS2_LEIMU]	3.19	1	1	1	1	0.931	1		2.304	313	34.463
P0C867	Putative uncharacterized protein LOC100130201 OS=Homo sapiens PE=5 SV=1 - [YB052_HUMAN]	5.83	1	1	1	1	1.459	1		2.303	120	13.318
H0YC06	PWWP domain-containing protein 2A (Fragment) OS=Homo sapiens GN=PWWP2A PE=4 SV=1 - [H0YC06_HUMAN]	15.94	2	1	1	1	1.000	1		2.303	69	7.948
B7Z9V2	cDNA, FLJ78966, highly similar to Homo sapiens RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B7.	0.93	1	1	1	1	0.670	1		2.302	749	85.165
B4E0X0	cDNA FLJ53844, highly similar to DNA-repair protein complementing XP-G cells OS=Homo sapiens PE=2 SV=1 - [B4E0X0_HUMAN]	3.5	7	1	1	1	1.000	1		2.302	429	47.343
D3DT44	Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=4 SV=1 - [D3DT44_HUMAN]	8.27	2	2	2	2	0.650	2	58.399	2.301	254	28.598
B4DR12	G-protein-coupled receptor 84 OS=Homo sapiens GN=GPR84 PE=2 SV=1 - [B4DR12_HUMAN]	8.13	8	2	2	2	1.375	2	32.061	2.301	320	36.159
Q9H6N6	cDNA: FLJ22037 fis, clone HEP08868 (Fragment) OS=Homo sapiens GN=MYH16 PE=2 SV=1 - [Q9H6N6_HUMAN]	1.47	1	1	1	1	1.140	1		2.300	746	86.940
E9ASX3	Putative serine/threonine protein phosphatase 2B catalytic subunit A2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1980 PE=4 SV=1 - [E9A	1.72	1	1	1	1	1.000	1		2.299	407	45.060
E9AML9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0200 PE=4 SV=1 - [E9AML9_LEIMU]	2.43	1	1	1	1	0.893	1		2.299	493	52.436
E9B2Z5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2150 PE=4 SV=1 - [E9B2Z5_LEIMU]	1.66	1	1	1	1	1.000	1		2.299	1082	117.446
Q86YG2	Similar to expressed sequence AI449432 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q86YG2_HUMAN]	3.38	3	1	1	1	1.000	1		2.298	622	68.878
J3KQY4	Transcription elongation factor A protein-like 4 (Fragment) OS=Homo sapiens GN=TCEAL4 PE=1 SV=1 - [J3KQY4_HUMAN]	22	7	1	1	1	1.000	1		2.297	50	5.815
E9AQM3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0640 PE=4 SV=1 - [E9AQM3_LEIMU]	1.09	1	1	1	1	1.115	1		2.297	640	68.253
Q96A46	Mitoferrin-2 OS=Homo sapiens GN=SLC25A28 PE=2 SV=1 - [MFRN2_HUMAN]	4.12	1	1	1	1	1.367	1		2.296	364	39.247
E9APH9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1550 PE=4 SV=1 - [E9APH9_LEIMU]	2.37	2	1	2	2	1.000	1		2.296	1182	124.440
E9ATR0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4760 PE=4 SV=1 - [E9ATR0_LEIMU]	1.4	1	1	1	1	0.893	1		2.295	645	71.168
C9JWF7	SRSF protein kinase 2 (Fragment) OS=Homo sapiens GN=SRPK2 PE=1 SV=1 - [C9JWF7_HUMAN]	4.33	1	1	1	1	0.980	1		2.295	231	25.848
E9AVE2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1555 PE=4 SV=1 - [E9AVE2_LEIMU]	2.28	1	1	1	2	1.000	2	0.000	2.294	395	46.545
Q9NPP4	NLR family CARD domain-containing protein 4 OS=Homo sapiens GN=NLRC4 PE=1 SV=2 - [NLRC4_HUMAN]	0.68	1	1	1	1	0.600	1		2.294	1024	116.085
Q7Z4Q2	HEAT repeat-containing protein 3 OS=Homo sapiens GN=HEATR3 PE=1 SV=2 - [HEAT3_HUMAN]	1.32	1	1	1	1	1.000	1		2.293	680	74.535
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3 - [DDAH1_HUMAN]	2.46	1	1	1	4	0.466	2	30.624	2.293	285	31.102
B7ZMI2	ARAP1 protein OS=Homo sapiens GN=ARAP1 PE=2 SV=1 - [B7ZMI2_HUMAN]	3.69	4	3	3	3	1.000	3	8.288	2.292	1194	134.621
Q0VF96	Cingulin-like protein 1 OS=Homo sapiens GN=CGNL1 PE=1 SV=2 - [CGNL1_HUMAN]	0.84	1	1	1	1	1.000	1		2.291	1302	148.989
E9AJK8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0460 PE=4 SV=1 - [E9AJK8_LEIMU]	2.75	1	1	1	1	2.959	1		2.290	291	31.944
Q9H8P0	Polyprenol reductase OS=Homo sapiens GN=SRD5A3 PE=1 SV=1 - [PORED_HUMAN]	5.66	2	2	2	2	1.228	2	2.623	2.290	318	36.497
A0A024R853	IQ motif containing E, isoform CRA_b OS=Homo sapiens GN=IQCE PE=4 SV=1 - [A0A024R853_HUMAN]	1.43	8	1	1	1	1.000	1		2.290	630	70.252
Q8WYK8	Sodium/hydrogen exchanger (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8WYK8_HUMAN]	2.67	2	1	1	1	1.000	1		2.289	374	41.437
A0A087X1P1	Protein LOC102725453 OS=Homo sapiens GN=LOC102725453 PE=4 SV=1 - [A0A087X1P1_HUMAN]	3.24	2	1	1	1	1.000	1		2.289	555	58.519
Q13571	Lysosomal-associated transmembrane protein 5 OS=Homo sapiens GN=LAPTM5 PE=1 SV=1 - [LAPM5_HUMAN]	3.44	3	1	1	1	1.000	1		2.289	262	29.917
Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 - [TOPK_HUMAN]	2.17	1	1	1	1	0.929	1		2.287	322	36.062
H0UI53	HD domain containing 2, isoform CRA_a OS=Homo sapiens GN=HDDC2 PE=4 SV=1 - [H0UI53_HUMAN]	13.13	3	1	1	3	1.000	3	0.000	2.287	99	11.439
B2RTQ5	LRRC16A protein OS=Homo sapiens GN=LRRC16A PE=2 SV=1 - [B2RTQ5_HUMAN]	0.88	2	1	1	1	1.000	1		2.287	1365	150.821
E9B5H5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3820 PE=4 SV=1 - [E9B5H5_LEIMU]	2.42	1	1	1	1	0.715	1		2.286	289	31.575
B3KV47	cDNA FLJ16122 fis, clone BLADE2008995 OS=Homo sapiens PE=2 SV=1 - [B3KV47_HUMAN]	3.05	4	1	1	1	1.000	1		2.286	361	40.838
B2RAT1	cDNA, FLJ95092, highly similar to Homo sapiens TRIAD3 protein (TRIAD3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAT1_HUMAN]	2.25	5	1	1	1	1.000	1		2.285	488	56.688
E9PSC3	Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens GN=C11orf54 PE=1 SV=3 - [E9PSC3_HUMAN]	7.29	10	1	1	1	1.040	1		2.285	96	10.431
B3KX94	cDNA FLJ44997 fis, clone BRAWH3010726, highly similar to Membrane-associated phosphatidylinositol transfer protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KX94_HU	4.37	3	1	1	1	1.000	1		2.285	526	57.717
E9PRQ4	NADH dehydrogenase [ubiquinone] 1 subunit C2, isoform 2 OS=Homo sapiens GN=NDUFC2-KCTD14 PE=1 SV=1 - [E9PRQ4_HUMAN]	33.33	7	1	2	2				2.283	66	7.481
E9AR11	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0420 PE=4 SV=1 - [E9AR11_LEIMU]	1.62	1	1	1	1	1.000	1		2.283	556	61.723
Q96ES7	SAGA-associated factor 29 homolog OS=Homo sapiens GN=CCDC101 PE=1 SV=1 - [SGF29_HUMAN]	4.44	1	1	1	1	1.066	1		2.282	293	33.217
H7C5J7	TPA-induced transmembrane protein (Fragment) OS=Homo sapiens GN=C3orf52 PE=4 SV=1 - [H7C5J7_HUMAN]	5.81	1	1	1	1	1.129	1		2.280	241	26.748
Q5UCC4	ER membrane protein complex subunit 10 OS=Homo sapiens GN=EMC10 PE=1 SV=1 - [EMC10_HUMAN]	3.05	2	1	1	2	1.656	2	128.592	2.280	262	27.330
B4DV06	cDNA FLJ55904, highly similar to Homo sapiens leucine rich repeat and coiled-coil domain containing 1 (LRRCC1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [l	1.6	2	1	1	1	1.096	1		2.278	751	87.352
E9AVK4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0210 PE=4 SV=1 - [E9AVK4_LEIMU]	0.59	1	1	1	1	1.000	1		2.278	1537	171.905
E9AKV9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0810 PE=4 SV=1 - [E9AKV9_LEIMU]	0.21	1	1	1	1	0.914	1		2.277	3269	345.803
K7EQ71	Periplakin (Fragment) OS=Homo sapiens GN=PPL PE=1 SV=1 - [K7EQ71_HUMAN]	0.81	3	1	1	1	1.000	1		2.276	1115	131.296
Q7Z7A3	Cytoplasmic tRNA 2-thiolation protein 1 OS=Homo sapiens GN=CTU1 PE=1 SV=1 - [CTU1_HUMAN]	4.31	1	1	1	1	0.686	1		2.276	348	36.427
E9B5V1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0710 PE=4 SV=1 - [E9B5V1_LEIMU]	2.64	1	1	1	1	1.000	1		2.276	531	59.823
A0A024R637	TBC1 domain family, member 4, isoform CRA_b OS=Homo sapiens GN=TBC1D4 PE=4 SV=1 - [A0A024R637_HUMAN]	0.46	2	1	1	1	0.796	1		2.276	1298	146.457
Q6T774	Cytosolic phospholipase A2 gamma OS=Homo sapiens GN=KLK2 PE=2 SV=1 - [Q6T774_HUMAN]	38.78	1	1	1	1	1.180	1		2.275	49	5.063
A0JNU9	TBC1 domain family member 1 OS=Homo sapiens GN=TBC1D1 PE=2 SV=1 - [A0JNU9_HUMAN]	2.55	5	1	1	1	1.000	1		2.275	432	50.001
E9APV7	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1110 PE=3 SV=1 - [E9APV7_LEIMU]	1.73	1	1	1	1	0.697	1		2.274	2307	254.231
B4DHJ7	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 OS=Homo sapiens GN=BNIP3 PE=1 SV=1 - [B4DHJ7_HUMAN]	5	5	1	1	1	1.000	1		2.274	180	19.931
E9ASN8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1180 PE=4 SV=1 - [E9ASN8_LEIMU]	2.99	1	1	1	1	1.000	1		2.273	334	35.883
E9PLD2	Mitochondrial fission regulator 1-like OS=Homo sapiens GN=MTFR1L PE=1 SV=1 - [E9PLD2_HUMAN]	3.59	4	1	1	1	1.099	1		2.273	195	21.178
H7C1N4	Protein shisa-7 (Fragment) OS=Homo sapiens GN=SHISA7 PE=4 SV=1 - [H7C1N4_HUMAN]	4.58	2	1	1	1	1.143	1		2.271	153	15.813
K7ERC8	3-ketodihydrosphingosine reductase (Fragment) OS=Homo sapiens GN=KDSR PE=3 SV=1 - [K7ERC8_HUMAN]	3.94	2	1	1	1	0.889	1		2.271	203	22.606
B7ZM61	Phosphoinositide phospholipase C OS=Homo sapiens GN=PLCE1 PE=2 SV=1 - [B7ZM61_HUMAN]	0.7	2	1	1	1	1.000	1		2.271	2286	256.941
B2R762	cDNA, FLJ93300, highly similar to Homo sapiens interferon regulatory factor 6 (IRF6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R762_HUMAN]	1.93	2	1	1	1	1.127	1		2.270	467	53.113
H7C529	PX domain-containing protein kinase-like protein (Fragment) OS=Homo sapiens GN=PXK PE=4 SV=1 - [H7C529_HUMAN]	24	11	1	1	1	1.000	1		2.269	50	5.157
I3L3C6	Coiled-coil domain-containing protein 43 (Fragment) OS=Homo sapiens GN=CCDC43 PE=4 SV=1 - [I3L3C6_HUMAN]	4.17	7	1	1	1	1.692	1		2.266	216	23.496
Q8N9V2	Probable E3 ubiquitin-protein ligase TRIML1 OS=Homo sapiens GN=TRIML1 PE=1 SV=1 - [TRIML_HUMAN]	2.14	1	1	1	1	0.938	1		2.265	468	52.968
B7Z6Q2	Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 - [B7Z6Q2_HUMAN]	5.93	1	1	1	1	2.098	1		2.265	135	15.042
H7BYJ3	Citron Rho-interacting kinase (Fragment) OS=Homo sapiens GN=CIT PE=1 SV=1 - [H7BYJ3_HUMAN]	0.61	2	2	2	2	1.000	2	0.000	2.264	1640	187.297
Q96DC9	Ubiquitin thioesterase OTUB2 OS=Homo sapiens GN=OTUB2 PE=1 SV=2 - [OTUB2_HUMAN]	2.99	1	1	1	4	1.000	2	0.000	2.264	234	27.196
E9B3W9	Cysteine conjugate beta-lyase,aminotransferase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1330 PE=4 SV=1 - [E9B3W9_LE	2.17	1	1	1	1	1.753	1		2.263	414	46.094
B4E2E8	cDNA FLJ61546 OS=Homo sapiens PE=2 SV=1 - [B4E2E8_HUMAN]	2.31	3	1	1	1	1.000	1		2.263	477	53.479
Q92560	Ubiquitin carboxyl-terminal hydrolase BAP1 OS=Homo sapiens GN=BAP1 PE=1 SV=2 - [BAP1_HUMAN]	1.92	1	1	1	1	1.002	1		2.263	729	80.312
E9AK25	Serine/threonine protein kinase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0440 PE=4 SV=1 - [E9AK25_LEIMU]	1.07	1	1	1	1	1.075	1		2.261	1311	138.748
E9B089	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2660 PE=4 SV=1 - [E9B089_LEIMU]	6.16	1	1	1	1	1.000	1		2.261	146	16.559
Q8TD98	MLL/AF4 fusion protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TD98_HUMAN]	3.69	27	1	2	2	1.096	1		2.259	624	68.146
B3KXS7	cDNA FLJ45975 fis, clone PLACE7018479, highly similar to 182 kDa tankyrase 1-binding protein OS=Homo sapiens PE=2 SV=1 - [B3KXS7_HUMAN]	1.02	2	1	1	1	0.705	1		2.259	1075	113.270
E9B187	Putative valyl-tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3130 PE=3 SV=1 - [E9B187_LEIMU]	0.72	1	1	1	1	1.913	1		2.259	967	109.717
B2R7X3	cDNA, FLJ93645, highly similar to Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B),mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7X3_HUMAN]	1.79	2	1	1	1	0.911	1		2.258	559	61.480
D6RAI0	Embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein (Fragment) OS=Homo sapiens GN=HMCES PE=1 SV=1 - [D6RAI0_HUMAN]	5	7	1	1	1	1.000	1		2.257	140	15.966
E9AZJ9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_0380 PE=4 SV=1 - [E9AZJ9_LEIMU]	2.81	1	1	1	1	1.000	1		2.257	392	41.800
J3QLF3	Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens GN=DRG2 PE=1 SV=1 - [J3QLF3_HUMAN]	8.89	10	1	1	1	0.928	1		2.256	90	9.829
Q9UP76	Rh50 (Fragment) OS=Homo sapiens GN=RH50 PE=4 SV=1 - [Q9UP76_HUMAN]	24.51	1	1	1	1	1.000	1		2.256	102	11.218
E9B352	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2730 PE=4 SV=1 - [E9B352_LEIMU]	1.89	1	1	1	1	1.000	1		2.256	1004	107.420
Q9BSF4	Uncharacterized protein C19orf52 OS=Homo sapiens GN=C19orf52 PE=1 SV=2 - [CS052_HUMAN]	2.69	1	1	1	1	1.019	1		2.255	260	29.215
A0A087WVD1	Leukocyte receptor cluster member 9 OS=Homo sapiens GN=LENG9 PE=4 SV=1 - [A0A087WVD1_HUMAN]	1.88	2	1	1	1	1.000	1		2.255	478	50.735
H9KV50	Selenoprotein N OS=Homo sapiens GN=SEPN1 PE=4 SV=1 - [H9KV50_HUMAN]	2.88	2	1	1	2	1.000	1		2.254	556	62.027
P22083	Alpha-(1,3)-fucosyltransferase 4 OS=Homo sapiens GN=FUT4 PE=1 SV=3 - [FUT4_HUMAN]	3.4	1	2	2	2	0.633	2	47.834	2.254	530	59.047
Q9BV81	ER membrane protein complex subunit 6 OS=Homo sapiens GN=EMC6 PE=1 SV=1 - [EMC6_HUMAN]	9.09	1	1	1	1	1.201	1		2.253	110	12.010
E9AN79	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0690 PE=4 SV=1 - [E9AN79_LEIMU]	0.66	1	1	1	1	1.000	1		2.252	1677	177.822
E9AY54	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0750 PE=4 SV=1 - [E9AY54_LEIMU]	1.09	2	1	2	2	1.233	1		2.252	1743	183.094
Q53QN0	Putative uncharacterized protein GTF3C2 (Fragment) OS=Homo sapiens GN=GTF3C2 PE=4 SV=1 - [Q53QN0_HUMAN]	4.87	3	2	2	3	0.898	3	18.610	2.252	534	58.421
A0A087WXN0	Uncharacterized protein KIAA1683 OS=Homo sapiens GN=KIAA1683 PE=4 SV=1 - [A0A087WXN0_HUMAN]	2.02	3	1	1	1	1.000	1		2.251	794	86.978
L7P8G6	Methylenetetrahydrofolate reductase OS=Homo sapiens GN=MTHFR PE=2 SV=1 - [L7P8G6_HUMAN]	1.7	3	1	1	1	1.000	1		2.250	411	47.334
G5E953	Myotubularin related protein 3, isoform CRA_e OS=Homo sapiens GN=MTMR3 PE=1 SV=1 - [G5E953_HUMAN]	1.22	5	1	1	1	1.000	1		2.248	1062	117.495
E9AYK8	Putative nitrilase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_2280 PE=4 SV=1 - [E9AYK8_LEIMU]	2.51	1	1	1	1	2.437	1		2.246	279	31.081
E9AVA0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1160 PE=4 SV=1 - [E9AVA0_LEIMU]	0.72	1	1	1	1	0.481	1		2.245	1105	113.676
H0Y915	Tetratricopeptide repeat protein 37 (Fragment) OS=Homo sapiens GN=TTC37 PE=4 SV=1 - [H0Y915_HUMAN]	24.24	3	1	1	2	0.337	1		2.243	33	3.717
Q6ZU65	Ubinuclein-2 OS=Homo sapiens GN=UBN2 PE=1 SV=2 - [UBN2_HUMAN]	0.82	1	1	1	1	1.000	1		2.243	1347	145.998
K7EIJ2	Mothers against decapentaplegic homolog 4 (Fragment) OS=Homo sapiens GN=SMAD4 PE=1 SV=1 - [K7EIJ2_HUMAN]	9.29	7	1	1	1	1.000	1		2.243	140	15.892
H0UI63	Zinc finger, NFX1-type containing 1, isoform CRA_b OS=Homo sapiens GN=ZNFX1 PE=4 SV=1 - [H0UI63_HUMAN]	2.14	7	4	4	5	1.000	5	0.000	2.242	1918	220.105
E9AX02	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1570 PE=4 SV=1 - [E9AX02_LEIMU]	1.01	1	1	1	1	0.757	1		2.241	696	72.616
Q9BRX5	DNA replication complex GINS protein PSF3 OS=Homo sapiens GN=GINS3 PE=1 SV=1 - [PSF3_HUMAN]	6.94	1	1	1	3	1.061	3	8.838	2.241	216	24.519
Q9NP62	Chorion-specific transcription factor GCMa OS=Homo sapiens GN=GCM1 PE=2 SV=1 - [GCM1_HUMAN]	2.06	1	1	1	1	2.975	1		2.240	436	49.237
K7EN58	Biogenesis of lysosome-related organelles complex 1 subunit 3 (Fragment) OS=Homo sapiens GN=BLOC1S3 PE=4 SV=1 - [K7EN58_HUMAN]	11.54	2	1	1	1	0.942	1		2.237	78	7.866
E9B545	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2540 PE=4 SV=1 - [E9B545_LEIMU]	1.04	1	1	1	1	0.715	1		2.237	869	100.083
G3V2R9	Prostaglandin reductase 2 OS=Homo sapiens GN=PTGR2 PE=1 SV=1 - [G3V2R9_HUMAN]	3.69	2	1	1	1	0.832	1		2.237	217	23.365
L7RER4	C-C chemokine receptor type 2 (Fragment) OS=Homo sapiens GN=CCR2 PE=3 SV=1 - [L7RER4_HUMAN]	4.15	4	1	1	1	1.000	1		2.236	313	35.684
Q86XZ4	Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens GN=SPATS2 PE=1 SV=1 - [SPAS2_HUMAN]	2.02	1	1	1	1	0.379	1		2.235	545	59.508
P62891	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]	19.61	2	1	1	1	0.855	1		2.234	51	6.403
E9AKH1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0650 PE=4 SV=1 - [E9AKH1_LEIMU]	2.11	1	1	1	1	1.000	1		2.233	854	90.795
A0A087WUL7	Nuclear receptor-binding factor 2 OS=Homo sapiens GN=NRBF2 PE=4 SV=1 - [A0A087WUL7_HUMAN]	7.33	2	2	2	2	0.922	1		2.233	273	31.467
Q59H56	Pre-mRNA splicing factor 17 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H56_HUMAN]	5.79	6	3	3	3	0.976	3	5.449	2.233	501	56.659
E9AYV1	Putative calpain-like cysteine peptidase (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0490 PE=4 SV=1 - [E9AYV1_LEIMU]	1.7	1	1	1	1	1.000	1		2.232	2355	268.888
H3BMP1	Paraplegin (Fragment) OS=Homo sapiens GN=SPG7 PE=4 SV=1 - [H3BMP1_HUMAN]	9.16	3	2	2	2	1.790	2	105.143	2.232	131	15.096
X5DP08	Tuberous sclerosis 2 isoform N (Fragment) OS=Homo sapiens GN=TSC2 PE=2 SV=1 - [X5DP08_HUMAN]	8.49	9	1	1	1	1.000	1		2.231	212	23.716
E9AVM7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0440 PE=4 SV=1 - [E9AVM7_LEIMU]	0.54	1	1	1	1	0.956	1		2.230	1286	140.417
H0Y8S6	Cytochrome c oxidase subunit 7A2, mitochondrial (Fragment) OS=Homo sapiens GN=COX7A2 PE=4 SV=1 - [H0Y8S6_HUMAN]	8.96	8	1	1	3	0.993	2	1.238	2.229	67	7.703
B7Z7P7	cDNA FLJ51397 OS=Homo sapiens PE=2 SV=1 - [B7Z7P7_HUMAN]	2.64	2	1	1	1	1.000	1		2.229	303	34.160
B4DEZ9	cDNA FLJ60453, highly similar to Proprotein convertase subtilisin/kexin type 9 (EC 3.4.21.-) OS=Homo sapiens PE=2 SV=1 - [B4DEZ9_HUMAN]	5.37	2	1	1	1	1.082	1		2.229	205	23.124
E9AP97	Ubiquitin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0730 PE=4 SV=1 - [E9AP97_LEIMU]	0.85	1	1	1	1	1.000	1		2.228	827	87.970
B4DN11	cDNA FLJ54270 OS=Homo sapiens PE=2 SV=1 - [B4DN11_HUMAN]	5.71	4	1	1	1	1.018	1		2.228	140	16.085
R4GN18	Membrane cofactor protein (Fragment) OS=Homo sapiens GN=CD46 PE=4 SV=1 - [R4GN18_HUMAN]	10.26	1	1	1	1				2.227	78	8.496
E9B270	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2715 PE=4 SV=1 - [E9B270_LEIMU]	5.48	1	1	1	1	1.000	1		2.227	146	16.392
Q9Y2S0	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Homo sapiens GN=POLR1D PE=1 SV=1 - [RPAC2_HUMAN]	8.27	1	1	1	1	0.741	1		2.226	133	15.227
Q5TEV0	Rho guanine nucleotide exchange factor 19 (Fragment) OS=Homo sapiens GN=ARHGEF19 PE=4 SV=1 - [Q5TEV0_HUMAN]	4.19	2	1	1	1	0.873	1		2.226	167	18.658
F5GXL6	Probable ATP-dependent RNA helicase DDX11 (Fragment) OS=Homo sapiens GN=DDX11 PE=4 SV=3 - [F5GXL6_HUMAN]	6.25	1	1	1	1	1.000	1		2.225	192	21.470
S4R302	Glucose-fructose oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=GFOD1 PE=1 SV=1 - [S4R302_HUMAN]	6.76	2	1	1	1	1.000	1		2.224	148	16.324
E9ALC0	Peptidyl-prolyl cis-trans isomerase/rotamase,putative (Putative ppiase) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_1030 PE=4 SV=1 - [E9	6.96	1	1	1	1	1.000	1		2.224	115	12.677
D3DVC4	Nestin, isoform CRA_c OS=Homo sapiens GN=NES PE=3 SV=1 - [D3DVC4_HUMAN]	0.86	2	1	1	1	1.000	1		2.224	1621	177.320
E9ASX1	Phosphomannomutase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1960 PE=3 SV=1 - [E9ASX1_LEIMU]	4.45	1	1	1	1	7.565	1		2.222	247	28.060
D6RJH2	Zinc finger protein 131 OS=Homo sapiens GN=ZNF131 PE=4 SV=1 - [D6RJH2_HUMAN]	4.35	5	1	1	1	1.000	1		2.222	253	28.549
E9ARZ1	Putative 40S ribosomal protein S13 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0390 PE=3 SV=1 - [E9ARZ1_LEIMU]	5.96	1	1	1	1	1.000	1		2.221	151	17.460
Q9HAF1	Chromatin modification-related protein MEAF6 OS=Homo sapiens GN=MEAF6 PE=1 SV=1 - [EAF6_HUMAN]	5.24	1	1	1	1	1.000	1		2.221	191	21.622
C9JKZ3	Transmembrane protease serine 2 (Fragment) OS=Homo sapiens GN=TMPRSS2 PE=3 SV=1 - [C9JKZ3_HUMAN]	2.86	3	1	1	1	1.000	1		2.219	489	53.581
J3KSL6	Period circadian protein homolog 1 (Fragment) OS=Homo sapiens GN=PER1 PE=4 SV=1 - [J3KSL6_HUMAN]	5.98	10	1	1	1	1.000	1		2.219	117	11.922
B7Z3V3	cDNA FLJ59556, highly similar to Tyrosine-protein phosphatase non-receptor type3 (EC 3.1.3.48) OS=Homo sapiens PE=2 SV=1 - [B7Z3V3_HUMAN]	2.08	4	1	1	1	1.000	1		2.218	626	70.934
O95559	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [O95559_HUMAN]	2.83	1	1	1	1	2.098	1		2.218	671	72.180
O43541	Mothers against decapentaplegic homolog 6 OS=Homo sapiens GN=SMAD6 PE=1 SV=2 - [SMAD6_HUMAN]	2.82	1	1	1	1	1.000	1		2.217	496	53.464
B4DUH2	cDNA FLJ51651, highly similar to Glucose-6-phosphate translocase OS=Homo sapiens PE=2 SV=1 - [B4DUH2_HUMAN]	2.81	10	1	1	1	1.403	1		2.217	356	38.204
B3KQS3	cDNA PSEC0114 fis, clone NT2RP2006543, highly similar to DI-N-ACETYLCHITOBIASE (EC 3.2.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KQS3_HUMAN]	3.4	4	1	1	1	0.353	1		2.215	294	33.517
Q8TCA8	Ankyrin repeat domain 5 OS=Homo sapiens GN=ANKRD5 PE=2 SV=1 - [Q8TCA8_HUMAN]	2.06	2	1	1	1	1.000	1		2.214	776	86.511
Q9ULM0	Pleckstrin homology domain-containing family H member 1 OS=Homo sapiens GN=PLEKHH1 PE=2 SV=2 - [PKHH1_HUMAN]	1.1	2	1	2	2	1.002	1		2.214	1364	151.137
Q53SB2	Putative uncharacterized protein RPIA (Fragment) OS=Homo sapiens GN=RPIA PE=4 SV=1 - [Q53SB2_HUMAN]	13.33	2	1	1	1	1.000	1		2.214	60	6.508
B2RMQ4	Cytoskeleton associated protein 2 OS=Homo sapiens GN=CKAP2 PE=2 SV=1 - [B2RMQ4_HUMAN]	1.17	2	1	1	1	0.919	1		2.213	682	76.838
E9AY65	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0870 PE=4 SV=1 - [E9AY65_LEIMU]	0.77	1	1	1	2	1.000	2	0.000	2.213	783	80.499
E9ATM8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4440 PE=4 SV=1 - [E9ATM8_LEIMU]	3.19	1	1	1	1	0.576	1		2.212	282	32.398
B4E0J9	cDNA FLJ57348, highly similar to Homo sapiens hexokinase domain containing 1 (HKDC1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4E0J9_HUMAN]	1.03	4	1	1	1	0.956	1		2.212	780	86.642
E9AYG2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1820 PE=4 SV=1 - [E9AYG2_LEIMU]	0.56	1	1	1	1	1.000	1		2.212	2303	237.156
R4GN39	Putative short-chain dehydrogenase/reductase family 42E member 2 (Fragment) OS=Homo sapiens GN=SDR42E2 PE=3 SV=1 - [R4GN39_HUMAN]	2.58	2	1	1	1	1.000	1		2.209	388	43.251
H3BUA7	Growth arrest-specific protein 8 (Fragment) OS=Homo sapiens GN=GAS8 PE=4 SV=1 - [H3BUA7_HUMAN]	10	10	1	1	1	0.868	1		2.209	60	7.285
Q5VV50	Zinc finger protein 691 OS=Homo sapiens GN=ZNF691 PE=1 SV=1 - [Q5VV50_HUMAN]	7.84	72	1	2	3				2.208	306	34.632
E9AXT9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_2070 PE=4 SV=1 - [E9AXT9_LEIMU]	1.47	1	1	1	1	0.879	1		2.207	543	58.451
A0A023HHL0	TET1 splice variant VP_DE4 OS=Homo sapiens PE=2 SV=1 - [A0A023HHL0_HUMAN]	0.86	3	1	1	1	1.238	1		2.206	694	75.556
A0A024RE18	Prominin 2, isoform CRA_a OS=Homo sapiens GN=PROM2 PE=4 SV=1 - [A0A024RE18_HUMAN]	1.8	3	1	1	1	1.000	1		2.205	834	91.853
D6R9W2	Glutathione S-transferase C-terminal domain-containing protein OS=Homo sapiens GN=GSTCD PE=4 SV=1 - [D6R9W2_HUMAN]	4.41	2	1	1	1	1.000	1		2.205	340	38.174
Q0GM93	P2X purinoceptor (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q0GM93_HUMAN]	5.69	6	1	1	1	1.011	1		2.203	123	14.046
B7Z7C0	cDNA FLJ53109, highly similar to Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform OS=Homo sapiens PE=2 SV=1 - [B7Z7C0_HUMAN	2.56	1	1	1	1	2.039	1		2.203	391	46.090
E9AWC0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1025 PE=4 SV=1 - [E9AWC0_LEIMU]	3.77	1	1	1	4	1.055	4	15.892	2.202	557	60.342
C9J2A2	Myotubularin (Fragment) OS=Homo sapiens GN=MTM1 PE=4 SV=1 - [C9J2A2_HUMAN]	11.65	3	1	1	1	0.859	1		2.202	103	11.903
F8WC38	Ribonuclease P protein subunit p40 OS=Homo sapiens GN=RPP40 PE=4 SV=1 - [F8WC38_HUMAN]	6.19	3	1	1	1	1.935	1		2.201	113	13.482
I3L2A4	NAD-dependent protein deacetylase sirtuin-7 OS=Homo sapiens GN=SIRT7 PE=4 SV=1 - [I3L2A4_HUMAN]	11.21	2	1	1	1	1.000	1		2.200	116	13.253
E9AYI7	Putative SUMO1/Ulp2 (Cysteine peptidase, clan ca, family c48,putative) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_2070 PE=4 SV=1 - [E	0.52	1	1	1	1	1.155	1		2.200	1348	143.643
E9AL81	Putative 40S ribosomal protein S9 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0680 PE=3 SV=1 - [E9AL81_LEIMU]	3.7	2	1	1	1	1.000	1		2.199	189	22.086
H0YGS7	Tripartite motif-containing protein 65 (Fragment) OS=Homo sapiens GN=TRIM65 PE=4 SV=1 - [H0YGS7_HUMAN]	6.15	2	1	1	1	1.580	1		2.198	244	27.088
Q9Y2Q5	Ragulator complex protein LAMTOR2 OS=Homo sapiens GN=LAMTOR2 PE=1 SV=1 - [LTOR2_HUMAN]	7.2	1	1	1	1	1.128	1		2.198	125	13.499
E9B075	Putative PIF1 helicase-like protein (Putative dna repair and recombination protein,mitochondrial) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_2	0.75	1	1	1	1	0.757	1		2.197	935	102.358
B3KUZ9	cDNA FLJ40997 fis, clone UTERU2016147, highly similar to Serine/threonine-protein kinase ULK2 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B3KUZ9_HUMAN]	0.63	3	1	1	1	0.913	1		2.196	952	102.980
Q9Y5A5	Putative kruppel-related zinc finger protein NY-REN-23 antigen (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9Y5A5_HUMAN]	2.38	3	1	1	1	1.331	1		2.196	547	62.029
A0A024R836	Uncharacterized protein (Fragment) OS=Homo sapiens GN=MGC11257 PE=4 SV=1 - [A0A024R836_HUMAN]	7.64	5	1	1	1	1.000	1		2.196	157	18.500
I3L3P9	Double C2-like domain-containing protein alpha (Fragment) OS=Homo sapiens GN=DOC2A PE=4 SV=1 - [I3L3P9_HUMAN]	92.31	4	1	1	1	0.973	1		2.196	13	1.482
B7Z8R4	cDNA FLJ51444, highly similar to ETS-related transcription factor Elf-2 OS=Homo sapiens PE=2 SV=1 - [B7Z8R4_HUMAN]	1.77	3	1	1	1	1.202	1		2.195	396	42.510
E9PJV3	RNA pseudouridylate synthase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=RPUSD4 PE=4 SV=2 - [E9PJV3_HUMAN]	6.25	3	1	1	1	1.121	1		2.194	176	19.363
A0A087WUD3	Oligosaccharyltransferase complex subunit OSTC OS=Homo sapiens GN=OSTC PE=4 SV=1 - [A0A087WUD3_HUMAN]	14.46	2	1	1	1	0.951	1		2.194	83	9.363
E9APD0	NADH-cytochrome b5 reductase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1060 PE=3 SV=1 - [E9APD0_LEIMU]	2.6	1	1	1	1	1.000	1		2.194	308	34.796
B2RWP0	Signal-induced proliferation-associated 1 like 3 OS=Homo sapiens GN=SIPA1L3 PE=2 SV=1 - [B2RWP0_HUMAN]	0.45	2	1	1	1	1.000	1		2.194	1781	194.504
B3KV53	cDNA FLJ16135 fis, clone BRACE2045445, highly similar to Tripartite motif-containing protein 3 OS=Homo sapiens PE=2 SV=1 - [B3KV53_HUMAN]	3.55	4	1	1	1	1.026	1		2.193	169	18.081
Q5TGS1	Transcription factor HES-3 OS=Homo sapiens GN=HES3 PE=2 SV=1 - [HES3_HUMAN]	4.84	1	1	1	1	1.334	1		2.193	186	19.955
Q5VV42	Threonylcarbamoyladenosine tRNA methylthiotransferase OS=Homo sapiens GN=CDKAL1 PE=1 SV=1 - [CDKAL_HUMAN]	1.38	1	1	1	1	0.482	1		2.193	579	65.070
Q02413	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2 - [DSG1_HUMAN]	0.95	1	1	1	1	1.632	1		2.192	1049	113.676
J3QQX3	NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR PE=1 SV=2 - [J3QQX3_HUMAN]	4.75	4	2	2	2	0.912	2	13.666	2.192	463	50.588
B4DLG0	cDNA FLJ58510, highly similar to Autism susceptibility gene 2 protein OS=Homo sapiens PE=2 SV=1 - [B4DLG0_HUMAN]	0.98	5	1	1	1	0.815	1		2.192	711	79.296
Q8NCE2	Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 PE=1 SV=2 - [MTMRE_HUMAN]	1.69	1	1	1	1	1.000	1		2.192	650	72.158
E9ALJ2	Putative mitogen activated protein kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2320 PE=4 SV=1 - [E9ALJ2_LEIMU]	2.69	1	1	1	1	9.003	1		2.191	372	41.443
P25874	Mitochondrial brown fat uncoupling protein 1 OS=Homo sapiens GN=UCP1 PE=1 SV=3 - [UCP1_HUMAN]	2.93	1	1	1	1	1.439	1		2.191	307	32.983
E9B037	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2160 PE=4 SV=1 - [E9B037_LEIMU]	7.41	1	1	1	1	1.000	1		2.190	243	27.475
B7ZA02	cDNA, FLJ79016, weakly similar to Mus musculus microtubule-associated protein 7 (Mtap7), mRNA OS=Homo sapiens PE=2 SV=1 - [B7ZA02_HUMAN]	2.04	4	1	2	2	0.931	1		2.189	687	76.968
F8W9W8	Solute carrier organic anion transporter family member 2A1 OS=Homo sapiens GN=SLCO2A1 PE=1 SV=1 - [F8W9W8_HUMAN]	1.45	4	1	1	1	0.891	1		2.188	415	44.967

E9AQU5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1340 PE=4 SV=1 - [E9AQU5_LEIMU]	0.16	1	1	1	1	0.842	1		2.187	3749	399.500
B4E223	cDNA FLJ52075, moderately similar to Mus musculus SPT2, Suppressor of Ty, domain containing 1, mRNA OS=Homo sapiens PE=2 SV=1 - [B4E223_HUMAN]	1.59	2	1	1	1	1.000	1		2.187	629	68.462
A8K8S6	cDNA FLJ77231, highly similar to Homo sapiens hemogen (HEMGN), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8S6_HUMAN]	2.27	2	1	1	1	1.000	1		2.187	484	55.273
B1ALD3	AP-4 complex subunit beta-1 (Fragment) OS=Homo sapiens GN=AP4B1 PE=4 SV=1 - [B1ALD3_HUMAN]	6.29	7	1	1	1	1.000	1		2.185	175	20.166
B3KRP2	cDNA FLJ34661 fis, clone KIDNE2018989, weakly similar to Homo sapiens centrosomal protein 170 kDa (CEP170), transcript variant alpha, mRNA OS=Homo sapiens P	5.42	4	1	1	1	1.011	1		2.185	203	22.951
Q96T49	Protein phosphatase 1 regulatory inhibitor subunit 16B OS=Homo sapiens GN=PPP1R16B PE=1 SV=1 - [PP16B_HUMAN]	2.82	1	1	1	4	1.064	4	0.698	2.184	567	63.511
E9PAM9	Bcl-2-like protein 11 (Fragment) OS=Homo sapiens GN=BCL2L11 PE=4 SV=3 - [E9PAM9_HUMAN]	15.28	4	1	1	1	1.000	1		2.183	72	7.369
Q6ZQX7	Uncharacterized protein C17orf97 OS=Homo sapiens GN=C17orf97 PE=2 SV=2 - [CQ097_HUMAN]	22.08	1	1	1	1	0.686	1		2.183	453	49.626
B7Z7S6	cDNA FLJ61723 OS=Homo sapiens PE=2 SV=1 - [B7Z7S6_HUMAN]	0.53	1	1	1	1	1.000	1		2.182	1323	145.426
B3KUP6	cDNA FLJ40351 fis, clone TESTI2033453, highly similar to Actin-like protein 7B OS=Homo sapiens PE=2 SV=1 - [B3KUP6_HUMAN]	2.17	2	1	1	1	1.482	1		2.182	415	45.165
E9APM2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0290 PE=4 SV=1 - [E9APM2_LEIMU]	3.21	1	1	1	1	0.991	1		2.182	280	30.175
Q0JRZ9	FCH domain only protein 2 OS=Homo sapiens GN=FCHO2 PE=1 SV=2 - [FCHO2_HUMAN]	1.23	1	1	1	1	2.744	1		2.182	810	88.869
E9AKL8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_1110 PE=4 SV=1 - [E9AKL8_LEIMU]	0.72	1	1	1	1	11.600	1		2.181	1245	132.960
B3KP13	cDNA FLJ30924 fis, clone FEBRA2006521, highly similar to Junctophilin-3 OS=Homo sapiens PE=2 SV=1 - [B3KP13_HUMAN]	2.36	3	1	1	1	1.000	1		2.181	423	46.552
B2R820	cDNA, FLJ93700, highly similar to Homo sapiens CD244 natural killer cell receptor 2B4 (CD244), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R820_HUMAN]	1.92	2	1	1	1	0.560	1		2.180	365	41.111
E9AL45	Putative ATP-dependent DEAD/H RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0340 PE=4 SV=1 - [E9AL45_LEIMU]	1.93	1	1	1	1	2.973	1		2.179	415	45.901
Q6ZV51	cDNA FLJ42984 fis, clone BRTHA2008335 OS=Homo sapiens PE=2 SV=1 - [Q6ZV51_HUMAN]	3.89	3	1	1	1	1.145	1		2.178	180	19.499
E9ARX5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0240 PE=4 SV=1 - [E9ARX5_LEIMU]	1.19	1	1	1	1	0.966	1		2.178	671	72.815
Q5TBG2	Serine/threonine-protein kinase Nek6 (Fragment) OS=Homo sapiens GN=NEK6 PE=1 SV=1 - [Q5TBG2_HUMAN]	5.26	7	1	1	1	0.827	1		2.178	171	19.668
E9B2C8	Glycylpeptide N-tetradecanoyltransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0080 PE=3 SV=1 - [E9B2C8_LEIMU]	1.9	1	1	1	1	1.000	1		2.178	421	48.588
Q7KYR7	Butyrophilin subfamily 2 member A1 OS=Homo sapiens GN=BTN2A1 PE=1 SV=3 - [BT2A1_HUMAN]	2.09	1	1	1	1	1.039	1		2.177	527	59.594
E9AKX1	2,4-dienoyl-coa reductase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0930 PE=4 SV=1 - [E9AKX1_LEIMU]	1.64	1	1	1	1	0.653	1		2.176	730	80.598
B7Z339	Phosphatase and actin regulator OS=Homo sapiens PE=2 SV=1 - [B7Z339_HUMAN]	1.74	3	1	1	1	1.000	1		2.176	518	58.500
A0A075B6H5	Protein TRBV20OR9-2 (Fragment) OS=Homo sapiens GN=TRBV20OR9-2 PE=4 SV=1 - [A0A075B6H5_HUMAN]	6.15	1	1	1	1	1.167	1		2.176	130	14.272
A0PJW6	Transmembrane protein 223 OS=Homo sapiens GN=TMEM223 PE=1 SV=1 - [TM223_HUMAN]	4.95	1	1	1	1	0.621	1		2.176	202	22.035
Q9UL40	Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 - [ZN346_HUMAN]	2.38	2	1	1	1	0.766	1		2.175	294	32.912
Q9P2J8	Zinc finger protein 624 OS=Homo sapiens GN=ZNF624 PE=2 SV=3 - [ZN624_HUMAN]	5.55	198	0	3	4				2.174	865	99.864
P0CB33	Putative zinc finger protein 735 OS=Homo sapiens GN=ZNF735P PE=5 SV=1 - [ZN735_HUMAN]	13.11	171	1	3	5	1.000	2	0.000	2.174	412	47.534
I0CMK8	Zinc finger protein 626 isoform 1 (Fragment) OS=Homo sapiens GN=ZNF626 PE=4 SV=1 - [I0CMK8_HUMAN]	28.9	175	1	3	4	0.762	1		2.174	218	25.148
I7HIK6	Zinc finger protein 311 (Fragment) OS=Homo sapiens GN=GD:ZNF311_2 PE=4 SV=1 - [I7HIK6_HUMAN]	8.75	173	1	3	4	1.000	1		2.174	606	69.930
A8K3D4	cDNA FLJ77979 OS=Homo sapiens PE=2 SV=1 - [A8K3D4_HUMAN]	4.18	42	1	2	2	0.758	1		2.174	502	57.583
C9JA99	Protocadherin alpha-13 OS=Homo sapiens GN=PCDHA13 PE=4 SV=1 - [C9JA99_HUMAN]	2.21	3	1	1	1	1.000	1		2.174	904	97.371
E9B3H1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3930 PE=4 SV=1 - [E9B3H1_LEIMU]	0.17	1	1	1	1	0.830	1		2.173	4087	453.583
Q3KRB8	Rho GTPase-activating protein 11B OS=Homo sapiens GN=ARHGAP11B PE=1 SV=1 - [RHGBB_HUMAN]	3.37	3	1	1	1	1.580	1		2.172	267	30.232
B7Z7G7	Vacuolar protein sorting-associated protein 45 OS=Homo sapiens GN=VPS45 PE=2 SV=1 - [B7Z7G7_HUMAN]	4.55	5	1	1	1	1.134	1		2.170	198	22.980
E9AR04	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0350 PE=4 SV=1 - [E9AR04_LEIMU]	1.36	1	1	1	1	1.790	1		2.170	660	73.648
Q15645	Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2 - [PCH2_HUMAN]	4.63	2	1	2	2	0.879	1		2.170	432	48.520
A4VCI6	HIP1 protein (Fragment) OS=Homo sapiens GN=HIP1 PE=2 SV=1 - [A4VCI6_HUMAN]	1.55	5	1	1	1	1.340	1		2.168	517	57.652
B3KN79	cDNA FLJ13894 fis, clone THYRO1001671, highly similar to 59 kDa 2'-5'-oligoadenylate synthetase-like protein OS=Homo sapiens PE=2 SV=1 - [B3KN79_HUMAN]	1.56	2	1	1	2	1.000	2	0.000	2.168	514	59.219
A0A087WTM7	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=4 SV=1 - [A0A087WTM7_HUMAN]	0.46	7	2	2	2	1.365	1		2.168	4344	489.527
B4DS83	cDNA FLJ53179, highly similar to Nucleolar protein 10 OS=Homo sapiens PE=2 SV=1 - [B4DS83_HUMAN]	1.1	2	1	1	1	1.000	1		2.167	638	74.366
Q7Z606	Breast and ovarian cancer susceptibility protein (Fragment) OS=Homo sapiens GN=BRCA1 PE=4 SV=1 - [Q7Z606_HUMAN]	1.58	11	2	2	2	1.000	2	0.000	2.167	1141	126.971
E9PPJ3	Smoothelin-like protein 1 OS=Homo sapiens GN=SMTNL1 PE=4 SV=1 - [E9PPJ3_HUMAN]	1.42	1	1	1	1	0.921	1		2.166	494	52.954
H0Y9V7	Calcium-transporting ATPase type 2C member 1 (Fragment) OS=Homo sapiens GN=ATP2C1 PE=1 SV=1 - [H0Y9V7_HUMAN]	1.77	7	2	2	2	1.033	2	4.789	2.166	903	98.985
E9AY30	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0480 PE=4 SV=1 - [E9AY30_LEIMU]	4.6	1	1	1	1	1.000	1		2.164	326	36.634
Q96I45	Transmembrane protein 141 OS=Homo sapiens GN=TMEM141 PE=1 SV=1 - [TM141_HUMAN]	7.41	1	1	1	1	0.877	1		2.163	108	11.867
E9B4C1	Transcription elongation factor-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2810 PE=4 SV=1 - [E9B4C1_LEIMU]	1.68	1	1	1	1	1.331	1		2.163	476	50.805
E9AVR1	Putative NADH-cytochrome b5 reductase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0770 PE=4 SV=1 - [E9AVR1_LEIMU]	5.54	1	2	2	2	0.918	2	12.703	2.161	289	31.848
L7REZ6	TRIM5 (Fragment) OS=Homo sapiens GN=TRIM5 PE=4 SV=1 - [L7REZ6_HUMAN]	14.52	13	1	1	1	0.314	1		2.161	62	6.875
E9B3Z9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1620 PE=4 SV=1 - [E9B3Z9_LEIMU]	0.77	1	1	1	1	1.978	1		2.160	905	100.960
Q8IXV0	HES1 protein OS=Homo sapiens GN=HES1 PE=2 SV=1 - [Q8IXV0_HUMAN]	3.25	2	1	1	1	1.000	1		2.160	277	29.253
H7C1F9	Ral GTPase-activating protein subunit alpha-2 (Fragment) OS=Homo sapiens GN=RALGAPA2 PE=1 SV=1 - [H7C1F9_HUMAN]	1.61	2	2	2	2	0.286	1		2.160	1740	194.918
B4DPL0	cDNA FLJ50827, highly similar to Huntingtin-interacting protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DPL0_HUMAN]	1.37	4	1	1	1	1.381	1		2.159	437	49.959
Q9Y2F5	Little elongation complex subunit 1 OS=Homo sapiens GN=ICE1 PE=1 SV=5 - [ICE1_HUMAN]	0.31	1	1	1	1	1.000	1		2.158	2266	247.737
E9AWU8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1070 PE=4 SV=1 - [E9AWU8_LEIMU]	1.39	1	2	2	2	1.000	2	0.000	2.158	2514	266.936
E9B6E6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2680 PE=4 SV=1 - [E9B6E6_LEIMU]	9.33	1	1	1	1	1.000	1		2.158	75	8.307
O75051	Plexin-A2 OS=Homo sapiens GN=PLXNA2 PE=1 SV=4 - [PLXA2_HUMAN]	0.42	1	1	2	2	0.889	1		2.158	1894	210.969
E9AXR5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1830 PE=4 SV=1 - [E9AXR5_LEIMU]	2.79	1	1	1	1	1.000	1		2.157	1002	103.872
B4DIM7	cDNA FLJ50168, highly similar to Peroxisome biogenesis factor 1 OS=Homo sapiens PE=2 SV=1 - [B4DIM7_HUMAN]	1.04	4	1	1	1	1.000	1		2.156	961	105.889
E9ARB5	Putative zinc-finger protein ZPR1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_1410 PE=4 SV=1 - [E9ARB5_LEIMU]	1.61	1	1	1	1	0.848	1		2.155	497	56.170
Q68D18	Putative uncharacterized protein DKFZp686J14194 OS=Homo sapiens GN=DKFZp686J14194 PE=2 SV=1 - [Q68D18_HUMAN]	8.7	4	1	1	1	1.000	1		2.154	92	10.472
E9AS21	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0690 PE=3 SV=1 - [E9AS21_LEIMU]	0.68	1	1	1	1	1.024	1		2.154	1034	117.037
E9AS64	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1130 PE=4 SV=1 - [E9AS64_LEIMU]	0.24	1	1	1	1	3.168	1		2.153	5789	614.523
E9AR98	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_1260 PE=4 SV=1 - [E9AR98_LEIMU]	1.56	1	1	1	1	1.000	1		2.153	449	47.462
B3KNI7	cDNA FLJ14669 fis, clone NT2RP2003243, highly similar to Homo sapiens activating transcription factor 7 interacting protein (ATF7IP), mRNA OS=Homo sapiens PE=2 S	4.8	3	2	2	2	0.835	1		2.153	709	75.904
E9B307	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2260 PE=4 SV=1 - [E9B307_LEIMU]	7.49	1	1	1	1	1.000	1		2.151	187	20.261
B4DG57	cDNA FLJ61230, highly similar to PHD finger protein 14 OS=Homo sapiens PE=2 SV=1 - [B4DG57_HUMAN]	1.66	2	1	1	1	1.000	1		2.150	603	68.527
E9AMR9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0680 PE=4 SV=1 - [E9AMR9_LEIMU]	1.89	1	1	1	1	0.998	1		2.150	370	40.432
E9PJ07	Erythroid differentiation-related factor 1 OS=Homo sapiens GN=EDRF1 PE=4 SV=1 - [E9PJ07_HUMAN]	4.08	2	1	1	1	1.000	1		2.150	343	37.570
A4D0Y1	Wiskott-Aldrich syndrome-like OS=Homo sapiens GN=WASL PE=4 SV=1 - [A4D0Y1_HUMAN]	1.65	3	1	1	1	0.955	1		2.150	485	52.652
H7C2L3	Cysteine-rich with EGF-like domain protein 1 (Fragment) OS=Homo sapiens GN=CRELD1 PE=4 SV=1 - [H7C2L3_HUMAN]	12	3	1	1	1	1.000	1		2.149	100	10.710
B7ZMC8	BarH-like homeobox 1 OS=Homo sapiens GN=BARHL1 PE=2 SV=1 - [B7ZMC8_HUMAN]	2.45	2	1	1	1	0.818	1		2.149	327	35.101
Q9NQW1	Protein transport protein Sec31B OS=Homo sapiens GN=SEC31B PE=1 SV=1 - [SC31B_HUMAN]	1.53	6	1	2	2	1.000	1		2.149	1179	128.615
E5RH51	Small integral membrane protein 12 OS=Homo sapiens GN=SMIM12 PE=4 SV=1 - [E5RH51_HUMAN]	14.86	2	1	1	1	0.550	1		2.149	74	8.673
B7ZBA8	Coiled-coil domain-containing protein 154 OS=Homo sapiens GN=CCDC154 PE=4 SV=1 - [B7ZBA8_HUMAN]	1.72	2	1	1	1	0.606	1		2.148	522	59.412
G3V5U8	Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma OS=Homo sapiens GN=PPP2R3C PE=4 SV=1 - [G3V5U8_HUMAN]	6.6	5	1	1	1	1.086	1		2.148	106	12.916
E9ANJ2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0460 PE=4 SV=1 - [E9ANJ2_LEIMU]	1.09	1	1	1	1	1.011	1		2.147	644	69.192
O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens GN=NDUFS5 PE=1 SV=3 - [NDUS5_HUMAN]	15.09	1	2	2	3	1.007	3	18.119	2.146	106	12.509
Q9BZS5	PNAS-122 OS=Homo sapiens PE=2 SV=1 - [Q9BZS5_HUMAN]	6.48	3	1	1	1	0.874	1		2.146	108	11.768
E9ATI5	Golgi SNARE protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4020 PE=4 SV=1 - [E9ATI5_LEIMU]	2.9	1	1	1	1	0.676	1		2.144	276	31.370
B2R7C2	cDNA, FLJ93375, highly similar to Homo sapiens ZW10, kinetochore associated, homolog (Drosophila) (ZW10), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7C2_HUM	1.93	8	2	2	3	0.909	2	10.537	2.144	779	88.783
P63128	Endogenous retrovirus group K member 9 Pol protein OS=Homo sapiens GN=ERVK-9 PE=3 SV=3 - [POK9_HUMAN]	0.54	1	1	1	1	0.975	1		2.144	1117	123.542
B3KY29	cDNA FLJ46695 fis, clone TRACH3013043, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA OS=Homo sapiens PE=2	1.64	6	1	1	1	1.125	1		2.144	731	78.487
B4DNQ4	cDNA FLJ56610 OS=Homo sapiens PE=2 SV=1 - [B4DNQ4_HUMAN]	6.77	1	1	1	1	1.243	1		2.143	133	14.552
C9J315	Lanosterol synthase (Fragment) OS=Homo sapiens GN=LSS PE=1 SV=1 - [C9J315_HUMAN]	3.44	3	1	1	1	0.862	1		2.143	262	29.561
Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial OS=Homo sapiens GN=PTRH2 PE=1 SV=1 - [PTH2_HUMAN]	3.91	2	1	1	1	0.925	1		2.143	179	19.181
K7ESJ9	Protein PROCA1 (Fragment) OS=Homo sapiens GN=PROCA1 PE=4 SV=1 - [K7ESJ9_HUMAN]	6.36	2	1	1	1	1.000	1		2.142	110	12.193
E9B480	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2410 PE=4 SV=1 - [E9B480_LEIMU]	0.9	1	1	1	1	1.730	1		2.142	667	71.427
E9AKF9	Kinetoplast-associated protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0530 PE=4 SV=1 - [E9AKF9_LEIMU]	0.34	1	1	1	1				2.141	2055	213.113
E9PKC0	Pleckstrin homology domain-containing family A member 7 OS=Homo sapiens GN=PLEKHA7 PE=1 SV=1 - [E9PKC0_HUMAN]	0.55	1	1	1	1	1.187	1		2.141	1271	144.335
E9B591	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3020 PE=4 SV=1 - [E9B591_LEIMU]	2.24	1	2	2	2	0.670	2	177.412	2.141	936	99.071
Q5CZC0	Fibrous sheath-interacting protein 2 OS=Homo sapiens GN=FSIP2 PE=2 SV=4 - [FSIP2_HUMAN]	0.1	2	1	1	1	1.151	1		2.140	6907	780.119
E9B0Z4	Putative endosomal trafficking protein RME-8 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2210 PE=4 SV=1 - [E9B0Z4_LEIMU]	0.33	1	1	1	1	1.000	1		2.140	2452	273.048
A8K7S0	cDNA FLJ75478, highly similar to Homo sapiens splicing factor 4 (SF4), transcript variant a, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K7S0_HUMAN]	5.43	9	2	2	2	0.954	2	6.999	2.140	645	72.397
Q96PN6	Adenylate cyclase type 10 OS=Homo sapiens GN=ADCY10 PE=1 SV=3 - [ADCYA_HUMAN]	0.87	1	1	1	1	1.000	1		2.137	1610	187.026
A8K724	cDNA FLJ76899, highly similar to Homo sapiens p21(CDKN1A)-activated kinase 4 (PAK4), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K724_HUMAN]	2.37	2	1	1	1	1.000	1		2.137	591	63.926
B4DYR7	cDNA FLJ57854, highly similar to Synaptophysin-like protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DYR7_HUMAN]	4.33	2	1	1	1	1.000	1		2.136	208	23.662
C9J2N5	Inositol polyphosphate 1-phosphatase (Fragment) OS=Homo sapiens GN=INPP1 PE=4 SV=1 - [C9J2N5_HUMAN]	26.67	13	1	1	1	1.198	1		2.136	30	3.406
H0YNT1	E3 ubiquitin-protein ligase RNF31 (Fragment) OS=Homo sapiens GN=RNF31 PE=4 SV=1 - [H0YNT1_HUMAN]	5	5	1	1	1	1.000	1		2.134	140	16.396
X6RII9	Protrudin (Fragment) OS=Homo sapiens GN=ZFYVE27 PE=4 SV=1 - [X6RII9_HUMAN]	3.05	2	1	1	1	1.000	1		2.134	394	44.019
A0A087X228	Tumor necrosis factor ligand superfamily member 8 OS=Homo sapiens GN=TNFSF8 PE=4 SV=1 - [A0A087X228_HUMAN]	7.93	2	1	1	1	1.000	1		2.132	164	17.822
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 PE=1 SV=1 - [FIP1_HUMAN]	2.36	1	1	1	1	1.000	1		2.132	594	66.487
E9B5I6	Expression site-associated protein 5 (ESAG5),putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3930 PE=4 SV=1 - [E9B5I6_LEIMU]	3.1	1	1	1	3	1.128	3	9.271	2.132	548	60.022
Q8NF99	Zinc finger protein 397 OS=Homo sapiens GN=ZNF397 PE=1 SV=2 - [ZN397_HUMAN]	3	71	1	2	3	1.000	1		2.131	534	61.100
B4DME6	cDNA FLJ57055 OS=Homo sapiens PE=2 SV=1 - [B4DME6_HUMAN]	1.06	2	1	1	1	1.030	1		2.131	753	83.179
B4DNG0	cDNA FLJ58142, highly similar to Olfactomedin-like protein 3 OS=Homo sapiens PE=2 SV=1 - [B4DNG0_HUMAN]	2.9	2	1	1	1	1.000	1		2.131	345	38.958
Q9NX09	DNA damage-inducible transcript 4 protein OS=Homo sapiens GN=DDIT4 PE=1 SV=1 - [DDIT4_HUMAN]	3.45	1	1	1	1	1.120	1		2.131	232	25.355
Q8N130	Sodium-dependent phosphate transport protein 2C OS=Homo sapiens GN=SLC34A3 PE=1 SV=2 - [NPT2C_HUMAN]	1.17	1	1	1	1	1.183	1		2.130	599	63.509
Q8N2R8	Protein FAM43A OS=Homo sapiens GN=FAM43A PE=2 SV=2 - [FA43A_HUMAN]	3.07	1	1	1	1	1.000	1		2.129	423	45.747
Q96JM4	Leucine-rich repeat and IQ domain-containing protein 1 OS=Homo sapiens GN=LRRIQ1 PE=2 SV=3 - [LRIQ1_HUMAN]	0.46	1	1	1	1	0.602	1		2.129	1722	199.176
O95958	Lost in inflammatory breast cancer tumor suppressor protein OS=Homo sapiens GN=LIBC PE=2 SV=1 - [O95958_HUMAN]	2.11	1	1	1	1	0.838	1		2.128	331	36.884
Q3KRG8	CEACAM1 protein (Fragment) OS=Homo sapiens GN=CEACAM1 PE=2 SV=1 - [Q3KRG8_HUMAN]	1.42	2	1	1	1	1.324	1		2.128	493	53.310
Q5CZB5	Putative uncharacterized protein DKFZp686M0430 OS=Homo sapiens GN=DKFZp686M0430 PE=2 SV=1 - [Q5CZB5_HUMAN]	0.52	2	1	1	1	0.333	1		2.128	1157	125.010
E9B5V5	Putative proteasome activator protein pa26 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0750 PE=4 SV=1 - [E9B5V5_LEIMU]	3.04	1	1	1	1	3.973	1		2.125	230	24.885
A9QM74	Importin subunit alpha-8 OS=Homo sapiens GN=KPNA7 PE=1 SV=1 - [IMA8_HUMAN]	3.49	1	1	1	1	1.129	1		2.124	516	56.902
H0Y9L8	Bifunctional lysine-specific demethylase and histidyl-hydroxylase MINA (Fragment) OS=Homo sapiens GN=MINA PE=1 SV=1 - [H0Y9L8_HUMAN]	8.33	2	1	1	1	1.225	1		2.124	108	12.185
H0YIE8	WD repeat domain-containing protein 83 (Fragment) OS=Homo sapiens GN=WDR83 PE=4 SV=1 - [H0YIE8_HUMAN]	5.69	2	1	1	1	1.000	1		2.123	211	23.509
B4DLS2	cDNA FLJ50803, highly similar to Zinc finger protein 23 OS=Homo sapiens PE=2 SV=1 - [B4DLS2_HUMAN]	3.08	14	1	2	2	0.312	1		2.123	585	67.144
E9B1R0	Putative N-acyl-L-amino acid amidohydrolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1130 PE=4 SV=1 - [E9B1R0_LEIMU]	4.44	1	1	2	2	1.896	1		2.121	405	43.814
Q8NA31	Telomere repeats-binding bouquet formation protein 1 OS=Homo sapiens GN=CCDC79 PE=2 SV=3 - [TERB1_HUMAN]	1.24	1	1	1	1	1.053	1		2.121	727	83.011
P12318	Low affinity immunoglobulin gamma Fc region receptor II-a OS=Homo sapiens GN=FCGR2A PE=1 SV=4 - [FCG2A_HUMAN]	3.15	3	1	1	1	0.889	1		2.119	317	34.978
Q9UIH9	Krueppel-like factor 15 OS=Homo sapiens GN=KLF15 PE=1 SV=1 - [KLF15_HUMAN]	1.44	5	1	1	1	1.323	1		2.118	416	43.964
Q8NHZ8	Anaphase-promoting complex subunit CDC26 OS=Homo sapiens GN=CDC26 PE=1 SV=1 - [CDC26_HUMAN]	8.24	1	1	1	1	0.679	1		2.118	85	9.771
B4DHZ3	cDNA FLJ61266 OS=Homo sapiens PE=2 SV=1 - [B4DHZ3_HUMAN]	2.67	2	1	1	1	1.000	1		2.118	300	31.565
Q96BD5	PHD finger protein 21A OS=Homo sapiens GN=PHF21A PE=1 SV=1 - [PF21A_HUMAN]	1.03	1	1	1	1	1.000	1		2.118	680	74.807
A7E2E5	Phosphodiesterase 3B, cGMP-inhibited OS=Homo sapiens GN=PDE3B PE=2 SV=1 - [A7E2E5_HUMAN]	1.44	2	1	1	1	1.001	1		2.117	1112	124.236
F8WEP8	Upstream-binding protein 1 OS=Homo sapiens GN=UBP1 PE=4 SV=1 - [F8WEP8_HUMAN]	8.54	4	1	1	1	1.000	1		2.115	164	18.029
E9AWT2	DNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0910 PE=3 SV=1 - [E9AWT2_LEIMU]	3.25	1	1	1	1				2.114	801	86.716
B7Z2D2	Centrosomal protein of 70 kDa OS=Homo sapiens GN=CEP70 PE=2 SV=1 - [B7Z2D2_HUMAN]	4.49	3	2	2	2	1.000	2	0.000	2.114	445	51.981
H3BU38	Uncharacterized protein C16orf59 (Fragment) OS=Homo sapiens GN=C16orf59 PE=4 SV=1 - [H3BU38_HUMAN]	9.94	1	1	1	1	1.000	1		2.114	171	18.723
B4DXD8	cDNA FLJ51369, highly similar to DNA repair endonuclease XPF (EC 3.1.-.-) OS=Homo sapiens PE=2 SV=1 - [B4DXD8_HUMAN]	2.58	2	1	1	1	1.000	1		2.113	466	52.809
E9AUP5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_1060 PE=4 SV=1 - [E9AUP5_LEIMU]	0.61	1	1	1	1	1.000	1		2.113	1317	136.653
E9AQH7	Mitochondrial ornithine carrier protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0200 PE=3 SV=1 - [E9AQH7_LEIMU]	2.68	1	1	1	1	0.945	1		2.112	299	32.781
F8VXK3	Carbohydrate sulfotransferase 11 (Fragment) OS=Homo sapiens GN=CHST11 PE=4 SV=1 - [F8VXK3_HUMAN]	5.06	2	1	1	1	1.000	1		2.112	158	18.457
Q9C0D4	Zinc finger protein 518B OS=Homo sapiens GN=ZNF518B PE=2 SV=2 - [Z518B_HUMAN]	2.23	1	2	2	2	1.000	2	0.000	2.111	1074	119.456
B7Z1M7	cDNA FLJ59478, highly similar to Liprin-beta-2 OS=Homo sapiens PE=2 SV=1 - [B7Z1M7_HUMAN]	4.75	10	2	2	2	1.507	2	55.592	2.110	400	45.018
B4DNX8	cDNA FLJ60744, moderately similar to B-cell lymphoma 9 protein OS=Homo sapiens PE=2 SV=1 - [B4DNX8_HUMAN]	3.13	2	1	1	2	1.000	2	0.000	2.109	416	44.578
E9B4U1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1180 PE=4 SV=1 - [E9B4U1_LEIMU]	1.37	1	1	1	1	1.000	1		2.109	656	69.255
Q8TE73	Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3 - [DYH5_HUMAN]	0.63	2	1	2	2	1.000	1		2.109	4624	528.684
H0YC68	Glutathione reductase, mitochondrial (Fragment) OS=Homo sapiens GN=GSR PE=1 SV=1 - [H0YC68_HUMAN]	6.11	2	1	1	1	2.749	1		2.107	131	14.185
E9AUK0	CTP synthase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_0560 PE=3 SV=1 - [E9AUK0_LEIMU]	1.68	1	1	1	1	1.000	1		2.106	596	65.871
E9AWX1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1290 PE=4 SV=1 - [E9AWX1_LEIMU]	0.58	1	1	1	1	1.000	1		2.106	1381	153.507
C9J5N2	Beta/gamma crystallin domain-containing protein 3 OS=Homo sapiens GN=CRYBG3 PE=4 SV=2 - [C9J5N2_HUMAN]	0.27	1	1	1	1	0.940	1		2.105	2970	330.427
Q8N8R3	Mitochondrial basic amino acids transporter OS=Homo sapiens GN=SLC25A29 PE=2 SV=2 - [MCATL_HUMAN]	2.31	1	1	1	1	1.007	1		2.105	303	32.042
E9AQD1	Actin-related protein 3, putative arp3 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_1360 PE=3 SV=1 - [E9AQD1_LEIMU]	3.46	1	1	1	1	1.000	1		2.104	405	43.858
K7ELF3	Transcription factor E2-alpha (Fragment) OS=Homo sapiens GN=TCF3 PE=1 SV=2 - [K7ELF3_HUMAN]	5.16	6	1	1	1	1.036	1		2.103	213	21.889
Q9HB66	Alternative protein MKKS OS=Homo sapiens GN=MKKS PE=2 SV=1 - [Q9HB66_HUMAN]	14.29	1	1	1	1	1.100	1		2.103	63	7.259
B3KY85	cDNA FLJ16031 fis, clone NT2RI2000313, highly similar to Polypeptide N-acetylgalactosaminyltransferase 13 (EC 2.4.1.41) OS=Homo sapiens PE=2 SV=1 - [B3KY85_H	2.16	3	2	2	2	1.042	2	41.553	2.103	556	63.949
E9ALL3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2100 PE=4 SV=1 - [E9ALL3_LEIMU]	0.94	1	1	1	1	1.094	1		2.100	640	69.501
Q96HJ9	UPF0562 protein C7orf55 OS=Homo sapiens GN=C7orf55 PE=1 SV=2 - [CG055_HUMAN]	10.62	1	1	1	1	1.000	1		2.100	113	12.741
B4E0U9	cDNA FLJ51594, highly similar to Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 15B (PPP1R15B), mRNA OS=Homo sapiens PE=2 SV=1 - [B4E0U9	1.12	2	1	1	1	1.000	1		2.099	623	69.175
K7ELF8	Inositol monophosphatase 2 OS=Homo sapiens GN=IMPA2 PE=1 SV=1 - [K7ELF8_HUMAN]	10.43	1	1	1	1				2.096	163	17.853
C9J6H0	Polyhomeotic-like protein 3 (Fragment) OS=Homo sapiens GN=PHC3 PE=1 SV=2 - [C9J6H0_HUMAN]	3.85	6	1	1	1	0.474	1		2.096	182	19.325
A4D227	Similar to 60S RIBOSOMAL PROTEIN L21 OS=Homo sapiens GN=LOC393079 PE=4 SV=1 - [A4D227_HUMAN]	8.93	1	1	1	1	1.000	1		2.095	112	12.590
B2RAM2	cDNA, FLJ94999, highly similar to Homo sapiens calpain 7 (CAPN7), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAM2_HUMAN]	0.98	3	1	1	1	1.586	1		2.095	813	92.566
E9B4M2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0530 PE=4 SV=1 - [E9B4M2_LEIMU]	3.88	1	1	1	1				2.094	490	52.091
V9GZ31	Ubiquitin-conjugating enzyme E2 U (Fragment) OS=Homo sapiens GN=UBE2U PE=4 SV=1 - [V9GZ31_HUMAN]	2.94	2	1	1	1	0.933	1		2.092	204	24.205
E9APA9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0850 PE=4 SV=1 - [E9APA9_LEIMU]	1.15	1	1	1	1	1.000	1		2.091	869	91.551
P02549	Spectrin alpha chain, erythrocytic 1 OS=Homo sapiens GN=SPTA1 PE=1 SV=5 - [SPTA1_HUMAN]	0.41	2	1	1	1	1.102	1		2.090	2419	279.842
E9B5B5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3260 PE=4 SV=1 - [E9B5B5_LEIMU]	1.34	1	1	1	1	1.000	1		2.090	670	72.590
Q6IEG0	U11/U12 small nuclear ribonucleoprotein 48 kDa protein OS=Homo sapiens GN=SNRNP48 PE=1 SV=2 - [SNR48_HUMAN]	2.36	1	1	1	1	1.000	1		2.090	339	39.941
P46108	Adapter molecule crk OS=Homo sapiens GN=CRK PE=1 SV=2 - [CRK_HUMAN]	2.63	1	1	1	1	3.155	1		2.090	304	33.810
E9AQU7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1360 PE=4 SV=1 - [E9AQU7_LEIMU]	1.84	1	1	1	1	1.000	1		2.089	599	65.953
E9AKF8	Nuclear receptor binding factor-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0520 PE=4 SV=1 - [E9AKF8_LEIMU]	3.82	1	1	1	1	1.291	1		2.088	340	35.969
Q5T7I8	SHC-transforming protein 3 OS=Homo sapiens GN=SHC3 PE=4 SV=1 - [Q5T7I8_HUMAN]	16.19	2	1	1	1	1.000	1		2.087	105	11.510
Q9NR48	Histone-lysine N-methyltransferase ASH1L OS=Homo sapiens GN=ASH1L PE=1 SV=2 - [ASH1L_HUMAN]	0.94	2	2	2	2	1.000	1		2.086	2969	332.582
J3KRR1	Protein Njmu-R1 (Fragment) OS=Homo sapiens GN=C17orf75 PE=1 SV=1 - [J3KRR1_HUMAN]	2.91	3	1	1	1	1.000	1		2.086	275	30.604
B3KMH8	Autophagy protein 5 OS=Homo sapiens PE=2 SV=1 - [B3KMH8_HUMAN]	5.09	2	1	1	1	1.000	1		2.085	275	32.354
E9B419	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1830 PE=4 SV=1 - [E9B419_LEIMU]	1.15	1	1	1	1				2.085	957	103.845
A0A024R3S6	HCG1984338, isoform CRA_a OS=Homo sapiens GN=hCG_1984338 PE=4 SV=1 - [A0A024R3S6_HUMAN]	4.55	1	1	1	1	1.224	1		2.084	154	16.899
E9ASS7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1570 PE=4 SV=1 - [E9ASS7_LEIMU]	1.89	1	1	1	1	0.511	1		2.084	476	52.788
X6R9U5	E3 ubiquitin-protein ligase TRIM13 (Fragment) OS=Homo sapiens GN=TRIM13 PE=4 SV=1 - [X6R9U5_HUMAN]	4.89	2	1	1	1	1.000	1		2.081	266	30.610
Q86VV4	Ran-binding protein 3-like OS=Homo sapiens GN=RANBP3L PE=2 SV=2 - [RNB3L_HUMAN]	2.15	1	1	1	1	0.711	1		2.080	465	52.178
E9B3C8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3440 PE=4 SV=1 - [E9B3C8_LEIMU]	0.81	1	1	1	1	0.970	1		2.080	864	92.198
Q9NZ23	Drug-sensitive protein 1 OS=Homo sapiens GN=YA61 PE=2 SV=1 - [Q9NZ23_HUMAN]	5.15	1	1	1	1	1.000	1		2.080	136	14.858
E9AQ08	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0110 PE=4 SV=1 - [E9AQ08_LEIMU]	2.01	1	1	1	1	1.062	1		2.080	795	84.940
E9B116	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2430 PE=4 SV=1 - [E9B116_LEIMU]	0.82	1	1	1	1	1.042	1		2.080	1215	128.009
E7EVC4	E3 ubiquitin-protein ligase TRAIP OS=Homo sapiens GN=TRAIP PE=4 SV=1 - [E7EVC4_HUMAN]	11.11	5	1	1	1	1.000	1		2.079	99	11.357
Q9BX69	Caspase recruitment domain-containing protein 6 OS=Homo sapiens GN=CARD6 PE=1 SV=2 - [CARD6_HUMAN]	0.96	1	1	1	1	1.000	1		2.078	1037	116.394
P13196	5-aminolevulinate synthase, nonspecific, mitochondrial OS=Homo sapiens GN=ALAS1 PE=1 SV=2 - [HEM1_HUMAN]	1.25	2	1	1	1	0.780	1		2.077	640	70.536
E9B0B0	Putative dynein heavy chain OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2880 PE=4 SV=1 - [E9B0B0_LEIMU]	0.19	1	1	1	1	0.593	1		2.077	4230	474.321
Q05923	Dual specificity protein phosphatase 2 OS=Homo sapiens GN=DUSP2 PE=1 SV=1 - [DUS2_HUMAN]	2.23	1	1	1	1	0.970	1		2.077	314	34.378
F4MHM4	Ubiquitously transcribed tetratricopeptide repeat protein Y-linked transcript variant 226 OS=Homo sapiens GN=UTY PE=2 SV=1 - [F4MHM4_HUMAN]	8.74	22	1	1	1				2.076	103	11.215
E9B3A4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3210 PE=4 SV=1 - [E9B3A4_LEIMU]	5.96	1	1	1	1	1.000	1		2.075	218	24.292
B3KU55	cDNA FLJ39219 fis, clone OCBBF2006849, weakly similar to Transmembrane protein 131 OS=Homo sapiens PE=2 SV=1 - [B3KU55_HUMAN]	1.79	4	1	1	2	1.000	2	0.000	2.074	895	99.463
Q6ZR86	cDNA FLJ46557 fis, clone THYMU3039846 OS=Homo sapiens PE=2 SV=1 - [Q6ZR86_HUMAN]	5.66	1	1	1	1	1.000	1		2.074	159	16.733
Q9P2D6	Protein FAM135A OS=Homo sapiens GN=FAM135A PE=1 SV=2 - [F135A_HUMAN]	0.46	1	1	1	1	3.457	1		2.074	1515	169.732
E9B2A8	Putative peptidase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_3090 PE=3 SV=1 - [E9B2A8_LEIMU]	1.02	1	1	1	1	1.000	1		2.073	1080	118.553
E9APC4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1000 PE=4 SV=1 - [E9APC4_LEIMU]	2.38	1	1	1	1	1.000	1		2.073	462	49.766

C9J388	Polypeptide N-acetylgalactosaminyltransferase 3 (Fragment) OS=Homo sapiens GN=GALNT3 PE=4 SV=1 - [C9J388_HUMAN]	14.44	4	1	1	1	1.000	1		2.073	90	10.787
H7C312	Thymidylate kinase (Fragment) OS=Homo sapiens GN=DTYMK PE=1 SV=1 - [H7C312_HUMAN]	5.88	4	1	1	1	0.860	1		2.073	170	19.466
B4DL63	cDNA FLJ51231, highly similar to Mitochondrial ornithine transporter 1 OS=Homo sapiens PE=2 SV=1 - [B4DL63_HUMAN]	2.9	3	1	1	1	0.482	1		2.072	241	25.928
Q5T5P0	Sickle tail protein homolog (Fragment) OS=Homo sapiens GN=KIAA1217 PE=1 SV=1 - [Q5T5P0_HUMAN]	1.28	5	1	1	2	1.000	1		2.071	783	86.676
E9AZS5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1080 PE=4 SV=1 - [E9AZS5_LEIMU]	0.83	1	1	1	1	0.954	1		2.071	723	80.891
Q6ZMK4	FLJ00323 protein (Fragment) OS=Homo sapiens GN=FLJ00323 PE=2 SV=1 - [Q6ZMK4_HUMAN]	2	2	1	1	1	1.050	1		2.071	450	49.917
V9GYS2	Diphthamide biosynthesis protein 1 (Fragment) OS=Homo sapiens GN=DPH1 PE=4 SV=1 - [V9GYS2_HUMAN]	38.46	8	1	1	1	1.000	1		2.071	52	5.513
E9B5Q6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0180 PE=4 SV=1 - [E9B5Q6_LEIMU]	0.7	1	1	1	1	1.000	1		2.069	862	98.044
E9PP47	Ubiquitin carboxyl-terminal hydrolase 33 (Fragment) OS=Homo sapiens GN=USP33 PE=4 SV=3 - [E9PP47_HUMAN]	12.33	4	1	1	1	1.000	1		2.069	73	8.174
M0QZU5	Glioma tumor suppressor candidate region gene 2 protein (Fragment) OS=Homo sapiens GN=GLTSCR2 PE=4 SV=1 - [M0QZU5_HUMAN]	8.08	11	1	1	1	0.921	1		2.069	99	11.957
Q8N9S9	Sorting nexin-31 OS=Homo sapiens GN=SNX31 PE=2 SV=3 - [SNX31_HUMAN]	2.05	1	1	1	1	0.834	1		2.068	440	50.769
E9ANW6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0390 PE=4 SV=1 - [E9ANW6_LEIMU]	2.75	1	1	1	1				2.068	400	42.269
Q86Y38	Xylosyltransferase 1 OS=Homo sapiens GN=XYLT1 PE=1 SV=1 - [XYLT1_HUMAN]	2.09	1	1	2	3	1.013	1		2.068	959	107.501
A0A024R857	F-box and leucine-rich repeat protein 18, isoform CRA_b OS=Homo sapiens GN=FBXL18 PE=4 SV=1 - [A0A024R857_HUMAN]	1.11	3	1	1	1	0.925	1		2.068	718	78.869
E9AW99	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0840 PE=4 SV=1 - [E9AW99_LEIMU]	1.52	1	1	1	1	0.852	1		2.068	527	57.032
E9AKT4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0550 PE=4 SV=1 - [E9AKT4_LEIMU]	3.47	1	2	2	2	1.000	1		2.066	1727	180.377
H0YER2	Activating signal cointegrator 1 complex subunit 1 (Fragment) OS=Homo sapiens GN=ASCC1 PE=1 SV=1 - [H0YER2_HUMAN]	5.52	7	1	1	1	1.942	1		2.066	145	16.713
E9B410	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1730 PE=4 SV=1 - [E9B410_LEIMU]	2.35	1	1	1	1	1.257	1		2.065	893	97.239
E9B6M3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3440 PE=4 SV=1 - [E9B6M3_LEIMU]	8.55	1	1	1	1	1.000	1		2.064	117	13.201
C9JHD8	RNA polymerase II elongation factor ELL3 (Fragment) OS=Homo sapiens GN=ELL3 PE=4 SV=1 - [C9JHD8_HUMAN]	3.4	2	1	1	1	0.758	1		2.064	206	22.874
K7EKB5	Troponin T, slow skeletal muscle (Fragment) OS=Homo sapiens GN=TNNT1 PE=4 SV=2 - [K7EKB5_HUMAN]	22.39	1	1	1	2	1.000	2	0.000	2.064	67	7.096
K7EQZ5	Membrane primary amine oxidase (Fragment) OS=Homo sapiens GN=AOC3 PE=3 SV=1 - [K7EQZ5_HUMAN]	16.96	3	1	1	1	3.380	1		2.063	112	12.931
B2R4K1	cDNA, FLJ92123, highly similar to Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R4K1_HU	25	2	1	1	1	1.000	1		2.062	76	7.926
F8WCU2	Peptidyl-prolyl cis-trans isomerase FKBP7 OS=Homo sapiens GN=FKBP7 PE=1 SV=1 - [F8WCU2_HUMAN]	12.16	6	1	1	1	1.454	1		2.062	74	8.848
E9AK52	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0690 PE=4 SV=1 - [E9AK52_LEIMU]	2.41	1	2	2	2	0.839	2	26.479	2.062	746	80.323
E8NHE3	Putative 60S ribosomal protein L28 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_1130 PE=4 SV=1 - [E8NHE3_LEIMU]	6.12	1	1	1	1	1.916	1		2.062	147	16.226
G3V5L7	Protein NDRG2 (Fragment) OS=Homo sapiens GN=NDRG2 PE=1 SV=1 - [G3V5L7_HUMAN]	3.21	7	1	1	1	1.000	1		2.060	218	24.124
Q8NCZ5	Putative uncharacterized protein DKFZp434E1119 (Fragment) OS=Homo sapiens GN=DKFZp434E1119 PE=2 SV=1 - [Q8NCZ5_HUMAN]	6.67	1	1	1	1	1.843	1		2.060	150	14.822
E9B6K5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3260 PE=4 SV=1 - [E9B6K5_LEIMU]	3.24	1	1	1	1	1.000	1		2.057	309	34.151
E9B736	60S ribosomal protein L37 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_5100 PE=4 SV=1 - [E9B736_LEIMU]	10.53	2	1	1	1	1.000	1		2.056	76	9.123
K7ERF7	Endoplasmic reticulum membrane-associated RNA degradation protein OS=Homo sapiens GN=ERMARD PE=4 SV=1 - [K7ERF7_HUMAN]	2.21	2	1	1	1	1.000	1		2.056	542	62.422
E9AMQ9	Surface antigen-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0580 PE=4 SV=1 - [E9AMQ9_LEIMU]	2.81	1	1	1	1	0.953	1		2.056	285	30.262
K7EIP4	Laminin subunit alpha-3 (Fragment) OS=Homo sapiens GN=LAMA3 PE=1 SV=2 - [K7EIP4_HUMAN]	3.23	5	2	2	2	1.780	2	103.711	2.056	1147	128.203
E9AXE4	Putative epsin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0670 PE=4 SV=1 - [E9AXE4_LEIMU]	1.26	1	1	1	1	1.000	1		2.056	635	70.577
E9AVG8	60S ribosomal protein L32 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1720 PE=4 SV=1 - [E9AVG8_LEIMU]	5.26	2	1	1	1	1.000	1		2.055	133	15.359
A0A087X1H4	Protein archease (Fragment) OS=Homo sapiens GN=ZBTB8OS PE=4 SV=1 - [A0A087X1H4_HUMAN]	9.09	5	1	1	1	1.000	1		2.055	88	10.183
H0Y892	Zinc finger protein 782 (Fragment) OS=Homo sapiens GN=ZNF782 PE=4 SV=1 - [H0Y892_HUMAN]	4.36	140	0	3	4				2.055	688	79.251
E9AUC7	Putative T-complex protein 1, theta subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6910 PE=3 SV=1 - [E9AUC7_LEIMU]	1.86	1	1	1	1	1.101	1		2.054	537	58.203
H3BT82	Syntaxin-1B (Fragment) OS=Homo sapiens GN=STX1B PE=3 SV=2 - [H3BT82_HUMAN]	2.94	2	1	1	1	1.052	1		2.054	204	23.432
E9B2F2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0310 PE=4 SV=1 - [E9B2F2_LEIMU]	0.6	1	1	1	1	1.000	1		2.053	1655	180.960
E9AXR0	Histone-lysine N-methyltransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1780 PE=4 SV=1 - [E9AXR0_LEIMU]	1.5	1	1	1	1	2.272	1		2.051	868	91.405
Q59GI1	Serum response factor (C-fos serum response element-binding transcription factor) variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GI1_HUMAN]	2.71	3	1	1	1	0.924	1		2.050	295	30.230
Q53RD8	Putative uncharacterized protein LOC84524 (Fragment) OS=Homo sapiens GN=LOC84524 PE=4 SV=1 - [Q53RD8_HUMAN]	4.89	2	1	1	1	1.000	1		2.049	266	30.793
Q6V0I7	Protocadherin Fat 4 OS=Homo sapiens GN=FAT4 PE=1 SV=2 - [FAT4_HUMAN]	0.44	1	1	1	1	1.000	1		2.049	4981	542.351
Q68DL7	Uncharacterized protein C18orf63 OS=Homo sapiens GN=C18orf63 PE=2 SV=2 - [CR063_HUMAN]	1.46	1	1	1	1	1.000	1		2.049	685	77.181
P43308	Translocon-associated protein subunit beta OS=Homo sapiens GN=SSR2 PE=1 SV=1 - [SSRB_HUMAN]	3.28	2	1	1	3	1.017	3	7.571	2.048	183	20.122
E7ETM6	Protein SYS1 homolog OS=Homo sapiens GN=SYS1 PE=4 SV=1 - [E7ETM6_HUMAN]	6.67	2	1	1	1	0.228	1		2.047	135	15.173
E9B028	Putative mitochondrial DEAD box protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2080 PE=3 SV=1 - [E9B028_LEIMU]	2.21	1	1	1	1	0.891	1		2.046	544	60.207
E5RIJ0	DNA polymerase beta OS=Homo sapiens GN=POLB PE=4 SV=1 - [E5RIJ0_HUMAN]	4.66	6	1	1	1				2.046	193	21.803
K7EL91	Protein rogdi homolog OS=Homo sapiens GN=ROGDI PE=1 SV=1 - [K7EL91_HUMAN]	19.12	5	1	1	1				2.045	68	7.453
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]	1.02	2	1	1	1	0.922	1		2.045	683	74.634
I3L4X7	G protein pathway suppressor 2 (Fragment) OS=Homo sapiens GN=GPS2 PE=4 SV=2 - [I3L4X7_HUMAN]	9.65	4	3	3	3	1.000	3	25.947	2.044	259	29.316
H7C1P2	Tetratricopeptide repeat protein 7A (Fragment) OS=Homo sapiens GN=TTC7A PE=4 SV=1 - [H7C1P2_HUMAN]	7.41	7	1	1	1	1.000	1		2.044	108	12.050
F1T0I3	Patched domain-containing protein 2 OS=Homo sapiens GN=PTCHD2 PE=2 SV=1 - [F1T0I3_HUMAN]	0.57	2	1	1	1	1.000	1		2.043	1392	152.964
E9AXP2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1620 PE=4 SV=1 - [E9AXP2_LEIMU]	9.66	1	1	1	1	2.955	1		2.042	145	16.678
A0A024R0G8	Sirtuin (Silent mating type information regulation 2 homolog) 2 (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=SIRT2 PE=4 SV=1 - [A0A024R0G8_HUMAN]	1.99	2	1	1	1	1.133	1		2.042	352	39.490
C9JRU6	DCN1-like protein (Fragment) OS=Homo sapiens GN=DCUN1D1 PE=1 SV=1 - [C9JRU6_HUMAN]	12	11	1	1	1	1.047	1		2.041	75	8.774
D0AB08	Lutheran blood group (Fragment) OS=Homo sapiens GN=LU PE=4 SV=1 - [D0AB08_HUMAN]	40.63	1	1	1	1				2.040	32	3.738
E9AS94	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_1400 PE=4 SV=1 - [E9AS94_LEIMU]	3.51	1	1	1	1	1.645	1		2.040	228	25.760
Q8HWS3	DNA-binding protein RFX6 OS=Homo sapiens GN=RFX6 PE=1 SV=2 - [RFX6_HUMAN]	0.75	1	1	1	1	0.946	1		2.040	928	102.396
E9API6	Squalene monooxygenase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1620 PE=4 SV=1 - [E9API6_LEIMU]	1.23	1	1	1	1	0.963	1		2.040	569	63.721
A8MVW0	Protein FAM171A2 OS=Homo sapiens GN=FAM171A2 PE=1 SV=1 - [F1712_HUMAN]	0.97	1	1	1	1	1.004	1		2.040	826	87.381
Q4G0X0	DMD protein OS=Homo sapiens GN=DMD PE=2 SV=1 - [Q4G0X0_HUMAN]	3.11	9	1	2	2	1.000	1		2.039	772	88.745
E9AT96	Receptor-type adenylate cyclase a-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3180 PE=4 SV=1 - [E9AT96_LEIMU]	0.5	1	1	1	1	0.921	1		2.038	1410	152.208
E9B5I7	Phosphatidylinositol 3-kinase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3940 PE=4 SV=1 - [E9B5I7_LEIMU]	0.3	1	1	1	1	0.843	1		2.037	2628	295.969
F5CNE9	Mutant RET proto-oncogene protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [F5CNE9_HUMAN]	18.82	1	1	1	1	1.000	1		2.037	85	9.400
E9AMM1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0220 PE=4 SV=1 - [E9AMM1_LEIMU]	0.98	1	1	1	1	1.462	1		2.037	813	93.327
J3QKX0	Fanconi anemia group J protein (Fragment) OS=Homo sapiens GN=BRIP1 PE=4 SV=1 - [J3QKX0_HUMAN]	7.22	4	1	1	1	1.066	1		2.037	180	19.723
H0YFI1	Ragulator complex protein LAMTOR1 (Fragment) OS=Homo sapiens GN=LAMTOR1 PE=1 SV=1 - [H0YFI1_HUMAN]	13.92	5	1	1	1	0.508	1		2.037	79	8.702
E9ARW3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0120 PE=4 SV=1 - [E9ARW3_LEIMU]	2.63	2	1	1	1				2.036	228	25.999
Q8NF09	FLJ00394 protein (Fragment) OS=Homo sapiens GN=FLJ00394 PE=2 SV=1 - [Q8NF09_HUMAN]	9.66	1	1	1	1	1.000	1		2.036	238	26.124
E9AQ58	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0600 PE=4 SV=1 - [E9AQ58_LEIMU]	0.8	1	1	1	1	0.818	1		2.035	1251	133.203
Q8NBV9	cDNA FLJ90717 fis, clone PLACE1008657, highly similar to Bovine adseverin OS=Homo sapiens PE=2 SV=1 - [Q8NBV9_HUMAN]	2.53	2	1	1	1	1.435	1		2.035	396	44.748
I3L3D9	XIAP-associated factor 1 (Fragment) OS=Homo sapiens GN=XAF1 PE=4 SV=1 - [I3L3D9_HUMAN]	9.02	4	1	1	1	1.156	1		2.034	133	15.499
Q8NE86	Calcium uniporter protein, mitochondrial OS=Homo sapiens GN=MCU PE=1 SV=1 - [MCU_HUMAN]	4.27	3	2	2	2	0.927	2	11.247	2.033	351	39.842
Q8N1Q1	Carbonic anhydrase 13 OS=Homo sapiens GN=CA13 PE=1 SV=1 - [CAH13_HUMAN]	3.44	1	1	1	1	1.000	1		2.033	262	29.425
F5GYI3	Ubiquitin-associated protein 1-like OS=Homo sapiens GN=UBAP1L PE=2 SV=1 - [UBA1L_HUMAN]	1.84	1	1	1	1	0.954	1		2.033	381	40.567
Q86W42	THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1 - [THOC6_HUMAN]	2.93	1	1	1	1	1.000	1		2.029	341	37.511
E9AU12	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5780 PE=4 SV=1 - [E9AU12_LEIMU]	1.94	1	1	1	1	0.361	1		2.028	464	51.045
E9B602	Putative short chain dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1230 PE=4 SV=1 - [E9B602_LEIMU]	3.15	1	1	1	1	1.277	1		2.027	254	28.058
E9B4K5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0370 PE=4 SV=1 - [E9B4K5_LEIMU]	1.49	1	1	1	1	1.000	1		2.027	1140	120.730
E9B3W3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1280 PE=4 SV=1 - [E9B3W3_LEIMU]	5.99	1	1	1	1	0.679	1		2.026	167	19.618
E9B5G4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3730 PE=4 SV=1 - [E9B5G4_LEIMU]	1.76	1	1	1	1				2.024	340	40.541
E9API5	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1610 PE=3 SV=1 - [E9API5_LEIMU]	1.38	1	1	1	1	1.000	1		2.024	724	80.433
A8K2T5	cDNA FLJ77047, highly similar to Homo sapiens zinc finger protein 217 (ZNF217), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K2T5_HUMAN]	1.58	3	1	1	1	1.000	1		2.024	1012	110.971
B4DTY4	cDNA FLJ57086, highly similar to RNA polymerase transcriptional regulation mediator, subunit 6 homolog OS=Homo sapiens PE=2 SV=1 - [B4DTY4_HUMAN]	6.25	5	1	1	1	1.000	1		2.024	128	14.663
E9AVG2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1670 PE=4 SV=1 - [E9AVG2_LEIMU]	2.03	1	1	1	1	0.947	1		2.023	443	48.286
B3KU51	cDNA FLJ39200 fis, clone OCBBF2005343, highly similar to Microtubule-associated serine/threonine-protein kinase 2 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B3I	3.97	17	1	2	2	1.000	1		2.023	630	71.637
E9AYF0	Putative cytochrome c oxidase subunit V OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1710 PE=4 SV=1 - [E9AYF0_LEIMU]	7.14	1	2	2	3	3.236	3	65.088	2.022	196	22.258
E9ALA4	Splicing factor ptsr1-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0870 PE=4 SV=1 - [E9ALA4_LEIMU]	1.88	1	1	1	2	0.994	2	0.936	2.022	372	41.658
O75691	Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3 - [UTP20_HUMAN]	0.32	1	1	1	1	1.000	1		2.022	2785	318.182
E9AL56	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0450 PE=4 SV=1 - [E9AL56_LEIMU]	7.23	1	1	1	1	0.958	1		2.021	166	19.529
E9PH88	PMS1 protein homolog 1 (Fragment) OS=Homo sapiens GN=PMS1 PE=1 SV=1 - [E9PH88_HUMAN]	2.63	1	1	1	1	1.000	1		2.021	266	31.038
Q7LGC8	Carbohydrate sulfotransferase 3 OS=Homo sapiens GN=CHST3 PE=1 SV=3 - [CHST3_HUMAN]	1.46	1	1	1	1	0.861	1		2.020	479	54.671
O94864	STAGA complex 65 subunit gamma OS=Homo sapiens GN=SUPT7L PE=1 SV=1 - [ST65G_HUMAN]	2.42	1	1	1	1	1.000	1		2.020	414	46.164
I3L3E4	Charged multivesicular body protein 6 (Fragment) OS=Homo sapiens GN=CHMP6 PE=1 SV=1 - [I3L3E4_HUMAN]	7.08	2	1	1	1	0.906	1		2.019	113	12.931
Q8NGX2	Olfactory receptor 2T35 OS=Homo sapiens GN=OR2T35 PE=2 SV=1 - [O2T35_HUMAN]	2.17	2	1	1	1	1.000	1		2.019	323	36.077
E9B4J6	Putative calpain-like cysteine peptidase (Putative cysteine peptidase, clan ca, family c2) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0280	0.77	1	1	2	2	0.531	1		2.018	1553	172.511
K7EN65	Methyl-CpG-binding domain protein 1 (Fragment) OS=Homo sapiens GN=MBD1 PE=1 SV=1 - [K7EN65_HUMAN]	5	8	1	1	2	0.748	2	45.227	2.017	240	25.708
H7C1M9	Myosin-IIIb (Fragment) OS=Homo sapiens GN=MYO3B PE=4 SV=1 - [H7C1M9_HUMAN]	2.22	4	1	1	1	0.897	1		2.017	360	41.064
B3KPG6	cDNA FLJ31769 fis, clone NT2RI2007956, highly similar to Chondroitin sulfate glucuronyltransferase (EC 2.4.1.226) OS=Homo sapiens PE=2 SV=1 - [B3KPG6_HUMAN]	1.18	3	1	1	1	1.336	1		2.016	764	85.108
X6RBL6	Methyl-CpG-binding domain protein 2 OS=Homo sapiens GN=MBD2 PE=1 SV=1 - [X6RBL6_HUMAN]	6.64	3	1	1	1	1.207	1		2.015	241	24.603
B7ZCA0	Ras/Rap GTPase-activating protein SynGAP (Fragment) OS=Homo sapiens GN=SYNGAP1 PE=4 SV=2 - [B7ZCA0_HUMAN]	1.8	2	1	1	1	1.000	1		2.015	1279	141.236
E9AR71	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0990 PE=4 SV=1 - [E9AR71_LEIMU]	0.12	1	1	1	1	1.000	1		2.014	6467	674.931
J3QSG3	Leucine-rich repeat-containing protein 36 (Fragment) OS=Homo sapiens GN=LRRC36 PE=4 SV=1 - [J3QSG3_HUMAN]	2.55	1	1	1	1	0.883	1		2.014	275	30.596
Q15542	Transcription initiation factor TFIID subunit 5 OS=Homo sapiens GN=TAF5 PE=1 SV=3 - [TAF5_HUMAN]	1.25	1	1	1	1	1.000	1		2.012	800	86.776
A0A087WUK4	Nuclear receptor subfamily 2 group C member 1 OS=Homo sapiens GN=NR2C1 PE=4 SV=1 - [A0A087WUK4_HUMAN]	2.3	3	1	1	1	1.442	1		2.012	434	47.386
E9PJ27	Poly [ADP-ribose] polymerase 2 OS=Homo sapiens GN=PARP2 PE=4 SV=2 - [E9PJ27_HUMAN]	9.09	3	1	1	1	0.843	1		2.011	110	12.031
J3KSX6	5'(3')-deoxyribonucleotidase, cytosolic type (Fragment) OS=Homo sapiens GN=NT5C PE=1 SV=1 - [J3KSX6_HUMAN]	13.73	3	2	2	2	0.885	2	1.285	2.011	153	17.753
C9JVN9	L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=L2HGDH PE=1 SV=1 - [C9JVN9_HUMAN]	2.27	3	1	1	1	1.000	1		2.010	441	48.444
B4DQ44	cDNA FLJ51274, highly similar to NACHT, LRR and PYD-containing protein 7 OS=Homo sapiens PE=2 SV=1 - [B4DQ44_HUMAN]	1.04	5	1	1	1	1.084	1		2.010	672	76.914
B3KX20	cDNA FLJ44510 fis, clone UTERU3001652, highly similar to Leiomodin-1 OS=Homo sapiens PE=2 SV=1 - [B3KX20_HUMAN]	1.22	5	1	1	1	0.971	1		2.010	491	55.017
E9AQU2	Putative cytochrome c OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1310 PE=3 SV=1 - [E9AQU2_LEIMU]	7.08	1	1	1	1	1.159	1		2.007	113	12.215
E9B5D3	DNA topoisomerase IB, large subunit OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_3440 PE=4 SV=1 - [E9B5D3_LEIMU]	2.2	1	1	1	1	1.000	1		2.007	637	73.830
A0A087WTN8	Ankyrin repeat domain-containing protein 11 OS=Homo sapiens GN=ANKRD11 PE=4 SV=1 - [A0A087WTN8_HUMAN]	3.28	6	1	1	1	1.088	1		2.006	366	40.064
E9B3U1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1070 PE=4 SV=1 - [E9B3U1_LEIMU]	3.29	1	1	1	1	1.000	1		2.006	243	27.764
E9ARR1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1240 PE=4 SV=1 - [E9ARR1_LEIMU]	0.79	2	1	1	1	0.872	1		2.006	764	80.344
E9B1T0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1320 PE=3 SV=1 - [E9B1T0_LEIMU]	1.17	1	2	2	2	1.020	2	2.996	2.005	2566	268.300
B3KQW5	cDNA FLJ33204 fis, clone ADRGL2007125, highly similar to Alpha-1,3-mannosyl-glycoprotein2-beta-N- acetylglucosaminyltransferase OS=Homo sapiens PE=2 SV=1 - [E	4.57	5	1	1	1	1.081	1		2.005	197	23.226
H3BRH4	Eukaryotic elongation factor 2 kinase OS=Homo sapiens GN=EEF2K PE=1 SV=1 - [H3BRH4_HUMAN]	1.94	2	1	1	1	1.029	1		2.005	412	46.717
O94986	Centrosomal protein of 152 kDa OS=Homo sapiens GN=CEP152 PE=1 SV=4 - [CE152_HUMAN]	0.53	1	1	1	1	1.440	1		2.004	1710	195.504
B4DUC9	cDNA FLJ53756, highly similar to SPRY domain-containing protein 4 OS=Homo sapiens PE=2 SV=1 - [B4DUC9_HUMAN]	6.98	2	1	1	1	1.000	1		2.004	129	14.447
M0R1H1	HAUS augmin-like complex subunit 8 OS=Homo sapiens GN=HAUS8 PE=1 SV=1 - [M0R1H1_HUMAN]	41.03	3	1	1	1	1.000	1		2.003	39	4.125
D3DUP4	RAD52 homolog (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=RAD52 PE=4 SV=1 - [D3DUP4_HUMAN]	5.44	4	1	1	1	1.000	1		2.000	147	16.172
B4E186	cDNA FLJ56834 OS=Homo sapiens PE=2 SV=1 - [B4E186_HUMAN]	1.95	2	1	1	1	1.000	1		2.000	410	46.654
A6NM43	Putative T-complex protein 1 subunit theta-like 1 OS=Homo sapiens GN=CCT8L1P PE=5 SV=1 - [TCPQL_HUMAN]	1.44	2	1	1	1	0.893	1		1.999	557	59.476
E9AV25	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0580 PE=4 SV=1 - [E9AV25_LEIMU]	1.74	1	1	1	1	0.729	1		1.999	461	48.183
Q8NC44	Protein FAM134A OS=Homo sapiens GN=FAM134A PE=1 SV=3 - [F134A_HUMAN]	1.66	1	1	1	1	0.634	1		1.998	543	57.794
E9B6A8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2280 PE=4 SV=1 - [E9B6A8_LEIMU]	3.23	2	2	2	2	0.985	1		1.998	465	53.515
E9ANK4	3-methylcrotonoyl-CoA carboxylase beta subunit,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0590 PE=4 SV=1 - [E9ANK4_LEIMU	1.87	1	1	1	1				1.997	534	58.162
A0A087WU05	C-Maf-inducing protein OS=Homo sapiens GN=CMIP PE=4 SV=1 - [A0A087WU05_HUMAN]	2.39	4	2	2	2	0.920	2	12.403	1.996	586	65.242
B4E2H5	cDNA FLJ58741, highly similar to JmjC domain-containing histone demethylation protein 2A (EC 1.14.11.-) OS=Homo sapiens PE=2 SV=1 - [B4E2H5_HUMAN]	1.34	6	2	2	3	1.000	1		1.995	1269	140.946
H7C5D5	Procollagen C-endopeptidase enhancer 2 (Fragment) OS=Homo sapiens GN=PCOLCE2 PE=4 SV=1 - [H7C5D5_HUMAN]	4.29	7	1	1	1				1.994	140	15.347
H0YD26	ATP-dependent RNA helicase DDX25 (Fragment) OS=Homo sapiens GN=DDX25 PE=4 SV=2 - [H0YD26_HUMAN]	5.24	5	1	1	1	1.000	1		1.993	191	20.991
E9APW6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1190 PE=3 SV=1 - [E9APW6_LEIMU]	1.98	1	1	1	1	1.000	1		1.993	556	58.062
Q2HIZ8	CSC1-like protein 1 OS=Homo sapiens GN=TMEM63A PE=2 SV=1 - [Q2HIZ8_HUMAN]	8.54	3	1	1	1	1.000	1		1.993	82	9.568
K7ELQ8	Amino-terminal enhancer of split OS=Homo sapiens GN=AES PE=4 SV=1 - [K7ELQ8_HUMAN]	18.75	3	1	1	1	0.906	1		1.992	48	5.606
E9AW81	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0660 PE=4 SV=1 - [E9AW81_LEIMU]	1.81	1	1	1	1	1.006	1		1.991	886	90.135
E9AL77	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0640 PE=4 SV=1 - [E9AL77_LEIMU]	2.39	1	1	1	1	1.690	1		1.989	335	37.991
Q05C85	CUL9 protein (Fragment) OS=Homo sapiens GN=CUL9 PE=1 SV=1 - [Q05C85_HUMAN]	0.92	3	1	1	1	1.000	1		1.989	763	84.450
Q96N67	Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4 - [DOCK7_HUMAN]	0.42	1	1	1	1	1.000	1		1.988	2140	242.407
K7EJ05	Syntaxin-10 (Fragment) OS=Homo sapiens GN=STX10 PE=1 SV=1 - [K7EJ05_HUMAN]	27.59	8	1	1	1	1.000	1		1.988	58	6.385
E9AV48	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0800 PE=4 SV=1 - [E9AV48_LEIMU]	0.4	1	1	1	1	0.977	1		1.987	2253	249.071
E9ASU5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_1730 PE=4 SV=1 - [E9ASU5_LEIMU]	0.73	1	1	1	1	0.952	1		1.986	961	103.675
E9ATM1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4370 PE=4 SV=1 - [E9ATM1_LEIMU]	0.43	1	1	1	1	1.000	1		1.981	2576	276.584
Q8NDH2	Coiled-coil domain-containing protein 168 OS=Homo sapiens GN=CCDC168 PE=2 SV=2 - [CC168_HUMAN]	0.49	1	1	1	1	1.000	1		1.981	2452	277.778
Q8IZ20	Zinc finger protein 683 OS=Homo sapiens GN=ZNF683 PE=2 SV=3 - [ZN683_HUMAN]	1.53	1	1	1	1	1.130	1		1.979	524	56.868
U3KQQ5	Membralin (Fragment) OS=Homo sapiens GN=TMEM259 PE=1 SV=1 - [U3KQQ5_HUMAN]	5.04	4	1	1	1	1.000	1		1.978	139	15.876
H0YAG1	WD repeat-containing protein 17 (Fragment) OS=Homo sapiens GN=WDR17 PE=4 SV=1 - [H0YAG1_HUMAN]	1.8	3	1	1	1	1.095	1		1.976	557	62.610
E9AKB0	Putative major vault protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0060 PE=4 SV=1 - [E9AKB0_LEIMU]	0.84	1	1	1	1				1.975	833	92.893
A6NC57	Ankyrin repeat domain-containing protein 62 OS=Homo sapiens GN=ANKRD62 PE=2 SV=4 - [ANR62_HUMAN]	1.09	1	1	1	1	1.000	1		1.975	917	106.379
E9AVM3	DNA primase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0390 PE=3 SV=1 - [E9AVM3_LEIMU]	1.33	1	1	1	3	1.000	3	0.000	1.974	451	51.045
Q96MC4	Protein DDC8 homolog OS=Homo sapiens GN=KIAA1731NL PE=2 SV=1 - [DDC8_HUMAN]	1.13	1	1	1	1	1.000	1		1.972	621	69.795
A0A024R6H6	Family with sequence similarity 35, member A, isoform CRA_a OS=Homo sapiens GN=FAM35A PE=4 SV=1 - [A0A024R6H6_HUMAN]	3.4	1	1	1	1	3.385	1		1.970	206	23.636
B2R8D2	cDNA, FLJ93842 OS=Homo sapiens PE=2 SV=1 - [B2R8D2_HUMAN]	3.21	2	1	1	1	0.734	1		1.969	280	32.403
J3KT60	Uncharacterized protein C17orf80 (Fragment) OS=Homo sapiens GN=C17orf80 PE=4 SV=1 - [J3KT60_HUMAN]	10.09	6	2	2	2	0.807	2	32.538	1.969	109	12.287
E9ARY5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0330 PE=4 SV=1 - [E9ARY5_LEIMU]	2.42	1	1	2	2	1.000	1		1.968	784	86.349
Q8TDR2	Serine/threonine-protein kinase 35 OS=Homo sapiens GN=STK35 PE=1 SV=2 - [STK35_HUMAN]	1.31	1	1	1	1	1.113	1		1.967	534	58.015
E9AXB9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0420 PE=4 SV=1 - [E9AXB9_LEIMU]	0.56	1	1	1	1	0.634	1		1.967	1601	172.657
E9AP22	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_1220 PE=4 SV=1 - [E9AP22_LEIMU]	0.64	1	1	1	1	1.000	1		1.966	1410	150.477
F5H1D4	Ankyrin repeat and LEM domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ANKLE2 PE=1 SV=1 - [F5H1D4_HUMAN]	3.49	2	1	1	1	1.000	1		1.965	258	28.366
P42680	Tyrosine-protein kinase Tec OS=Homo sapiens GN=TEC PE=1 SV=2 - [TEC_HUMAN]	1.11	1	1	1	1	1.000	1		1.964	631	73.534
A0A087X1N6	Biogenesis of lysosome-related organelles complex 1 subunit 2 OS=Homo sapiens GN=BLOC1S2 PE=4 SV=1 - [A0A087X1N6_HUMAN]	8.42	3	1	1	1	1.119	1		1.964	95	11.118
P56378	6.8 kDa mitochondrial proteolipid OS=Homo sapiens GN=MP68 PE=1 SV=1 - [68MP_HUMAN]	12.07	2	1	1	1	1.112	1		1.963	58	6.658
E9B3M5	Putative deoxyribodipyrimidine photolyase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_0470 PE=4 SV=1 - [E9B3M5_LEIMU]	1.48	1	1	1	1	1.000	1		1.963	541	61.776
E9AXL5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1360 PE=4 SV=1 - [E9AXL5_LEIMU]	0.83	1	1	1	1	0.622	1		1.963	965	105.137
D6R9A8	Catenin delta-2 OS=Homo sapiens GN=CTNND2 PE=4 SV=3 - [D6R9A8_HUMAN]	2.19	9	1	1	1	0.924	1		1.963	320	35.826
V5M404	Mutant thrombospondin receptor (Fragment) OS=Homo sapiens GN=CD36 PE=4 SV=1 - [V5M404_HUMAN]	21.21	13	1	1	1	1.078	1		1.962	33	3.941
P60602	Reactive oxygen species modulator 1 OS=Homo sapiens GN=ROMO1 PE=1 SV=1 - [ROMO1_HUMAN]	10.13	1	1	1	1	1.144	1		1.962	79	8.177
P08253	72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2 - [MMP2_HUMAN]	1.06	1	1	1	1	1.198	1		1.960	660	73.835
E5RJX3	Metastasis suppressor protein 1 (Fragment) OS=Homo sapiens GN=MTSS1 PE=1 SV=1 - [E5RJX3_HUMAN]	5.31	9	1	1	1	0.741	1		1.959	207	22.420
E9ANI3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0370 PE=4 SV=1 - [E9ANI3_LEIMU]	1.63	1	1	1	1	1.000	1		1.955	615	67.590
Q5T9F4	Extracellular matrix protein 2 (Fragment) OS=Homo sapiens GN=ECM2 PE=4 SV=1 - [Q5T9F4_HUMAN]	3.75	12	1	1	1				1.955	160	18.302
Q05BT9	COL6A1 protein (Fragment) OS=Homo sapiens GN=COL6A1 PE=2 SV=1 - [Q05BT9_HUMAN]	5.61	6	1	1	1	1.330	1		1.955	107	12.268
E9B0E9	Putative ubiquitin hydrolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_0250 PE=4 SV=1 - [E9B0E9_LEIMU]	0.53	2	1	1	1	1.000	1		1.954	1127	125.952
E9PRF4	Histone-lysine N-methyltransferase SETDB1 (Fragment) OS=Homo sapiens GN=SETDB1 PE=1 SV=1 - [E9PRF4_HUMAN]	1.27	2	2	2	2	0.855	2	23.454	1.954	1259	139.300
E9ASJ5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0750 PE=4 SV=1 - [E9ASJ5_LEIMU]	0.86	1	1	1	1	1.000	1		1.954	1285	137.878
E9AQ75	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0770 PE=4 SV=1 - [E9AQ75_LEIMU]	1.07	1	1	1	1	1.000	1		1.953	656	72.488
K7ESP4	Dephospho-CoA kinase domain-containing protein (Fragment) OS=Homo sapiens GN=DCAKD PE=1 SV=1 - [K7ESP4_HUMAN]	4.31	2	1	1	1	1.000	1		1.952	209	24.162
H7C1D1	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 - [H7C1D1_HUMAN]	3.09	3	1	1	1	1.000	1		1.951	291	31.291
B2R8E4	cDNA, FLJ93859, highly similar to Homo sapiens protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform (PPM1A), mRNA OS=Homo sapiens PE=2	2.36	3	1	1	1	1.663	1		1.949	382	42.407
E9B047	Putative glycosomal membrane protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2260 PE=4 SV=1 - [E9B047_LEIMU]	3.6	1	1	1	1	1.000	1		1.948	222	24.126
E9AT83	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3050 PE=4 SV=1 - [E9AT83_LEIMU]	4.93	1	1	1	1	1.020	1		1.948	142	15.890
B4DKP8	cDNA FLJ52317, highly similar to tRNA-dihydrouridine synthase 2-like (EC 1.-.-.-) OS=Homo sapiens PE=2 SV=1 - [B4DKP8_HUMAN]	2.4	3	1	1	1	1.093	1		1.946	458	51.345
Q5HYW3	Retrotransposon gag domain-containing protein 4 OS=Homo sapiens GN=RGAG4 PE=2 SV=1 - [RGAG4_HUMAN]	1.23	1	1	1	1	1.000	1		1.945	569	64.671
B3KW95	cDNA FLJ42616 fis, clone BRACE3014317, highly similar to Homo sapiens vacuolar protein sorting 37A (yeast) (VPS37A), mRNA OS=Homo sapiens PE=2 SV=1 - [B3K\	6.55	3	1	1	1	1.000	1		1.944	168	19.290
O14907	Tax1-binding protein 3 OS=Homo sapiens GN=TAX1BP3 PE=1 SV=2 - [TX1B3_HUMAN]	13.71	1	1	1	1				1.944	124	13.726
E9AZ24	Putative translation initiation factor eIF2B subunit-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1210 PE=3 SV=1 - [E9AZ24_LEI	1.85	1	1	1	1	0.831	1		1.944	541	57.927
D6RAP6	Anaphase-promoting complex subunit 4 (Fragment) OS=Homo sapiens GN=ANAPC4 PE=4 SV=1 - [D6RAP6_HUMAN]	4.32	3	1	1	1	1.106	1		1.942	162	18.315

A1ECB1	NK2 transcription factor related locus 5 (Fragment) OS=Homo sapiens GN=NKX2-5 PE=4 SV=1 - [A1ECB1_HUMAN]	8	7	1	1	1	1.036	1		1.942	100	11.536
E9PJM4	Polyribonucleotide 5'-hydroxyl-kinase Clp1 (Fragment) OS=Homo sapiens GN=CLP1 PE=1 SV=1 - [E9PJM4_HUMAN]	8.33	3	1	1	1	1.000	1		1.942	132	14.880
C9J1X3	Activated CDC42 kinase 1 OS=Homo sapiens GN=TNK2 PE=1 SV=1 - [C9J1X3_HUMAN]	1.25	1	1	1	1	1.012	1		1.942	1040	114.878
D3DS91	A kinase (PRKA) anchor protein 6, isoform CRA_b OS=Homo sapiens GN=AKAP6 PE=4 SV=1 - [D3DS91_HUMAN]	0.34	3	1	1	1	1.899	1		1.942	2077	229.322
E9AWV5	Actin-interacting protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1130 PE=4 SV=1 - [E9AWV5_LEIMU]	0.81	1	1	1	1	2.183	1		1.941	985	108.201
Q9NVH6	Trimethyllysine dioxygenase, mitochondrial OS=Homo sapiens GN=TMLHE PE=1 SV=1 - [TMLH_HUMAN]	1.9	1	1	1	1	1.000	1		1.937	421	49.486
A8K6A8	cDNA FLJ76304, highly similar to Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 4 (ADAMTS4), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K	0.72	2	1	1	1	1.000	1		1.934	837	90.109
B4DWT9	cDNA FLJ55432, highly similar to Probable ATP-dependent RNA helicase DDX58 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DWT9_HUMAN]	1.49	4	1	1	1	0.269	1		1.932	536	60.663
C9JG35	Zinc finger protein 668 (Fragment) OS=Homo sapiens GN=ZNF668 PE=1 SV=2 - [C9JG35_HUMAN]	8.7	6	1	1	1	0.440	1		1.931	92	9.736
E9AMS7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0760 PE=4 SV=1 - [E9AMS7_LEIMU]	0.24	3	1	2	2				1.928	5461	566.976
F5H3X8	Poly [ADP-ribose] polymerase 8 OS=Homo sapiens GN=PARP8 PE=4 SV=1 - [F5H3X8_HUMAN]	1.62	7	1	1	1	1.000	1		1.927	494	55.113
Q5SQQ1	Arginyl-tRNA--protein transferase 1 (Fragment) OS=Homo sapiens GN=ATE1 PE=1 SV=1 - [Q5SQQ1_HUMAN]	3.6	8	1	1	1	0.733	1		1.922	222	24.927
E9B1W9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1690 PE=4 SV=1 - [E9B1W9_LEIMU]	0.77	1	1	1	1	0.931	1		1.921	1420	151.406
C9JVH1	Vesicular, overexpressed in cancer, prosurvival protein 1 OS=Homo sapiens GN=VOPP1 PE=4 SV=1 - [C9JVH1_HUMAN]	5.29	2	1	1	1	1.000	1		1.921	170	19.113
D6RB59	Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=1 - [D6RB59_HUMAN]	1.95	6	1	1	1	0.986	1		1.919	462	53.208
P62304	Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 - [RUXE_HUMAN]	11.96	1	1	1	1	0.972	1		1.919	92	10.797
E9B2L2	60S ribosomal protein L18a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0880 PE=3 SV=1 - [E9B2L2_LEIMU]	4.47	2	1	1	3	1.041	3	5.987	1.918	179	20.792
E9B393	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3090 PE=4 SV=1 - [E9B393_LEIMU]	0.59	1	1	1	1	1.686	1		1.917	1515	159.654
Q96FT7	Acid-sensing ion channel 4 OS=Homo sapiens GN=ASIC4 PE=1 SV=2 - [ASIC4_HUMAN]	1.85	1	1	1	1	0.728	1		1.917	647	70.060
Q53T40	Putative uncharacterized protein FHL2 (Fragment) OS=Homo sapiens GN=FHL2 PE=4 SV=1 - [Q53T40_HUMAN]	11.31	6	2	2	2	1.028	2	4.074	1.917	168	19.294
Q5T370	Arrestin domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ARRDC1 PE=4 SV=1 - [Q5T370_HUMAN]	4.06	3	1	1	1	1.141	1		1.917	271	29.236
P01275	Glucagon OS=Homo sapiens GN=GCG PE=1 SV=3 - [GLUC_HUMAN]	4.44	1	1	1	1	1.000	1		1.915	180	20.896
A2A2N0	Cystatin-8 (Fragment) OS=Homo sapiens GN=CST8 PE=4 SV=1 - [A2A2N0_HUMAN]	5.22	2	1	1	1	1.000	1		1.914	134	15.330
B4DPI4	cDNA FLJ53456, highly similar to Homo sapiens solute carrier family 22 (organic anion transporter), member 8 (SLC22A8), mRNA OS=Homo sapiens PE=2 SV=1 - [B4D	1.33	4	1	1	1	1.612	1		1.914	528	58.309
E9AVS8	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0960 PE=3 SV=1 - [E9AVS8_LEIMU]	0.57	1	1	1	1	0.062	1		1.914	1223	136.016
F2Z3J2	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=1 - [F2Z3J2_HUMAN]	12.5	3	1	1	1	1.000	1		1.913	72	8.216
B4E1T4	cDNA FLJ53955, highly similar to Secreted frizzled-related protein 4 OS=Homo sapiens PE=2 SV=1 - [B4E1T4_HUMAN]	6.41	2	1	2	2	1.000	1		1.912	343	39.190
B4DGV0	cDNA FLJ60251, highly similar to Contactin-6 OS=Homo sapiens PE=2 SV=1 - [B4DGV0_HUMAN]	1.15	2	1	1	1	1.000	1		1.911	956	105.772
Q5VZM0	Ras-related GTP-binding protein B (Fragment) OS=Homo sapiens GN=RRAGB PE=4 SV=1 - [Q5VZM0_HUMAN]	4.64	3	1	1	1	1.000	1		1.910	194	22.905
E9AZ02	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1010 PE=4 SV=1 - [E9AZ02_LEIMU]	0.86	1	1	1	1	1.877	1		1.910	934	105.323
D6W5X5	Solute carrier family 12 (Potassium/chloride transporters), member 9, isoform CRA_c OS=Homo sapiens GN=SLC12A9 PE=4 SV=1 - [D6W5X5_HUMAN]	2.02	8	1	1	1				1.910	446	47.425
Q9Y6V0	Protein piccolo OS=Homo sapiens GN=PCLO PE=1 SV=4 - [PCLO_HUMAN]	0.53	2	2	3	3	0.896	2	16.355	1.910	5065	552.937
F8VWR7	25-hydroxyvitamin D-1 alpha hydroxylase, mitochondrial (Fragment) OS=Homo sapiens GN=CYP27B1 PE=3 SV=1 - [F8VWR7_HUMAN]	6.37	2	1	1	1	1.000	1		1.909	157	17.444
E9AU78	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6420 PE=4 SV=1 - [E9AU78_LEIMU]	4.37	1	1	1	1	1.000	1		1.906	206	22.854
G3V2I3	RCC1 domain-containing protein 1 OS=Homo sapiens GN=RCCD1 PE=1 SV=1 - [G3V2I3_HUMAN]	2.94	1	1	1	1	0.925	1		1.906	374	39.882
E9AW69	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1665 PE=4 SV=1 - [E9AW69_LEIMU]	2.94	1	1	1	1	0.794	1		1.906	238	25.551
Q9BXI2	Mitochondrial ornithine transporter 2 OS=Homo sapiens GN=SLC25A2 PE=1 SV=3 - [ORNT2_HUMAN]	3.99	1	1	1	1	1.000	1		1.906	301	32.559
P0C7P0	CDGSH iron-sulfur domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CISD3 PE=1 SV=1 - [CISD3_HUMAN]	5.51	1	1	1	1	1.237	1		1.905	127	14.206
E9AJX9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_03_0950 PE=4 SV=1 - [E9AJX9_LEIMU]	2.88	1	1	1	1	1.000	1		1.905	556	62.071
A0A087WZE0	Semaphorin-3B (Fragment) OS=Homo sapiens GN=SEMA3B PE=4 SV=1 - [A0A087WZE0_HUMAN]	3.74	3	1	1	1	1.000	1		1.904	214	23.501
E9AS32	Putative ABC transporter OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0800 PE=3 SV=1 - [E9AS32_LEIMU]	1.47	1	1	1	2	1.000	2	0.000	1.903	612	68.538
Q5TCH7	Meiotic recombination protein SPO11 OS=Homo sapiens GN=SPO11 PE=4 SV=1 - [Q5TCH7_HUMAN]	2.54	2	1	1	1	0.452	1		1.903	354	39.910
K7ELI9	Stromal cell-derived factor 2 (Fragment) OS=Homo sapiens GN=SDF2 PE=1 SV=1 - [K7ELI9_HUMAN]	7.69	2	1	1	1	1.000	1		1.901	104	11.283
K7ERI3	Metallophosphoesterase 1 (Fragment) OS=Homo sapiens GN=MPPE1 PE=4 SV=3 - [K7ERI3_HUMAN]	15.94	9	1	1	1	1.000	1		1.899	69	7.932
A8KA24	cDNA FLJ78648, highly similar to Homo sapiens vacuolar protein sorting 54 (yeast) (VPS54), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [A8KA24_HUM	1.24	3	1	1	1				1.899	965	109.264
E9B6U8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4180 PE=4 SV=1 - [E9B6U8_LEIMU]	1.01	1	1	1	1	1.000	1		1.897	592	64.388
E9PKB7	Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=4 SV=1 - [E9PKB7_HUMAN]	3.94	10	1	1	1				1.894	330	37.057
E9B203	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2040 PE=4 SV=1 - [E9B203_LEIMU]	1.2	1	1	1	1	1.000	1		1.894	500	53.350
A8K7G2	cDNA FLJ75762, highly similar to Homo sapiens protease, serine, 25 (PRSS25), nuclear gene encodingmitochondrial protein, transcript variant 1, mRNA OS=Homo sapie	2.4	2	1	1	1	1.000	1		1.893	458	48.768
E9AYG7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_1870 PE=4 SV=1 - [E9AYG7_LEIMU]	0.76	2	1	2	2	1.000	1		1.893	2617	274.662
H0YNY7	Zinc fingers and homeoboxes protein 3 OS=Homo sapiens GN=ZHX3 PE=4 SV=2 - [H0YNY7_HUMAN]	2.54	1	1	1	1	0.861	1		1.893	315	33.959
X5DP92	Benzodiazapine receptor peripheral-associated protein 1 isoform G OS=Homo sapiens GN=BZRAP1 PE=2 SV=1 - [X5DP92_HUMAN]	2.09	12	1	1	1	1.000	1		1.892	719	80.188
E9B2E3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0220 PE=4 SV=1 - [E9B2E3_LEIMU]	0.78	1	1	1	1	1.000	1		1.892	1027	114.694
E9ANK3	Putative cytochrome b5 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0580 PE=3 SV=1 - [E9ANK3_LEIMU]	5.63	1	2	2	2	1.369	2	49.177	1.890	142	15.851
Q15397	Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3 - [K0020_HUMAN]	1.23	1	1	1	1	1.000	1		1.889	648	73.538
H0Y412	Protein PRRC2B (Fragment) OS=Homo sapiens GN=PRRC2B PE=1 SV=1 - [H0Y412_HUMAN]	1.7	2	1	1	1	1.000	1		1.888	588	63.270
B4DP44	cDNA FLJ60751, highly similar to Protein arginine N-methyltransferase 3 (EC 2.1.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DP44_HUMAN]	1.32	4	1	1	1				1.887	454	51.557
E8NHS4	WGS CADB00000000 data, contig 97 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_15_0440b_1 PE=4 SV=1 - [E8NHS4_LEIMU]	3.04	3	1	2	2	1.000	1		1.884	657	73.324
P31629	Transcription factor HIVEP2 OS=Homo sapiens GN=HIVEP2 PE=1 SV=2 - [ZEP2_HUMAN]	0.33	2	1	1	1	1.000	1		1.883	2446	268.885
E9PJ42	Transmembrane protein 41B OS=Homo sapiens GN=TMEM41B PE=1 SV=1 - [E9PJ42_HUMAN]	3.06	3	1	1	1	0.852	1		1.878	196	21.706
B2Z4H6	Cytochrome b OS=Homo sapiens GN=CYTB PE=3 SV=1 - [B2Z4H6_HUMAN]	7.94	254	2	2	2				1.878	378	42.384
B7Z2E2	cDNA FLJ54671, highly similar to Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens PE=2 SV=1 - [B7Z2E2_HUMAN]	1.41	5	1	1	1	1.457	1		1.878	567	62.248
O15014	Zinc finger protein 609 OS=Homo sapiens GN=ZNF609 PE=1 SV=2 - [ZN609_HUMAN]	0.64	1	1	1	1	1.690	1		1.877	1411	151.098
P38936	Cyclin-dependent kinase inhibitor 1 OS=Homo sapiens GN=CDKN1A PE=1 SV=3 - [CDN1A_HUMAN]	10.98	4	1	1	1				1.876	164	18.108
E9AVJ6	Putative GMP synthase (Putative glutamine amidotransferase) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0110 PE=4 SV=1 - [E9AVJ6_LI	2.44	2	1	2	2				1.875	656	71.212
M0R389	Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=3 - [M0R389_HUMAN]	4.24	3	1	1	1	0.927	1		1.875	165	18.402
E9AN27	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0195 PE=4 SV=1 - [E9AN27_LEIMU]	3.17	1	1	1	1	1.000	1		1.874	221	23.501
E9AVA6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1220 PE=4 SV=1 - [E9AVA6_LEIMU]	0.58	1	1	1	1	0.915	1		1.872	1371	146.697
Q86UK5	Limbin OS=Homo sapiens GN=EVC2 PE=1 SV=1 - [LBN_HUMAN]	0.54	1	1	1	1	0.911	1		1.872	1308	147.856
Q5TDG9	DnaJ (Hsp40) homolog, subfamily C, member 16, isoform CRA_a OS=Homo sapiens GN=DNAJC16 PE=2 SV=1 - [Q5TDG9_HUMAN]	3.53	7	2	2	2	1.041	2	6.011	1.870	595	69.270
Q9HBM8	cDNA, FLJ78849, highly similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase alpha (EC 2.3.1.51) OS=Homo sapiens PE=2 SV=1 - [Q9HBM8_HUMAN]	5.26	5	1	1	1	1.288	1		1.869	171	18.744
L8E749	Alternative protein MS4A13 OS=Homo sapiens GN=MS4A13 PE=4 SV=1 - [L8E749_HUMAN]	11.11	1	1	1	1	1.168	1		1.868	63	7.608
G3V2T6	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 - [G3V2T6_HUMAN]	5.18	2	1	1	1	1.102	1		1.867	193	22.649
B3KWR9	Toll-like receptor OS=Homo sapiens PE=2 SV=1 - [B3KWR9_HUMAN]	1.02	2	1	1	1	1.100	1		1.865	784	89.768
F8VQF2	Transmembrane and coiled-coil domains protein 3 (Fragment) OS=Homo sapiens GN=TMCC3 PE=4 SV=1 - [F8VQF2_HUMAN]	5.3	3	1	1	1	0.616	1		1.864	132	15.069
Q8IVH4	Methylmalonic aciduria type A protein, mitochondrial OS=Homo sapiens GN=MMAA PE=1 SV=1 - [MMAA_HUMAN]	5.26	4	2	2	2	1.000	2	0.000	1.863	418	46.509
E9AW28	ABC-thiol transporter OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0250 PE=3 SV=1 - [E9AW28_LEIMU]	0.7	1	1	1	1	1.000	1		1.862	1571	173.850
E9B1X5	Nucleosome assembly protein-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1750 PE=3 SV=1 - [E9B1X5_LEIMU]	5.41	1	2	2	2	2.393	2	22.433	1.861	407	45.152
Q5VWA0	Volume-regulated anion channel subunit LRRC8D (Fragment) OS=Homo sapiens GN=LRRC8D PE=4 SV=3 - [Q5VWA0_HUMAN]	10.26	8	1	1	1	1.000	1		1.860	117	12.874
Q8WX70	Centriolin OS=Homo sapiens GN=CNTRL PE=4 SV=1 - [Q8WX70_HUMAN]	0.89	3	1	1	1	0.451	1		1.859	1007	118.155
Q13257	Mitotic spindle assembly checkpoint protein MAD2A OS=Homo sapiens GN=MAD2L1 PE=1 SV=1 - [MD2L1_HUMAN]	3.41	1	1	1	1	0.944	1		1.858	205	23.495
Q9BXJ4	Complement C1q tumor necrosis factor-related protein 3 OS=Homo sapiens GN=C1QTNF3 PE=1 SV=1 - [C1QT3_HUMAN]	9.35	4	2	2	2				1.852	246	26.977
E9AT37	Cyclin-e binding protein 1-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2600 PE=4 SV=1 - [E9AT37_LEIMU]	0.97	1	1	1	1	1.014	1		1.850	720	75.113
E9AXJ0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1110 PE=4 SV=1 - [E9AXJ0_LEIMU]	0.12	1	1	1	1	1.189	1		1.849	6542	679.131
Q5SQ12	Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=3 SV=1 - [Q5SQ12_HUMAN]	10	4	1	1	1	1.000	1		1.848	160	16.861
E9AVQ8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0740 PE=4 SV=1 - [E9AVQ8_LEIMU]	1.35	1	1	1	1	0.637	1		1.848	592	61.885
E9AUX8	Putative calpain OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0120 PE=4 SV=1 - [E9AUX8_LEIMU]	0.49	1	1	1	1				1.847	1626	180.275
E9PN19	Galectin OS=Homo sapiens GN=LGALS8 PE=4 SV=1 - [E9PN19_HUMAN]	5.86	10	2	2	2	1.000	2	0.000	1.846	290	32.612
E9B2D5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0150 PE=4 SV=1 - [E9B2D5_LEIMU]	1.3	1	1	1	1	1.000	1		1.844	999	110.992
J3QR78	STE20-related kinase adapter protein alpha OS=Homo sapiens GN=STRADA PE=4 SV=1 - [J3QR78_HUMAN]	17.5	3	1	1	1	1.000	1		1.844	40	4.735
C9JB34	55 kDa erythrocyte membrane protein (Fragment) OS=Homo sapiens GN=MPP1 PE=1 SV=1 - [C9JB34_HUMAN]	8.97	6	1	2	2	0.516	1		1.842	156	17.473
E9AMX5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_1240 PE=4 SV=1 - [E9AMX5_LEIMU]	0.36	1	1	1	1	0.961	1		1.842	2475	265.028
Q8N9B5	Junction-mediating and -regulatory protein OS=Homo sapiens GN=JMY PE=1 SV=2 - [JMY_HUMAN]	0.71	1	1	1	1	1.000	1		1.842	988	111.376
E9AMW7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_1160 PE=4 SV=1 - [E9AMW7_LEIMU]	1.08	1	1	1	1	0.721	1		1.840	739	81.591
Q56A86	AKT1 protein (Fragment) OS=Homo sapiens GN=AKT3 PE=2 SV=1 - [Q56A86_HUMAN]	8.37	32	1	3	3	0.390	1		1.840	466	54.253
B7Z1M2	cDNA FLJ53720, highly similar to Interferon regulatory factor 5 OS=Homo sapiens PE=2 SV=1 - [B7Z1M2_HUMAN]	15	13	1	2	2				1.840	140	16.357
E9PKV2	39S ribosomal protein L17, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL17 PE=1 SV=1 - [E9PKV2_HUMAN]	7.75	2	1	1	1	0.940	1		1.838	142	16.361
F5H2P7	Zinc finger protein 26 (Fragment) OS=Homo sapiens GN=ZNF26 PE=4 SV=1 - [F5H2P7_HUMAN]	5.88	1	1	1	1	0.973	1		1.837	153	17.656
Q96BQ5	Coiled-coil domain-containing protein 127 OS=Homo sapiens GN=CCDC127 PE=1 SV=1 - [CC127_HUMAN]	3.08	1	1	1	1	1.000	1		1.837	260	30.815
A0A024RAM5	Protein S100 OS=Homo sapiens GN=S100Z PE=3 SV=1 - [A0A024RAM5_HUMAN]	9.09	2	1	1	1	1.004	1		1.835	99	11.554
Q96JG9	Zinc finger protein 469 OS=Homo sapiens GN=ZNF469 PE=2 SV=3 - [ZN469_HUMAN]	0.51	2	2	2	2	1.000	1		1.835	3925	409.949
E9AKJ5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_05_0890 PE=4 SV=1 - [E9AKJ5_LEIMU]	0.5	1	1	1	1	0.855	1		1.834	1982	208.536
B3KR79	cDNA FLJ33827 fis, clone CTONG2003524 OS=Homo sapiens PE=2 SV=1 - [B3KR79_HUMAN]	1.71	4	2	2	2	1.036	2	5.279	1.833	817	91.988
Q4VC05	B-cell CLL/lymphoma 7 protein family member A OS=Homo sapiens GN=BCL7A PE=1 SV=1 - [BCL7A_HUMAN]	4.29	1	1	1	1	0.118	1		1.833	210	22.796
K7EQ93	RING finger protein unkempt homolog (Fragment) OS=Homo sapiens GN=UNK PE=1 SV=1 - [K7EQ93_HUMAN]	3.64	2	1	1	1				1.830	220	23.725
B3KVM5	cDNA FLJ16751 fis, clone BEAST2001444, highly similar to Orphan nuclear receptor PXR OS=Homo sapiens PE=2 SV=1 - [B3KVM5_HUMAN]	2.8	7	1	1	1	1.097	1		1.829	322	36.926
Q7Z2D7	Pex26pT35insC OS=Homo sapiens GN=PEX26T35insC PE=2 SV=1 - [Q7Z2D7_HUMAN]	8.85	1	1	1	1	1.000	1		1.829	113	10.590
E9AWF8	DNA polymerase theta (Helicase domain only),putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1380 PE=4 SV=1 - [E9AWF8_LEIMU]	0.53	1	1	1	1	1.188	1		1.829	1882	195.686
E9AK82	Putative chloride channel protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_1000 PE=4 SV=1 - [E9AK82_LEIMU]	1.23	1	1	1	1	1.000	1		1.828	1135	122.380
Q8IYE1	Coiled-coil domain-containing protein 13 OS=Homo sapiens GN=CCDC13 PE=2 SV=2 - [CCD13_HUMAN]	1.12	1	1	1	1	1.000	1		1.826	715	80.834
E9AZX4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1540 PE=4 SV=1 - [E9AZX4_LEIMU]	0.81	1	1	1	1	1.000	1		1.826	865	92.689
O14772	Fucose-1-phosphate guanylyltransferase OS=Homo sapiens GN=FPGT PE=1 SV=2 - [FPGT_HUMAN]	1.68	2	1	1	1	1.000	1		1.826	594	66.556
Q12882	Dihydropyrimidine dehydrogenase [NADP(+)] OS=Homo sapiens GN=DPYD PE=1 SV=2 - [DPYD_HUMAN]	1.56	2	2	2	2	0.942	2	8.910	1.825	1025	111.329
Q9BRD4	ZCCHC2 protein OS=Homo sapiens GN=ZCCHC2 PE=2 SV=1 - [Q9BRD4_HUMAN]	2.76	4	1	1	1				1.823	362	38.672
E9ALL4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2090 PE=4 SV=1 - [E9ALL4_LEIMU]	0.44	1	1	1	1	1.121	1		1.822	1602	175.936
Q7Z3C9	Putative uncharacterized protein DKFZp451F1711 (Fragment) OS=Homo sapiens GN=DKFZp451F1711 PE=2 SV=1 - [Q7Z3C9_HUMAN]	0.81	1	1	1	2	1.307	1		1.822	865	93.357
E9AR80	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_1080 PE=4 SV=1 - [E9AR80_LEIMU]	0.96	1	1	1	1	1.000	1		1.817	732	76.887
E9AR53	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0810 PE=4 SV=1 - [E9AR53_LEIMU]	2.64	1	1	1	1	1.410	1		1.817	379	39.367
A6NLP5	Tetratricopeptide repeat protein 36 OS=Homo sapiens GN=TTC36 PE=2 SV=1 - [TTC36_HUMAN]	5.29	1	1	1	1	0.426	1		1.812	189	20.884
Q5T8U5	Surfeit 4 OS=Homo sapiens GN=SURF4 PE=1 SV=1 - [Q5T8U5_HUMAN]	4.3	6	1	1	1	0.886	1		1.810	186	21.114
E9AX29	Putative lysophospholipase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1840 PE=4 SV=1 - [E9AX29_LEIMU]	2.52	1	1	1	1	1.000	1		1.808	278	30.215
B3KMU3	cDNA FLJ12639 fis, clone NT2RM4001938, highly similar to Tripartite motif-containing protein 37 OS=Homo sapiens PE=2 SV=1 - [B3KMU3_HUMAN]	3	5	1	1	1	1.000	1		1.808	300	31.962
B4DY78	cDNA FLJ59827, highly similar to Homo sapiens translin-associated factor X interacting protein 1 (TSNAXIP1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DY78_HUMAI	2.29	7	1	1	1	0.726	1		1.807	350	40.605
E9AKW6	Putative acyl-coenzyme a dehydrogenase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0880 PE=3 SV=1 - [E9AKW6_LEIMU]	1.68	1	1	1	1	1.000	1		1.806	416	45.128
E9APL4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0210 PE=4 SV=1 - [E9APL4_LEIMU]	1.81	1	1	1	1	1.000	1		1.803	443	50.835
E9B4N1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0620 PE=4 SV=1 - [E9B4N1_LEIMU]	0.29	1	1	1	1	0.643	1		1.803	2400	253.797
H7C488	Leucine zipper transcription factor-like protein 1 (Fragment) OS=Homo sapiens GN=LZTFL1 PE=1 SV=1 - [H7C488_HUMAN]	3.4	2	1	1	1	0.681	1		1.802	235	26.889
Q9P2W3	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-13 OS=Homo sapiens GN=GNG13 PE=2 SV=1 - [GBG13_HUMAN]	14.93	1	1	1	1	1.000	1		1.802	67	7.944
E9AXH6	Putative dynein heavy chain OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0980 PE=4 SV=1 - [E9AXH6_LEIMU]	0.23	1	1	1	1	0.932	1		1.802	4702	536.206
A0A024RBL4	RNA binding motif protein 19, isoform CRA_a OS=Homo sapiens GN=RBM19 PE=4 SV=1 - [A0A024RBL4_HUMAN]	0.9	2	1	1	1	1.000	1		1.802	777	86.757
Q99797	Mitochondrial intermediate peptidase OS=Homo sapiens GN=MIPEP PE=1 SV=2 - [MIPEP_HUMAN]	1.12	1	1	1	1				1.801	713	80.589
E9AN07	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_1540 PE=4 SV=1 - [E9AN07_LEIMU]	1.48	1	1	1	1	1.166	1		1.801	607	68.783
E9ANG1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0150 PE=4 SV=1 - [E9ANG1_LEIMU]	0.92	1	1	1	1	1.071	1		1.800	867	92.254
M0R3H2	Inactive serine/threonine-protein kinase VRK3 (Fragment) OS=Homo sapiens GN=VRK3 PE=4 SV=1 - [M0R3H2_HUMAN]	5.13	5	1	1	1	0.877	1		1.798	117	13.223
C9J9T8	Uncharacterized protein C6orf10 OS=Homo sapiens GN=C6orf10 PE=4 SV=2 - [C9J9T8_HUMAN]	1.5	7	1	1	1	1.000	1		1.798	468	50.889
C9J031	E3 ubiquitin-protein ligase makorin-1 (Fragment) OS=Homo sapiens GN=MKRN1 PE=4 SV=1 - [C9J031_HUMAN]	11.52	9	2	2	2	1.000	2	0.000	1.798	165	17.964
Q9HB96	Fanconi anemia group E protein OS=Homo sapiens GN=FANCE PE=1 SV=1 - [FANCE_HUMAN]	1.12	1	1	1	1	0.861	1		1.797	536	58.674
C9JPG5	Semaphorin-3F OS=Homo sapiens GN=SEMA3F PE=4 SV=1 - [C9JPG5_HUMAN]	0.87	4	1	1	1	1.294	1		1.794	686	77.263
M0R2E1	Protein GPR108 (Fragment) OS=Homo sapiens GN=GPR108 PE=4 SV=1 - [M0R2E1_HUMAN]	6.59	7	1	1	1	0.940	1		1.794	167	18.862
H0YA53	Claudin domain-containing protein 1 (Fragment) OS=Homo sapiens GN=CLDND1 PE=4 SV=1 - [H0YA53_HUMAN]	15.28	1	1	1	1	1.000	1		1.792	72	7.530
E9B2E6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0250 PE=4 SV=1 - [E9B2E6_LEIMU]	0.47	1	1	1	1	1.203	1		1.789	1702	185.842
E9AXN7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1570 PE=4 SV=1 - [E9AXN7_LEIMU]	0.39	1	1	1	1	1.000	1		1.788	2289	244.859
E9B2I2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_0590 PE=4 SV=1 - [E9B2I2_LEIMU]	2.53	1	1	1	1	0.949	1		1.788	316	36.679
B3KVB0	cDNA FLJ16322 fis, clone SPLEN2037678, highly similar to Protein D11Lgp1 homolog OS=Homo sapiens PE=2 SV=1 - [B3KVB0_HUMAN]	6.12	5	3	3	3	1.000	3	4.226	1.787	474	50.934
Q7Z6J8	E3 ubiquitin-protein ligase E3D OS=Homo sapiens GN=UBE3D PE=1 SV=2 - [UBE3D_HUMAN]	2.31	1	1	1	1	0.820	1		1.786	389	43.628
B4DTY6	cDNA FLJ59983, highly similar to Zinc finger protein 586 OS=Homo sapiens PE=2 SV=1 - [B4DTY6_HUMAN]	3.47	1	1	1	1	0.887	1		1.786	259	27.922
E9ALB3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_07_0960 PE=4 SV=1 - [E9ALB3_LEIMU]	0.95	1	1	1	1	1.000	1		1.784	1155	128.408
O75063	Glycosaminoglycan xylosylkinase OS=Homo sapiens GN=FAM20B PE=1 SV=1 - [XYLK_HUMAN]	2.44	1	1	1	1	1.000	1		1.784	409	46.403
C9JZA7	Protein SSUH2 homolog (Fragment) OS=Homo sapiens GN=SSUH2 PE=4 SV=1 - [C9JZA7_HUMAN]	5.78	3	1	1	1	0.840	1		1.783	173	19.844
E9AQI8	tRNA (guanine(37)-N1)-methyltransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0310 PE=3 SV=1 - [E9AQI8_LEIMU]	1.6	1	1	1	1	1.000	1		1.782	688	74.071
Q8N9P0	Putative uncharacterized protein FLJ36797 OS=Homo sapiens PE=5 SV=1 - [YF006_HUMAN]	2.56	1	1	1	1	1.000	1		1.781	234	25.143
Q99611	Selenide, water dikinase 2 OS=Homo sapiens GN=SEPHS2 PE=1 SV=3 - [SPS2_HUMAN]	3.13	6	1	2	2	0.795	1		1.780	448	47.276
P15056	Serine/threonine-protein kinase B-raf OS=Homo sapiens GN=BRAF PE=1 SV=4 - [BRAF_HUMAN]	3	6	1	2	2	1.000	1		1.779	766	84.384
F1T0A1	Germ cell-specific gene 1 protein OS=Homo sapiens GN=GSG1 PE=2 SV=1 - [F1T0A1_HUMAN]	2.15	2	1	1	1	0.921	1		1.777	326	36.717
E9AY60	Glutathione peroxidase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0810 PE=3 SV=1 - [E9AY60_LEIMU]	4.6	2	1	1	1	8.042	1		1.776	174	19.244
C9JZN9	Troponin T, fast skeletal muscle OS=Homo sapiens GN=TNNT3 PE=4 SV=1 - [C9JZN9_HUMAN]	2.51	4	1	1	1	1.000	1		1.776	239	28.306
R4GN60	Enkurin domain-containing protein 1 OS=Homo sapiens GN=ENKD1 PE=4 SV=1 - [R4GN60_HUMAN]	3.11	2	1	1	1	1.321	1		1.774	225	24.089
Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 - [SPEB_HUMAN]	2.84	1	1	1	1	1.060	1		1.772	352	37.636
E8NHH1	WGS CADB00000000 data, contig 26 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_15_0440c_1 PE=4 SV=1 - [E8NHH1_LEIMU]	1.14	1	1	1	1	0.866	1		1.771	703	76.859
E9B604	Thioredoxin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1250 PE=4 SV=1 - [E9B604_LEIMU]	3.51	1	1	1	1	1.335	1		1.770	228	25.393
C9K0K2	Cleavage and polyadenylation-specificity factor subunit 4 (Fragment) OS=Homo sapiens GN=CPSF4 PE=4 SV=1 - [C9K0K2_HUMAN]	6.25	4	1	1	1	1.453	1		1.768	112	13.267
E9B1Z5	Tryparedoxin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1960 PE=4 SV=1 - [E9B1Z5_LEIMU]	3.14	1	1	1	1	1.000	1		1.767	191	21.918
P15514	Amphiregulin OS=Homo sapiens GN=AREG PE=1 SV=2 - [AREG_HUMAN]	4.37	2	1	1	1	1.000	1		1.766	252	27.878
Q5VVP1	Spermatogenesis-associated protein 31A6 OS=Homo sapiens GN=SPATA31A6 PE=3 SV=1 - [S31A6_HUMAN]	0.74	8	1	1	1	0.848	1		1.766	1343	147.725
E9APK5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0110 PE=4 SV=1 - [E9APK5_LEIMU]	1.72	1	1	1	1	0.845	1		1.765	523	59.068
Q14209	Transcription factor E2F2 OS=Homo sapiens GN=E2F2 PE=1 SV=1 - [E2F2_HUMAN]	2.52	2	1	1	1	1.043	1		1.760	437	47.476
B3KSM9	Transmembrane channel-like protein OS=Homo sapiens PE=2 SV=1 - [B3KSM9_HUMAN]	1.39	6	1	1	1	1.000	1		1.759	504	58.538
K4DI81	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1 - [K4DI81_HUMAN]	22	4	1	1	1	1.080	1		1.759	50	5.114
Q2YEL0	Preprodynorphin (Fragment) OS=Homo sapiens GN=PDYN PE=4 SV=1 - [Q2YEL0_HUMAN]	2.84	2	1	1	1	0.933	1		1.759	211	23.823
B4DPP8	cDNA FLJ53075, highly similar to Kininogen-1 OS=Homo sapiens PE=2 SV=1 - [B4DPP8_HUMAN]	3.86	5	2	2	2	1.473	1		1.758	415	46.467
P0C7P3	Schlafen family member 14 OS=Homo sapiens GN=SLFN14 PE=2 SV=2 - [SLN14_HUMAN]	0.99	1	1	1	1	0.769	1		1.757	912	103.840
Q9NVH0	Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2 - [EXD2_HUMAN]	3.86	4	2	2	2	1.000	2	0.000	1.757	621	70.308
B3KNL1	cDNA FLJ14826 fis, clone OVARC1000850, highly similar to Large neutral amino acids transporter small subunit 3 OS=Homo sapiens PE=2 SV=1 - [B3KNL1_HUMAN]	1.86	2	1	1	1	1.000	1		1.755	485	52.941
E9ASG7	Putative DNAJ domain protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0500 PE=4 SV=1 - [E9ASG7_LEIMU]	2.16	1	1	1	1	1.000	1		1.755	510	56.423
E9B4L4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0460 PE=4 SV=1 - [E9B4L4_LEIMU]	0.37	1	1	1	1	1.345	1		1.753	2403	253.501
B4DEX0	cDNA FLJ60447, weakly similar to Sorting nexin-6 OS=Homo sapiens PE=2 SV=1 - [B4DEX0_HUMAN]	5.06	1	1	1	1	2.661	1		1.751	158	17.579
A0A087X026	RING finger and transmembrane domain-containing protein 2 OS=Homo sapiens GN=RNFT2 PE=4 SV=1 - [A0A087X026_HUMAN]	2.6	4	1	1	1	1.000	1		1.749	231	25.690
Q53XS6	Antigen p97 (Melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 OS=Homo sapiens GN=MFI2 PE=2 SV=1 - [Q53XS6_HUMAN]	3.64	2	1	1	1	1.000	1		1.748	302	32.702
Q9BYI3	Hyccin OS=Homo sapiens GN=FAM126A PE=1 SV=2 - [HYCCI_HUMAN]	1.92	1	2	2	2	1.000	2	0.000	1.748	521	57.589
H7BZR5	IQ and AAA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=IQCA1 PE=4 SV=1 - [H7BZR5_HUMAN]	1.31	3	1	1	1	1.316	1		1.748	536	63.553
E9B1B8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3430 PE=4 SV=1 - [E9B1B8_LEIMU]	1.25	1	1	1	2				1.745	799	90.606
E9AMG7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0930 PE=4 SV=1 - [E9AMG7_LEIMU]	0.95	1	1	1	2	0.911	2	13.922	1.745	1160	121.038
E9AS31	Putative signal recognition particle protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0790 PE=4 SV=1 - [E9AS31_LEIMU]	1.08	1	1	1	1	1.000	1		1.743	741	80.938
E9B479	Putative GTPase protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2400 PE=4 SV=1 - [E9B479_LEIMU]	1.41	1	1	1	1	0.841	1		1.743	566	62.384
E9B372	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2920 PE=4 SV=1 - [E9B372_LEIMU]	0.83	1	1	1	1	0.729	1		1.743	727	80.459
B2R8K8	cDNA, FLJ93949, highly similar to Homo sapiens NIMA (never in mitosis gene a)-related kinase 7 (NEK7), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8K8_HUMAN]	5.63	4	2	2	2	0.998	2	47.668	1.741	302	34.514
O94993	Transcription factor SOX-30 OS=Homo sapiens GN=SOX30 PE=1 SV=1 - [SOX30_HUMAN]	0.8	1	1	1	1	1.000	1		1.740	753	81.804
E9AT06	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2290 PE=4 SV=1 - [E9AT06_LEIMU]	1.25	1	1	1	1	1.292	1		1.737	481	52.992
A8KA77	cDNA FLJ78669, highly similar to Homo sapiens tetratricopeptide repeat domain 21B (TTC21B), mRNA OS=Homo sapiens PE=2 SV=1 - [A8KA77_HUMAN]	0.46	2	1	1	1	1.039	1		1.737	1316	150.741

O95342	Bile salt export pump OS=Homo sapiens GN=ABCB11 PE=1 SV=2 - [ABCBB_HUMAN]	0.68	1	1	1	1	0.761	1		1.736	1321	146.314
Q8N7A7	cDNA FLJ25861 fis, clone CBR01776 OS=Homo sapiens PE=1 SV=1 - [Q8N7A7_HUMAN]	2.34	1	1	1	2	0.983	2	2.558	1.736	299	31.879
B3KSU1	cDNA FLJ36952 fis, clone BRACE2005773, highly similar to L-seryl-tRNA(Ser/Sec) kinase OS=Homo sapiens PE=2 SV=1 - [B3KSU1_HUMAN]	5.84	1	1	1	1	1.057	1		1.735	257	29.607
H0YK36	Dipeptidyl peptidase 8 (Fragment) OS=Homo sapiens GN=DPP8 PE=4 SV=2 - [H0YK36_HUMAN]	1.94	6	1	1	1	1.000	1		1.735	361	41.169
E9AVG4	RNA-binding regulatory protein (Pumilio family),putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1680 PE=4 SV=1 - [E9AVG4_LEIMU]	1.23	1	1	1	1	1.000	1		1.731	568	63.561
Q7Z4T8	Inactive polypeptide N-acetylgalactosaminyltransferase-like protein 5 OS=Homo sapiens GN=GALNTL5 PE=2 SV=3 - [GLTL5_HUMAN]	1.81	1	1	1	1	1.000	1		1.729	443	51.395
O43753	NK receptor OS=Homo sapiens PE=2 SV=1 - [O43753_HUMAN]	2.31	1	1	1	1	0.874	1		1.728	303	33.304
E9B3B3	Putative chaperone protein DNAj OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3300 PE=4 SV=1 - [E9B3B3_LEIMU]	2.25	1	1	1	1				1.727	400	44.606
B7ZBM4	Syntaxin-16 (Fragment) OS=Homo sapiens GN=STX16 PE=4 SV=3 - [B7ZBM4_HUMAN]	6.61	9	1	1	1				1.726	121	13.374
O94817	Ubiquitin-like protein ATG12 OS=Homo sapiens GN=ATG12 PE=1 SV=1 - [ATG12_HUMAN]	6.43	2	1	1	1	0.912	1		1.726	140	15.104
B2RAJ0	cDNA, FLJ94946, highly similar to Homo sapiens cartilage intermediate layer protein 2 (CILP2), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RAJ0_HUMAN]	0.78	3	1	1	1	1.000	1		1.726	1156	126.223
H0UI04	Epilepsy, progressive myoclonus type 2A, Lafora disease (Laforin), isoform CRA_a OS=Homo sapiens GN=EPM2A PE=4 SV=1 - [H0UI04_HUMAN]	4.15	2	1	1	1	1.000	1		1.725	193	22.145
B4E0A4	cDNA FLJ57023, highly similar to Homo sapiens collagen, type VI, alpha 3 (COL6A3), transcript variant 3, mRNA OS=Homo sapiens PE=2 SV=1 - [B4E0A4_HUMAN]	0.66	5	1	1	1	1.303	1		1.723	1207	132.477
B4DWM8	cDNA FLJ56259, highly similar to Vacuolar ATP synthase subunit S1 (EC 3.6.3.14) OS=Homo sapiens PE=2 SV=1 - [B4DWM8_HUMAN]	2.38	4	1	1	1	1.761	1		1.722	294	32.851
F8W659	RNA-binding protein Nova-1 OS=Homo sapiens GN=NOVA1 PE=1 SV=1 - [F8W659_HUMAN]	2.84	1	1	1	1	1.362	1		1.722	211	22.837
A8K619	cDNA FLJ77751, highly similar to Homo sapiens SREBP cleavage-activating protein (SCAP), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K619_HUMAN]	1.13	3	1	1	1				1.721	886	95.600
Q0MQR4	Poly (ADP-ribose) glycohydrolase OS=Homo sapiens GN=PARG PE=2 SV=1 - [Q0MQR4_HUMAN]	1.02	2	1	1	1	1.000	1		1.719	976	110.901
F6VJC3	Bromodomain adjacent to zinc finger domain protein 2B (Fragment) OS=Homo sapiens GN=BAZ2B PE=4 SV=1 - [F6VJC3_HUMAN]	6.32	5	1	1	1	1.000	1		1.719	95	9.083
A0A087WWN3	RNA exonuclease 1 homolog (Fragment) OS=Homo sapiens GN=REXO1 PE=4 SV=1 - [A0A087WWN3_HUMAN]	4.88	2	1	1	1				1.712	123	14.069
F8VRS5	Meiosis arrest female protein 1 (Fragment) OS=Homo sapiens GN=KIAA0430 PE=4 SV=1 - [F8VRS5_HUMAN]	3.66	4	1	1	1	1.215	1		1.708	164	17.565
H0Y9M1	Spermatogenesis-associated protein 20 (Fragment) OS=Homo sapiens GN=SPATA20 PE=4 SV=1 - [H0Y9M1_HUMAN]	3.24	6	1	1	1	3.439	1		1.708	247	27.772
E9B715	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4870 PE=4 SV=1 - [E9B715_LEIMU]	1.5	1	1	2	2	0.622	1		1.707	999	112.120
E9B4H8	Putative adenylate kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_0110 PE=3 SV=1 - [E9B4H8_LEIMU]	5.05	1	1	1	1				1.705	218	24.514
Q9P0C7	HSPC254 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9P0C7_HUMAN]	4.02	1	1	1	1	1.000	1		1.705	174	19.032
R9RV30	Androgen-induced 1/Golgi SNAP receptor complex member 1 variant 1 fusion protein (Fragment) OS=Homo sapiens GN=AIG1 PE=2 SV=1 - [R9RV30_HUMAN]	11.25	4	1	1	2	1.000	1		1.705	80	9.003
P62875	DNA-directed RNA polymerases I, II, and III subunit RPABC5 OS=Homo sapiens GN=POLR2L PE=1 SV=1 - [RPAB5_HUMAN]	13.43	1	1	1	1	1.000	1		1.703	67	7.640
E9AQ05	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0080 PE=4 SV=1 - [E9AQ05_LEIMU]	4.08	1	1	1	1	1.000	1		1.703	319	36.602
B4DH05	cDNA FLJ60512, highly similar to Tetratricopeptide repeat protein 16 OS=Homo sapiens PE=2 SV=1 - [B4DH05_HUMAN]	1.63	3	1	1	1	1.000	1		1.703	369	42.003
D6R9M7	RNA-binding protein 47 (Fragment) OS=Homo sapiens GN=RBM47 PE=4 SV=3 - [D6R9M7_HUMAN]	7.55	8	1	1	1	0.940	1		1.702	159	17.389
E9AW42	ABC transporter-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0380 PE=3 SV=1 - [E9AW42_LEIMU]	0.89	1	1	1	1	1.000	1		1.701	1235	135.003
E9B1T5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1370 PE=4 SV=1 - [E9B1T5_LEIMU]	1.81	1	1	2	2	1.000	1		1.700	1326	141.697
B7Z8U0	Palmitoyltransferase OS=Homo sapiens PE=2 SV=1 - [B7Z8U0_HUMAN]	4.28	3	1	1	1	0.898	1		1.699	187	21.982
E9AR00	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_17_0310 PE=4 SV=1 - [E9AR00_LEIMU]	0.51	1	1	1	1	1.000	1		1.698	1384	142.121
E9PLD3	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [E9PLD3_HUMAN]	7.07	2	1	1	1	0.954	1		1.693	99	11.593
B3KR25	cDNA FLJ33522 fis, clone BRAMY2006375, highly similar to PIAS-like protein Zimp7 OS=Homo sapiens PE=2 SV=1 - [B3KR25_HUMAN]	1.66	5	1	1	1	1.208	1		1.691	543	58.836
G3V144	SH3 and PX domain-containing protein 2B OS=Homo sapiens GN=SH3PXD2B PE=1 SV=1 - [G3V144_HUMAN]	2.09	2	1	1	1	1.000	1		1.690	430	49.139
Q7Z5M8	Abhydrolase domain-containing protein 12B OS=Homo sapiens GN=ABHD12B PE=2 SV=1 - [AB12B_HUMAN]	1.66	1	1	1	1	2.120	1		1.688	362	40.750
F2Z2B0	Mitochondrial import inner membrane translocase subunit Tim10 B OS=Homo sapiens GN=TIMM10B PE=1 SV=1 - [F2Z2B0_HUMAN]	12.68	2	1	1	2	1.000	1		1.688	71	7.723
E8NHG6	Putative uncharacterized protein LmxM_30_0440_1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LmxM_30_0440_1 PE=4 SV=1 - [E8NHG6_LEIMU]	1.38	1	1	1	1	0.795	1		1.687	724	79.790
Q59GL6	Mitogen-activated protein kinase kinase kinase 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59GL6_HUMAN]	0.48	1	1	1	1				1.686	1455	162.856
B3KQH5	Integrator complex subunit 6 OS=Homo sapiens GN=INTS6 PE=1 SV=1 - [B3KQH5_HUMAN]	2.4	5	2	2	2	0.684	2	27.359	1.683	709	80.461
K7ES72	Calcyphosin (Fragment) OS=Homo sapiens GN=CAPS PE=4 SV=1 - [K7ES72_HUMAN]	8.47	2	1	1	1	1.000	1		1.682	118	12.848
G4V2I8	Anion exchanger-1 variant OS=Homo sapiens PE=2 SV=1 - [G4V2I8_HUMAN]	0.99	4	1	1	1	1.000	1		1.681	911	101.683
H7BZH9	Protein prune homolog 2 (Fragment) OS=Homo sapiens GN=PRUNE2 PE=4 SV=1 - [H7BZH9_HUMAN]	0.38	9	1	1	1	1.000	1		1.681	2384	262.632
Q96BY7	Autophagy-related protein 2 homolog B OS=Homo sapiens GN=ATG2B PE=1 SV=5 - [ATG2B_HUMAN]	0.72	1	2	2	4	1.000	4	3.419	1.679	2078	232.616
Q8N567	Zinc finger CCHC domain-containing protein 9 OS=Homo sapiens GN=ZCCHC9 PE=2 SV=2 - [ZCHC9_HUMAN]	6.27	1	2	2	3	1.022	1		1.679	271	30.457
Q8WXX0	Dynein heavy chain 7, axonemal OS=Homo sapiens GN=DNAH7 PE=1 SV=2 - [DYH7_HUMAN]	0.32	1	1	1	1				1.678	4024	460.862
E9ALF1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2730 PE=4 SV=1 - [E9ALF1_LEIMU]	1.91	1	1	1	1	1.550	1		1.677	366	41.613
Q96N11	Uncharacterized protein C7orf26 OS=Homo sapiens GN=C7orf26 PE=2 SV=1 - [CG026_HUMAN]	1.56	1	1	1	1	0.767	1		1.674	449	50.014
Q8WWL2	Protein spire homolog 2 OS=Homo sapiens GN=SPIRE2 PE=1 SV=3 - [SPIR2_HUMAN]	1.54	1	1	1	1	1.000	1		1.672	714	79.620
Q9BTM9	Ubiquitin-related modifier 1 OS=Homo sapiens GN=URM1 PE=1 SV=1 - [URM1_HUMAN]	12.87	1	1	1	1	1.000	1		1.671	101	11.373
Q15253	F2 protein (Fragment) OS=Homo sapiens GN=F2 PE=2 SV=1 - [Q15253_HUMAN]	8	4	1	1	1				1.670	100	11.295
E9AVF6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1610 PE=4 SV=1 - [E9AVF6_LEIMU]	4.4	1	1	1	1	1.000	1		1.669	159	17.125
J3QLM2	SAP30-binding protein (Fragment) OS=Homo sapiens GN=SAP30BP PE=1 SV=1 - [J3QLM2_HUMAN]	7.53	6	1	1	1	1.053	1		1.667	93	11.004
Q8TF09	Dynein light chain roadblock-type 2 OS=Homo sapiens GN=DYNLRB2 PE=1 SV=1 - [DLRB2_HUMAN]	12.5	5	1	1	1	0.657	1		1.666	96	10.848
Q6UWF7	NXPE family member 4 OS=Homo sapiens GN=NXPE4 PE=2 SV=1 - [NXPE4_HUMAN]	1.29	1	1	1	1	1.000	1		1.663	544	62.223
Q9UK39	Nocturnin OS=Homo sapiens GN=CCRN4L PE=2 SV=2 - [NOCT_HUMAN]	2.78	1	1	1	1				1.660	431	48.165
E9AXH3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0950 PE=4 SV=1 - [E9AXH3_LEIMU]	2.04	1	1	1	1				1.659	441	49.188
B3KPJ4	Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 - [B3KPJ4_HUMAN]	1.51	3	1	1	1	0.313	1		1.659	464	50.371
C4TNW4	Pituitary tumor-transforming protein 1 (Fragment) OS=Homo sapiens GN=PTTG1 PE=4 SV=1 - [C4TNW4_HUMAN]	48.39	4	1	1	1				1.659	31	3.486
B4DWD0	cDNA FLJ50716 OS=Homo sapiens PE=2 SV=1 - [B4DWD0_HUMAN]	10.09	1	1	1	1	1.005	1		1.658	109	13.178
E9AUA4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6680 PE=4 SV=1 - [E9AUA4_LEIMU]	6.21	1	1	1	1	1.000	1		1.655	161	18.421
Q9H176	ZNF143 protein (Fragment) OS=Homo sapiens GN=ZNF143 PE=4 SV=1 - [Q9H176_HUMAN]	1.51	3	1	1	1	1.091	1		1.653	531	57.230
E9AV00	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0330 PE=4 SV=1 - [E9AV00_LEIMU]	0.67	1	1	1	1	1.000	1		1.652	1047	112.037
Q9BV35	Calcium-binding mitochondrial carrier protein SCaMC-3 OS=Homo sapiens GN=SLC25A23 PE=1 SV=2 - [SCMC3_HUMAN]	1.71	1	1	1	1	1.000	1		1.651	468	52.345
B7Z7S9	cDNA FLJ61724, highly similar to Shugoshin-like 2 OS=Homo sapiens PE=2 SV=1 - [B7Z7S9_HUMAN]	3.02	2	3	3	3	1.000	1		1.651	1260	143.886
C9JRT7	Kelch domain-containing protein 10 (Fragment) OS=Homo sapiens GN=KLHDC10 PE=4 SV=1 - [C9JRT7_HUMAN]	22.79	2	2	2	2	1.000	2	0.000	1.650	136	14.363
Q96Q61	Mitochondrial ribosomal protein S14 (Fragment) OS=Homo sapiens GN=MRPS14 PE=4 SV=1 - [Q96Q61_HUMAN]	23.08	3	1	1	1	1.000	1		1.649	39	4.960
B2REA4	PR domain zinc finger protein 1 (Fragment) OS=Homo sapiens GN=PRDM1 PE=4 SV=1 - [B2REA4_HUMAN]	4.09	8	1	1	1	0.764	1		1.649	171	19.973
A4UHR0	C2ORF3 variant 3 OS=Homo sapiens GN=C2orf3 PE=2 SV=1 - [A4UHR0_HUMAN]	2.04	3	1	1	1	1.057	1		1.648	343	39.763
Q9Y468	Lethal(3)malignant brain tumor-like protein 1 OS=Homo sapiens GN=L3MBTL1 PE=1 SV=3 - [LMBL1_HUMAN]	0.8	3	1	1	1	1.502	1		1.647	752	83.830
D6RHX8	G protein-coupled receptor kinase 6 OS=Homo sapiens GN=GRK6 PE=3 SV=1 - [D6RHX8_HUMAN]	1.89	5	1	1	1	1.000	1		1.643	475	54.449
E9AWZ7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1520 PE=4 SV=1 - [E9AWZ7_LEIMU]	1.31	1	1	1	1	1.000	1		1.642	1148	119.785
B4DXZ3	cDNA FLJ54201, highly similar to Homo sapiens peptidase inhibitor 16 (PI16), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DXZ3_HUMAN]	3.85	4	1	1	1	1.000	1		1.641	234	23.859
Q5RHP9	Glutamate-rich protein 3 OS=Homo sapiens GN=ERICH3 PE=2 SV=1 - [ERIC3_HUMAN]	1.05	1	1	2	2	0.938	1		1.640	1530	168.363
E5RJM6	Ankyrin repeat domain-containing protein 65 OS=Homo sapiens GN=ANKRD65 PE=2 SV=2 - [ANR65_HUMAN]	2.51	1	1	1	1				1.638	399	41.472
E9B4U6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1230 PE=4 SV=1 - [E9B4U6_LEIMU]	0.82	1	1	1	1				1.638	1590	174.134
E9AN59	Mitogen-activated protein kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0490 PE=3 SV=1 - [E9AN59_LEIMU]	1.55	1	1	1	1	0.959	1		1.635	388	43.678
F2Z2K5	Janus kinase and microtubule-interacting protein 1 OS=Homo sapiens GN=JAKMIP1 PE=1 SV=1 - [F2Z2K5_HUMAN]	1.05	3	1	1	1	1.353	1		1.635	569	66.365
Q96MK7	cDNA FLJ32214 fis, clone PLACE6003705 OS=Homo sapiens PE=2 SV=1 - [Q96MK7_HUMAN]	3.13	3	1	1	1	1.012	1		1.631	224	24.241
B4DFX7	cDNA FLJ50132, highly similar to F-box only protein 22 OS=Homo sapiens PE=2 SV=1 - [B4DFX7_HUMAN]	2.68	3	1	1	1	1.000	1		1.630	299	32.852
O95169	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Homo sapiens GN=NDUFB8 PE=1 SV=1 - [NDUB8_HUMAN]	15.59	3	2	2	2	0.898	2	15.992	1.628	186	21.751
F8WAX7	Selenoprotein K OS=Homo sapiens GN=SELK PE=4 SV=1 - [F8WAX7_HUMAN]	12.5	4	1	1	1	0.429	1		1.624	72	8.286
E9APF8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1340 PE=4 SV=1 - [E9APF8_LEIMU]	0.52	1	1	1	1	1.443	1		1.624	1345	140.139
E9B755	p21 antigen protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_5290 PE=4 SV=1 - [E9B755_LEIMU]	3.66	1	1	1	1	1.135	1		1.620	191	21.345
K7EP94	Neurofibromin truncated (Fragment) OS=Homo sapiens GN=NF1 PE=4 SV=1 - [K7EP94_HUMAN]	8.55	7	1	1	1	1.000	1		1.619	117	13.290
A6NFI3	Zinc finger protein 316 OS=Homo sapiens GN=ZNF316 PE=1 SV=1 - [ZN316_HUMAN]	1.39	1	2	2	2	1.000	2	0.000	1.618	1004	108.370
E9B6A7	ATP-dependent RNA helicase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2270 PE=4 SV=1 - [E9B6A7_LEIMU]	0.61	1	1	1	1	0.549	1		1.617	1150	127.025
H7C530	Protein KRBA1 (Fragment) OS=Homo sapiens GN=KRBA1 PE=4 SV=1 - [H7C530_HUMAN]	4.79	2	1	1	1	0.913	1		1.616	167	17.647
E9AKP3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0150 PE=4 SV=1 - [E9AKP3_LEIMU]	10.09	1	1	1	1	1.360	1		1.615	109	13.166
P19784	Casein kinase II subunit alpha' OS=Homo sapiens GN=CSNK2A2 PE=1 SV=1 - [CSK22_HUMAN]	9.14	3	3	3	4	0.941	4	11.203	1.613	350	41.187
E9AM42	Protein kinase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0370 PE=4 SV=1 - [E9AM42_LEIMU]	0.43	1	1	1	1	1.000	1		1.610	1389	147.863
E9AJD5	Beta eliminating lyase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_01_0480 PE=4 SV=1 - [E9AJD5_LEIMU]	2.44	1	1	1	1	1.052	1		1.610	369	40.445
B3KRD1	Syntabulin OS=Homo sapiens GN=SYBU PE=2 SV=1 - [B3KRD1_HUMAN]	1.75	4	1	1	1	0.569	1		1.608	457	50.431
Q8IWY9	Codanin-1 OS=Homo sapiens GN=CDAN1 PE=1 SV=4 - [CDAN1_HUMAN]	0.73	1	1	1	1	0.957	1		1.608	1227	134.035
E9APS4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0790 PE=4 SV=1 - [E9APS4_LEIMU]	0.21	1	1	1	1	0.862	1		1.608	4216	449.038
P19387	DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens GN=POLR2C PE=1 SV=2 - [RPB3_HUMAN]	9.82	3	2	2	3	1.000	1		1.608	275	31.422
Q8NH19	Olfactory receptor 10AG1 OS=Homo sapiens GN=OR10AG1 PE=2 SV=1 - [O10AG_HUMAN]	2.33	1	1	1	1	1.382	1		1.604	301	34.081
Q92547	DNA topoisomerase 2-binding protein 1 OS=Homo sapiens GN=TOPBP1 PE=1 SV=3 - [TOPB1_HUMAN]	1.31	5	2	2	3	1.000	1		1.603	1522	170.571
B1AKK6	Uncharacterized protein C1orf21 (Fragment) OS=Homo sapiens GN=C1orf21 PE=1 SV=1 - [B1AKK6_HUMAN]	8.05	1	1	1	1	1.000	1		1.603	87	10.186
P09917	Arachidonate 5-lipoxygenase OS=Homo sapiens GN=ALOX5 PE=1 SV=2 - [LOX5_HUMAN]	2.23	1	2	2	2	1.077	2	5.985	1.603	674	77.933
Q53TS8	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 11 protein OS=Homo sapiens GN=ALS2CR11 PE=2 SV=1 - [AL2SA_HUMAN]	0.96	1	1	1	2	1.000	1		0.000	623	71.114
Q69YW0	Uncharacterized protein C1orf222 OS=Homo sapiens GN=C1orf222 PE=2 SV=1 - [CA222_HUMAN]	2.3	2	1	1	1	1.036	1		0.000	305	33.133
Q8IXQ3	Uncharacterized protein C9orf40 OS=Homo sapiens GN=C9orf40 PE=1 SV=1 - [CI040_HUMAN]	6.7	1	1	1	1	1.000	1		0.000	194	21.050
Q8WW14	Uncharacterized protein C10orf82 OS=Homo sapiens GN=C10orf82 PE=2 SV=2 - [CJ082_HUMAN]	3.04	2	1	1	1	1.000	1		0.000	230	25.906
Q6NT55	Cytochrome P450 4F22 OS=Homo sapiens GN=CYP4F22 PE=2 SV=1 - [CP4FN_HUMAN]	3.77	1	1	1	1	1.000	1		0.000	531	61.918
Q9UK59	Lariat debranching enzyme OS=Homo sapiens GN=DBR1 PE=1 SV=2 - [DBR1_HUMAN]	4.23	3	2	2	2	1.000	2	0.000	0.000	544	61.516
Q8IV48	3'-5' exoribonuclease 1 OS=Homo sapiens GN=ERI1 PE=1 SV=3 - [ERI1_HUMAN]	4.58	3	2	2	3	1.000	3	9.343	0.000	349	40.038
Q9NQ30	Endothelial cell-specific molecule 1 OS=Homo sapiens GN=ESM1 PE=1 SV=2 - [ESM1_HUMAN]	6.52	2	1	1	1	1.000	1		0.000	184	20.081
Q17R55	Protein FAM187B OS=Homo sapiens GN=FAM187B PE=2 SV=2 - [F187B_HUMAN]	4.61	1	1	1	1				0.000	369	42.359
Q9UBI6	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3 - [GBG12_HUMAN]	15.28	1	1	1	1	1.000	1		0.000	72	8.001
Q8IZA3	Histone H1oo OS=Homo sapiens GN=H1FOO PE=2 SV=1 - [H1FOO_HUMAN]	1.73	2	1	1	1	1.877	1		0.000	346	35.792
O94927	HAUS augmin-like complex subunit 5 OS=Homo sapiens GN=HAUS5 PE=1 SV=2 - [HAUS5_HUMAN]	2.05	1	1	1	1				0.000	633	71.638
P01769	Ig heavy chain V-III region GA OS=Homo sapiens PE=1 SV=1 - [HV308_HUMAN]	18.03	1	1	1	1				0.000	122	13.157
Q6DN90	IQ motif and SEC7 domain-containing protein 1 OS=Homo sapiens GN=IQSEC1 PE=1 SV=1 - [IQEC1_HUMAN]	0.83	3	1	1	1	1.000	1		0.000	963	108.247
Q9P266	Junctional protein associated with coronary artery disease OS=Homo sapiens GN=KIAA1462 PE=1 SV=3 - [JCAD_HUMAN]	1.18	1	1	1	1				0.000	1359	148.260
Q9UMN6	Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1 - [KMT2B_HUMAN]	0.48	1	1	1	1	1.000	1		0.000	2715	293.330
Q8N7C0	Leucine-rich repeat-containing protein 52 OS=Homo sapiens GN=LRRC52 PE=1 SV=2 - [LRC52_HUMAN]	7.67	1	1	1	1				0.000	313	35.104
Q6ZN28	Metastasis-associated in colon cancer protein 1 OS=Homo sapiens GN=MACC1 PE=1 SV=2 - [MACC1_HUMAN]	0.82	1	1	1	1	1.000	1		0.000	852	96.578
Q8TE49	OTU domain-containing protein 7A OS=Homo sapiens GN=OTUD7A PE=1 SV=1 - [OTU7A_HUMAN]	0.86	1	1	1	1	1.285	1		0.000	926	100.614
Q8WVD5	RING finger protein 141 OS=Homo sapiens GN=RNF141 PE=1 SV=1 - [RN141_HUMAN]	2.61	3	1	1	1	1.000	1		0.000	230	25.518
A6NCQ9	RING finger protein 222 OS=Homo sapiens GN=RNF222 PE=3 SV=1 - [RN222_HUMAN]	2.73	1	1	1	1				0.000	220	23.751
Q9NZJ4	Sacsin OS=Homo sapiens GN=SACS PE=1 SV=2 - [SACS_HUMAN]	0.17	1	1	1	1	1.074	1		0.000	4579	520.795
O75971	snRNA-activating protein complex subunit 5 OS=Homo sapiens GN=SNAPC5 PE=1 SV=1 - [SNPC5_HUMAN]	17.35	1	1	1	1				0.000	98	11.322
Q9BX66	Sorbin and SH3 domain-containing protein 1 OS=Homo sapiens GN=SORBS1 PE=1 SV=3 - [SRBS1_HUMAN]	0.93	1	1	1	1	1.000	1		0.000	1292	142.426
Q8TBP0	TBC1 domain family member 16 OS=Homo sapiens GN=TBC1D16 PE=2 SV=1 - [TBC16_HUMAN]	1.04	1	1	1	1	1.000	1		0.000	767	86.317
Q9P273	Teneurin-3 OS=Homo sapiens GN=TENM3 PE=2 SV=3 - [TEN3_HUMAN]	0.26	1	1	1	1				0.000	2699	300.760
Q32P41	tRNA (guanine(37)-N1)-methyltransferase OS=Homo sapiens GN=TRMT5 PE=1 SV=2 - [TRM5_HUMAN]	1.77	1	1	1	1	0.913	1		0.000	509	58.209
O43379	WD repeat-containing protein 62 OS=Homo sapiens GN=WDR62 PE=1 SV=4 - [WDR62_HUMAN]	0.72	1	1	1	1	1.000	1		0.000	1518	165.849
Q68DK2	Zinc finger FYVE domain-containing protein 26 OS=Homo sapiens GN=ZFYVE26 PE=1 SV=3 - [ZFY26_HUMAN]	1.18	4	1	2	2	1.000	1		0.000	2539	284.395
D6RA97	Probable E3 SUMO-protein ligase RNF212 OS=Homo sapiens GN=RNF212 PE=4 SV=1 - [D6RA97_HUMAN]	17.31	3	1	1	1	1.000	1		0.000	52	6.108
B4DKD1	Protein tweety homolog OS=Homo sapiens GN=TTYH2 PE=1 SV=1 - [B4DKD1_HUMAN]	1.75	1	1	1	1	1.392	1		0.000	513	56.284
Q5FC08	IL4R nirs variant 1 OS=Homo sapiens GN=IL4R PE=2 SV=1 - [Q5FC08_HUMAN]	9.09	1	1	1	1				0.000	66	7.326
B4DT96	Nucleoporin-like protein 2 OS=Homo sapiens GN=NUPL2 PE=1 SV=1 - [B4DT96_HUMAN]	7.74	5	1	1	1				0.000	155	17.377
J3QKX5	Metalloendopeptidase OS=Homo sapiens GN=MEP1B PE=3 SV=1 - [J3QKX5_HUMAN]	1.86	2	1	1	2	1.000	1		0.000	700	79.393
B9A012	Myosin VIIA, isoform CRA_a OS=Homo sapiens GN=MYO7A PE=4 SV=1 - [B9A012_HUMAN]	0.85	3	1	1	1				0.000	1178	135.713
A8K2L3	Chromosome 9 open reading frame 152 OS=Homo sapiens GN=C9orf152 PE=2 SV=1 - [A8K2L3_HUMAN]	5.96	2	1	1	1	1.000	1		0.000	218	23.884
G3V171	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2 OS=Homo sapiens GN=TPTE2 PE=4 SV=1 - [G3V171_HUMAN]	3.26	2	1	1	1				0.000	337	39.025
Q05DB8	POLR3F protein OS=Homo sapiens GN=POLR3F PE=2 SV=1 - [Q05DB8_HUMAN]	3.27	3	1	1	1	1.000	1		0.000	275	31.001
F1T0K3	Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha OS=Homo sapiens GN=PDE6A PE=2 SV=1 - [F1T0K3_HUMAN]	0.77	2	1	1	1	1.000	1		0.000	779	90.074
A8MYR7	Discs, large (Drosophila) homolog-associated protein 1, isoform CRA_a OS=Homo sapiens GN=DLGAP1 PE=4 SV=1 - [A8MYR7_HUMAN]	1.05	5	1	1	1	0.910	1		0.000	667	74.338
A0A024R3K8	Rho GTPase-activating protein, isoform CRA_c OS=Homo sapiens GN=RICS PE=4 SV=1 - [A0A024R3K8_HUMAN]	1.34	5	1	1	1	1.000	1		0.000	671	73.735
D3DRX8	HCG2017386, isoform CRA_a OS=Homo sapiens GN=hCG_2017386 PE=4 SV=1 - [D3DRX8_HUMAN]	7.21	3	1	1	1	0.944	1		0.000	111	12.638
D3DNM3	HCG1658560, isoform CRA_a OS=Homo sapiens GN=hCG_1658560 PE=4 SV=1 - [D3DNM3_HUMAN]	10	1	1	1	1	1.000	1		0.000	70	7.551
Q9UPJ7	PkB-like (Fragment) OS=Homo sapiens GN=PkB-like 2 PE=4 SV=1 - [Q9UPJ7_HUMAN]	3.13	4	1	1	1	1.764	1		0.000	319	36.597
Q6ZT31	cDNA FLJ45014 fis, clone BRAWH3014609 OS=Homo sapiens PE=2 SV=1 - [Q6ZT31_HUMAN]	1.54	5	1	1	1	1.000	1		0.000	518	59.031
B4DTZ5	cDNA FLJ60157, highly similar to Interferon-induced protein with tetratricopeptide repeats 2 OS=Homo sapiens PE=2 SV=1 - [B4DTZ5_HUMAN]	3.81	5	1	2	2	1.000	1		0.000	472	54.670
Q5SYF9	HAUS augmin-like complex subunit 6 (Fragment) OS=Homo sapiens GN=HAUS6 PE=1 SV=1 - [Q5SYF9_HUMAN]	12.57	3	2	2	2	1.000	2	0.000	0.000	183	20.619
F5H876	Transcription factor SOX-5 OS=Homo sapiens GN=SOX5 PE=4 SV=1 - [F5H876_HUMAN]	4.56	8	1	1	1	1.000	1		0.000	241	26.692
F8WCM7	Thiamin pyrophosphokinase 1 OS=Homo sapiens GN=TPK1 PE=4 SV=1 - [F8WCM7_HUMAN]	7.44	4	1	1	1	1.000	1		0.000	121	14.076
H0YBW3	Integrator complex subunit 10 (Fragment) OS=Homo sapiens GN=INTS10 PE=1 SV=1 - [H0YBW3_HUMAN]	5.11	2	1	1	1				0.000	235	27.520
A8K6N4	cDNA FLJ77152, highly similar to Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1 - [A8K6N4_HUMAN]	1.7	2	1	1	1	1.000	1		0.000	881	100.003
X6RL26	DDB1- and CUL4-associated factor 12 (Fragment) OS=Homo sapiens GN=DCAF12 PE=4 SV=1 - [X6RL26_HUMAN]	4.76	3	1	1	1	1.556	1		0.000	189	21.257
F8W0J4	YEATS domain-containing protein 4 OS=Homo sapiens GN=YEATS4 PE=1 SV=1 - [F8W0J4_HUMAN]	6.36	3	1	1	1	0.598	1		0.000	173	20.118
A0A024RAC6	Transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A), isoform CRA_a OS=Homo sapiens GN=TCEB3 PE=4 SV=1 - [A0A024RAC6_HUMAN]	1.04	2	1	1	1	0.992	1		0.000	772	87.176
A8MQD4	Mesoderm induction early response protein 3 (Fragment) OS=Homo sapiens GN=MIER3 PE=1 SV=1 - [A8MQD4_HUMAN]	6.21	2	1	1	1	1.000	1		0.000	145	16.024
Q9HBZ5	Transcription factor (Fragment) OS=Homo sapiens GN=NKX2B PE=4 SV=1 - [Q9HBZ5_HUMAN]	8.14	2	1	1	1				0.000	86	9.240
B8ZZF2	WD repeat, SAM and U-box domain-containing protein 1 OS=Homo sapiens GN=WDSUB1 PE=1 SV=2 - [B8ZZF2_HUMAN]	1.86	3	1	1	1	1.174	1		0.000	429	47.536
H0Y4B0	ERI1 exoribonuclease 3 (Fragment) OS=Homo sapiens GN=ERI3 PE=1 SV=1 - [H0Y4B0_HUMAN]	3.43	1	1	1	2	1.112	2	15.892	0.000	204	22.875
M0R0B6	Pyroglutamyl-peptidase 1 (Fragment) OS=Homo sapiens GN=PGPEP1 PE=4 SV=2 - [M0R0B6_HUMAN]	6.9	1	1	1	1	1.000	1		0.000	87	8.616
A0A087WY09	Transcription termination factor 1 OS=Homo sapiens GN=TTF1 PE=4 SV=1 - [A0A087WY09_HUMAN]	2.82	3	1	1	1	1.000	1		0.000	390	45.594
E7ER08	Cytochrome P450 26B1 OS=Homo sapiens GN=CYP26B1 PE=3 SV=1 - [E7ER08_HUMAN]	2.49	3	1	1	1	1.000	1		0.000	321	35.978
A6PVK2	Alpha-tocopherol transfer protein-like OS=Homo sapiens GN=TTPAL PE=4 SV=1 - [A6PVK2_HUMAN]	5.84	4	1	1	1	0.981	1		0.000	154	17.662
A5JUM9	Truncated adenomatosis polyposis coli tumor suppressor (Fragment) OS=Homo sapiens GN=APC PE=4 SV=1 - [A5JUM9_HUMAN]	7.14	1	1	1	1	1.000	1		0.000	98	11.114
E5RGJ7	Regulator of G-protein-signaling 22 (Fragment) OS=Homo sapiens GN=RGS22 PE=4 SV=1 - [E5RGJ7_HUMAN]	2.23	1	1	1	1	1.000	1		0.000	269	31.613
H0YHE2	Intraflagellar transport protein 81 homolog (Fragment) OS=Homo sapiens GN=IFT81 PE=1 SV=1 - [H0YHE2_HUMAN]	0.96	3	1	1	1	1.000	1		0.000	624	73.431
A8K8X5	cDNA FLJ76447, highly similar to Homo sapiens cell division cycle associated 7-like (CDCA7L), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8X5_HUMAN]	1.98	2	1	1	1	1.000	1		0.000	454	52.162
H7C175	Serine/threonine-protein kinase LMTK1 OS=Homo sapiens GN=AATK PE=3 SV=2 - [H7C175_HUMAN]	0.87	2	1	1	1	1.254	1		0.000	1271	133.764
F5H6D6	Ubiquitin-protein ligase E3B OS=Homo sapiens GN=UBE3B PE=1 SV=1 - [F5H6D6_HUMAN]	7.69	4	1	1	1				0.000	247	29.235
Q8IWJ3	ATAD2B protein (Fragment) OS=Homo sapiens GN=ATAD2B PE=2 SV=2 - [Q8IWJ3_HUMAN]	7.08	3	1	1	1				0.000	212	25.280
B7Z5D1	cDNA FLJ52020, highly similar to DNA mismatch repair protein Mlh3 OS=Homo sapiens PE=2 SV=1 - [B7Z5D1_HUMAN]	9.6	2	1	1	1				0.000	198	22.402
F8WE49	E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=1 - [F8WE49_HUMAN]	2.26	4	1	1	1	1.000	1		0.000	310	34.892
Q9H7N7	FLJ00031 protein (Fragment) OS=Homo sapiens GN=FLJ00031 PE=2 SV=1 - [Q9H7N7_HUMAN]	4.26	3	1	1	1				0.000	188	21.212
E7EQS8	Methylcytosine dioxygenase TET2 OS=Homo sapiens GN=TET2 PE=1 SV=1 - [E7EQS8_HUMAN]	1.29	1	1	1	1				0.000	2023	225.938
H0YI15	Histone deacetylase 7 (Fragment) OS=Homo sapiens GN=HDAC7 PE=1 SV=1 - [H0YI15_HUMAN]	16.39	3	1	1	1	1.050	1		0.000	61	6.104
I3L4A6	Mixed lineage kinase domain-like protein (Fragment) OS=Homo sapiens GN=MLKL PE=1 SV=1 - [I3L4A6_HUMAN]	4	1	1	1	1	1.117	1		0.000	175	20.032
B2R7W7	cDNA, FLJ93638, Homo sapiens NADPH cytochrome B5 oxidoreductase (NCB5OR), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R7W7_HUMAN]	1.44	2	1	1	3				0.000	487	55.791
W0NTM2	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [W0NTM2_HUMAN]	4.97	1	1	1	1	1.393	1		0.000	181	21.144
B4DLR4	cDNA FLJ55280, highly similar to Heat shock 70 kDa protein 12B OS=Homo sapiens PE=2 SV=1 - [B4DLR4_HUMAN]	1.15	6	1	1	2	1.000	2	0.000	0.000	520	57.549
F8WCC4	Uncharacterized protein C3orf18 OS=Homo sapiens GN=C3orf18 PE=4 SV=1 - [F8WCC4_HUMAN]	16.35	1	1	1	1	1.000	1		0.000	104	10.922
H0YB67	Ribonuclease 3 (Fragment) OS=Homo sapiens GN=DROSHA PE=1 SV=1 - [H0YB67_HUMAN]	7.18	1	1	1	1	1.000	1		0.000	195	23.420
B9DI78	Protein FAM184A (Fragment) OS=Homo sapiens GN=FAM184A PE=4 SV=1 - [B9DI78_HUMAN]	4.24	1	1	1	1	1.000	1		0.000	165	19.144
H0YJN5	Receptor-interacting serine/threonine-protein kinase 3 (Fragment) OS=Homo sapiens GN=RIPK3 PE=4 SV=1 - [H0YJN5_HUMAN]	10.49	3	1	1	1				0.000	162	17.658
K7EN13	Ubiquitin carboxyl-terminal hydrolase 32 (Fragment) OS=Homo sapiens GN=USP32 PE=4 SV=1 - [K7EN13_HUMAN]	4.02	5	1	1	1	0.969	1		0.000	174	19.297
Q59H02	Suppression of tumorigenicity variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H02_HUMAN]	1.39	2	1	1	1	1.000	1		0.000	793	87.852
H0YGW0	B-cell CLL/lymphoma 6 member B protein (Fragment) OS=Homo sapiens GN=BCL6B PE=4 SV=2 - [H0YGW0_HUMAN]	5.19	3	1	1	1	1.594	1		0.000	135	15.244
H0YFB8	Natural killer cells antigen CD94 (Fragment) OS=Homo sapiens GN=KLRD1 PE=4 SV=1 - [H0YFB8_HUMAN]	37.25	6	1	1	1				0.000	51	5.826
D6RHH3	Cyclin-dependent kinase 10 OS=Homo sapiens GN=CDK10 PE=4 SV=1 - [D6RHH3_HUMAN]	12.5	1	1	1	2	1.000	1		0.000	56	6.290
B4DHM9	cDNA FLJ59517, highly similar to SNF-related serine/threonine-protein kinase (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4DHM9_HUMAN]	3.04	4	1	1	1				0.000	559	61.064

F2Z2M5	Centrosome and spindle pole-associated protein 1 OS=Homo sapiens GN=CSPP1 PE=4 SV=1 - [F2Z2M5_HUMAN]	2.23	2	1	1	1	1.000	1		0.000	404	47.492
G1EMV5	MHC class II antigen (Fragment) OS=Homo sapiens GN=HLA-DQB1 PE=4 SV=1 - [G1EMV5_HUMAN]	18.84	4	1	1	1	0.933	1		0.000	69	8.232
D6RA80	Sodium/hydrogen exchanger 9B1 OS=Homo sapiens GN=SLC9B1 PE=4 SV=1 - [D6RA80_HUMAN]	33.33	2	1	1	1				0.000	48	5.548
Q6PH87	CCDC18 protein (Fragment) OS=Homo sapiens GN=CCDC18 PE=2 SV=1 - [Q6PH87_HUMAN]	2.21	5	1	1	1	1.000	1		0.000	362	41.253
Q5TCS5	Polyphosphoinositide phosphatase (Fragment) OS=Homo sapiens GN=FIG4 PE=4 SV=2 - [Q5TCS5_HUMAN]	3.8	3	1	1	1	1.000	1		0.000	237	27.458
E5RKA7	Small integral membrane protein 19 (Fragment) OS=Homo sapiens GN=SMIM19 PE=4 SV=1 - [E5RKA7_HUMAN]	61.11	2	1	1	1				0.000	36	4.331
C9J3B5	Rho GDP-dissociation inhibitor 3 (Fragment) OS=Homo sapiens GN=ARHGDIG PE=4 SV=1 - [C9J3B5_HUMAN]	6.03	4	1	1	2	1.098	2	13.943	0.000	116	13.364
H0Y4R5	Transmembrane protein 201 (Fragment) OS=Homo sapiens GN=TMEM201 PE=1 SV=1 - [H0Y4R5_HUMAN]	2.36	2	1	1	1	1.000	1		0.000	552	59.802
C9JDA1	Follicle-stimulating hormone receptor (Fragment) OS=Homo sapiens GN=FSHR PE=4 SV=1 - [C9JDA1_HUMAN]	5.76	1	1	1	1				0.000	278	31.498
F8WAW5	ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=4 SV=1 - [F8WAW5_HUMAN]	5.88	2	1	1	1	1.000	1		0.000	102	11.120
Q96EG4	LOC646903 protein (Fragment) OS=Homo sapiens GN=LOC646903 PE=2 SV=1 - [Q96EG4_HUMAN]	4.58	1	1	1	1	1.022	1		0.000	153	15.828
F5H2Z7	Coiled-coil domain-containing protein 92 (Fragment) OS=Homo sapiens GN=CCDC92 PE=4 SV=1 - [F5H2Z7_HUMAN]	11.46	4	1	1	1				0.000	96	10.986
H0YE66	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [H0YE66_HUMAN]	3.86	5	1	1	2	1.000	2	0.000	0.000	207	25.016
H0YBT2	Clathrin coat assembly protein AP180 (Fragment) OS=Homo sapiens GN=SNAP91 PE=4 SV=1 - [H0YBT2_HUMAN]	4.5	6	1	1	1	1.000	1		0.000	222	22.055
S4R3Z9	IGF-like family receptor 1 (Fragment) OS=Homo sapiens GN=IGFLR1 PE=4 SV=1 - [S4R3Z9_HUMAN]	13.33	5	1	1	1	1.000	1		0.000	60	6.647
Q5STR5	Death domain-associated protein 6 (Fragment) OS=Homo sapiens GN=DAXX PE=4 SV=3 - [Q5STR5_HUMAN]	6.15	9	1	1	1	1.000	1		0.000	130	14.196
Q59EV2	P2X purinoceptor (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EV2_HUMAN]	2.08	1	1	1	1	1.000	1		0.000	385	43.987
Q8V9L0	E6 protein (Fragment) OS=Homo sapiens GN=E6 PE=4 SV=1 - [Q8V9L0_HUMAN]	18	1	1	1	1				0.000	50	6.131
E9PJ00	ATP-binding cassette sub-family G member 4 (Fragment) OS=Homo sapiens GN=ABCG4 PE=4 SV=1 - [E9PJ00_HUMAN]	7.24	1	1	1	1	1.000	1		0.000	152	16.827
D6R9R7	S-phase kinase-associated protein 2 (Fragment) OS=Homo sapiens GN=SKP2 PE=1 SV=1 - [D6R9R7_HUMAN]	3.53	3	1	1	1	0.943	1		0.000	255	28.628
H0YBN5	Protein virilizer homolog (Fragment) OS=Homo sapiens GN=KIAA1429 PE=1 SV=1 - [H0YBN5_HUMAN]	0.96	2	1	1	1	1.217	1		0.000	730	81.927
K7EJK5	Probable proline dehydrogenase 2 (Fragment) OS=Homo sapiens GN=PRODH2 PE=4 SV=2 - [K7EJK5_HUMAN]	5.04	3	1	1	1	1.000	1		0.000	119	13.185
D6RFH5	Folliculin-interacting protein 2 (Fragment) OS=Homo sapiens GN=FNIP2 PE=4 SV=1 - [D6RFH5_HUMAN]	1.19	2	1	1	1	5.660	1		0.000	673	74.668
E5RK67	Neuronal acetylcholine receptor subunit alpha-2 (Fragment) OS=Homo sapiens GN=CHRNA2 PE=4 SV=1 - [E5RK67_HUMAN]	6.48	1	1	1	2				0.000	108	11.937
Q8N3T5	Putative uncharacterized protein DKFZp761P0818 (Fragment) OS=Homo sapiens GN=DKFZp761P0818 PE=2 SV=2 - [Q8N3T5_HUMAN]	4.24	4	1	1	1	1.000	1		0.000	236	27.306
C9JSR4	Non-syndromic hearing impairment protein 5 (Fragment) OS=Homo sapiens GN=DFNA5 PE=4 SV=1 - [C9JSR4_HUMAN]	66.67	6	1	1	1	1.000	1		0.000	18	2.035
B9EGN3	SYNJ1 protein OS=Homo sapiens GN=SYNJ1 PE=2 SV=1 - [B9EGN3_HUMAN]	0.71	5	1	1	1	1.000	1		0.000	1264	139.855
V9H0T1	cDNA FLJ12219 fis, clone MAMMA1001078 OS=Homo sapiens PE=2 SV=1 - [V9H0T1_HUMAN]	5.65	1	1	1	1	1.000	1		0.000	124	14.216
B4DJW5	cDNA FLJ51979, highly similar to Tumor necrosis factor receptor superfamily member 27 OS=Homo sapiens PE=2 SV=1 - [B4DJW5_HUMAN]	8.09	3	1	1	1	1.000	1		0.000	173	19.207
B4DZD8	cDNA FLJ56183, weakly similar to Mucin-like protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DZD8_HUMAN]	1.08	2	1	1	1	1.000	1		0.000	929	98.381
L0B3M6	RE1-silencing transcription factor variant E1a/E2/E5 OS=Homo sapiens GN=REST PE=2 SV=1 - [L0B3M6_HUMAN]	2.28	12	1	1	1	1.000	1		0.000	307	34.399
B2R7Q9	cDNA, FLJ93562 OS=Homo sapiens PE=2 SV=1 - [B2R7Q9_HUMAN]	1.47	2	1	1	1	1.000	1		0.000	543	59.553
Q9NXL7	cDNA FLJ20173 fis, clone COL09814 OS=Homo sapiens PE=2 SV=1 - [Q9NXL7_HUMAN]	5.88	2	1	1	1	1.000	1		0.000	153	15.972
B4DT76	cDNA FLJ59752, highly similar to Homo sapiens radical S-adenosyl methionine domain containing 2 (RSAD2), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DT76_HUMAN	4.72	3	1	1	1	1.000	1		0.000	254	29.765
B4E0N6	cDNA FLJ56280, highly similar to Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens PE=2 SV=1 - [B4E0N6_HUMAN]	8.94	6	2	2	2	1.170	2	23.554	0.000	235	26.242
B4E2N3	cDNA FLJ52151, highly similar to 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial (EC 1.2.4.4) OS=Homo sapiens PE=2 SV=1 - [B4E2N3_HUMAN]	2.17	3	1	1	1	0.325	1		0.000	322	35.470
B4DMY2	cDNA FLJ55388 OS=Homo sapiens PE=2 SV=1 - [B4DMY2_HUMAN]	6.9	1	1	1	1	1.000	1		0.000	116	13.539
A8KA30	Oxysterol-binding protein OS=Homo sapiens PE=2 SV=1 - [A8KA30_HUMAN]	1.89	4	2	2	2	1.389	2	51.755	0.000	950	108.370
B3KQZ8	cDNA FLJ33349 fis, clone BRACE2003905 OS=Homo sapiens PE=2 SV=1 - [B3KQZ8_HUMAN]	0.86	2	1	1	3	1.000	2	0.000	0.000	811	86.461
L8E9G2	Alternative protein DYZ1L5 OS=Homo sapiens GN=DYZ1L5 PE=4 SV=1 - [L8E9G2_HUMAN]	18.75	2	1	1	1	1.000	1		0.000	64	7.708
L8E7H9	Alternative protein CNTNAP1 OS=Homo sapiens GN=CNTNAP1 PE=4 SV=1 - [L8E7H9_HUMAN]	48.94	1	1	1	2				0.000	47	5.204
Q96NH7	cDNA FLJ30870 fis, clone FEBRA2004237 OS=Homo sapiens PE=2 SV=1 - [Q96NH7_HUMAN]	5.08	1	1	1	1	1.000	1		0.000	295	32.086
B3KV14	cDNA FLJ16042 fis, clone BRAMY2021498, highly similar to ADAMTS-19 OS=Homo sapiens PE=2 SV=1 - [B3KV14_HUMAN]	1	2	1	1	1				0.000	599	67.108
Q9UMP7	G4 protein OS=Homo sapiens GN=G4 PE=2 SV=1 - [Q9UMP7_HUMAN]	8.33	2	2	2	2	1.000	2	0.000	0.000	312	33.852
B4E195	cDNA FLJ51442, highly similar to Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (AASDH), mRNA OS=Homo sapiens PE=2 SV=1 - [B4E195_HUMAN]	0.76	1	1	1	1	1.000	1		0.000	789	88.964
B4DE07	cDNA FLJ52472 OS=Homo sapiens PE=2 SV=1 - [B4DE07_HUMAN]	3.51	4	1	1	1	1.000	1		0.000	171	19.136
A4D1N7	Plexin A4 OS=Homo sapiens GN=PLXNA4 PE=4 SV=1 - [A4D1N7_HUMAN]	1.65	2	1	1	1				0.000	850	93.552
E9ALJ4	Ubiquitin carboxyl-terminal hydrolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2300 PE=3 SV=1 - [E9ALJ4_LEIMU]	1.07	1	1	1	1	1.000	1		0.000	748	81.447
E9B406	DNA polymerase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1690 PE=3 SV=1 - [E9B406_LEIMU]	0.78	1	1	1	1	1.416	1		0.000	1032	116.387
E9AV56	Methionine aminopeptidase 2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0840 PE=3 SV=1 - [E9AV56_LEIMU]	1.51	1	1	1	1	1.000	1		0.000	465	51.228
E9B1F0	Aquaglyceroporin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_0020 PE=3 SV=1 - [E9B1F0_LEIMU]	7.01	1	1	1	1				0.000	314	34.761
E9AXL6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1370 PE=4 SV=1 - [E9AXL6_LEIMU]	2.11	1	1	1	1	1.000	1		0.000	473	53.058
E9AZD1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_2250 PE=4 SV=1 - [E9AZD1_LEIMU]	3.25	1	1	1	1	1.000	1		0.000	246	26.469
E9ATP2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_4580 PE=4 SV=1 - [E9ATP2_LEIMU]	1.33	1	1	1	1	1.000	1		0.000	452	48.784
E9AV88	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1040 PE=3 SV=1 - [E9AV88_LEIMU]	0.33	1	1	1	1				0.000	2129	230.371
E9AZZ7	Putative DNA topoisomerase III OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_1780 PE=3 SV=1 - [E9AZZ7_LEIMU]	0.92	1	1	1	1				0.000	866	96.197
E9B207	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2080 PE=4 SV=1 - [E9B207_LEIMU]	2.11	1	1	1	1	1.000	1		0.000	807	87.055
E9AUT4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_1450 PE=4 SV=1 - [E9AUT4_LEIMU]	2.3	1	1	1	1	1.000	1		0.000	392	42.973
E9ARQ5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_1180 PE=4 SV=1 - [E9ARQ5_LEIMU]	0.45	1	1	1	1	1.016	1		0.000	1551	163.999
E9B3K2	Adenosine deaminase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_0235 PE=4 SV=1 - [E9B3K2_LEIMU]	3.49	1	1	1	1				0.000	601	65.183
E9AZ09	Putative vesicular-fusion ATPase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1070 PE=4 SV=1 - [E9AZ09_LEIMU]	1.01	1	1	1	1				0.000	993	107.516
E9ALS4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1490 PE=4 SV=1 - [E9ALS4_LEIMU]	0.57	1	1	1	1				0.000	1232	132.239
E9AJQ8	Putative long chain fatty Acyl CoA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_03_0230 PE=4 SV=1 - [E9AJQ8_LEIMU]	1.37	1	1	1	1	1.000	1		0.000	656	73.575
E9AQF6	Anti-silencing protein a-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0005 PE=4 SV=1 - [E9AQF6_LEIMU]	7.03	1	1	1	1				0.000	185	20.568
E9AP82	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0580 PE=4 SV=1 - [E9AP82_LEIMU]	0.45	1	1	1	1				0.000	1553	161.958
E9AP61	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_0270 PE=4 SV=1 - [E9AP61_LEIMU]	0.46	1	1	1	1				0.000	1746	189.993
E9AM19	Putative DNA repair helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0590 PE=4 SV=1 - [E9AM19_LEIMU]	0.63	1	1	1	1	1.000	1		0.000	1103	121.253
E9AVD0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1460 PE=4 SV=1 - [E9AVD0_LEIMU]	1.17	1	1	1	1	1.000	1		0.000	682	71.656
E9B0C5	Putative uncharacterized protein LMXM_28_3030 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_3030 PE=4 SV=1 - [E9B0C5_LEIMU]	0.61	1	1	1	1	0.323	1		0.000	1468	147.242
E9ATH9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3970 PE=4 SV=1 - [E9ATH9_LEIMU]	0.9	1	1	1	1	1.000	1		0.000	1333	144.212
E9AS09	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0540 PE=4 SV=1 - [E9AS09_LEIMU]	1.32	1	1	1	1	1.285	1		0.000	530	58.511
E9APX1	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_1240 PE=4 SV=1 - [E9APX1_LEIMU]	2.27	1	1	1	1	1.111	1		0.000	309	31.941
E9APT9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0940 PE=4 SV=1 - [E9APT9_LEIMU]	0.74	1	1	1	1				0.000	815	86.145
E9B1S5	p-glycoprotein e OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1270 PE=3 SV=1 - [E9B1S5_LEIMU]	0.36	1	1	1	1	1.000	1		0.000	1661	181.374
E9AXA8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_0310 PE=4 SV=1 - [E9AXA8_LEIMU]	0.55	1	1	1	1	1.000	1		0.000	1082	116.378
E9AK92	Putative proton motive ATPase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_1110 PE=4 SV=1 - [E9AK92_LEIMU]	0.66	1	1	1	1	1.000	1		0.000	910	96.763
E9ANX4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0460 PE=4 SV=1 - [E9ANX4_LEIMU]	5.36	1	2	2	2	1.000	2	0.000	0.000	784	80.517
E9AT60	Putative pre-mRNA splicing factor ATP-dependent RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2830 PE=4 SV=1 - [E9AT60_	1.47	1	2	2	2	1.230	1		0.000	1088	123.276
E9AVZ2	Putative ser/thr protein phosphatase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_1600 PE=4 SV=1 - [E9AVZ2_LEIMU]	0.99	1	1	1	1	0.337	1		0.000	808	85.537
E9AQR4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1060 PE=4 SV=1 - [E9AQR4_LEIMU]	3.27	5	1	2	2	1.164	1		0.000	979	107.818
E9AYL6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_2350 PE=4 SV=1 - [E9AYL6_LEIMU]	0.81	1	1	1	1	1.000	1		0.000	860	90.583
E9AKX3	Putative glucosamine-fructose-6-phosphate aminotransferase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0950 PE=4 SV=1 - [E9AKX3_LI	1.19	1	1	1	1	1.000	1		0.000	670	73.087
E9AXY5	Methylmalonyl-coa epimerase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_0020 PE=4 SV=1 - [E9AXY5_LEIMU]	8.61	1	1	1	1	1.027	1		0.000	151	16.397
E9B2Z9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2180 PE=4 SV=1 - [E9B2Z9_LEIMU]	4.72	1	1	1	1	1.000	1		0.000	233	26.181
E9AW71	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0560 PE=3 SV=1 - [E9AW71_LEIMU]	0.91	1	1	1	1	1.000	1		0.000	656	75.138
E9B0Z3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2200 PE=4 SV=1 - [E9B0Z3_LEIMU]	7.69	1	1	1	1				0.000	169	18.062
E9B6R8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3900 PE=4 SV=1 - [E9B6R8_LEIMU]	2.64	1	1	1	1	1.000	1		0.000	341	39.987
E9AW31	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0280 PE=4 SV=1 - [E9AW31_LEIMU]	0.64	1	1	1	1	1.000	1		0.000	1098	117.848
E9AMW3	Mitochondrial RNA binding protein 2 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_1120 PE=4 SV=1 - [E9AMW3_LEIMU]	3.31	1	1	1	2	1.000	1		0.000	242	26.875
E9AWQ2	Ubiquitin carboxyl-terminal hydrolase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0620 PE=3 SV=1 - [E9AWQ2_LEIMU]	1.24	1	1	1	1	1.000	1		0.000	807	89.152
E9B288	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2890 PE=4 SV=1 - [E9B288_LEIMU]	0.48	1	1	1	1				0.000	1240	135.208
E9AUR4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_1240 PE=4 SV=1 - [E9AUR4_LEIMU]	2.33	1	3	3	4	1.026	2	3.771	0.000	2751	293.758
E9AU84	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_6500 PE=4 SV=1 - [E9AU84_LEIMU]	1.23	1	1	1	1				0.000	652	71.048
E9AQR2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1020 PE=4 SV=1 - [E9AQR2_LEIMU]	3.16	6	2	3	3				0.000	950	103.478
E9APN0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_14_0370 PE=4 SV=1 - [E9APN0_LEIMU]	0.37	1	1	1	1	0.943	1		0.000	2672	278.560
E9B6Y8	Putative phosphatidylserine decarboxylase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4590 PE=4 SV=1 - [E9B6Y8_LEIMU]	1.7	1	1	1	1				0.000	352	39.469
E9AMS0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_09_0690 PE=4 SV=1 - [E9AMS0_LEIMU]	2.61	1	1	1	1				0.000	306	33.928
E9ASB8	Phosphoglycan beta 1,3 galactosyltransferase 4 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0010 PE=4 SV=1 - [E9ASB8_LEIMU]	3.07	4	2	2	2	1.000	2	0.000	0.000	815	91.568
E9AK77	Putative adenylate kinase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0960 PE=3 SV=1 - [E9AK77_LEIMU]	4.83	1	1	1	1	1.000	1		0.000	207	22.736
E9B041	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_28_2200 PE=4 SV=1 - [E9B041_LEIMU]	0.74	1	1	1	1				0.000	947	108.014
E9AVD5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_1510 PE=4 SV=1 - [E9AVD5_LEIMU]	1.03	1	1	1	1				0.000	1458	152.079
E9AM72	Putative syntaxin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0070 PE=4 SV=1 - [E9AM72_LEIMU]	4.33	1	1	1	1				0.000	254	29.788
E9ANR1	Putative ATP-binding cassette protein subfamily A, member 2 (Fragment) OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_1220 PE=3 SV=1 - [I	0.42	2	1	1	1	1.000	1		0.000	1686	185.987
E9AM80	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_0020 PE=4 SV=1 - [E9AM80_LEIMU]	5.13	1	1	1	1	1.000	1		0.000	273	30.321
Q12974	Protein tyrosine phosphatase type IVA 2 OS=Homo sapiens GN=PTP4A2 PE=1 SV=1 - [TP4A2_HUMAN]	11.38	1	1	1	1	1.000	1		0.000	167	19.115
Q86UQ4	ATP-binding cassette sub-family A member 13 OS=Homo sapiens GN=ABCA13 PE=2 SV=3 - [ABCAD_HUMAN]	0.22	1	1	1	1	1.268	1		0.000	5058	575.791
Q8NC06	Acyl-CoA-binding domain-containing protein 4 OS=Homo sapiens GN=ACBD4 PE=1 SV=2 - [ACBD4_HUMAN]	13.81	4	1	1	1				0.000	268	30.288
Q5TGY3	AT-hook DNA-binding motif-containing protein 1 OS=Homo sapiens GN=AHDC1 PE=1 SV=1 - [AHDC1_HUMAN]	1.5	1	1	1	1	1.000	1		0.000	1603	168.245
Q9UKA4	A-kinase anchor protein 11 OS=Homo sapiens GN=AKAP11 PE=1 SV=1 - [AKA11_HUMAN]	0.37	1	1	1	1	0.836	1		0.000	1901	210.380
Q5JPF3	Ankyrin repeat domain-containing protein 36C OS=Homo sapiens GN=ANKRD36C PE=2 SV=3 - [AN36C_HUMAN]	0.67	2	1	1	1	1.000	1		0.000	1778	199.626
Q75V66	Anoctamin-5 OS=Homo sapiens GN=ANO5 PE=1 SV=1 - [ANO5_HUMAN]	0.66	1	1	1	1	0.860	1		0.000	913	107.118
Q8IW93	Rho guanine nucleotide exchange factor 19 OS=Homo sapiens GN=ARHGEF19 PE=1 SV=1 - [ARHGJ_HUMAN]	2.99	1	2	2	2	1.000	2	0.000	0.000	802	89.142
Q8IZT6	Abnormal spindle-like microcephaly-associated protein OS=Homo sapiens GN=ASPM PE=1 SV=2 - [ASPM_HUMAN]	0.32	1	1	1	1	1.000	1		0.000	3477	409.540
Q9BSB4	Autophagy-related protein 101 OS=Homo sapiens GN=ATG101 PE=1 SV=1 - [ATGA1_HUMAN]	8.26	1	1	1	1	1.000	1		0.000	218	24.987
Q8TE60	A disintegrin and metalloproteinase with thrombospondin motifs 18 OS=Homo sapiens GN=ADAMTS18 PE=1 SV=3 - [ATS18_HUMAN]	1.72	1	1	1	1				0.000	1221	135.079
O15072	A disintegrin and metalloproteinase with thrombospondin motifs 3 OS=Homo sapiens GN=ADAMTS3 PE=2 SV=4 - [ATS3_HUMAN]	0.66	1	1	1	1	1.000	1		0.000	1205	135.515
Q9UMQ3	Homeobox protein BarH-like 2 OS=Homo sapiens GN=BARX2 PE=1 SV=3 - [BARX2_HUMAN]	3.58	1	1	1	1	1.000	1		0.000	279	31.168
Q96NH3	Protein broad-minded OS=Homo sapiens GN=TBC1D32 PE=2 SV=4 - [BROMI_HUMAN]	0.95	1	1	1	1	1.968	1		0.000	1257	144.663
Q4AC94	C2 domain-containing protein 3 OS=Homo sapiens GN=C2CD3 PE=1 SV=4 - [C2CD3_HUMAN]	0.93	1	1	1	1	1.000	1		0.000	2353	260.226
Q9P1Y5	Calmodulin-regulated spectrin-associated protein 3 OS=Homo sapiens GN=CAMSAP3 PE=1 SV=2 - [CAMP3_HUMAN]	1.44	1	1	1	2	1.000	2	0.000	0.000	1249	134.666
Q8NDL9	Cytosolic carboxypeptidase-like protein 5 OS=Homo sapiens GN=AGBL5 PE=2 SV=1 - [CBPC5_HUMAN]	1.47	1	1	1	1	1.022	1		0.000	886	97.472
Q7Z3E2	Coiled-coil domain-containing protein 186 OS=Homo sapiens GN=CCDC186 PE=1 SV=2 - [CC186_HUMAN]	0.78	2	1	1	1	1.176	1		0.000	898	103.623
Q6UXH8	Collagen and calcium-binding EGF domain-containing protein 1 OS=Homo sapiens GN=CCBE1 PE=1 SV=1 - [CCBE1_HUMAN]	11.08	1	1	1	1				0.000	406	44.074
Q9H6F5	Coiled-coil domain-containing protein 86 OS=Homo sapiens GN=CCDC86 PE=1 SV=1 - [CCD86_HUMAN]	2.5	1	1	1	1	1.012	1		0.000	360	40.211
P32246	C-C chemokine receptor type 1 OS=Homo sapiens GN=CCR1 PE=1 SV=1 - [CCR1_HUMAN]	1.97	1	1	1	1	1.143	1		0.000	355	41.146
O43866	CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1 - [CD5L_HUMAN]	5.48	1	1	1	1	1.000	1		0.000	347	38.063
Q9NX76	CKLF-like MARVEL transmembrane domain-containing protein 6 OS=Homo sapiens GN=CMTM6 PE=1 SV=1 - [CKLF6_HUMAN]	3.83	1	1	1	3	1.145	3	7.679	0.000	183	20.406
Q2KHT3	Protein CLEC16A OS=Homo sapiens GN=CLEC16A PE=2 SV=2 - [CL16A_HUMAN]	1.71	1	1	1	1				0.000	1053	117.640
Q8N2M8	CLK4-associating serine/arginine rich protein OS=Homo sapiens GN=CLASRP PE=1 SV=4 - [CLASR_HUMAN]	1.19	1	1	1	1	1.171	1		0.000	674	77.115
Q15846	Clusterin-like protein 1 OS=Homo sapiens GN=CLUL1 PE=1 SV=1 - [CLUL1_HUMAN]	2.15	4	1	1	1	0.855	1		0.000	466	54.180
P24311	Cytochrome c oxidase subunit 7B, mitochondrial OS=Homo sapiens GN=COX7B PE=1 SV=2 - [COX7B_HUMAN]	8.75	1	1	1	3	1.015	3	0.096	0.000	80	9.155
Q86TM3	Probable ATP-dependent RNA helicase DDX53 OS=Homo sapiens GN=DDX53 PE=1 SV=3 - [DDX53_HUMAN]	1.9	1	1	1	1	1.444	1		0.000	631	71.110
Q8IY21	Probable ATP-dependent RNA helicase DDX60 OS=Homo sapiens GN=DDX60 PE=1 SV=3 - [DDX60_HUMAN]	0.93	1	2	2	2	1.134	2	18.826	0.000	1712	197.727
Q8IV53	DENN domain-containing protein 1C OS=Homo sapiens GN=DENND1C PE=1 SV=1 - [DEN1C_HUMAN]	1.12	1	1	1	1	0.997	1		0.000	801	87.010
Q7L5Y6	DET1 homolog OS=Homo sapiens GN=DET1 PE=1 SV=2 - [DET1_HUMAN]	3.45	1	1	1	1	1.000	1		0.000	550	63.808
Q3MIW9	Diffuse panbronchiolitis critical region protein 1 OS=Homo sapiens GN=DPCR1 PE=2 SV=2 - [DPCR1_HUMAN]	1.35	2	1	1	1	0.956	1		0.000	517	56.312
Q9H4B8	Dipeptidase 3 OS=Homo sapiens GN=DPEP3 PE=2 SV=2 - [DPEP3_HUMAN]	7.17	1	1	1	1				0.000	488	53.654
O60673	DNA polymerase zeta catalytic subunit OS=Homo sapiens GN=REV3L PE=1 SV=2 - [DPOLZ_HUMAN]	0.8	1	1	1	1	1.000	1		0.000	3130	352.554
Q05215	Early growth response protein 4 OS=Homo sapiens GN=EGR4 PE=2 SV=3 - [EGR4_HUMAN]	2.55	1	1	1	1	1.000	1		0.000	589	61.584
Q6PCB8	Embigin OS=Homo sapiens GN=EMB PE=1 SV=1 - [EMB_HUMAN]	9.17	1	1	1	1	1.000	1		0.000	327	36.858
Q9UKH3	Endogenous retrovirus group K member 9 Env polyprotein OS=Homo sapiens GN=ERVK-9 PE=1 SV=1 - [ENK9_HUMAN]	5.87	2	1	1	1				0.000	698	78.965
Q14534	Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=1 SV=3 - [ERG1_HUMAN]	5.4	5	3	3	3	0.892	3	13.413	0.000	574	63.882
Q96PZ2	Protein FAM111A OS=Homo sapiens GN=FAM111A PE=1 SV=2 - [F111A_HUMAN]	2.45	1	1	1	1	1.000	1		0.000	611	70.151
A6NFH5	Fatty acid-binding protein 12 OS=Homo sapiens GN=FABP12 PE=2 SV=2 - [FBP12_HUMAN]	4.29	1	1	1	1	1.281	1		0.000	140	15.555
P49356	Protein farnesyltransferase subunit beta OS=Homo sapiens GN=FNTB PE=1 SV=1 - [FNTB_HUMAN]	3.66	2	1	1	1	1.027	1		0.000	437	48.742
Q05932	Folylpolyglutamate synthase, mitochondrial OS=Homo sapiens GN=FPGS PE=1 SV=3 - [FOLC_HUMAN]	1.7	1	1	1	1	0.495	1		0.000	587	64.568
Q12948	Forkhead box protein C1 OS=Homo sapiens GN=FOXC1 PE=1 SV=3 - [FOXC1_HUMAN]	4.16	2	1	1	2	1.203	1		0.000	553	56.753
Q9H461	Frizzled-8 OS=Homo sapiens GN=FZD8 PE=1 SV=1 - [FZD8_HUMAN]	1.01	1	1	1	2	0.873	1		0.000	694	73.252
Q9HDB9	Endogenous retrovirus group K member 5 Gag polyprotein OS=Homo sapiens GN=ERVK-5 PE=1 SV=3 - [GAK5_HUMAN]	1.05	1	1	1	1	0.532	1		0.000	667	73.542
Q8N292	Protein GAPT OS=Homo sapiens GN=GAPT PE=1 SV=1 - [GAPT_HUMAN]	10.83	1	1	1	1	0.840	1		0.000	157	17.872
Q86UU5	Gametogenetin OS=Homo sapiens GN=GGN PE=2 SV=2 - [GGN_HUMAN]	4.14	1	1	1	1				0.000	652	66.657
Q8NCI6	Beta-galactosidase-1-like protein 3 OS=Homo sapiens GN=GLB1L3 PE=2 SV=3 - [GLBL3_HUMAN]	2.6	1	1	1	1	1.435	1		0.000	653	74.775
Q8TDV2	Probable G-protein coupled receptor 148 OS=Homo sapiens GN=GPR148 PE=2 SV=2 - [GP148_HUMAN]	5.48	1	1	1	1	1.000	1		0.000	347	38.263
Q9C091	GREB1-like protein OS=Homo sapiens GN=GREB1L PE=2 SV=2 - [GRB1L_HUMAN]	0.94	1	1	1	1	1.000	1		0.000	1923	214.219
A4D1B5	Gamma-secretase-activating protein OS=Homo sapiens GN=GSAP PE=1 SV=2 - [GSAP_HUMAN]	1.17	1	1	1	1	3.450	1		0.000	854	97.739
P02008	Hemoglobin subunit zeta OS=Homo sapiens GN=HBZ PE=1 SV=2 - [HBAZ_HUMAN]	10.56	2	1	1	1	1.000	1		0.000	142	15.627
Q6UWX4	HHIP-like protein 2 OS=Homo sapiens GN=HHIPL2 PE=2 SV=1 - [HIPL2_HUMAN]	1.24	1	1	1	1	0.879	1		0.000	724	80.728
Q96RW7	Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2 - [HMCN1_HUMAN]	0.18	1	1	1	1	1.161	1		0.000	5635	613.001
O95256	Interleukin-18 receptor accessory protein OS=Homo sapiens GN=IL18RAP PE=1 SV=1 - [I18RA_HUMAN]	1.34	1	1	1	1	1.000	1		0.000	599	68.266
Q9H2X8	Interferon alpha-inducible protein 27-like protein 2 OS=Homo sapiens GN=IFI27L2 PE=2 SV=1 - [I27L2_HUMAN]	10.77	1	1	1	1	1.271	1		0.000	130	12.402
P27987	Inositol-trisphosphate 3-kinase B OS=Homo sapiens GN=ITPKB PE=1 SV=5 - [IP3KB_HUMAN]	2.54	1	1	1	1	1.000	1		0.000	946	102.312
Q96I82	Kazal-type serine protease inhibitor domain-containing protein 1 OS=Homo sapiens GN=KAZALD1 PE=1 SV=1 - [KAZD1_HUMAN]	6.25	1	1	1	1	0.769	1		0.000	304	32.924
Q96EK5	KIF1-binding protein OS=Homo sapiens GN=KIAA1279 PE=1 SV=1 - [KBP_HUMAN]	4.35	1	2	2	2	1.129	2	18.121	0.000	621	71.768
Q15058	Kinesin-like protein KIF14 OS=Homo sapiens GN=KIF14 PE=1 SV=1 - [KIF14_HUMAN]	1.15	1	1	1	1				0.000	1648	186.375
O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	1.16	4	1	1	1	0.937	1		0.000	517	57.097
Q9Y6N6	Laminin subunit gamma-3 OS=Homo sapiens GN=LAMC3 PE=1 SV=3 - [LAMC3_HUMAN]	2.16	2	1	1	1	1.000	1		0.000	1575	171.117
Q6UWE0	E3 ubiquitin-protein ligase LRSAM1 OS=Homo sapiens GN=LRSAM1 PE=1 SV=1 - [LRSM1_HUMAN]	0.97	1	1	1	1	1.158	1		0.000	723	83.541
Q8N2S1	Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens GN=LTBP4 PE=1 SV=2 - [LTBP4_HUMAN]	0.99	1	1	1	1	1.000	1		0.000	1624	173.320
Q9P2G4	Microtubule-associated protein 10 OS=Homo sapiens GN=MAP10 PE=1 SV=2 - [MAP10_HUMAN]	2.76	1	1	1	1	1.000	1		0.000	905	100.283
Q96EH3	Mitochondrial assembly of ribosomal large subunit protein 1 OS=Homo sapiens GN=MALSU1 PE=1 SV=1 - [MASU1_HUMAN]	8.97	1	1	1	2	1.000	2	0.000	0.000	234	26.153
Q9Y3D2	Methionine-R-sulfoxide reductase B2, mitochondrial OS=Homo sapiens GN=MSRB2 PE=2 SV=2 - [MSRB2_HUMAN]	5.49	1	1	1	1	1.141	1		0.000	182	19.524
Q9HC84	Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3 - [MUC5B_HUMAN]	0.57	2	1	1	1				0.000	5762	595.960
Q86W25	NACHT, LRR and PYD domains-containing protein 13 OS=Homo sapiens GN=NLRP13 PE=2 SV=2 - [NAL13_HUMAN]	1.92	1	1	1	1	1.000	1		0.000	1043	118.807
P52961	GPI-linked NAD(P)(+)--arginine ADP-ribosyltransferase 1 OS=Homo sapiens GN=ART1 PE=2 SV=2 - [NAR1_HUMAN]	3.67	1	1	1	1	1.000	1		0.000	327	36.311
Q9HCH0	Nck-associated protein 5-like OS=Homo sapiens GN=NCKAP5L PE=1 SV=2 - [NCK5L_HUMAN]	1.43	1	1	1	1	1.000	1		0.000	1330	138.927
Q8IXH7	Negative elongation factor C/D OS=Homo sapiens GN=NELFCD PE=1 SV=2 - [NELFD_HUMAN]	1.02	3	1	1	1	0.911	1		0.000	590	66.204
Q96T66	Nicotinamide mononucleotide adenylyltransferase 3 OS=Homo sapiens GN=NMNAT3 PE=1 SV=2 - [NMNA3_HUMAN]	4.76	1	1	1	1	1.000	1		0.000	252	28.304
Q9Y4C0	Neurexin-3 OS=Homo sapiens GN=NRXN3 PE=1 SV=4 - [NRX3A_HUMAN]	1.34	1	1	1	1	1.000	1		0.000	1643	180.484
Q5VST9	Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3 - [OBSCN_HUMAN]	0.23	3	1	1	1	1.000	1		0.000	7968	867.940
Q56VL3	OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 - [OCAD2_HUMAN]	12.99	1	2	2	3	1.074	3	19.067	0.000	154	16.943
Q96R48	Olfactory receptor 2A5 OS=Homo sapiens GN=OR2A5 PE=2 SV=2 - [OR2A5_HUMAN]	8.68	1	1	1	1	1.000	1		0.000	311	35.184
Q96R27	Olfactory receptor 2M4 OS=Homo sapiens GN=OR2M4 PE=2 SV=2 - [OR2M4_HUMAN]	8.68	1	1	1	1	1.348	1		0.000	311	35.047
Q96FX8	p53 apoptosis effector related to PMP-22 OS=Homo sapiens GN=PERP PE=2 SV=1 - [PERP_HUMAN]	8.81	1	1	1	1	1.000	1		0.000	193	21.372
Q75T13	GPI inositol-deacylase OS=Homo sapiens GN=PGAP1 PE=1 SV=1 - [PGAP1_HUMAN]	3.9	1	1	1	1				0.000	922	105.315
Q9NXJ5	Pyroglutamyl-peptidase 1 OS=Homo sapiens GN=PGPEP1 PE=1 SV=1 - [PGPI_HUMAN]	2.87	1	1	1	1	0.986	1		0.000	209	23.123
O15428	Putative PIN1-like protein OS=Homo sapiens GN=PIN1P1 PE=5 SV=1 - [PINL_HUMAN]	31	1	1	1	1				0.000	100	11.014
Q9NWT1	p21-activated protein kinase-interacting protein 1 OS=Homo sapiens GN=PAK1IP1 PE=1 SV=2 - [PK1IP_HUMAN]	2.81	1	1	1	1	1.334	1		0.000	392	43.936
Q14088	Ras-related protein Rab-33A OS=Homo sapiens GN=RAB33A PE=1 SV=2 - [RB33A_HUMAN]	7.17	1	1	1	1	1.000	1		0.000	237	26.576
O00287	Regulatory factor X-associated protein OS=Homo sapiens GN=RFXAP PE=1 SV=1 - [RFXAP_HUMAN]	7.35	1	1	1	1	1.000	1		0.000	272	28.215

Q9NWS8	Required for meiotic nuclear division protein 1 homolog OS=Homo sapiens GN=RMND1 PE=1 SV=2 - [RMND1_HUMAN]	4.23	3	2	2	3	1.016	3	37.293	0.000	449	51.571
Q9NTX7	E3 ubiquitin-protein ligase RNF146 OS=Homo sapiens GN=RNF146 PE=1 SV=1 - [RN146_HUMAN]	3.9	1	1	1	1	1.000	1		0.000	359	38.926
O15235	28S ribosomal protein S12, mitochondrial OS=Homo sapiens GN=MRPS12 PE=1 SV=1 - [RT12_HUMAN]	12.32	1	3	3	3	1.032	3	24.914	0.000	138	15.163
Q8WXD0	Relaxin receptor 2 OS=Homo sapiens GN=RXFP2 PE=1 SV=1 - [RXFP2_HUMAN]	2.12	1	1	1	1	1.000	1		0.000	754	86.396
Q86VL8	Multidrug and toxin extrusion protein 2 OS=Homo sapiens GN=SLC47A2 PE=1 SV=1 - [S47A2_HUMAN]	1.99	1	1	1	1	1.000	1		0.000	602	65.042
O95025	Semaphorin-3D OS=Homo sapiens GN=SEMA3D PE=2 SV=2 - [SEM3D_HUMAN]	4.63	1	1	1	1				0.000	777	89.594
Q13796	Protein Shroom2 OS=Homo sapiens GN=SHROOM2 PE=1 SV=1 - [SHRM2_HUMAN]	1.18	1	1	1	1	0.905	1		0.000	1616	176.303
Q7Z3B0	Small integral membrane protein 15 OS=Homo sapiens GN=SMIM15 PE=2 SV=1 - [SIM15_HUMAN]	9.46	1	1	1	1	1.028	1		0.000	74	8.620
Q9C093	Sperm flagellar protein 2 OS=Homo sapiens GN=SPEF2 PE=1 SV=2 - [SPEF2_HUMAN]	2.03	4	2	2	2	0.987	2	2.005	0.000	1822	209.680
Q9HCB6	Spondin-1 OS=Homo sapiens GN=SPON1 PE=1 SV=2 - [SPON1_HUMAN]	3.35	1	1	1	1	1.117	1		0.000	807	90.914
Q6ZRS2	Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3 - [SRCAP_HUMAN]	0.43	1	1	1	1	1.000	1		0.000	3230	343.343
A2VEC9	SCO-spondin OS=Homo sapiens GN=SSPO PE=2 SV=1 - [SSPO_HUMAN]	0.25	1	1	1	1				0.000	5147	547.133
O95210	Starch-binding domain-containing protein 1 OS=Homo sapiens GN=STBD1 PE=1 SV=1 - [STBD1_HUMAN]	4.47	1	1	1	1	1.000	1		0.000	358	38.983
Q96BN2	Transcriptional adapter 1 OS=Homo sapiens GN=TADA1 PE=1 SV=1 - [TADA1_HUMAN]	3.58	1	1	1	1	0.879	1		0.000	335	37.358
Q16514	Transcription initiation factor TFIID subunit 12 OS=Homo sapiens GN=TAF12 PE=1 SV=1 - [TAF12_HUMAN]	4.97	1	1	1	1	1.000	1		0.000	161	17.913
Q9P2M4	TBC1 domain family member 14 OS=Homo sapiens GN=TBC1D14 PE=1 SV=3 - [TBC14_HUMAN]	2.31	1	1	1	1	1.000	1		0.000	693	78.088
O75443	Alpha-tectorin OS=Homo sapiens GN=TECTA PE=1 SV=3 - [TECTA_HUMAN]	1.62	1	1	1	1	1.000	1		0.000	2155	239.370
Q8IWB6	Inactive serine/threonine-protein kinase TEX14 OS=Homo sapiens GN=TEX14 PE=1 SV=2 - [TEX14_HUMAN]	0.53	1	1	1	1	1.193	1		0.000	1497	167.796
Q9NRE2	Teashirt homolog 2 OS=Homo sapiens GN=TSHZ2 PE=1 SV=3 - [TSH2_HUMAN]	3.19	1	1	1	1	1.000	1		0.000	1034	114.933
Q16864	V-type proton ATPase subunit F OS=Homo sapiens GN=ATP6V1F PE=1 SV=2 - [VATF_HUMAN]	6.72	1	1	1	1	1.074	1		0.000	119	13.362
Q7Z5H4	Vomeronasal type-1 receptor 5 OS=Homo sapiens GN=VN1R5 PE=2 SV=2 - [VN1R5_HUMAN]	10.92	1	1	1	1				0.000	357	40.752
Q9Y2I8	WD repeat-containing protein 37 OS=Homo sapiens GN=WDR37 PE=1 SV=2 - [WDR37_HUMAN]	1.82	1	1	1	1	1.000	1		0.000	494	54.632
Q6UXN9	WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1 - [WDR82_HUMAN]	2.24	1	1	1	1	0.663	1		0.000	313	35.056
O75132	Zinc finger BED domain-containing protein 4 OS=Homo sapiens GN=ZBED4 PE=1 SV=2 - [ZBED4_HUMAN]	1.11	1	1	1	1	1.000	1		0.000	1171	130.239
Q5T1R4	Transcription factor HIVEP3 OS=Homo sapiens GN=HIVEP3 PE=2 SV=1 - [ZEP3_HUMAN]	0.54	1	1	1	1	1.000	1		0.000	2406	259.304
Q5H9K5	Zinc finger matrin-type protein 1 OS=Homo sapiens GN=ZMAT1 PE=2 SV=1 - [ZMAT1_HUMAN]	3.45	1	1	1	1	1.000	1		0.000	638	74.708
Q9C0G0	Zinc finger protein 407 OS=Homo sapiens GN=ZNF407 PE=1 SV=2 - [ZN407_HUMAN]	0.49	1	1	1	1	1.000	1		0.000	2248	247.211
Q9UEG4	Zinc finger protein 629 OS=Homo sapiens GN=ZNF629 PE=1 SV=2 - [ZN629_HUMAN]	2.76	71	1	2	3	1.139	1		0.000	869	96.559
Q96IR2	Zinc finger protein 845 OS=Homo sapiens GN=ZNF845 PE=2 SV=3 - [ZN845_HUMAN]	14.85	79	1	2	5	1.000	1		0.000	970	113.060
P17040	Zinc finger and SCAN domain-containing protein 20 OS=Homo sapiens GN=ZSCAN20 PE=2 SV=3 - [ZSC20_HUMAN]	9.01	108	1	3	4				0.000	1043	117.467
F2Z2L5	VIP36-like protein OS=Homo sapiens GN=LMAN2L PE=4 SV=1 - [F2Z2L5_HUMAN]	16.26	1	1	1	1	1.000	1		0.000	123	13.516
E9PJX1	Zinc finger protein-like 1 OS=Homo sapiens GN=ZFPL1 PE=1 SV=1 - [E9PJX1_HUMAN]	21.54	7	1	1	1	1.141	1		0.000	65	7.112
Q5S8W6	ATP synthase protein 8 OS=Homo sapiens GN=ATP8 PE=3 SV=1 - [Q5S8W6_HUMAN]	52.94	127	1	2	2	1.000	1		0.000	68	7.958
Q69YV6	Putative uncharacterized protein DKFZp564C0716 (Fragment) OS=Homo sapiens GN=DKFZp564G1016 PE=2 SV=1 - [Q69YV6_HUMAN]	4.49	4	1	1	1	1.084	1		0.000	245	27.621
G5E968	Chromogranin A (Parathyroid secretory protein 1), isoform CRA_b OS=Homo sapiens GN=CHGA PE=1 SV=1 - [G5E968_HUMAN]	6.21	3	1	1	1	1.000	1		0.000	306	34.248
D9N2U4	Immunity-related GTPase family, M (Fragment) OS=Homo sapiens GN=IRGM PE=4 SV=1 - [D9N2U4_HUMAN]	17.24	2	1	1	1	1.000	1		0.000	116	12.967
B7ZLG2	HCG1642804, isoform CRA_c OS=Homo sapiens GN=TRIM50 PE=2 SV=1 - [B7ZLG2_HUMAN]	5.14	3	1	1	1	1.000	1		0.000	486	54.565
B3KUV7	Phosphatidylinositol glycan, class A (Paroxysmal nocturnal hemoglobinuria), isoform CRA_b OS=Homo sapiens GN=PIGA PE=2 SV=1 - [B3KUV7_HUMAN]	7.1	3	1	1	1	1.000	1		0.000	169	18.782
B8ZZ67	SMT3 suppressor of mif two 3 homolog 1 (Yeast), isoform CRA_b OS=Homo sapiens GN=SUMO1 PE=1 SV=1 - [B8ZZ67_HUMAN]	12.9	3	1	1	1	0.851	1		0.000	62	7.161
X5CF57	BRD2 OS=Homo sapiens GN=BRD2 PE=4 SV=1 - [X5CF57_HUMAN]	1.46	3	1	1	1	1.238	1		0.000	754	83.100
Q6P4F9	RASAL2 protein (Fragment) OS=Homo sapiens GN=RASAL2 PE=2 SV=1 - [Q6P4F9_HUMAN]	8.92	2	1	1	1	1.000	1		0.000	370	41.717
K7EQ86	KIAA0100, isoform CRA_a OS=Homo sapiens GN=KIAA0100 PE=1 SV=1 - [K7EQ86_HUMAN]	0.72	3	1	1	1	1.000	1		0.000	2092	237.148
Q69YW4	Anoctamin-2 OS=Homo sapiens GN=DKFZp434P102 PE=2 SV=1 - [Q69YW4_HUMAN]	29.07	3	1	1	1				0.000	86	9.443
D3DNC7	HCG1648279, isoform CRA_a OS=Homo sapiens GN=hCG_1648279 PE=3 SV=1 - [D3DNC7_HUMAN]	15.71	4	1	1	1				0.000	191	21.632
G5EA49	Glycosyltransferase-like domain containing 1, isoform CRA_a OS=Homo sapiens GN=GTDC1 PE=4 SV=1 - [G5EA49_HUMAN]	3.04	4	1	1	1	2.010	1		0.000	329	37.657
Q8WYW5	Phospholipase D1 OS=Homo sapiens GN=pp13439 PE=2 SV=1 - [Q8WYW5_HUMAN]	12.5	1	1	1	1	1.000	1		0.000	152	16.494
B8ZZG1	MAGUK p55 subfamily member 6 OS=Homo sapiens GN=MPP6 PE=1 SV=1 - [B8ZZG1_HUMAN]	2.34	2	1	1	1	1.031	1		0.000	428	48.727
B8ZZ99	Coiled-coil domain-containing protein 115 OS=Homo sapiens GN=CCDC115 PE=4 SV=1 - [B8ZZ99_HUMAN]	6.86	3	1	1	1	1.000	1		0.000	175	19.044
G5E9U9	Poly (ADP-ribose) polymerase family, member 12, isoform CRA_a OS=Homo sapiens GN=PARP12 PE=1 SV=1 - [G5E9U9_HUMAN]	2.14	1	1	1	1	1.000	1		0.000	420	47.454
B4DMD6	Ring finger protein 185, isoform CRA_h OS=Homo sapiens GN=RNF185 PE=2 SV=1 - [B4DMD6_HUMAN]	11.54	3	1	1	1	1.000	1		0.000	130	14.052
A0A024R9L5	Mitogen activated protein kinase binding protein 1, isoform CRA_a OS=Homo sapiens GN=MAPKBP1 PE=4 SV=1 - [A0A024R9L5_HUMAN]	2.66	3	1	1	1	1.000	1		0.000	1015	109.087
B4DG45	cDNA FLJ53877, highly similar to Sortilin-related receptor OS=Homo sapiens PE=2 SV=1 - [B4DG45_HUMAN]	1.93	10	1	1	1	1.000	1		0.000	829	92.224
Q9Y348	HCG2012339 OS=Homo sapiens GN=hCG_2012339 PE=2 SV=1 - [Q9Y348_HUMAN]	6.54	1	1	1	1	0.379	1		0.000	107	12.407
A0A024RA82	HCG37272, isoform CRA_b OS=Homo sapiens GN=hCG_37272 PE=4 SV=1 - [A0A024RA82_HUMAN]	2.65	2	1	1	1	0.801	1		0.000	528	58.823
D3DU61	Coiled-coil domain containing 78, isoform CRA_b OS=Homo sapiens GN=CCDC78 PE=4 SV=1 - [D3DU61_HUMAN]	5.02	3	1	1	1	0.877	1		0.000	319	35.421
A0A024R8B3	Family with sequence similarity 73, member B, isoform CRA_e OS=Homo sapiens GN=FAM73B PE=4 SV=1 - [A0A024R8B3_HUMAN]	9.29	3	1	1	1				0.000	323	34.061
Q8N7S3	cDNA FLJ40411 fis, clone TESTI2037845 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8N7S3_HUMAN]	2.33	2	1	1	1	1.000	1		0.000	644	72.609
Q6IPQ7	NR1H4 protein (Fragment) OS=Homo sapiens GN=NR1H4 PE=2 SV=1 - [Q6IPQ7_HUMAN]	5.26	1	1	1	1	1.000	1		0.000	475	54.569
D6R9P1	Ectonucleotide pyrophosphatase/phosphodiesterase family member 6 soluble form (Fragment) OS=Homo sapiens GN=ENPP6 PE=4 SV=1 - [D6R9P1_HUMAN]	10.31	2	1	1	1	1.000	1		0.000	194	22.333
E5E129	ATP synthase protein 8 OS=Homo sapiens GN=ATP8 PE=3 SV=1 - [E5E129_HUMAN]	36.76	127	1	2	2				0.000	68	7.968
Q5R3B4	Mitochondrial pyruvate carrier 2 (Fragment) OS=Homo sapiens GN=MPC2 PE=1 SV=1 - [Q5R3B4_HUMAN]	11.43	3	1	1	1	1.091	1		0.000	105	11.673
F8WF54	Exostosin-1 OS=Homo sapiens GN=EXT1 PE=4 SV=1 - [F8WF54_HUMAN]	85.37	1	1	1	1	1.000	1		0.000	41	4.581
H0YLS2	Aromatase (Fragment) OS=Homo sapiens GN=CYP19A1 PE=4 SV=3 - [H0YLS2_HUMAN]	13.33	14	1	1	1	1.000	1		0.000	165	18.456
R4GN54	Protein COMMD3-BMI1 (Fragment) OS=Homo sapiens GN=COMMD3-BMI1 PE=4 SV=1 - [R4GN54_HUMAN]	13.64	7	1	1	1	1.000	1		0.000	110	12.320
X6RFN3	E3 ubiquitin-protein ligase RING2 (Fragment) OS=Homo sapiens GN=RNF2 PE=1 SV=2 - [X6RFN3_HUMAN]	5.71	2	1	1	1	1.171	1		0.000	245	27.260
B4DU33	cDNA FLJ58110, highly similar to Homo sapiens glycine-N-acyltransferase-like 1 (GLYATL1), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DU33_HUMAN]	2.15	3	1	1	1				0.000	279	32.254
C9K0C9	CDK5 regulatory subunit-associated protein 2 (Fragment) OS=Homo sapiens GN=CDK5RAP2 PE=1 SV=1 - [C9K0C9_HUMAN]	8.27	13	1	1	1	0.796	1		0.000	133	15.093
C9JDX1	Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1 (Fragment) OS=Homo sapiens GN=C1GALT1 PE=4 SV=1 - [C9JDX1_HUMAN]	15	3	1	1	1	0.999	1		0.000	100	11.266
A6NHN7	Zinc finger MYM-type protein 3 OS=Homo sapiens GN=ZMYM3 PE=1 SV=1 - [A6NHN7_HUMAN]	0.55	3	1	1	1	1.168	1		0.000	1280	141.697
H3BS02	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial OS=Homo sapiens GN=BCKDK PE=1 SV=1 - [H3BS02_HUMAN]	3.23	4	2	2	2	0.882	2	48.516	0.000	217	24.433
Q5T088	MORN repeat-containing protein 1 (Fragment) OS=Homo sapiens GN=MORN1 PE=4 SV=1 - [Q5T088_HUMAN]	8.65	1	1	1	1	1.000	1		0.000	185	19.686
F8WA26	Palladin (Fragment) OS=Homo sapiens GN=PALLD PE=1 SV=1 - [F8WA26_HUMAN]	4.88	3	1	1	1	1.000	1		0.000	164	18.482
A0A087WYJ1	Glutamine synthetase OS=Homo sapiens GN=GLUL PE=4 SV=1 - [A0A087WYJ1_HUMAN]	16.74	1	1	1	1				0.000	233	26.396
A0A087WU64	DNA polymerase alpha catalytic subunit OS=Homo sapiens GN=POLA1 PE=4 SV=1 - [A0A087WU64_HUMAN]	1.3	3	1	1	1	1.000	1		0.000	1461	165.663
Q9UF71	Putative uncharacterized protein DKFZp434J1672 (Fragment) OS=Homo sapiens GN=DKFZp434J1672 PE=2 SV=1 - [Q9UF71_HUMAN]	2.07	4	1	1	1	1.000	1		0.000	580	65.989
H9KVB3	Otogelin OS=Homo sapiens GN=OTOG PE=4 SV=1 - [H9KVB3_HUMAN]	1.33	2	1	1	1	1.000	1		0.000	2852	306.742
K7EIJ1	Zinc phosphodiesterase ELAC protein 1 OS=Homo sapiens GN=ELAC1 PE=4 SV=1 - [K7EIJ1_HUMAN]	4.93	3	1	1	1	0.412	1		0.000	223	25.146
Q4VBL9	TACR3 protein (Fragment) OS=Homo sapiens GN=TACR3 PE=2 SV=1 - [Q4VBL9_HUMAN]	1.29	3	1	1	1	0.784	1		0.000	464	52.132
M0QZD8	Protein LOC388210 OS=Homo sapiens GN=LOC388210 PE=4 SV=2 - [M0QZD8_HUMAN]	0.56	1	1	1	3	1.000	3	0.000	0.000	3231	354.000
H0YDG4	Melatonin receptor type 1B (Fragment) OS=Homo sapiens GN=MTNR1B PE=4 SV=1 - [H0YDG4_HUMAN]	7.96	1	1	1	1	1.126	1		0.000	113	12.593
H3BRQ1	Kinesin-like protein KIFC3 (Fragment) OS=Homo sapiens GN=KIFC3 PE=4 SV=3 - [H3BRQ1_HUMAN]	12.26	1	1	1	1	1.000	1		0.000	155	16.714
Q17RV3	Leucine-rich repeat kinase 2 OS=Homo sapiens GN=LRRK2 PE=2 SV=1 - [Q17RV3_HUMAN]	0.55	2	1	1	1				0.000	2527	285.884
E9PIQ7	HCLS1-associated protein X-1 OS=Homo sapiens GN=HAX1 PE=1 SV=1 - [E9PIQ7_HUMAN]	7.28	3	1	1	1	0.838	1		0.000	151	17.156
K7EMP7	Coiled-coil domain-containing protein 106 (Fragment) OS=Homo sapiens GN=CCDC106 PE=4 SV=1 - [K7EMP7_HUMAN]	4.65	3	1	1	1	1.000	1		0.000	172	19.449
E9PSE9	Uncharacterized protein C14orf105 OS=Homo sapiens GN=C14orf105 PE=4 SV=1 - [E9PSE9_HUMAN]	3.05	5	1	1	1	1.000	1		0.000	295	34.541
C9WCR6	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [C9WCR6_HUMAN]	12.71	1	1	1	1	1.000	1		0.000	181	20.811
H0YD47	Synaptotagmin-13 (Fragment) OS=Homo sapiens GN=SYT13 PE=4 SV=1 - [H0YD47_HUMAN]	9.68	2	1	1	1				0.000	186	20.770
B1AH48	Thiosulfate sulfurtransferase (Fragment) OS=Homo sapiens GN=TST PE=1 SV=1 - [B1AH48_HUMAN]	4.84	7	1	1	1				0.000	124	14.227
F8W8Y8	U6 snRNA-associated Sm-like protein LSm5 OS=Homo sapiens GN=LSM5 PE=4 SV=1 - [F8W8Y8_HUMAN]	25.35	1	1	1	1	1.000	1		0.000	71	7.540
B3KSA1	cDNA FLJ35817 fis, clone TESTI2006120, moderately similar to Rattus norvegicus Na+ dependent glucose transporter 1 (Naglt1), mRNA OS=Homo sapiens PE=2 SV=1	8.11	2	1	1	1	1.000	1		0.000	518	56.240
Q71U42	Benzodiazepine receptor ligand OS=Homo sapiens GN=BRL PE=1 SV=1 - [Q71U42_HUMAN]	8.05	2	1	1	1	1.489	1		0.000	87	9.994
B4DHA1	cDNA FLJ59020, highly similar to WD repeat protein 47 OS=Homo sapiens PE=2 SV=1 - [B4DHA1_HUMAN]	1.35	2	1	1	1	1.000	1		0.000	817	90.020
B4DXK4	cDNA FLJ50908, highly similar to Homo sapiens keratin protein K6irs (K6IRS2), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DXK4_HUMAN]	4.95	2	1	1	1	1.000	1		0.000	323	35.689
Q6LDX5	Pro-gastrin releasing peptide type 3 (Fragment) OS=Homo sapiens PE=4 SV=1 - [Q6LDX5_HUMAN]	65	1	1	1	1	1.000	1		0.000	20	2.201
H0YF78	Vacuolar protein sorting-associated protein 13A (Fragment) OS=Homo sapiens GN=VPS13A PE=4 SV=1 - [H0YF78_HUMAN]	6.21	5	1	1	1	1.000	1		0.000	177	19.735
M0QZW2	CD70 antigen (Fragment) OS=Homo sapiens GN=CD70 PE=1 SV=2 - [M0QZW2_HUMAN]	12.31	2	1	1	1	0.543	1		0.000	65	7.100
F6TX30	Ankyrin repeat and SOCS box protein 6 OS=Homo sapiens GN=ASB6 PE=4 SV=1 - [F6TX30_HUMAN]	4.08	3	1	1	1	0.769	1		0.000	392	44.055
A0A087WTP7	Nitrogen permease regulator 3-like protein OS=Homo sapiens GN=NPRL3 PE=4 SV=1 - [A0A087WTP7_HUMAN]	23.38	5	1	1	1	1.000	1		0.000	77	8.628
Q8WU11	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8WU11_HUMAN]	8.55	7	1	1	1	1.000	1		0.000	304	33.025
B4DGA3	cDNA FLJ55898, highly similar to Receptor-type tyrosine-protein phosphatase mu (EC 3.1.3.48) OS=Homo sapiens PE=2 SV=1 - [B4DGA3_HUMAN]	1.69	4	1	1	1	1.000	1		0.000	1239	140.017
G8FV57	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1 - [G8FV57_HUMAN]	5.86	1	1	1	1	0.920	1		0.000	273	31.563
Q5R3E6	Mitogen-activated protein kinase 13 OS=Homo sapiens GN=MAPK13 PE=4 SV=1 - [Q5R3E6_HUMAN]	6.58	6	1	1	1	1.000	1		0.000	152	17.332
H3BPP8	Transmembrane protein 62 OS=Homo sapiens GN=TMEM62 PE=4 SV=1 - [H3BPP8_HUMAN]	67.74	2	1	1	2				0.000	62	6.385
H0Y8E9	TSC22 domain family protein 2 (Fragment) OS=Homo sapiens GN=TSC22D2 PE=4 SV=1 - [H0Y8E9_HUMAN]	23.46	2	1	1	1	0.992	1		0.000	81	9.213
Q96LW0	cDNA FLJ25012 fis, clone CBL01290 OS=Homo sapiens PE=2 SV=1 - [Q96LW0_HUMAN]	4.67	3	1	1	1	0.971	1		0.000	407	44.495
A0A087X120	Polycystic kidney disease protein 1-like 2 OS=Homo sapiens GN=PKD1L2 PE=4 SV=1 - [A0A087X120_HUMAN]	0.69	2	1	1	1	1.000	1		0.000	2458	272.211
Q54AJ0	GDS-related protein OS=Homo sapiens GN=HKE1.5 PE=2 SV=1 - [Q54AJ0_HUMAN]	23.77	5	1	1	1	1.000	1		0.000	122	12.931
H0YEM3	KDEL motif-containing protein 2 (Fragment) OS=Homo sapiens GN=KDELC2 PE=1 SV=1 - [H0YEM3_HUMAN]	5	3	1	1	1	1.000	1		0.000	160	18.700
C9JAG2	Protein C-ets-2 (Fragment) OS=Homo sapiens GN=ETS2 PE=1 SV=1 - [C9JAG2_HUMAN]	10	2	1	1	1	0.993	1		0.000	270	30.332
C9JLH5	Elongator complex protein 6 (Fragment) OS=Homo sapiens GN=ELP6 PE=4 SV=1 - [C9JLH5_HUMAN]	15	8	1	1	1	0.961	1		0.000	80	8.959
H0YJR8	Dehydrogenase/reductase SDR family member 7 (Fragment) OS=Homo sapiens GN=DHRS7 PE=1 SV=1 - [H0YJR8_HUMAN]	5.19	5	1	1	1	0.603	1		0.000	212	23.463
H3BNF4	Transcription factor 12 (Fragment) OS=Homo sapiens GN=TCF12 PE=4 SV=1 - [H3BNF4_HUMAN]	16.67	1	1	1	1	1.000	1		0.000	48	5.191
A0A087WUZ9	Diacylglycerol kinase delta OS=Homo sapiens GN=DGKD PE=4 SV=1 - [A0A087WUZ9_HUMAN]	1.03	2	1	1	2	0.503	1		0.000	1168	129.965
A0A087WYS9	Surfeit locus protein 1 OS=Homo sapiens GN=SURF1 PE=4 SV=1 - [A0A087WYS9_HUMAN]	3.66	2	1	1	1	0.762	1		0.000	191	21.696
Q96JF4	KIAA1873 protein (Fragment) OS=Homo sapiens GN=KIAA1873 PE=2 SV=1 - [Q96JF4_HUMAN]	2.52	5	1	1	1	1.252	1		0.000	477	53.498
K7EID0	Max-like protein X (Fragment) OS=Homo sapiens GN=MLX PE=4 SV=1 - [K7EID0_HUMAN]	7.26	2	1	1	1	1.695	1		0.000	248	27.960
U6C5D7	Beta-1,4-galactosyltransferase 5 (Fragment) OS=Homo sapiens GN=B4GalT5 PE=2 SV=1 - [U6C5D7_HUMAN]	4.49	2	1	1	1	1.000	1		0.000	379	44.027
X6RGB1	Protein maelstrom homolog (Fragment) OS=Homo sapiens GN=MAEL PE=4 SV=1 - [X6RGB1_HUMAN]	6.96	3	1	1	1	1.000	1		0.000	316	36.074
Q4ZG84	Putative uncharacterized protein LRP2 (Fragment) OS=Homo sapiens GN=LRP2 PE=4 SV=1 - [Q4ZG84_HUMAN]	0.18	4	1	1	1	1.056	1		0.000	3881	435.470
H0YM92	Low-density lipoprotein receptor (Fragment) OS=Homo sapiens GN=LDLR PE=1 SV=1 - [H0YM92_HUMAN]	2.91	5	1	1	1	1.000	1		0.000	309	34.302
A0PJD3	C14orf43 protein (Fragment) OS=Homo sapiens GN=C14orf43 PE=2 SV=1 - [A0PJD3_HUMAN]	0.78	2	1	1	1	1.000	1		0.000	1025	112.618
B1AHR5	Beta-crystallin B3 OS=Homo sapiens GN=CRYBB3 PE=4 SV=1 - [B1AHR5_HUMAN]	15.04	1	1	1	1	1.000	1		0.000	113	12.522
H3BU61	Hydroxyacylglutathione hydrolase-like protein (Fragment) OS=Homo sapiens GN=HAGHL PE=4 SV=2 - [H3BU61_HUMAN]	28.72	1	1	1	1				0.000	94	10.160
B3KP28	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1 - [B3KP28_HUMAN]	1.02	5	1	1	1	0.944	1		0.000	689	78.949
E9PKG2	Low-density lipoprotein receptor-related protein 8 OS=Homo sapiens GN=LRP8 PE=4 SV=1 - [E9PKG2_HUMAN]	7.65	4	2	2	2	1.000	2	0.000	0.000	392	42.333
M0QZ43	Sarcoplasmic reticulum histidine-rich calcium-binding protein OS=Homo sapiens GN=HRC PE=4 SV=1 - [M0QZ43_HUMAN]	4.73	3	1	1	1				0.000	676	77.526
B3KRK9	cDNA FLJ34500 fis, clone HLUNG2005479, highly similar to Phosphoinositide 3-kinase regulatory subunit 6 OS=Homo sapiens PE=2 SV=1 - [B3KRK9_HUMAN]	5.32	3	1	1	1	1.000	1		0.000	376	42.041
C9JUI1	Intraflagellar transport protein 80 homolog (Fragment) OS=Homo sapiens GN=IFT80 PE=4 SV=1 - [C9JUI1_HUMAN]	20.31	5	1	1	1	1.000	1		0.000	64	7.539
M0R0U0	Protein SMG9 (Fragment) OS=Homo sapiens GN=SMG9 PE=1 SV=1 - [M0R0U0_HUMAN]	11.46	3	1	1	2	1.000	1		0.000	157	17.203
E9PNW4	CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1 - [E9PNW4_HUMAN]	11.11	3	1	1	1	1.000	1		0.000	108	11.977
B4DH28	Sodium channel protein OS=Homo sapiens PE=2 SV=1 - [B4DH28_HUMAN]	3.13	1	1	1	1	1.002	1		0.000	575	65.746
C9JPV1	Transporter (Fragment) OS=Homo sapiens GN=SLC6A6 PE=3 SV=1 - [C9JPV1_HUMAN]	15.6	7	1	1	1	1.050	1		0.000	109	12.055
E7EWM1	Nuclear receptor coactivator 2 OS=Homo sapiens GN=NCOA2 PE=1 SV=2 - [E7EWM1_HUMAN]	1.9	2	1	1	1	1.000	1		0.000	946	102.664
G3V3U6	39S ribosomal protein L52, mitochondrial OS=Homo sapiens GN=MRPL52 PE=4 SV=1 - [G3V3U6_HUMAN]	17.65	3	1	1	1	1.000	1		0.000	51	5.925
H9KVD6	Lysine-specific demethylase 7A (Fragment) OS=Homo sapiens GN=KDM7A PE=4 SV=1 - [H9KVD6_HUMAN]	7.67	2	1	1	1	1.000	1		0.000	404	46.168
C7FDR3	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [C7FDR3_HUMAN]	6.63	1	2	2	2	1.091	2	0.075	0.000	181	21.018
H7C0N0	Inter-alpha-trypsin inhibitor heavy chain H1 (Fragment) OS=Homo sapiens GN=ITIH1 PE=4 SV=1 - [H7C0N0_HUMAN]	4.31	5	1	1	1	1.000	1		0.000	464	51.831
Q59FX1	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FX1_HUMAN]	3	1	1	1	1	1.000	1		0.000	400	45.265
H7C3V1	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [H7C3V1_HUMAN]	14.29	1	1	1	1	1.000	1		0.000	112	12.581
E9PNM2	Bestrophin-3 OS=Homo sapiens GN=BEST3 PE=4 SV=1 - [E9PNM2_HUMAN]	9.14	2	1	1	1	1.000	1		0.000	197	22.766
H0Y9Y7	Transforming acidic coiled-coil-containing protein 2 (Fragment) OS=Homo sapiens GN=TACC2 PE=1 SV=1 - [H0Y9Y7_HUMAN]	7.88	11	1	1	1	1.161	1		0.000	165	18.472
B3KRQ8	DNA-directed RNA polymerase OS=Homo sapiens PE=2 SV=1 - [B3KRQ8_HUMAN]	1.19	3	1	1	1	1.000	1		0.000	838	94.309
M0QYK8	Aurora kinase C (Fragment) OS=Homo sapiens GN=AURKC PE=4 SV=1 - [M0QYK8_HUMAN]	4.38	1	1	1	1	4.940	1		0.000	137	15.962
F5H5P8	cGMP-dependent 3',5'-cyclic phosphodiesterase (Fragment) OS=Homo sapiens GN=PDE2A PE=4 SV=3 - [F5H5P8_HUMAN]	21.84	2	1	1	2	0.687	2	25.059	0.000	87	9.456
T1R7N3	MUC5AC (Fragment) OS=Homo sapiens GN=MUC5AC PE=4 SV=1 - [T1R7N3_HUMAN]	1.23	7	1	1	1				0.000	4066	413.617
H0YMI8	TNF receptor-associated factor 3 (Fragment) OS=Homo sapiens GN=TRAF3 PE=4 SV=1 - [H0YMI8_HUMAN]	14.89	4	1	1	1	1.000	1		0.000	94	10.309
B4DGC7	cDNA FLJ60081, highly similar to Zinc finger protein 106 (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DGC7_HUMAN]	1.23	4	1	1	1	0.647	1		0.000	816	89.767
E9PN78	Cell adhesion molecule-related/down-regulated by oncogenes OS=Homo sapiens GN=CDON PE=4 SV=1 - [E9PN78_HUMAN]	5.77	2	1	1	1				0.000	641	69.764
F8WBE2	Cytochrome P450 20A1 OS=Homo sapiens GN=CYP20A1 PE=4 SV=1 - [F8WBE2_HUMAN]	3.37	5	1	1	1	1.250	1		0.000	208	23.309
Q75MQ2	Putative uncharacterized protein SEMA3A (Fragment) OS=Homo sapiens GN=SEMA3A PE=4 SV=1 - [Q75MQ2_HUMAN]	2.09	2	1	1	1	0.898	1		0.000	287	33.527
B3KYA3	cDNA FLJ16320 fis, clone SPLEN2036702, highly similar to Homo sapiens tensin like C1 domain containing phosphatase (tensin 2) (TENC1), transcript variant 2, mRNA	4.48	5	2	2	2	1.000	1		0.000	781	86.588
C9JWE6	E3 ubiquitin-protein ligase PDZRN3 (Fragment) OS=Homo sapiens GN=PDZRN3 PE=4 SV=1 - [C9JWE6_HUMAN]	3.66	9	1	1	1	1.000	1		0.000	492	55.374
J3KNV1	Zinc finger protein 292 OS=Homo sapiens GN=ZNF292 PE=1 SV=1 - [J3KNV1_HUMAN]	0.44	2	1	1	1	1.000	1		0.000	2718	304.021
H0YHI9	Myelin regulatory factor-like protein (Fragment) OS=Homo sapiens GN=MYRFL PE=4 SV=1 - [H0YHI9_HUMAN]	2.93	1	1	1	1	1.000	1		0.000	375	42.524
Q0IJ72	LCE3D protein (Fragment) OS=Homo sapiens GN=LCE3D PE=2 SV=1 - [Q0IJ72_HUMAN]	37.36	3	1	1	1	1.000	1		0.000	91	9.397
B4DEQ1	cDNA FLJ53846, highly similar to Kinesin-like protein KIF3C OS=Homo sapiens PE=2 SV=1 - [B4DEQ1_HUMAN]	5.51	9	1	1	1	0.824	1		0.000	599	67.597
H7C5B7	Armadillo repeat-containing protein 8 (Fragment) OS=Homo sapiens GN=ARMC8 PE=4 SV=1 - [H7C5B7_HUMAN]	5.31	8	1	1	1	1.172	1		0.000	113	12.524
J3QRP2	CKLF-like MARVEL transmembrane domain-containing protein 4 (Fragment) OS=Homo sapiens GN=CMTM4 PE=1 SV=1 - [J3QRP2_HUMAN]	7.14	2	1	1	1	0.528	1		0.000	140	15.760
J3QT61	GTPase Era, mitochondrial OS=Homo sapiens GN=ERAL1 PE=1 SV=1 - [J3QT61_HUMAN]	6.43	4	1	1	1	0.827	1		0.000	171	18.401
X6RKY7	Cell division cycle protein 123 homolog (Fragment) OS=Homo sapiens GN=CDC123 PE=1 SV=1 - [X6RKY7_HUMAN]	7.01	4	1	1	1	1.223	1		0.000	157	17.766
O43550	Cdc25B phosphatase (Fragment) OS=Homo sapiens GN=CDC25B PE=4 SV=1 - [O43550_HUMAN]	5.25	1	1	1	1	1.000	1		0.000	305	33.837
B4DYV1	Tyrosine-protein kinase OS=Homo sapiens PE=2 SV=1 - [B4DYV1_HUMAN]	2.44	5	1	1	1	0.570	1		0.000	983	113.675
H3BRS3	Telomere length regulation protein TEL2 homolog OS=Homo sapiens GN=TELO2 PE=1 SV=1 - [H3BRS3_HUMAN]	1.88	4	1	1	1	0.978	1		0.000	426	47.350
E7ESY0	Type II inositol 1,4,5-trisphosphate 5-phosphatase OS=Homo sapiens GN=INPP5B PE=4 SV=2 - [E7ESY0_HUMAN]	1.47	3	1	1	3	1.100	3	14.254	0.000	748	85.004
B3KVC6	cDNA FLJ16395 fis, clone TRACH2024139, highly similar to DNA polymerase eta (EC 2.7.7.7) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KVC6_HUMAN]	2.92	5	1	1	1	1.000	1		0.000	617	67.610
Q59G51	Transient receptor potential cation channel, subfamily C, member 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G51_HUMAN]	1.93	1	1	1	1	1.000	1		0.000	725	84.062
Q5SXQ8	Uncharacterized protein C10orf67 (Fragment) OS=Homo sapiens GN=C10orf67 PE=4 SV=1 - [Q5SXQ8_HUMAN]	7.77	1	1	1	1				0.000	296	34.836
E5RGC7	28S ribosomal protein S28, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS28 PE=1 SV=1 - [E5RGC7_HUMAN]	7.77	6	1	1	1	0.823	1		0.000	103	11.740
B4DJR9	cDNA FLJ60603, highly similar to Anaphase-promoting complex subunit 2 (APC2)(Cyclosome subunit 2) OS=Homo sapiens PE=2 SV=1 - [B4DJR9_HUMAN]	5.26	3	1	1	1	1.000	1		0.000	247	27.683
B3KSK2	cDNA FLJ36470 fis, clone THYMU2015918, highly similar to Nucleotide-binding protein-like OS=Homo sapiens PE=2 SV=1 - [B3KSK2_HUMAN]	14.71	4	1	1	1	1.000	1		0.000	136	14.692
H7BZA5	Arf-GAP domain and FG repeat-containing protein 2 (Fragment) OS=Homo sapiens GN=AGFG2 PE=4 SV=1 - [H7BZA5_HUMAN]	11.66	1	1	1	1	1.000	1		0.000	223	21.834
Q658W3	Putative uncharacterized protein DKFZp666N1710 (Fragment) OS=Homo sapiens GN=DKFZp666N1710 PE=2 SV=1 - [Q658W3_HUMAN]	8.44	1	1	1	1				0.000	403	46.050
K7ENC1	Purine-rich element-binding protein gamma (Fragment) OS=Homo sapiens GN=PURG PE=4 SV=1 - [K7ENC1_HUMAN]	3.68	2	1	1	1	0.339	1		0.000	163	17.875
Q59FN4	LATS homolog 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FN4_HUMAN]	0.96	2	1	1	1	1.000	1		0.000	830	92.303
F5H1T8	Teratocarcinoma-derived growth factor 1 OS=Homo sapiens GN=TDGF1 PE=4 SV=1 - [F5H1T8_HUMAN]	8.14	5	1	1	1				0.000	172	19.167
E0WMV9	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1 - [E0WMV9_HUMAN]	4.4	2	1	1	1	0.986	1		0.000	273	31.432
B7ZKV0	Potassium voltage-gated channel, Shal-related subfamily, member 3 OS=Homo sapiens GN=KCND3 PE=2 SV=1 - [B7ZKV0_HUMAN]	3.93	1	1	1	1	1.000	1		0.000	636	71.293
J3KRA9	Serine/threonine-protein kinase SMG1 (Fragment) OS=Homo sapiens GN=SMG1 PE=1 SV=1 - [J3KRA9_HUMAN]	0.68	2	1	1	1	1.000	1		0.000	3551	398.588
I3L204	Unconventional myosin-Ic (Fragment) OS=Homo sapiens GN=MYO1C PE=1 SV=2 - [I3L204_HUMAN]	4.87	1	1	1	1	1.000	1		0.000	267	30.664
F5GZF6	Tyrosine-protein kinase STYK1 (Fragment) OS=Homo sapiens GN=STYK1 PE=4 SV=1 - [F5GZF6_HUMAN]	43.08	4	1	1	1				0.000	65	7.486
B9A019	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [B9A019_HUMAN]	13.13	1	1	1	1	1.000	1		0.000	99	11.404
H9KVC4	Interferon-induced GTP-binding protein Mx1 (Fragment) OS=Homo sapiens GN=MX1 PE=1 SV=1 - [H9KVC4_HUMAN]	37.66	2	1	1	1				0.000	77	8.005
L0R5D5	Alternative protein TMEM70 OS=Homo sapiens GN=TMEM70 PE=4 SV=1 - [L0R5D5_HUMAN]	9.73	2	1	1	1	1.000	1		0.000	113	13.248
D6RH12	Ankyrin repeat domain-containing protein 34B (Fragment) OS=Homo sapiens GN=ANKRD34B PE=4 SV=1 - [D6RH12_HUMAN]	94.12	2	1	1	1	1.000	1		0.000	17	1.810
C9K0D3	Myeloid leukemia factor 1 (Fragment) OS=Homo sapiens GN=MLF1 PE=4 SV=1 - [C9K0D3_HUMAN]	24.71	2	1	1	1	1.000	1		0.000	174	19.486
E7EVZ6	Pecanex-like protein 2 OS=Homo sapiens GN=PCNXL2 PE=4 SV=1 - [E7EVZ6_HUMAN]	3.77	4	1	1	1	0.797	1		0.000	424	48.239
H3BU99	Vacuolar fusion protein MON1 homolog B (Fragment) OS=Homo sapiens GN=MON1B PE=1 SV=1 - [H3BU99_HUMAN]	28.71	10	1	1	1	1.000	1		0.000	101	10.105
C9JFF0	Kinesin-like protein KIF26A OS=Homo sapiens GN=KIF26A PE=3 SV=1 - [C9JFF0_HUMAN]	1.66	3	2	2	2	1.000	2	0.000	0.000	1743	180.039
B0V3J0	tRNA-splicing endonuclease subunit Sen34 (Fragment) OS=Homo sapiens GN=TSEN34 PE=1 SV=1 - [B0V3J0_HUMAN]	8.26	5	1	1	1	1.000	1		0.000	242	26.086

H3BTK4	SH2B adapter protein 1 (Fragment) OS=Homo sapiens GN=SH2B1 PE=4 SV=3 - [H3BTK4_HUMAN]	14.04	6	1	1	1	1.089	1		0.000	57	6.156
B9A035	Cytosolic 5'-nucleotidase 3A OS=Homo sapiens GN=NT5C3A PE=1 SV=1 - [B9A035_HUMAN]	5.85	4	1	1	1	1.001	1		0.000	205	23.513
Q53S35	Putative uncharacterized protein SLC4A5 (Fragment) OS=Homo sapiens GN=SLC4A5 PE=4 SV=1 - [Q53S35_HUMAN]	3.5	3	1	1	1	1.000	1		0.000	714	78.614
H7C2N5	UPF0577 protein KIAA1324-like (Fragment) OS=Homo sapiens GN=KIAA1324L PE=4 SV=1 - [H7C2N5_HUMAN]	3.71	1	1	1	1				0.000	971	106.310
Q8TAR8	LRCH1 protein (Fragment) OS=Homo sapiens GN=LRCH1 PE=2 SV=1 - [Q8TAR8_HUMAN]	2.48	2	1	1	1	0.546	1		0.000	323	36.314
Q59EE7	Pro-alpha-1 type V collagen variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59EE7_HUMAN]	1	4	1	1	1	1.000	1		0.000	1792	178.407
Q6ZNE1	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1 - [Q6ZNE1_HUMAN]	2.51	1	1	2	2	1.000	1		0.000	957	111.707
B3KP15	cDNA FLJ30940 fis, clone FEBRA2007436, highly similar to Rap guanine nucleotide exchange factor 3 OS=Homo sapiens PE=2 SV=1 - [B3KP15_HUMAN]	6.48	6	1	1	1	1.000	1		0.000	216	25.134
J3QR65	Myotubularin-related protein 4 OS=Homo sapiens GN=MTMR4 PE=4 SV=1 - [J3QR65_HUMAN]	2.37	2	1	1	1	1.000	1		0.000	1138	126.589
Q8NH47	Olfactory receptor OS=Homo sapiens PE=3 SV=1 - [Q8NH47_HUMAN]	12.72	1	1	1	1				0.000	283	31.885
G3V368	GSK3-beta interaction protein (Fragment) OS=Homo sapiens GN=GSKIP PE=4 SV=1 - [G3V368_HUMAN]	39.74	3	1	1	1				0.000	78	8.806
Q32MQ5	MAP3K6 protein OS=Homo sapiens GN=MAP3K6 PE=2 SV=1 - [Q32MQ5_HUMAN]	4.31	3	1	1	1	0.904	1		0.000	441	48.379
B7Z398	cDNA FLJ50012, highly similar to Potassium voltage-gated channel subfamily H member 8 OS=Homo sapiens PE=2 SV=1 - [B7Z398_HUMAN]	4.98	2	1	1	1	1.000	1		0.000	542	62.051
Q9UEH6	A6(IV) collagen (Fragment) OS=Homo sapiens GN=COL4A6 PE=4 SV=1 - [Q9UEH6_HUMAN]	0.44	8	1	1	2	1.000	2	0.000	0.000	1600	153.707
J3KTQ2	ATP-dependent DNA helicase Q5 (Fragment) OS=Homo sapiens GN=RECQL5 PE=4 SV=1 - [J3KTQ2_HUMAN]	2.5	7	1	1	1	1.000	1		0.000	480	53.202
Q50KM3	Taste receptor type 2 (Fragment) OS=Homo sapiens GN=Hosa(Adygei)-T2R38 PE=3 SV=1 - [Q50KM3_HUMAN]	1.94	6	1	1	1	1.117	1		0.000	309	35.078
H7C009	cGMP-dependent 3',5'-cyclic phosphodiesterase (Fragment) OS=Homo sapiens GN=PDE2A PE=4 SV=1 - [H7C009_HUMAN]	6.42	6	1	1	1	1.000	1		0.000	327	37.379
Q9H678	cDNA: FLJ22530 fis, clone HRC12866 OS=Homo sapiens PE=2 SV=1 - [Q9H678_HUMAN]	1.97	4	1	1	1	0.921	1		0.000	406	45.330
Q8NEX1	Ells2 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8NEX1_HUMAN]	6.67	2	1	1	1	0.948	1		0.000	180	18.809
C9J3M8	Uncharacterized protein C3orf67 OS=Homo sapiens GN=C3orf67 PE=4 SV=1 - [C9J3M8_HUMAN]	6.29	2	1	1	1	1.000	1		0.000	334	36.978
M0R175	Nuclear receptor subfamily 2 group F member 6 (Fragment) OS=Homo sapiens GN=NR2F6 PE=1 SV=1 - [M0R175_HUMAN]	14.4	3	1	1	1	1.000	1		0.000	125	12.806
D6R9N5	Interferon regulatory factor 2 (Fragment) OS=Homo sapiens GN=IRF2 PE=4 SV=1 - [D6R9N5_HUMAN]	8.03	4	1	1	1	1.817	1		0.000	137	16.210
H7C2P2	Protein sidekick-2 (Fragment) OS=Homo sapiens GN=SDK2 PE=1 SV=1 - [H7C2P2_HUMAN]	2.41	2	1	1	1				0.000	1329	146.574
B4DKV6	cDNA FLJ60084, highly similar to Pericentrin (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DKV6_HUMAN]	2.14	2	1	1	1	0.601	1		0.000	888	101.204
A0A087WU50	Spermatogenesis-associated protein 3 OS=Homo sapiens GN=SPATA3 PE=4 SV=1 - [A0A087WU50_HUMAN]	10.5	3	1	1	1	1.000	1		0.000	181	19.761
Q5SZP1	Paired box protein Pax-2 (Fragment) OS=Homo sapiens GN=PAX2 PE=4 SV=1 - [Q5SZP1_HUMAN]	17.76	2	1	1	1				0.000	214	23.032
F5H6Q4	Transient receptor potential cation channel subfamily V member 4 OS=Homo sapiens GN=TRPV4 PE=4 SV=1 - [F5H6Q4_HUMAN]	1.45	2	1	1	1	1.231	1		0.000	552	61.769
H3BR95	WD repeat-containing protein 59 (Fragment) OS=Homo sapiens GN=WDR59 PE=4 SV=1 - [H3BR95_HUMAN]	8.97	3	1	1	1	1.345	1		0.000	156	17.570
A0A087WV52	28S ribosomal protein S30, mitochondrial OS=Homo sapiens GN=MRPS30 PE=4 SV=1 - [A0A087WV52_HUMAN]	3.56	5	1	1	2	1.176	2	20.795	0.000	337	38.869
Q9HBV8	Germ cell-less protein (Fragment) OS=Homo sapiens GN=GCL PE=2 SV=1 - [Q9HBV8_HUMAN]	3.1	4	1	1	1	1.000	1		0.000	387	44.594
H7C1P9	Titin (Fragment) OS=Homo sapiens GN=TTN PE=4 SV=1 - [H7C1P9_HUMAN]	0.62	1	1	1	1	1.000	1		0.000	962	109.167
D6RID7	Lymphoid enhancer-binding factor 1 OS=Homo sapiens GN=LEF1 PE=1 SV=1 - [D6RID7_HUMAN]	24.81	4	1	1	1				0.000	133	14.603
H0YH86	DCC-interacting protein 13-beta (Fragment) OS=Homo sapiens GN=APPL2 PE=4 SV=1 - [H0YH86_HUMAN]	19.68	1	1	1	1	1.000	1		0.000	188	21.147
E9PNW1	Harmonin (Fragment) OS=Homo sapiens GN=USH1C PE=4 SV=3 - [E9PNW1_HUMAN]	5.03	3	1	1	1	1.000	1		0.000	318	35.273
H0YLX3	Calcium and integrin-binding family member 2 (Fragment) OS=Homo sapiens GN=CIB2 PE=4 SV=3 - [H0YLX3_HUMAN]	49.09	1	1	1	1	1.000	1		0.000	55	6.371
X1WI30	DPY30 domain-containing protein 2 (Fragment) OS=Homo sapiens GN=DYDC2 PE=4 SV=2 - [X1WI30_HUMAN]	10.32	2	1	1	1	1.000	1		0.000	126	14.914
B4DTS3	cDNA FLJ50213, highly similar to Calpain-6 (Calpamodulin) OS=Homo sapiens PE=2 SV=1 - [B4DTS3_HUMAN]	2.07	3	1	1	1				0.000	386	45.038
Q5T3L7	Uroporphyrinogen-III synthase OS=Homo sapiens GN=UROS PE=4 SV=1 - [Q5T3L7_HUMAN]	10.53	4	1	1	1	0.898	1		0.000	133	14.685
B3KNV9	cDNA FLJ30554 fis, clone BRAWH2003693 OS=Homo sapiens PE=2 SV=1 - [B3KNV9_HUMAN]	1.18	3	1	1	1	1.338	1		0.000	1016	111.928
Q9BR35	Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1 - [Q9BR35_HUMAN]	15.79	1	1	1	1				0.000	133	14.534
B4E199	cDNA FLJ56283, highly similar to Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3F (PPP1R3F), mRNA OS=Homo sapiens PE=2 SV=1 - [B4E199_H	8.3	1	1	1	1				0.000	470	48.627
L8EAL3	Alternative protein NID2 OS=Homo sapiens GN=NID2 PE=4 SV=1 - [L8EAL3_HUMAN]	21.29	1	1	1	1	1.000	1		0.000	155	16.276
B3KTA9	cDNA FLJ37974 fis, clone CTONG2010024, highly similar to Homo sapiens radial spokehead-like 3 (RSHL3), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KTA9_HUMAN	3.33	2	1	1	1				0.000	511	58.407
B4DQN5	cDNA FLJ59958, highly similar to Homo sapiens ornithine aminotransferase-like 1 (OATL1), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1 - [B4DQN5_HUM	23.74	5	1	1	1	1.000	1		0.000	139	15.017
B2R6A9	cDNA, FLJ92868, highly similar to Homo sapiens HIRA interacting protein 3 (HIRIP3), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R6A9_HUMAN]	1.44	2	1	1	1	0.979	1		0.000	556	61.848
B4DHV8	cDNA FLJ57111, highly similar to Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase (EC 2.4.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DHV8_HUMAN]	10.63	3	1	1	1				0.000	254	29.472
B7Z5K0	cDNA FLJ52445, highly similar to Homo sapiens membrane-associated ring finger (C3HC4) 7 (MARCH7), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z5K0_HUMAN]	2.68	4	1	1	1	1.000	1		0.000	635	70.110
B7Z9C7	cDNA FLJ55885, highly similar to Homo sapiens zinc finger protein 423 (ZNF423), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z9C7_HUMAN]	1.37	3	1	1	1	1.000	1		0.000	1167	131.559
A0A075B6H2	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=4 SV=1 - [A0A075B6H2_HUMAN]	0.62	3	1	1	1	1.000	1		0.000	3548	387.260
Q8N7I6	CDNA FLJ25506 fis, clone CBR05185 OS=Homo sapiens PE=2 SV=1 - [Q8N7I6_HUMAN]	4.53	1	1	1	1	0.737	1		0.000	243	24.755
B4DMI5	cDNA FLJ56027, highly similar to Glutamate-rich protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DMI5_HUMAN]	3.79	2	1	1	1	1.000	1		0.000	422	46.439
A7E2V7	TUBGCP6 protein OS=Homo sapiens GN=TUBGCP6 PE=2 SV=1 - [A7E2V7_HUMAN]	1.88	4	1	1	1	0.937	1		0.000	1493	163.779
A8K1B1	cDNA FLJ75211, highly similar to Homo sapiens ubiquitin specific peptidase like 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K1B1_HUMAN]	2.47	2	1	1	1	1.055	1		0.000	1092	120.306
B2RC43	cDNA, FLJ95844, highly similar to Homo sapiens loss of heterozygosity, 11, chromosomal region 2, gene A (LOH11CR2A), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R(	2.97	3	1	1	1	1.325	1		0.000	437	47.982
O43245	Protein p65 OS=Homo sapiens GN=p65 PE=2 SV=2 - [O43245_HUMAN]	2.61	1	1	1	1	1.000	1		0.000	614	68.576
B4DVC0	cDNA FLJ60904, highly similar to Ras GTPase-activating protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DVC0_HUMAN]	4.69	2	1	1	1	1.072	1		0.000	277	31.718
A0A024RDH3	Uncharacterized protein OS=Homo sapiens GN=MGC16169 PE=4 SV=1 - [A0A024RDH3_HUMAN]	1.79	2	1	1	1	0.948	1		0.000	893	100.616
A8K073	cDNA FLJ78517, highly similar to Homo sapiens FK506 binding protein 9, 63 kDa (FKBP9), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K073_HUMAN]	4.93	9	1	1	1	0.951	1		0.000	142	15.551
B4DNS6	cDNA FLJ54278, highly similar to SPARC-like protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DNS6_HUMAN]	3.47	1	1	1	1	1.000	1		0.000	519	58.471
L8EAV7	Alternative protein DEF8 OS=Homo sapiens GN=DEF8 PE=4 SV=1 - [L8EAV7_HUMAN]	7.41	1	1	1	1	1.000	1		0.000	81	8.546
Q9BX88	Magphinin delta OS=Homo sapiens GN=TRO PE=2 SV=1 - [Q9BX88_HUMAN]	6.47	10	1	1	1	1.000	1		0.000	309	35.503
A8K383	cDNA FLJ75428, highly similar to Homo sapiens activating transcription factor 6 (ATF6), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K383_HUMAN]	3.28	2	1	1	1				0.000	670	74.547
B4DGW2	cDNA FLJ51627, highly similar to Rho guanine nucleotide exchange factor 12 OS=Homo sapiens PE=2 SV=1 - [B4DGW2_HUMAN]	1.86	4	1	1	1				0.000	1078	121.533
B3KTV1	cDNA FLJ38782 fis, clone LIVER2001113, highly similar to Leucine-rich repeat-containing protein 29 OS=Homo sapiens PE=2 SV=1 - [B3KTV1_HUMAN]	6.73	2	1	1	1	1.168	1		0.000	223	23.736
Q76L88	Putative G-protein coupled receptor OS=Homo sapiens GN=GPCR PE=4 SV=1 - [Q76L88_HUMAN]	3.74	2	1	1	1	0.735	1		0.000	321	36.465
Q9H986	cDNA FLJ12923 fis, clone NT2RP2004681, weakly similar to NEUROFILAMENT TRIPLET H PROTEIN OS=Homo sapiens PE=2 SV=1 - [Q9H986_HUMAN]	2.76	9	1	1	2	1.000	1		0.000	725	78.581
A5YKK5	KIAA0232 OS=Homo sapiens GN=KIAA0232 PE=2 SV=1 - [A5YKK5_HUMAN]	1.72	2	1	1	1	1.000	1		0.000	1395	154.706
A8K342	cDNA FLJ77706, highly similar to Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 (ALS2CR2), mRNA OS=Homo sapiens PE=2	1.67	2	1	1	1	0.708	1		0.000	418	47.006
B2R6H6	cDNA, FLJ92954, highly similar to Homo sapiens TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa (TAF9L), mRNA OS=Homo sapi	3.98	2	1	1	1	0.841	1		0.000	251	27.572
B7Z8Q7	cDNA FLJ53871, highly similar to Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens PE=2 SV=1 - [B7Z8Q7_HUMAN]	1.43	9	1	1	1	1.138	1		0.000	560	62.123
Q8N8L8	cDNA FLJ39246 fis, clone OCBBF2008466 OS=Homo sapiens PE=2 SV=1 - [Q8N8L8_HUMAN]	3.69	5	1	1	1	1.000	1		0.000	515	57.185
Q6ICA4	DJ402G11.5 protein OS=Homo sapiens GN=dJ402G11.5 PE=2 SV=1 - [Q6ICA4_HUMAN]	2.95	3	1	1	1	2.764	1		0.000	509	57.199
Q8N839	cDNA FLJ40081 fis, clone TESTI2001823 OS=Homo sapiens PE=2 SV=1 - [Q8N839_HUMAN]	7.56	1	1	1	1	1.000	1		0.000	172	19.233
E9ALP9	Histone H2A OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1720 PE=3 SV=1 - [E9ALP9_LEIMU]	7.58	1	1	1	1	13.351	1		0.000	132	13.952
E9AVM6	Putative 40S ribosomal protein S15 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_0420 PE=3 SV=1 - [E9AVM6_LEIMU]	3.95	1	1	1	1	1.149	1		0.000	152	17.424
E9AKS5	ATP-NAD kinase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0460 PE=4 SV=1 - [E9AKS5_LEIMU]	2.32	1	1	1	1	1.000	1		0.000	1249	132.471
E9AQ88	Putative ABC transporter OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_15_0890 PE=3 SV=1 - [E9AQ88_LEIMU]	1.35	1	1	1	1	0.938	1		0.000	743	83.469
E9AT28	Nucleoporin interacting component (NUP93),putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2510 PE=4 SV=1 - [E9AT28_LEIMU]	2	1	1	1	1	1.000	1		0.000	900	97.184
E9ATD7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3580 PE=4 SV=1 - [E9ATD7_LEIMU]	6.42	1	1	1	1	1.000	1		0.000	467	53.507
E9ALV5	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1180 PE=4 SV=1 - [E9ALV5_LEIMU]	0.7	1	1	1	1	1.000	1		0.000	2440	251.244
E9B1U0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1410 PE=4 SV=1 - [E9B1U0_LEIMU]	0.95	1	1	1	1	1.000	1		0.000	2414	256.412
E9AKR6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_06_0380 PE=4 SV=1 - [E9AKR6_LEIMU]	4.81	1	1	1	1	1.000	1		0.000	374	41.675
E9AJF3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_01_0660 PE=4 SV=1 - [E9AJF3_LEIMU]	1.44	1	1	1	1	1.051	1		0.000	1455	152.429
E9AV44	Proteasome regulatory non-ATP-ase subunit 5,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_21_0760 PE=4 SV=1 - [E9AV44_LEIMU]	2.32	1	1	1	1	1.000	1		0.000	474	54.394
E9ANM2	Putative 40S ribosomal protein S21 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0770 PE=4 SV=1 - [E9ANM2_LEIMU]	20.13	2	1	1	2	4.569	2	404.720	0.000	159	16.627
E9B6G5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2860 PE=4 SV=1 - [E9B6G5_LEIMU]	15.23	1	1	1	1	1.000	1		0.000	151	17.272
E9B534	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2473 PE=4 SV=1 - [E9B534_LEIMU]	10.14	1	1	1	1	1.000	1		0.000	138	14.855
E9B3Z4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_1575 PE=4 SV=1 - [E9B3Z4_LEIMU]	2.73	1	1	1	1	1.000	1		0.000	513	56.202
E9B1B7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3420 PE=4 SV=1 - [E9B1B7_LEIMU]	3.44	1	1	1	1				0.000	873	96.970
E9ARE7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0100 PE=4 SV=1 - [E9ARE7_LEIMU]	2.88	1	1	1	1	1.000	1		0.000	452	49.534
E9ARJ2	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0550 PE=4 SV=1 - [E9ARJ2_LEIMU]	6.46	1	1	1	1	1.000	1		0.000	356	40.810
E9AW09	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0090 PE=4 SV=1 - [E9AW09_LEIMU]	12.72	1	1	1	1				0.000	346	36.587
E9AW70	Putative ubiquitin-activating enzyme e1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_0550 PE=3 SV=1 - [E9AW70_LEIMU]	0.86	1	1	1	1	1.000	1		0.000	1044	115.070
E9ALT5	Putative RNA binding protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1370 PE=4 SV=1 - [E9ALT5_LEIMU]	1.3	1	1	1	1	1.000	1		0.000	1384	141.318
E9B103	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_2300 PE=4 SV=1 - [E9B103_LEIMU]	0.77	1	1	1	1	1.000	1		0.000	1306	139.740
E9AN13	Putative ribosomal protein l35a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0070 PE=4 SV=1 - [E9AN13_LEIMU]	4.86	2	1	1	1	3.202	1		0.000	144	16.470
E9B4T4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1130 PE=4 SV=1 - [E9B4T4_LEIMU]	0.89	1	1	1	1	1.000	1		0.000	2367	252.231
E9B6A9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2290 PE=4 SV=1 - [E9B6A9_LEIMU]	1.25	1	1	1	1	0.325	1		0.000	1514	158.675
E9ATV4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5200 PE=4 SV=1 - [E9ATV4_LEIMU]	1.52	1	1	1	1	1.000	1		0.000	986	106.850
E9ANM9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0850 PE=4 SV=1 - [E9ANM9_LEIMU]	4.03	1	1	1	1				0.000	472	52.331
E9B6N3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3540 PE=4 SV=1 - [E9B6N3_LEIMU]	8.14	1	1	1	1	1.000	1		0.000	221	24.430
E9B1S3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_1250 PE=4 SV=1 - [E9B1S3_LEIMU]	0.92	1	1	1	1	0.841	1		0.000	1090	117.236
E9B223	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2220 PE=4 SV=1 - [E9B223_LEIMU]	0.26	1	1	1	1	1.271	1		0.000	2291	239.576
E9B722	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4950 PE=4 SV=1 - [E9B722_LEIMU]	1.26	1	1	1	2	1.000	2	0.000	0.000	1032	107.214
E9B2Q7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_1320 PE=4 SV=1 - [E9B2Q7_LEIMU]	4.24	1	1	1	1				0.000	543	61.197
E9AQQ4	Sucrose-phosphate synthase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0950 PE=4 SV=1 - [E9AQQ4_LEIMU]	1.94	1	1	1	1	1.000	1		0.000	464	52.334
E9AXK4	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_25_1260 PE=4 SV=1 - [E9AXK4_LEIMU]	1.22	1	1	1	1				0.000	2294	233.384
E9B642	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1640 PE=4 SV=1 - [E9B642_LEIMU]	8.68	1	1	1	3	1.000	3	0.000	0.000	357	38.940
E9AU01	Putative RNA helicase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5670 PE=4 SV=1 - [E9AU01_LEIMU]	1.87	1	1	1	1	1.000	1		0.000	697	77.282
E9ATZ8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_5640 PE=4 SV=1 - [E9ATZ8_LEIMU]	4.05	1	1	1	1	1.000	1		0.000	494	54.181
E9AUQ0	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_1110 PE=4 SV=1 - [E9AUQ0_LEIMU]	0.96	1	1	1	1	1.000	1		0.000	1142	124.168
E9B5P8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_0100 PE=4 SV=1 - [E9B5P8_LEIMU]	4.95	1	1	1	1	0.737	1		0.000	202	24.223
E9AN22	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_0160 PE=4 SV=1 - [E9AN22_LEIMU]	5.62	1	1	1	1	1.000	1		0.000	498	53.936
E9AWR3	Putative signal recognition particle OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0730 PE=3 SV=1 - [E9AWR3_LEIMU]	7.32	1	1	1	1				0.000	519	56.590
E9AZ68	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_1650 PE=4 SV=1 - [E9AZ68_LEIMU]	1.93	1	1	1	1	1.000	1		0.000	1294	137.009
E9B5J6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_4010 PE=4 SV=1 - [E9B5J6_LEIMU]	8.65	1	1	1	1	1.000	1		0.000	104	12.180
E9ASL1	Mitogen-activated protein kinase-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0910 PE=4 SV=1 - [E9ASL1_LEIMU]	0.96	1	1	1	3	1.000	3	0.000	0.000	1563	171.956
E9B369	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_2890 PE=4 SV=1 - [E9B369_LEIMU]	8.59	1	1	1	4	1.000	3	0.000	0.000	291	32.948
E9B4W2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1380 PE=4 SV=1 - [E9B4W2_LEIMU]	1.62	1	1	1	1	1.000	1		0.000	1299	138.143
E9ARX7	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_19_0260 PE=3 SV=1 - [E9ARX7_LEIMU]	1.55	1	1	1	1				0.000	841	93.780
E9ANB2	Putative carrier protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_10_1020 PE=3 SV=1 - [E9ANB2_LEIMU]	2.28	1	1	1	1	2.239	1		0.000	395	43.389
E9B583	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_2940 PE=4 SV=1 - [E9B583_LEIMU]	2.04	1	1	1	1	1.000	1		0.000	294	33.072
E9B204	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_30_2050 PE=4 SV=1 - [E9B204_LEIMU]	4.43	1	1	1	1	1.000	1		0.000	519	58.554
E9AQQ2	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0930 PE=4 SV=1 - [E9AQQ2_LEIMU]	7.27	1	1	1	1	1.000	1		0.000	220	24.941
E9B0S8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1540 PE=4 SV=1 - [E9B0S8_LEIMU]	5.54	1	1	1	1	1.000	1		0.000	325	35.501
E9AM12	Putative flagellar radial spoke protein-like OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0660 PE=4 SV=1 - [E9AM12_LEIMU]	5.61	1	1	1	1	1.000	1		0.000	588	63.862
E9B491	UDP-N-acetylglucosamine pyrophosphorylase,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2520 PE=4 SV=1 - [E9B491_LEIMU]	3.21	1	1	1	1	0.647	1		0.000	560	59.295
E9ARF4	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_18_0170 PE=4 SV=1 - [E9ARF4_LEIMU]	6.05	1	1	1	2	1.010	2	1.446	0.000	347	38.484
E9B199	Putative glutamyl-tRNA synthetase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_3240 PE=3 SV=1 - [E9B199_LEIMU]	1.85	1	1	1	1	1.000	1		0.000	594	67.881
E9ASL6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_0960 PE=4 SV=1 - [E9ASL6_LEIMU]	2.19	1	1	1	1	1.000	1		0.000	915	98.743
E9B6H0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_2910 PE=4 SV=1 - [E9B6H0_LEIMU]	15.45	1	1	1	1				0.000	123	14.384
E9AYK6	Putative syntaxin binding protein 1 OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_26_2260 PE=4 SV=1 - [E9AYK6_LEIMU]	4.73	1	1	1	1	1.000	1		0.000	740	80.071
E9AT95	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_3170 PE=4 SV=1 - [E9AT95_LEIMU]	1.74	1	1	1	1	0.910	1		0.000	344	38.311
E9B3A3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3200 PE=4 SV=1 - [E9B3A3_LEIMU]	0.45	1	1	1	2	1.059	2	6.043	0.000	1321	143.091
E9AK10	Putative adenosine monophosphate deaminase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_04_0280 PE=4 SV=1 - [E9AK10_LEIMU]	1.43	1	1	1	1				0.000	2030	218.660
E9B4B3	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2730 PE=4 SV=1 - [E9B4B3_LEIMU]	3.78	1	1	1	1	1.000	1		0.000	502	56.996
E9AJN6	Putative peptidyl dipeptidase OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0740 PE=3 SV=1 - [E9AJN6_LEIMU]	1.77	1	1	1	1	7.268	1		0.000	678	76.578
E9ANN3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_11_0890 PE=4 SV=1 - [E9ANN3_LEIMU]	1.69	1	1	1	1	1.041	1		0.000	1007	106.090
E9AYS9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_27_0270 PE=4 SV=1 - [E9AYS9_LEIMU]	2.33	1	1	1	1	1.000	1		0.000	1071	118.182
E9B4U7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_33_1240 PE=4 SV=1 - [E9B4U7_LEIMU]	3.66	1	1	1	2	1.000	1		0.000	547	61.574
E9ALE8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_2760 PE=4 SV=1 - [E9ALE8_LEIMU]	4.75	1	1	1	1	1.000	1		0.000	568	64.611
E9AQS7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_1160 PE=4 SV=1 - [E9AQS7_LEIMU]	2.26	1	1	1	1	1.668	1		0.000	487	51.634
E9AM69	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_0100 PE=4 SV=1 - [E9AM69_LEIMU]	2.43	1	1	1	1	1.000	1		0.000	536	59.075
E9AMI8	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_1180 PE=4 SV=1 - [E9AMI8_LEIMU]	3.59	1	1	1	1	1.000	1		0.000	418	46.564
E9AWR6	DNA repair and recombination protein RAD54,putative OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0760 PE=4 SV=1 - [E9AWR6_LEIMU]	0.53	1	1	1	1	1.257	1		0.000	1130	123.552
E9B640	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_1620 PE=4 SV=1 - [E9B640_LEIMU]	0.56	1	1	1	1	0.733	1		0.000	1949	212.123
E9ANU3	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_12_0160 PE=4 SV=1 - [E9ANU3_LEIMU]	1.63	1	1	1	1	0.297	1		0.000	797	88.300
E9ALU5	Putative lipase domain protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_08_29_1280 PE=4 SV=1 - [E9ALU5_LEIMU]	1.01	1	1	1	1	1.000	1		0.000	1877	204.546
E9AUS7	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_20_1380 PE=4 SV=1 - [E9AUS7_LEIMU]	1.12	1	1	1	1	2.101	1		0.000	1247	128.844
E9B388	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_31_3050 PE=4 SV=1 - [E9B388_LEIMU]	2.42	1	1	1	1				0.000	825	93.147
E9B6W8	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4380 PE=4 SV=1 - [E9B6W8_LEIMU]	2.53	1	1	1	1	1.000	1		0.000	553	58.147
E9AWY6	Kinesin-like protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1430 PE=3 SV=1 - [E9AWY6_LEIMU]	0.43	1	1	1	1	1.000	1		0.000	3289	343.101
E9AWB5	Hydrophilic acylated surface protein a OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_23_1040 PE=4 SV=1 - [E9AWB5_LEIMU]	43.48	2	1	1	1	1.000	1		0.000	69	7.138
E9AX09	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1640 PE=4 SV=1 - [E9AX09_LEIMU]	2.42	1	1	1	1	0.966	1		0.000	579	64.715
E9AVT7	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_22_1050 PE=4 SV=1 - [E9AVT7_LEIMU]	4.25	1	1	1	1				0.000	964	100.370
E9AX45	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_1990 PE=4 SV=1 - [E9AX45_LEIMU]	5.97	1	1	1	1	1.000	1		0.000	352	38.619
E9APF0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_13_1260 PE=4 SV=1 - [E9APF0_LEIMU]	9.69	1	1	1	1	0.516	1		0.000	196	21.810
E9B451	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_2130 PE=4 SV=1 - [E9B451_LEIMU]	4.44	1	1	1	1	1.000	1		0.000	923	94.101
E9AJK9	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_02_0470 PE=4 SV=1 - [E9AJK9_LEIMU]	0.95	1	1	1	1	1.000	1		0.000	2936	296.819
E9AWL9	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_24_0300 PE=4 SV=1 - [E9AWL9_LEIMU]	0.9	1	1	1	2	0.803	2	39.692	0.000	1787	193.077
E9AQG5	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_16_0090 PE=4 SV=1 - [E9AQG5_LEIMU]	3.38	1	1	1	1	1.000	1		0.000	325	36.243
E9AT20	Putative caltractin OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_36_2430 PE=4 SV=1 - [E9AT20_LEIMU]	17.36	1	1	1	1				0.000	265	28.621
E9B6V6	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_4260 PE=4 SV=1 - [E9B6V6_LEIMU]	2.65	1	1	1	1	1.000	1		0.000	377	43.264
E9B3M6	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_32_0480 PE=4 SV=1 - [E9B3M6_LEIMU]	1.36	1	1	1	1	0.924	1		0.000	663	71.370
E9B6Q0	Putative uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_34_3720 PE=4 SV=1 - [E9B6Q0_LEIMU]	5.91	1	1	1	1	1.000	1		0.000	440	50.653
E9B0Q1	Uncharacterized protein OS=Leishmania mexicana (strain MHOM/GT/2001/U1103) GN=LMXM_29_1220 PE=4 SV=1 - [E9B0Q1_LEIMU]	0.65	1	1	1	1	1.000	1		0.000	930	98.578

Appendix IV – Published and Presented work

Hide and Spread for intracellular *Leishmania* parasites – from infection to apoptosis

Rajeev Rai and Giulia Getti
School of Science, University of Greenwich, Kent, ME4 4TB

Leishmania is a protozoan parasite responsible for human disease called leishmaniasis. The parasite life cycle alternates between two stages. The promastigotes stage develops inside the sandfly vector and once injected into a mammalian host, enters macrophages and establish itself as intracellular replicating amastigotes. The dissemination of amastigotes to uninfected macrophages is crucial for the development of the disease. However, the molecular mechanism of spreading is largely unknown.

Natural infection studies in mice have shown that early phase of infection occurs silently without accompanying immunopathological changes. A process resembling cell death via apoptosis, which involves the removal of damaged cells by macrophages without eliciting an inflammatory response, speculated us that *Leishmania* parasites could leave the host cell within apoptotic bodies, evading the host immune defense system.

Our study investigates the infection with four GFP expressing species of *Leishmania* on apoptosis of the host cells. Terminally differentiated THP-1 monocyte was employed to model the *in vitro Leishmania* infection. Through flow cytometry, infection and early apoptotic features were detected simultaneously for four days both on apoptosis induced and non-induced infected cells. Our results revealed higher level of early apoptosis upon parasite infection compared to uninfected cells. Remarkably apoptotic induction caused a 4 fold increase in percentage of infection when compared with non-induced infected cell. Moreover an increase in the level of apoptosis was also detected, further demonstrating a link between infection and apoptosis. Overall, the results support the hypothesis that apoptosis induction could participate in parasites spreading between human host cells.

Presented at British Society for Parasitology (BSP) Annual Spring meeting, Poster presentation, University of Cambridge, 2014

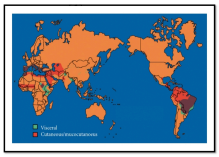
Hide and spread for intracellular *Leishmania* parasite – from infection to apoptosis

Rajeev Rai and Giulia Getti
School of Life Science, University of Greenwich, Kent, UK

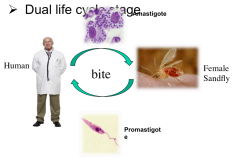
INTRODUCTION

- *Leishmania* is a protozoan parasite responsible for human diseases called leishmanisais

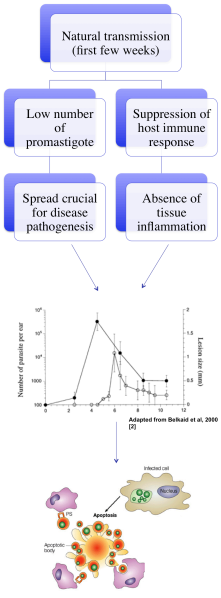
- Leishmaniasis is endemic in tropical and sub-tropical regions of the world with two million cases



- Dual life cycle/stage



RESEARCH BACKGROUND



Possible mechanism for exiting host cell?

AIMS OF THE STUDY

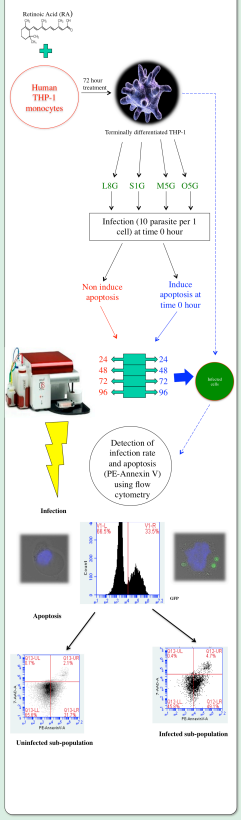
Study the link between apoptosis of terminally differentiated THP-1 monocytes (human monocyte cell line) and infection for four species of GFP expressing *Leishmania* parasites

- *L. aethiopica* (L8G)
- *L. major* (S1G)
- *L. mexicana* (M5G)
- *L. tropica* (O5G)

This will involve:

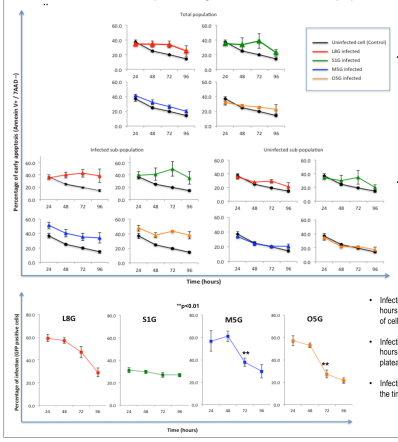
1. Investigating the effect of infection on host cells' apoptosis (24 to 96 hours).
2. Investigating the effect of apoptotic induction on infection (24 to 96 hours)
3. Developing an in vitro model to study late infection (72 to 120)

EXPERIMENTAL MODELS



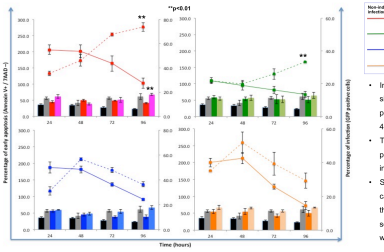
RESULTS and DISCUSSION

1. Effect of *Leishmania* promastigote infection on the apoptosis of differentiated THP-1



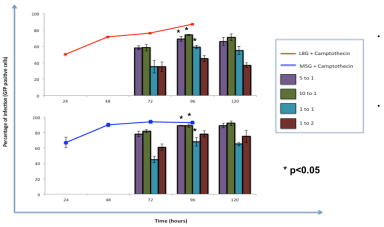
- In total and non infected sub… population, no significant….both the control and infected cells showed 40% of early apoptotic death at 24 hours Statistically significant difference???. Uninfected sub-population displayed no significant differences in apoptosis between infected cells and the control,
- A significant increase in early apoptosis was detected in the sub-population of infected cells when compared to uninfected control from 48 to 96 hours
- Infection of 60% were detected at 24 and 48 hours for L8G, M5G and O5G, whereas only 30% of cells were infected by S1G.
- Infection rate reduced significantly from 48 to 72 hours for M5G and O5G (**p<0.01), until it plateaus off at 96 hours post infection.
- Infection by S1G remained constant throughout the time course.

2. Effect of Camptothecin induced apoptosis on infection and host cell viability



- Induction with camptothecin caused a significant increase (**p<0.01) in the percentage of L8G and S1G infection from 48 to 96 hours.
- This was directly correlated with a higher percentage of early apoptotic cells for L8G infected cells only.
- Surprisingly, 24h treatment with..microM camptothecin induction negatively affected the infection % for M5G and O5G. This seemed to change when camp treatment was adjusted (data not shown)

3. Infection of autologous cells with an infected cells



- Significant rise in infection was detected only in 5/1, 10/1 and 1/1 ratio for healthy cells infected with L8G and M5G infected cell at 96 hours.
- Early apoptotic death was correlated with the above trend (data not shown)

CONCLUSIONS

- The apoptosis of THP-1 cell remains higher during *Leishmania* infection
- Induction of apoptosis could possibly transform the ability of amastigote to spread between cell.
- Preliminary studies of cell associated infection suggest a strong link between infection and apoptosis.

REFERENCE

1. World Health Organisation website (www.who.int/leishmaniasis)
2. Belkaid, Y., Mendez, S., Lira, R., Kadambi, N., Milon, G and Sacks, D. (2000). A natural model of Leishmania major infection reveals a prolonged silent phase of parasite amplification in the skin before the onset of lesion formation and immunity. 165; 969-977

THANK YOU

- Giulia Getti
- Lawrence Harbige
- University of Greenwich
- BSP Travel awards 2014

The *in vitro* development of *Leishmania* parasite dissemination during late stage of macrophage infection

Rajeev Rai and Giulia Getti

School of Science, University of Greenwich, Kent, ME4 4TB

The ability of replicating *Leishmania* parasite inside macrophage to spread their progeny towards naïve macrophages is of a paramount importance to initiate the pathogenesis of leishmaniasis. However, the mechanism of parasite spread has not been characterized yet. Research in this area has been largely hindered by the lack of infection models for this stage of the parasitic life cycle. We have developed an *in vitro* model to enhance our understanding on the dissemination of *Leishmania* that occurs during late stage of macrophage infection.

Terminally differentiated THP-1 monocytes were infected with two GFP expressing species, *Leishmania mexicana* (M5G) and *Leishmania aethiopica* (L8G) and treated with an apoptotic inducer. Following 72 hours from infection, both infected cells were used to infect a newly differentiated population of THP-1 cells at different infection ratios. Flow cytometric analysis was carried out to detect the percentage of GFP positive parasite residing in the cell.

We found that 80% of cells were infected by M5G and L8G at 72 hours, under apoptotic induction. Re-infection of the healthy cells at 72 hours with both infected cells at a ratio of 10/1, 5/1 and 1/1 resulted in a significant increase ($p<0.05$) in the percentage of infection post 24 hours. This infection remained constant from 48 to 72 hours, eventually lowering at 96 hours. Importantly, there was no significant reduction in the total number of viable cell before and after re-infection. This indicated that the infection rise observed was related to the possible spread of the parasites and not caused by death of uninfected THP-1 monocytes.

Our development of an *in vitro* model of *Leishmania* infection of macrophage revealed a potential time frame for parasite dissemination during late infective stage. This would allow further investigation into whether apoptosis could be involved in "hiding" and "spreading" this lethal parasite during leishmaniasis.

Presented at 13th International Congress for Parasitology (ICOPA), Oral presentation, Mexico City, 2014

Leishmania modulates host apoptotic signaling pathway in order to disseminate from cell-to-cell during human macrophage infection

Rajeev Rai and Giulia Getti

School of Science, University of Greenwich, Kent, ME4 4TB

The initiation for the pathogenesis of human leishmaniasis is dependent on the ability of *Leishmania* amastigotes to disseminate from infected to uninfected macrophages. However, the molecular and cellular mechanism behind this unique form of cell-to-cell spreading is one of the least explored topics in the field of *Leishmania* biology. This slow advancement has been largely due to the lack of effective model system to represent the late stage of host-parasite interaction *in vitro*. In this work, we have reported the development of a human cell-based *in vitro* model representative of *Leishmania aethiopica* dissemination in human cells.

The model is based on infecting a healthy population of terminally differentiated THP-1 macrophage with previously (72 hours) infected THP-1 macrophage. Such model showed an increase in *L. aethiopica* (GFP expressing) infection from 35% to 50% after 24 hours of co-culture. This was confirmed using real time lapse microscopy which revealed inter-cellular extrusion and subsequent transfer of amastigotes from infected to a healthy THP-1 macrophage. Interestingly, this form of cell-to-cell spreading appeared to be correlated with apoptotic induction, as there was a significant increase in the percentage of Annexin V and active caspase-3 expression as compared to uninfected control.

Western blot analysis further demonstrated that the above effect within this time period was associated with de-phosphorylation and reduced expression of anti-apoptotic protein AKT, and increased expression of cytochrome C protein. In conclusion, this could indicate that *L. aethiopica* promotes the host cell apoptosis by interfering with AKT pathways resulting in the release of cytochrome C and subsequent caspase-3 activation. This could represent one of the critical and novel mechanisms behind the dissemination of *Leishmania* species during human macrophage infection.

Presented at British Society for Parasitology (BSP) Annual Autumn meeting, Poster presentation, Royal Veterinary College, 2015

Leishmania modulates host apoptotic signaling pathway in order to disseminate from cell-to-cell during human macrophage infection

Rajeev Rai and Giulia Getti
School of Life Science, University of Greenwich, Kent, UK

INTRODUCTION

- *Leishmania* is a protozoan parasite responsible for human diseases called leishmaniasis (Figure 1)

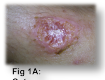


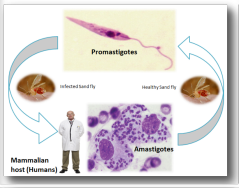
Fig 1A: Cutaneous

Fig 1B: Visceral

- The disease remains endemic in tropical and sub-tropical regions of the world (Figure 2) with two million cases per year [1]

Fig 2: Leishmaniasis world map

- Dimorphic life cycle of *Leishmania*



RESEARCH BACKGROUND

- The dissemination of *Leishmania* amastigotes from infected to uninfected macrophage represents a critical step in the establishment of human leishmaniasis

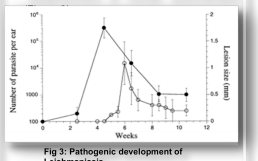


Fig 3: Pathogenic development of Leishmaniasis

- Activation of host cell apoptotic death have been suggested as a potential mode of escape route for intracellular amastigotes [2].
- However, the exact cellular and molecular mechanism behind this form of cell-to-cell spreading is one of the least explored topics in the field of *Leishmania* biology.
- This investigation has been largely due to the lack of effective model system to represent the late stage of host-parasite interaction in vitro.

RESEARCH AIMS

1. Validate our newly developed in vitro model (Figure 4) of *L. aethiopica* dissemination during human macrophage infection via real time lapse microscopy.

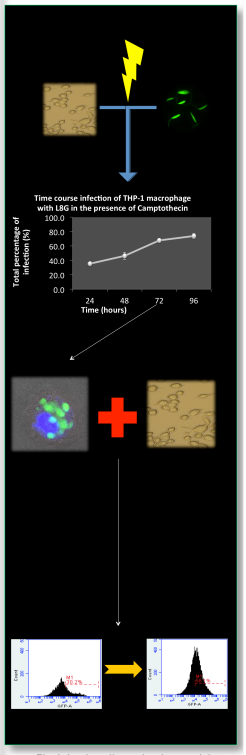


Fig 4: In vitro dissemination model for *L. aethiopica* during human macrophage infection

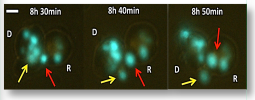
2. Utilize the above model in order to examine two critical aspects responsible for driving *Leishmania* infection spreading:

   i. Investigate the potential role of parasite mediated host cell apoptosis via Annexin V and Caspase-3 assay.

   ii. Analyze the molecular expression of host intracellular proteins associated with apoptosis regulation, including AKT and cytochrome C

RESULTS

1. Real time-lapse microscopy of amastigote transmission

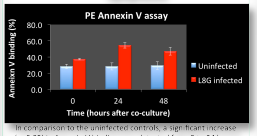


The recipient (R) THP-1 macrophage was pre-stained with Cell mask orange dye for 5 minutes and extensively washed with 1x PBS. This fresh population was then co-cultured with 72h LBG infected donor cells (D) and live imaged for a period of 12 hours every 10 minutes under TRITC laser (Scale: 25 µm).

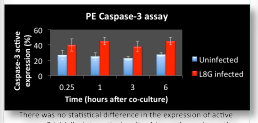
At 8h 30min, the red arrowed amastigote begin to migrate from the peripheral membrane of D. After 10-20minutes, the amastigote is completely extruded and transfers into R.

In addition, the yellow arrowed amastigote is possibly observed to be packaged within apoptotic bodies of D.

2. Link between infection spreading and host cell apoptosis

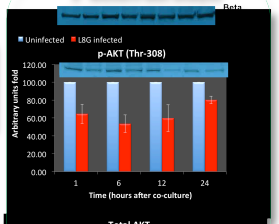


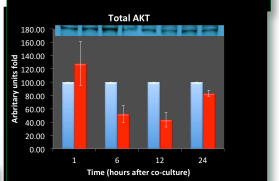
In comparison to the uninfected controls, a significant increase ($p<0.05$) in Annexin V binding was detected from 0 to 24 hours of co-culture in LBG infected cells.

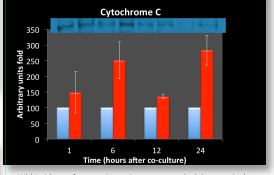


There was no statistical difference in the expression of active caspase-3 initially. Interestingly, after 1 hour of co-culture, the expression of active caspase-3 within the infected cells increased by two fold in relative to uninfected controls.

3. Western blot analysis

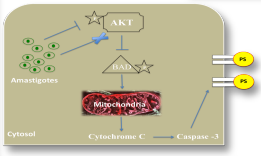






Within 1 hour after co-culture, there was a marked decrease in the phosphorylation of AKT (Thr 308) within the infected cells as compared to uninfected controls. However, no significant differences in the expression of total AKT and cytochrome C were observed. This level of reduced AKT inactivation was detected till 24 hours. Surprisingly, from 6 hours onwards, the expression of total AKT in infected cells remained significantly lower than the control, as cytochrome C expression was instead found to be higher. Overall, these results potentially suggest parasite mediated apoptotic protein modulation during the cell-to-cell dissemination of *Leishmania* infection.

DISCUSSION



This schematic diagram illustrates the probable apoptotic pathways induced by *Leishmania* amastigotes during cell-to-cell spreading. The parasite could interfere with AKT signalling by either inactivation or degradation of AKT. This could stimulate the release of cytochrome C from mitochondria via BAD activation. This in turn could promote the activation of caspase-3 resulting in the exposure of phosphatidylserine (PS) and subsequent induction of apoptosis.

CONCLUSIONS

1. Validation of our in vitro dissemination model was achieved following the visual evidence of *L. aethiopica* amastigotes transfer from cell-to-cell through real time lapse microscopy.
2. Induction of host cell apoptosis by amastigotes appeared to play an instrumental role behind this cell-to-cell dissemination.
3. Western blot analysis further demonstrated that the above effect was associated with de-phosphorylation and reduced expression of anti-apoptotic protein AKT, and increased expression of cytochrome C protein.

REFERENCES

1. Handman, E. (2001). Leishmaniasis: current status of vaccine development. Clinical Microbiology Reviews, 14, 229-243.
2. Real, F. (2014). Cell-to-cell transfer of *L.amazonensis* amastigotes is mediated by immunomodulatory LAMP rich parsitophorous extrusions. Cellular Microbiology 16, 1549-1564.