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Discovering and Drugging Anti-Cancer Targets of  
Natural Compounds Using Chemoproteomics

by

Elizabeth Anne Moore

A dissertation submitted in partial satisfaction of the

requirements for the degree of

Doctor of Philosophy

in

Chemistry

in the

Graduate Division

of the

University of California, Berkeley

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## Abstract

### Discovering and Drugging Anti-Cancer Targets of Natural Compounds Using Chemoproteomics

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Doctor of Philosophy in Chemistry

University of California, Berkeley

Professor Daniel K. Nomura, Chair

Though many proteins have been identified as relevant to cancer pathogenicity, very few are now targeted clinically due to a lack of both a mechanistic understanding of the protein(s) and the identification of small molecule modifiers. Even highly-studied oncogenes are rarely therapeutically utilized, since solvent-accessible amino acid residues to which small molecule drugs can bind have often not yet been identified. In fact, it is currently thought that such small molecule binding pockets have only been identified on 10-15% of human genes, and less than 5% are currently exploited therapeutically.<sup>1</sup> In order to develop targeted cancer therapies, it is imperative to both identify and effectively pharmacologically manipulate small molecule binding pockets on disease-relevant protein targets.

Many existing targeted cancer therapies utilize or build upon naturally-occurring compounds that exert anti-cancer activity. Many of these natural products contain electrophilic moieties, reacting covalently with nucleophilic amino acids. While the use of natural products themselves as drugs seems like a promising idea, such complex compounds often interact widely in the proteome, resulting in non-therapeutic interactions that could potentially result in unwanted physiological side effects. A more effective route toward natural product-based drug development, therefore, requires identifying the particular covalent modification responsible for the anti-cancer activity and developing a compound that binds to the same residue more selectively. A variety of approaches to identifying targets of natural products have arisen, but most rely on piecemeal methods, such as derivatizing the natural product or assessing its reactivity one protein at a time.

Chemoproteomics have arisen as strategies to address these two challenges, allowing for proteome-wide assessment of a compound's reactivity directly in biological systems. The use of chemoproteomic technologies has contributed to a deeper understanding of natural products' protein interactions while also allowing for the identification of more selective, covalently-acting small molecules, whose smaller size also renders them more synthetically accessible.

In this work I provide a comprehensive discussion of the current understanding of metabolic pathways implicated in cancer and the associated therapies in development and use. In addition, I demonstrate the efficacy of chemoproteomic technologies in a study that identifies a novel protein target and druggable site targeted by an anti-cancer natural product, followed by the discovery and development of small molecules that bind more selectively to the protein target.

*For my family, innate and chosen.*

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## LIST OF ABBREVIATIONS

1,3-BPG	1,3-bisphosphoglyceric acid
2-DG	2-deoxy-D-glucose
2-HG	alpha-hydroxyglutaric acid
3BP	bromopyruvic acid
5-FU	fluorouracil
ABPP	activity-based protein profiling
ACC	adrenocortical carcinoma
ACL	ATP citrate lyase
ACP	acyl carrier protein
ACS	acyl-CoA synthetase
ACSL(1-5)	long-chain acyl-CoA synthetase
AGPS	alkyl-glycerone phosphate synthase
a-KG	alpha-ketoglutarate
AKR(1B10)	aldo-keto reductase
Akt	protein kinase B
ALK	anaplastic lymphoma kinase
ALL	acute lymphoblastic leukemia
AML	acute myeloid leukemia
ATCC	American Type Culture Collection
ATP	adenosine triphosphate
BAK	bcl-2 homologous antagonist/killer
BAX	bcl-2-associated X protein
BCA	bicinchoninic acid assay
BCH	2-aminobicyclo(2,2,1)-heptane-2-carboxylic acid
BPTES	bis-2-[5-phenyl-acetamido-1,2,4-thiadiazol-2-yl] ethyl sulfide
BRCA1	breast cancer type 1 susceptibility protein
BRD(2-4)	bromodomain-containing protein
ccRCC	clear-cell renal carcinoma
CDK	cyclin-dependent kinase
CoA	coenzyme A
CPT1(A/B/C)	carnitine palmitoyltransferase I
CuACC	copper-catalyzed azide-alkyne cycloaddition
CYP450	cytochrome P450
DAG	diacylglycerol
DCA	dichloroacetate
DFMO	2-difluoromethyl ornithine
DHAP	dihydroxyacetone phosphate
DMEM	Dulbecco's modified Eagle's medium
DMSO	dimethyl sulfoxide
DNA	deoxyribonucleic acid
DTT	dithiothreitol
EC <sub>50</sub>	half maximal effective concentration
EDTA	ethylenediaminetetraacetic acid
EGFR	epidermal growth factor receptor

EGTA	ethylene glycol-bis( $\beta$ -aminoethyl ether)-N,N,N',N'-tetraacetic acid
ER	estrogen receptors
ErbB2	see HER2
ETC	electron transport chain
F1,6BP	fructose-1,6-bisphosphate
F2,6BP	fructose 2,6-bisphosphate
F6P	fructose-6-phosphate
FA	fatty acid
FAD	flavin adenine dinucleotide
FAO	fatty acid oxidation
FASN	fatty acid synthase
FBS	fetal bovine serum
FDA	Federal Drug Administration
FH	fumarate hydratase
G3P	glucose-3-phosphate
G6P	glucose-6-phosphate
G6PDH	glucose-6-phosphate dehydrogenase
GAPDH	glyceraldehyde-3-phosphate dehydrogenase
GDP	guanosine diphosphate
GIST	gastrointestinal stromal tumors
GLDH	glutamate dehydrogenase
GLS	glutaminase
GLUT(1-4)	glucose transporter
GPNA	l- $\gamma$ -glutamyl-p-nitroanilide
GPx1	glutathione peroxidase 1
Grb2	growth factor receptor-bound protein 2
GSH	glutathione
GSTP1	glutathione S-transferase Pi 1
GTP	guanosine triphosphate
HDAC	histone deacetylases
HER2	human epidermal growth factor receptor 2
HIF(1a-3a)	hypoxia-inducible factor
HK(1-4,DC1)	hexokinase
HLRCC	hereditary leiomyomatosis and renal cell carcinoma
HR	hormone receptor
Hsp90	heat shock protein 90
IA	iodoacetamide
IAyne	iodoacetamide alkyne
IC <sub>50</sub>	half maximal inhibitory power
IDH(1/2)	isocitrate dehydrogenase
IDO(1/2)	indole- amine (2,3)-dioxygenase
IKK $\beta$	inhibitor of nuclear factor kappa-B kinase subunit beta
isoTOP-ABPP	isotopic tandem orthogonal proteolysis-enabled activity based protein profiling
JAK	Janus kinase
KEAP1	Kelch-like ECH-associated protein 1

KO	knock out
LDH(A/B)	lactate dehydrogenase
LOA	loss of attachment
MAPK	mitogen-activated protein kinase
MAT	methionine adenytransferase
MAX	myc-associated factor X
MCT(1-4)	monocarboxylate transporter
me-THF	5,10-methylene-tetrahydrofolate
mTHF	5-methyltetrahydrofolate
MTHFR	methylene- tetrahydrofolate reductase
mTOR	mammalian target of rapamycin
mTORC(1/2)	mammalian target of rapamycin complex
NAD(H)	nicotinamide adenine dinucleotide
NADP(H)	nicotinamide adenine dinucleotide phosphate
NS	not significant
NSCLC	nonsmall cell lung cancer
ODC	ornithine decarboxylase
PAF	platelet-activating factor
PAFAH(1B1/2/3)	platelet-activating factor acetylhydrolases
PBS	phosphate-buffered saline
PD1	programmed cell death protein 1
PDB	Protein Data Bank
PDC	pyruvate dehydrogenase complex
PDK(-1/-3)	pyruvate dehydrogenase kinase
PFK(-1/-2)	phosphofructokinase
PFKFB(1-4)	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase
PHGDH	3-phosphoglycerate dehydrogenase
PI3K	phosphoinositide 3-kinase
PIP2	phosphatidylinositol 4,5-bisphosphate
PIP3	phosphatidylinositol 3,4,5-triphosphate
PK	pyruvate kinase
PKC	protein kinase C
PKM(1/2)	PK muscle isozyme M1, 2
PP2A	protein phosphatase 2A
PPP	pentose phosphate pathway
PTEN	phosphatase and tensin homologue
qPCR	quantitative PCR
R5P	ribose-5-phosphate
RCC	renal cell carcinoma
RNA	ribonucleic acid
RNAi	RNA interference
ROS	reactive oxygen species
SAM	S-adenosylmethionine
SCC	squamous cell carcinoma
SCCHN	squamous cell carcinoma of the head and neck
SCD	stearoyl-CoA desaturase

SCID	severe combined immunodeficiency
SCLC	small-cell lung cancer
SDH(B/C/D)	succinate dehydrogenase
SDS-PAGE	sodium dodecyl sulfate-polyacrylamide gel electrophoresis
SGOC	serine, glycine, and one-carbon
SHMT	serine hydroxymethyl transferase
shRNA	short hairpin RNA
siRNA	small interfering RNA
SIRT1	sirtuin 1
SOS	Son of Sevenless
STAT5	signal transducer and activator of transcription 5
TBST	tris-buffered saline with Tween 20
TCA	tricarboxylic acid
TCEP	tris(2-carboxyethyl)phosphine
TEV	tobacco etch virus
THF	tetrahydrofolate
TKTL1	transketolase-like protein 1
TNBC	triple negative breast cancer
TSC(1/2)	tuberous sclerosis complex
UQCRH	ubiquinol-cytochrome c reductase hinge protein
VEGF	vascular endothelial growth factor
VHL	von Hippel-Lindau

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“Now to Him who is able to do far more abundantly than all that we ask or think, according to the power at work within us, to Him be glory...forever and ever.”<sup>2</sup>

**CHAPTER 1**  
Cancer Metabolism: Current Understanding and Therapies

This chapter is based on the *Chemical Reviews* publication “Cancer Metabolism: Current Understanding and Therapies”<sup>3</sup> and is adapted with permission from all co-authors.

## **1. INTRODUCTION**

The development of cancer depends on alterations or mutations arising within the cell, driving aberrant behavior that can bypass the typical checkpoints required for normal cell health. Mutations or expression changes in oncogenes and tumor suppressors are known to alter cellular metabolism to fuel cancer pathogenicity, and the genomic landscape of cancer is highly complex and heterogeneous<sup>4-6</sup>. It has been determined, however, that many of the mutational or somatic changes in cancer cells commonly and fundamentally impact cancer metabolism. In this review, we will discuss many aspects of altered cancer cell metabolism and the current therapies developed to target these alterations. We will first discuss the major mutated oncogenes and tumor suppressors that impact cancer cell metabolism. We will then discuss the major alterations in nutrient metabolism and changes of associated proteins within various metabolic pathways. Along the way, we consider current targeted therapies, either in preclinical or clinical trials that are currently being researched and developed to target metabolic dysregulations.

## **2 ONCOGENES AND TUMOR SUPPRESSORS**

### **2.1 The Warburg Effect: The Link Between Oncogenesis and Metabolism**

A well-known dysregulation in cancer metabolism is Warburg's observation that cancer cells upregulate their use of glucose and produce more lactic acid than normal tissues<sup>7</sup>. Recent research has implicated oncogenic activation as the main cause, though not the only cause, of the 'Warburg effect'<sup>8</sup>. The Warburg effect, also more broadly called fermentation or aerobic glycolysis (though it takes place under anaerobic conditions in cancer cells as well), is considered a hallmark of dysregulated metabolism in many types of cancer cells. While resting cells typically rely on mitochondrial oxidation to meet their bioenergetic needs, cancer cells often utilize aerobic glycolysis for both energy and proliferative pathogenesis. Even though mitochondrial oxidation yields much more energy for a cell per glucose, tumor cells are thought to utilize aerobic glycolysis to allow diversion of glycolytic intermediates to biosynthetic pathways to generate species necessary for cell growth and division, such as nucleotides, lipids, and amino acids<sup>9</sup>. Though this is generally how the Warburg effect is canonically understood, recent studies of biosynthetic precursors have revealed that glucose and glutamine – and their associated increase due to the Warburg effect – are not the main providers of material for mass accumulation<sup>10</sup>. A full understanding of the Warburg effect's impact on cancer cell metabolism is yet to be elucidated.

Altered metabolism is found across many different cancer cell types. Although cells that are functioning under the Warburg effect produce about 20 times less ATP per glucose molecule than with oxidative respiration, ATP is rarely limiting in cancer cells. Further, the building blocks needed for tumorigenesis, including the reducing power NADPH, nucleotides, lipids, and amino acids, increase in availability with increased flux through glycolysis via the Warburg effect. Thus, increasing glycolysis and fermentation while simultaneously decreasing mitochondrial oxidation enables cells to balance their energetic requirements with their capacity to divide. Additionally, it has been shown that the production of lactate happens anywhere from ten to one hundred times faster than glucose oxidation<sup>11,12</sup>. In order for cancer cells to utilize the advantageous Warburg



effect, they must undergo genetic mutations or possess some form of varying transcriptional profiles<sup>13,14</sup>. Of note, the Warburg effect is most likely an primary event in oncogenesis and does not happen in all cancer cells. For example, it is an immediate result of an initial oncogenic KRAS mutation in pancreatic cancer and of BRAF in melanoma<sup>11,15,16</sup>.

One well-researched connection between tumorigenesis and glucose metabolism is the serine/threonine kinase AKT/phosphoinositide 3-kinase (PI3K)/mammalian target of rapamycin (mTOR) signaling pathway. PI3K signaling can directly upregulate glucose intake and metabolism via various mechanisms, including increased localization of the glucose transporter, namely GLUT1, to the plasma membrane and increasing hexokinase (HK), phosphofructokinase-1 (PFK-1), and phosphofructokinase-2 (PFK-2) activities<sup>13,17-19</sup>. PI3K also phosphorylates phosphatidylinositol 4,5-bisphosphate (PIP2) to phosphatidylinositol 3,4,5-triphosphate (PIP3). PIP3 can then stimulate AKT, which plays numerous important biological roles within the cell. For example, AKT regulates cellular growth via its effects on the tuberous sclerosis (TSC1/TSC2) complex and mTOR signaling<sup>20,21</sup>. AKT can also regulate cell proliferation and survival through phosphorylation of cyclin-dependent kinase (CDK) inhibitors for the former and inhibition of pro-apoptotic proteins and signals, such as Bad or the transcription factor FoxO, for the latter<sup>21-23</sup>.

AKT/PI3K's downstream effector, mTOR, is crucial for cellular proliferation and growth. mTOR belongs to two separate complexes, mTOR complex 1 (mTORC1) and mTOR complex 2 (mTORC2), which are structurally similar but functionally different. mTORC1 positively regulates protein translation and plays roles in lipid synthesis and glucose metabolism, while mTORC2, on the other hand, regulates AKT phosphorylation<sup>24-26</sup>.

Due to altered AKT/PI3K/mTOR signaling frequently contributing to human disease, researchers have been keen to develop small molecule inhibitors for AKT, PI3K, and mTOR<sup>27-29</sup>. For example, upregulation of the AKT/PI3K/mTOR pathway occurs in approximately 70% of breast cancers<sup>30</sup>. Data from a randomized phase II clinical trial, called the FERGI trial (NCT01437566), evaluated the role of adding pictilisib, also called GDC-0941 (Genentech), a PI3K inhibitor, to fulvestrant, a steroidal anti-estrogen hormone therapy drug, to treat patients with advanced ER+, aromatase inhibitor (AI)-resistant or metastatic breast cancer (Table 1). In preliminary results, the combination of pictilisib and fulvestrant was correlated to a progression-free survival that increased from 5.1 to 6.6 months<sup>31</sup>. Pictilisib is currently undergoing trials to treat non-small cell lung cancer (NSCLC) as well. BKM120, also called buparlisib (Novartis Pharmaceuticals), is another PI3K inhibitor that is more advanced in clinical development. The BELLE-2 study (NCT01610284) is a phase III trial which randomized 1,148 postmenopausal women with HR+/HER2- advanced breast cancer after progression on AI to fulvestrant and buparlisib or fulvestrant and placebo. Another trial, the BELLE-3 study (NCT01633060), looks at the same treatment combination in patients whose cancer has progressed after an AI and mTOR inhibitor.

The first mTOR inhibitor in clinical use was rapamycin, which was initially given as an immunosuppressant medication after transplant surgeries. Later, Temsirolimus, a rapamycin derivative, was developed and is currently approved to treat renal cell carcinoma (RCC). Everolimus, another rapamycin analogue and mTOR inhibitor, is

approved for treatment in post-menopausal women with HR+ breast cancer among other cancer types, including RCC, pancreatic, subependymal giant cell astrocytomas, and neuroendocrine tumors<sup>28</sup> (Figure 1.1). These analogues, cleverly called “rapalogues”, exert their effect mainly as mTORC1 allosteric inhibitors. However, since only the mTORC1 complex is inhibited, their use is sometimes accompanied with resistance, such as negative feedback regulatory mechanisms, leading to paradoxical AKT activation and downstream proliferative effects<sup>32</sup>.

mTOR is constitutively activated in some forms of cancer, such as acute myeloid leukemia (AML), and is also a target for inhibitor development. Many mTOR kinase inhibitors can suppress protein translation and synthesis and induce cell apoptosis<sup>33,34</sup>. For example, the mTORC1 pathway is normally rapamycin-sensitive; in AML, however, the leukemia cells are rapamycin-resistant and protein translation becomes dysregulated. Treatment of AML with NVP-BEZ235 (Novartis Pharmaceuticals), a dual PI3K/mTOR inhibitor, has been shown to inhibit protein translation, PI3K signaling, mTORC1 signaling, and mTORC2 activity<sup>33</sup>. Additionally, the proliferation rate in AML cells was reduced and induction of an apoptotic response occurred, without affecting normal CD34(+) survival, when treated with NVP-BEZ235<sup>33</sup>. It has additionally been shown that another inhibitor, AZD8055, which is a specific mTOR inhibitor, was able to block both mTORC1 and mTORC2 signaling in AML cells. Significantly, AZD8055 blocked PI3K/AKT feedback activation, which is mTORC1-dependent, in AML cells *in situ*<sup>34</sup>. Although clinical trials are not yet underway in treating AML, AZD8055 is undergoing testing in numerous phase I clinical trials for other tumor types, including one to treat recurrent gliomas (NCT01316809), another to treat advanced solid tumors (NCT00731263), and also one to treat liver cancer (NCT00999882). Due to the critical role of the AKT/PI3K/mTOR signaling pathway in cancer metabolism, this signaling pathway remains an important therapeutic target.

The Warburg effect is positively regulated by oncogenes, such as KRAS and MYC<sup>35</sup>. Activation of the oncogenic RAS has been shown to significantly impact various aspects of cancer cell malignancy, including the dysregulation of cell growth, apoptosis, and invasiveness, among others<sup>36</sup>. Three canonical members of the RAS family – HRAS, KRAS, and NRAS – have been found to be oncogenic<sup>37</sup>. The HRAS, KRAS, and NRAS enzymes are broadly expressed; KRAS, for example, is expressed in nearly every human cell type. In addition to its ubiquitous expression, KRAS has also been shown in previous knockout mice studies to be essential for normal development<sup>38</sup>.

Many receptor types, including tyrosine kinases and G-protein-coupled receptors, can activate RAS<sup>39</sup>. For example, the epidermal growth-factor receptor (EGFR), through growth factor receptor-bound protein 2 (Grb2) and the Son of Sevenless (SOS) proteins, can activate RAS via increased exchange of GDP with GTP. GTP-bound RAS is then able to activate various effector enzymes, such as the serine/threonine kinase RAF (i.e. c-RAF1, BRAF and ARAF), which promotes cell cycle progression through the mitogen-activated protein kinase (MAPK) pathway, PI3K, which promotes apoptosis evasion through the AKT/PI3K pathway, and the RAS-related RAL proteins, which evade cell cycle arrest and apoptosis by inhibiting transcription factors of the FoxO family<sup>40-43</sup>. These pathways, among others, enable activated RAS to significantly contribute to tumorigenesis. Targeting RAS and its associated downstream effector pathways is, therefore, an attractive therapeutic ambition.

RAS and its effector pathways often undergo aberrant signaling in cancer via mutational damage, including the RAS genes themselves. More than 20% of tumors have mutations in RAS, and KRAS comprises approximately 85% of the total RAS mutations<sup>39,44</sup>. These mutations all prevent GTP hydrolysis on RAS, causing accumulation of GTP-bound (active) RAS. As mentioned previously, overexpression of EGFR activates RAS signaling pathways; overexpression of HER2 is another common example. EGFR and HER2 are frequently overexpressed in many types of cancers, including ovarian, breast, and stomach carcinomas<sup>45</sup>.

Receptor tyrosine kinases, such as EGFR and HER2, activate downstream signal transduction pathways that coordinate tumor cell growth<sup>46</sup>. Lapatinib is an FDA-approved tyrosine kinase inhibitor that targets both EGFR and HER2<sup>47</sup>. At least six other EGFR small-molecule inhibitors are presently under evaluation in clinical trials. Two of these drugs have shown especially great potential and are at an advanced stage of development: ZD1839, also called Gefitinib or Iressa (AstraZeneca), and OSI-774, also called Tarceva or Erlotinib (OSI Pharmaceuticals/Genentech). ZD1839 has been tested in several phase I and II clinical trials, and has shown little toxicity. Encouragingly, its use against numerous cancer types, including advanced NSCLC (NCT00259064; NCT00770588; NCT01017679), metastatic squamous cell carcinoma (SCC) (NCT00054691), and adrenocortical carcinoma (ACC) (NCT00215202) has shown promising anti-tumor activity. Some combinatorial studies have also occurred, including comparing ZD1839 with anastrozole to ZD1839 with fulvestrant in postmenopausal women with metastatic breast cancer (NCT00057941). Phase I, II, and III clinical trials are also currently underway for OSI-774 and have shown promising results in NSCLC (NCT00036647; NCT00072631; NCT00137800; NCT00063895), ovarian cancer (NCT00063895), and head and neck cancer (NCT00063895)<sup>48</sup>. OSI-774 has been studied in combination as well, including OSI-774 plus gemcitabine in pancreatic cancer (NCT00040183). Other EGFR inhibitors in clinical trials include GW2016 (GlaxoSmithKline), PKI116 (Novartis), EKB-569 (Wyeth-Ayerst/Genetics Institute), and CI-1033 (Pfizer). Taken together, EGFR inhibitors seem to be a promising step towards the treatment of numerous carcinomas.

For RAS proteins to function normally, they must first be post-translationally modified via prenylation, most often by the covalent addition of a farnesyl isoprenoid group<sup>49</sup>. Prenylation serves to localize RAS proteins to the plasma membrane or another subcellular compartment. Since mislocalized RAS proteins are inactive, the enzymes involved in post-translational modification of RAS are attractive therapeutic targets<sup>39,50</sup>. Alternatively, some RAS proteins, including KRAS and NRAS, but not HRAS, can also undergo geranylgeranylation<sup>51-53</sup>. By using high-throughput screening of compound libraries, a large number of highly effective farnesyl transferase inhibitors that are specifically effective against HRAS mutations, which cannot be alternatively modified via geranylgeranylation, have been identified and developed as potential cancer therapies<sup>54,55</sup>. Tipifarnib, also called Zarnestra (Kura Oncology), is currently being evaluated in phase II clinical trials, including a trial that targets advanced thyroid and squamous head and neck tumors with HRAS mutations (NCT02383927). For those RAS proteins, such as KRAS, that can gain resistance against farnesyl transferase inhibitors via geranylgeranylation, geranylgeranyl transferase inhibitors are also being developed. For example, co-treatment with FTI-277, a farnesyl transferase inhibitor, and

GGTI-298, a geranylgeranyl transferase inhibitor, inhibited KRAS prenylation in multiple human cancer cell lines that were initially resistant to FTI-277 alone<sup>56,57</sup>.

As mentioned previously, MYC also positively regulates the Warburg effect. MYC is an important transcription factor within cells and is involved in numerous processes including proliferation, cellular differentiation, metabolism, and apoptosis<sup>58,59</sup>. MYC can promote activation or repression of genes that are part of the aforementioned processes on a global scale within cells<sup>60,61</sup>. In normal cells, MYC expression is tightly regulated; in cancer cells, however, various abnormalities, such as gene amplification, chromosomal translocation, or mutations in signaling pathways, can stimulate MYC overexpression, leading to cell proliferation and tumorigenesis<sup>62-64</sup>. When MYC becomes oncogenic, it drives cancer cell growth, cell metabolism (including promoting glutaminolysis, which is detailed later), and cell survival. Importantly, MYC is dysregulated in about 70% of human cancers<sup>60</sup>. Furthermore, it has been shown that tumor regression and cell differentiation occur when MYC activity is inhibited<sup>65</sup>. The widespread activation of MYC, as well as observed tumor regression when MYC is inhibited, has driven researchers to explore MYC as a target for cancer therapy.

Many efforts have been made to discover compounds that can deliberately target MYC for cancer therapy. This has proved an immense challenge, however, since MYC lacks known functional binding pockets to which small-molecules may bind and is localized within the nucleus, which makes it inaccessible to any antibody-based therapies. Researchers have then taken advantage of MYC's heterodimerization with MAX, which is essential for MYC DNA-binding activity, developing drugs that will disrupt this interaction. Compounds such as 10058-F4, KJ-Pyr-9, and Omomyc all disrupt the MYC/MAX interaction and have shown efficacy in *in vivo* experiments<sup>66</sup>.

Compound	Target	Clinical trial phase	Relevant cancer(s)
pictilisib (GDC0941)	PI3K inhibitor	phase II	breast, NSCLC
buparlisib (BKM120)	PI3K inhibitor	phase III	breast, cervical, NSCLC, colorectal, prostate
Temsirolimus	mTOR inhibitor	approved	
Everolimus	mTOR inhibitor	approved	
NVP-BEZ235	PI3K/mTOR inhibitor	phase II	breast, pancreatic, renal, endometrial, glioblastoma
AZD8055	mTOR kinase inhibitor	phase I	glioma, solid tumors
Lapatinib	TK inhibitor (HER2, EGFR)	approved	
Iressa (ZD1839, gefitinib)	EGFR inhibitor	approved	
Tarceva (OSI-774)	EGFR inhibitor	approved	
PKI116	EGFR inhibitor	NA	
GW2016	EGFR inhibitor	phase II	breast, prostate, ovarian, peritoneal, stomach, liver
EKB-569	EGFR inhibitor	phase II	NSCLC, colorectal
CI-1033 (PD183805)	EGFR inhibitor	phase II	breast, lung, NSCLC
Zarnestra (Tipifarnib)	farnesyltransferase inhibitors	phase III	pancreatic, lung, breast, colorectal, thyroid, prostate
FTI-277	farnesyl transferase inhibitor	NA	
GGTI-298	geranylgeranyl transferase inhibitor	NA	
10058-F4	MYC/MAX interaction disruptor	NA	
KJ-Pry-9	MYC/MAX interaction disruptor	NA	
Omomyc	MYC/MAX interaction disruptor	NA	

**TABLE 1:** Summary of oncogene-related drugs with clinical status.

## 2.2. Tumor Suppressor Loss

A well-known and well-researched tumor suppressor is p53, which is integral to apoptosis and cell cycle regulation and implicated in DNA damage sensing. Furthermore, p53 has been shown to counteract the Warburg effect, working to stimulate respiration and reduce glycolytic flux. p53 plays an integral role in blocking the formation of tumors and therefore, when a point mutation or deletion leads to loss of p53 function, cancer cells are better able to evade apoptosis and gain insensitivity to antigrowth signals, leading to immortalization and cancer<sup>67-69</sup>. Of importance, it has previously been observed that roughly 50% of cancers have p53 gene mutations<sup>70</sup>. Two key strategies have been employed to target cancer cells with a p53 mutation: first, developing drugs that reinstate wild-type p53 activity, and second, developing drugs that deplete mutant p53.

Most p53 mutants are no longer able to bind with p53-specific response elements and lose their transcriptional activity and tumor suppressive functions<sup>71</sup>. However, it has previously been shown that p53 transcriptional activity can be restored from mutant p53<sup>72</sup>. CP-31398 was the first drug identified with this function<sup>71</sup>. Since then, researchers have been developing compounds that restore p53 activity (Table 2). CP-31398, along with another p53-reactivating compound, STIMA-1, bind to the mutated p53 and stabilize the wild-type p53 conformation; now in its active-form conformation, p53's transcriptional activity is restored<sup>73</sup>. Other p53 wild-type restoration compounds include PRIMA-1<sup>MET</sup> (or APR-246), MIRA-1, NSC652287, NSC319726/ZMC1, NSC87511, Chetomin, PK7088, and SCH529074<sup>72</sup>. Currently, PRIMA-1<sup>MET</sup> is the only compound listed here presently undergoing clinical trials; it has been shown to be safe and has a favorable pharmacokinetic profile thus far (NCT02999893; NCT00900614)<sup>74</sup>.

The second main approach to drugging mutant p53 relies on discovering and developing compounds that specifically deplete mutant p53 while leaving wild-type p53 unscathed. Although the mechanism still remains unclear, several mutant p53-depleting compounds have been found. Two Hsp90 inhibitors, 17-AAG and Ganetespib, are able to deplete mutant p53, along with Raf-1 and ErbB2, since Hsp90 has been previously shown to contribute to the accumulation of mutant p53<sup>70,75,76</sup>. An analog of 17-AAG, IPI-504, has been tested in clinical trials focusing on NSCLC and gastrointestinal stromal tumors (GIST)<sup>77,78</sup>. However, a recent phase II clinical trial looking at IPI-504 in NSCLC patients with ALK mutations was terminated due to slow patient accrual (NCT01228435). The GIST trials were also terminated; there were multiple observed mortalities in patients given IPI-504 (NCT00688766). Ganetespib (Synta Pharmaceuticals Corp.) is also currently undergoing clinical trials, including phase II for metastatic breast cancer and phase III for NSCLC<sup>79,80</sup>. Ganetespib was also granted Fast Track status by the FDA in two clinical trials, GALAXY-1 (NCT01348126) and GALAXY-2 (NCT01798485), which are currently examining the use of ganetespib in combination with Taxotere for treating advanced lung adenocarcinoma (a type of NSCLC). Unfortunately, despite positive results in the phase II GALAXY-1 study, the phase III GALAXY-2 study did not show improved overall or progression-free survival, and was ultimately terminated after the first interim analysis<sup>81</sup>.

Inhibitors of histone deacetylases (HDAC), which prevent Hsp90 from complexing with p53, have also been developed<sup>70,82</sup>. In fact, one compound, Vorinostat, is already FDA-approved for use in relapsed or refractory cutaneous T cell lymphoma.

Other drugs in development to deplete mutant p53 include the natural product Gambogic acid, Spautin-1, YK-3-237, and NSC59984<sup>72</sup>.

Another significant tumor suppressor is phosphatase and tensin homologue (PTEN). PTEN is absent in approximately 40% of tumors, which is second only to p53<sup>83</sup>. PTEN normally antagonizes the AKT/PI3K/mTOR pathway to block tumor cell growth and survival; loss of PTEN's tumor suppressor activity activates the PI3K pathway in cancer cells. Specifically, the PTEN gene encodes a lipid phosphatase that removes one phosphate group from phosphatidylinositol (3,4,5)-trisphosphate (PIP3) and phosphatidylinositol (4,5)-bisphosphate (PIP2), reversing their accumulation which is caused by PI3K. PTEN also promotes DNA repair and chromosome stability within the nucleus.

Since loss of PTEN activity leads to PIP3 accumulation, and subsequently an activated AKT/PI3K/mTOR cascade researchers are interested in finding therapeutics that target this pathway<sup>84</sup>. For example, it has been shown in mouse models that genetic loss of PTEN is associated with increased sensitivity to Temsirolimus (an mTORC1 inhibitor), AZD6482 (a PI3K inhibitor), MK-2206 (an AKT inhibitor), and 17-AAG (a HSP90 inhibitor)<sup>85</sup>.

Another high-profile tumor suppressor, the von Hippel-Lindau tumor suppressor, is involved in the regulation of gene expression. Deletion of the von Hippel-Lindau (VHL) tumor suppressor gene predisposes individuals to a variety of cancers and was identified in the 1990's as the genetic source for VHL disease<sup>86</sup>. The *VHL* gene product, protein VHL (pVHL), plays an integral role in oxygen sensing; it specifically targets hypoxia-inducible factors (HIF), including HIF-1 $\alpha$ , HIF-2 $\alpha$ , and HIF-3 $\alpha$ , for ubiquitination and proteasomal degradation<sup>87-90</sup>. Since its discovery, researchers have identified that early loss of VHL function is frequently seen in clear-cell renal cell carcinoma (ccRCC), and patients with VHL disease are more likely to develop ccRCC. This finding led to the development of compounds that inhibit HIF, or associated downstream targets, to treat ccRCC. Although suitable inhibitors against HIF itself do not yet exist, multiple drugs have been reported to indirectly downregulate HIF. For example, it has been previously shown that rapamycin, the mTOR inhibitor, can downregulate HIF, in addition to Hsp90 inhibitors such as geldenamycin and 17-(allylamino)-17-demethoxygeldanamycin<sup>89,91-95</sup>. Alternatively, HIF-responsive gene products, including vascular endothelial growth factor (VEGF), can be targeted. In fact, the VEGF-neutralizing antibody bevacizumab is approved to treat ccRCC<sup>95,96</sup>. Bevacizumab, when used in combination (often with interferon- $\alpha$ ) has produced prolonged progression-free survival in RCC patients<sup>95,97</sup>. Sorafenib and pazopanib, anti-VEGF tyrosine kinase inhibitors, are also approved ccRCC drugs<sup>95,98,99</sup>.

Compound	Target	Clinical trial phase	Relevant cancer(s)
CP-31398	p53 reactivator	NA	
STIMA-1	p53 reactivator	NA	
PRIMA-1MET (APR-246)	p53 reactivator	phase II	ovarian, esophageal, AML, melanoma
MIRA-1	p53 reactivator	NA	
NSC652287	p53 reactivator	NA	
NSC319726 (ZMC1)	p53 reactivator	NA	
NSC87511	p53 reactivator	NA	
Chetomin	p53 reactivator	NA	
PK7088	p53 reactivator	NA	
SCH529074	p53 reactivator	NA	
17-AAG (tanespimycin)	Hsp90 inhibitor	phase III	gastrointestinal, ovarian, pancreatic, prostate, NSCLC
IPI-504	Hsp90 inhibitor	phase II	breast, prostate, NSCLC, lung, kidney, gastrointestinal
Ganetespib	Hsp90 inhibitor	phase III	NSCLC, breast, ovarian, lung, rectal
Vorinostat	HDAC inhibitor	approved	
Gambogic acid	(p53?)	NA	
Spautin-1	(p53?)	NA	
YK-3-237	(p53?)	NA	
NSC59984	(p53?)	NA	
Temsirolimus	mTORC1 inhibitor	approved	
AZD6482	PI3K/p110B inhibitor	NA	
MK-2206	AKT inhibitor	phase II	colon, rectal, breast, NSCLC
rapamycin	mTOR inhibitor	approved	
geldenamycin	Hsp90 inhibitor	NA	
17-(allylamino)-17-demethoxygeldanamycin	Hsp90 inhibitor	phase II	leukemia, lymphoma
bevacizumab	VEGF antibody	approved	
sorafenib	anti-VEGF tyrosine kinase inhibitor	approved	
pazopanib	anti-VEGF tyrosine kinase inhibitor	approved	

**TABLE 2:** Summary of tumor suppressor-related drugs with clinical status.



### 3. GLUCOSE METABOLISM

#### 3.1. Glycolysis

Glycolysis is the initial step in glucose metabolism and involves nine reactions, each of which is catalyzed by a distinct enzyme. Of these, three are highly regulated: hexokinase (HK), phosphofructokinase (PFK), and pyruvate kinase (PK). All three enzymes have been shown to be altered in cancer (Figure 1.2)<sup>13</sup>. Of these three rate-limiting steps in the glycolytic pathway, one may exert greater control over glycolytic flux depending on the context, such as the presence of the Warburg effect or a distinct lack of precursors<sup>100</sup>.

Glucose uptake, and associated lactate production, is increased in tumors regardless of hypoxia<sup>7</sup>. Glucose uptake is regulated and facilitated by glucose transporters (GLUT), of which there are four main isoforms, GLUT1-4. GLUT1 is overexpressed in most cancers; though other isoforms are also present in cancer cells, GLUT1 overexpression is correlated with poor prognosis<sup>101</sup>. GLUT1 transporters are upregulated by AKT/PI3K, HIF, KRAS, and BRAF in many cancers<sup>102,103</sup>. Attempts to target these transporters have resulted in identification of the cytotoxic small molecules fasentin and STF-31536, which inhibit GLUT1-mediated glucose transport (Table 3)<sup>104,105</sup>.

HK catalyzes the first reaction in glycolysis, the phosphorylation of glucose to glucose-6-phosphate (G6P). G6P feedback then inhibits HK. There are five hexokinases: HK1-4 and HKDC1, of which the latter is poorly characterized<sup>106</sup>. HK1 is the most ubiquitous, whereas HK2-4 are found in specific tissues. Though HK1 and HK2 operate in very similar ways, only HK2 is upregulated in cancers; the reason for this is unknown, but its occurrence drives the coupling of glycolysis and oxidative phosphorylation by increasing the glucose flux into a variety of other metabolic pathways<sup>106</sup>. While HK1 and HK2 are allosterically regulated by their product, G6P, HK1 activity can also be regulated via PI3K. HK2, bound to the outer mitochondrial membrane, has been shown to impair glycolytic rate when removed<sup>13</sup>. Targeting HK2 has been shown to effectively kill various cancer cell types, including hepatocellular carcinoma, as the small molecule 3-bromopyruvate (3BP) causes cell death by covalently binding to HK2, resulting in its dissociation from the mitochondrial membrane<sup>107</sup>. Interfering with HK2 activity is a viable option for cancer therapy, as HK2 ablation *in vivo* inhibited mouse tumor growth without noticeable physiological consequence or an induction in HK1 activity<sup>108</sup>.

2-Deoxyglucose (2-DG), a glucose analog without the 2-hydroxyl group, is taken up into cells and phosphorylated by HK. However, the phosphorylated 2-DG cannot continue through the glycolytic pathway, and competes against glucose to inhibit HK<sup>109</sup>. 2-DG's glycolytic blocking abilities have made it a widely pursued clinical candidate. However, its use in clinical trials has shown very little efficacy in solid tumors (NCT00633087; NCT00096707)<sup>110-112</sup>.

PFK catalyzes the third reaction in glycolysis: the transfer of a phosphate group from ATP to fructose-6-phosphate (F6P) to form fructose-1,6-bisphosphate (F1,6BP). The reaction catalyzed by PFK is extremely thermodynamically favorable, with a large negative  $\Delta G$ , and is the practically irreversible "committed step" in glycolysis. Therefore, PFK is the key biochemical "valve" controlling the flow of substrate to product in

glycolysis and is a crucial regulatory point in the glycolytic pathway. PFK can be regulated in a variety of ways: by ATP, where a high ATP concentration in the cell inhibits PFK activity by binding to an allosteric regulatory site; by PI3K, whose activation increases glycolytic flux to affect PFK-1 and PFK-2 specifically; and by fructose 2,6-bisphosphate (F2,6BP), which activates PFK. In regard to the latter, levels of F2,6BP are regulated by bifunctional enzymes with phosphofructo-2-kinase and fructose 2,6-bisphosphatase (PFKFB) activities. Of the PFKFB isoforms, PFKFB3 (which is regulated by the JAK/STAT5 pathway and phosphorylated by various kinases such as PTEN and HIF-1 $\alpha$ ) is upregulated in many aggressive cancers such as leukemia<sup>113–117</sup>.

Various inhibitors of PFKFB3 have been developed based off the scaffold of the weak inhibitor 3PO, with the latest iteration, PFK-158 (Advanced Cancer Therapeutics), having recently undergone phase 1 clinical trials (NCT02044861)<sup>113,114,118</sup>. PFKFB3 inhibitors are of particular interest in the context of combinatorial therapy, as resistance to targeted cancer therapies can be seen in the MAPK and PI3K/AKT-mediated activation of PFKFB3, restoring survival and proliferative defects induced by drugs such as B-raf inhibitors<sup>119</sup>. For example, it was found that treatment of ER+ breast cancer with both palbociclib and PFK-158 produced a combinatorial effect, causing greater cell death than either drug alone<sup>120</sup>.

PK catalyzes the final step of glycolysis. Of the four isoforms, PK muscle isozyme M2 (PKM2) is the dominant isoform in cancer cells, as well as fetal and proliferating cells in general. PKM2 activity is relatively low, attenuating the final irreversible glycolytic step and creating a buildup of glycolytic intermediates that can be shuttled elsewhere for use in biosynthetic pathways necessary for proliferation<sup>9</sup>. PKM2 is implicated in only some cancers, most notably breast and colon cancer<sup>121–123</sup>. PKM2 is activated by both F1,6BP and serine<sup>122</sup>. PKM2 is also a co-activator of HIF-1 $\alpha$ ; HIF-1 $\alpha$  is activated by PKM2 hydroxylation, participating in a positive feedback loop that activates its own production<sup>124</sup>. Though one might anticipate that a loss of PKM2 activity could impair the development of cancer, the absence of PKM2 has not been shown to inhibit tumor metabolism<sup>121</sup>. Rather, it was found that PKM2 exerts its pro-cancerous effect by becoming the dominant isoform over PKM1, which is more constitutively active, in order to control the production of ATP more closely<sup>13</sup>. Dominance of PKM2 results in the production of NADPH by shuttling glycolytic intermediates into the pentose phosphate pathway (PPP). One approach to cancer treatment focuses on activating PKM2 to make it more similar to PKM1, which has been shown to inhibit tumor growth and sensitize cells to oxidative stress<sup>125</sup>. It has even been postulated that PKM2 could be used as a potential biomarker in early tumor detection<sup>126</sup>.

The glycolytic intermediate F1,6BP can then be converted to dihydroxyacetone phosphate (DHAP) or glucose-3-phosphate (G3P), to continue downstream toward the production of pyruvate. Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) catalyzes the next step in this pathway, converting G3P to 1,3-bisphosphoglyceric acid (1,3-BPG). GAPDH has been reported to be a mechanism of metabolic control in cancer cells exhibiting the Warburg effect via its precursor, glutathione S-transferase Pi 1 (GSTP1)<sup>127,128</sup>. GSTP1 affects cancer pathogenicity via its control over glycolytic metabolism; a small molecule inhibitor of GSTP1, LAS17, lowers production of lipids and nucleotides, lowers ATP levels, and impairs oncogenic signaling<sup>127</sup>. Inhibitors of GAPDH itself, such as the natural product koniginic acid, also impair cancer cell

proliferation in those cancers exhibiting the Warburg effect<sup>128</sup>. Interestingly, GAPDH has also been shown to exert control over the entirety of glycolytic flux in cells operating under the Warburg effect, given that there is an abundance of precursor material<sup>100</sup>.

### 3.2. Lactate Metabolism

In a normal, non-diseased cell, under aerobic conditions the pyruvate produced in glycolysis enters the pyruvate dehydrogenase complex (PDC) and the tricarboxylic acid (TCA) cycle to be oxidized completely to CO<sub>2</sub>. The NADH produced in glycolysis and the PDC, as well as the NADH and the FADH<sub>2</sub> produced in the TCA cycle, are all re-oxidized in the electron transport chain (ETC), where O<sub>2</sub> is the final electron acceptor. In anaerobic conditions, however, electron transport is not functional, and the scarce supply of NAD<sup>+</sup> is entirely converted to NADH, inhibiting glycolysis if there is too little NAD<sup>+</sup> left in the cell.

Glycolysis can continue even when O<sub>2</sub> is absent; fermentation can regenerate NAD<sup>+</sup> in anaerobic conditions, which is a central feature of the Warburg effect. Fermentation allows pyruvate to accept high-energy electrons from NADH and simultaneously reduces pyruvate to lactate in muscle cells via lactate dehydrogenase (LDH) enzymes, which happens to a much higher percentage of metabolized glucose in tumors. The NAD<sup>+</sup> produced by pyruvate reduction is now available for reuse in glycolysis, so more ATP and other glucose by-products can be produced. In cancerous cells, the oft-increased expression of LDHA produces greater amounts of NAD<sup>+</sup>, affecting the opposite response and allowing glycolysis to continue<sup>129</sup>. Cancer exploits this fermentation step in multifarious ways, with one indication being that the expression of the LDHB isoform is inconsistently up- or down-regulated in various cancers<sup>130</sup>. Several groups have shown that the knockdown of LDHA is effective in preventing cancer cell proliferation, reporting that LDHA-deficient cells limit anchorage-independent and *in vivo* growth of breast tumors<sup>131,132</sup>. Various inhibitors have been identified; however, selectivity has caused issues for drugs in clinical trials. For example, the LDHA inhibitor AT-101 (Ascenta Therapeutics), an enantiomer of the naturally-derived phenol gossypol, is also a BCL-2 domain 3 mimetic and has only shown mild effectiveness in phase I and II trials (NCT01285635; NCT00286793; NCT00286806)<sup>133-136</sup>. Also, a class of compounds called the 3-hydroxycyclohex-2-enone series (Genentech) is currently being optimized for inhibition of LDHA over the B isoform<sup>137</sup>.

If lactate builds up to high enough concentrations, however, it can act as a poison to the cell, and lactate production, alongside CO<sub>2</sub> production, is a contributor to tumor acidity<sup>138</sup>. As cancer cells take in more glucose, more lactate is secreted by monocarboxylate transporters 1-4 (MCT1-4)<sup>106,139</sup>. Extracellular lactate has been shown to inhibit immune responses to tumorigenic cells by both inactivating cytokine release in cytotoxic T cells and increasing the extracellular pool of lactate to such a great extent that T cell glycolysis is impaired, as the imbalanced concentration gradient does not allow for further excretion of lactate<sup>140</sup>. Extracellular lactate can also act as a signaling molecule, as several membrane receptors respond to fluctuations in H<sup>+</sup> concentration/extracellular pH to effect changes within the cell. Targeting these membrane receptors holds potential for drug development, and researchers are looking at inhibiting the function of G-protein coupled receptors 4, 65, 68, and 132 via knockdown<sup>16,141</sup>.

### 3.3. The Pyruvate Dehydrogenase Complex

The pyruvate produced from glycolysis and not used in lactate production is transported into the mitochondrial matrix where it is oxidized to CO<sub>2</sub>. Pyruvate does not enter the Krebs cycle directly, but instead is oxidatively decarboxylated by the PDC. The PDC oxidizes pyruvate to release a CO<sub>2</sub> and produce NADH, converting pyruvate into acetyl-CoA. The bond between sulfur and the acetyl group in acetyl-CoA is high energy, making it easy for acetyl-CoA to transfer the acetyl fragment into the TCA for further oxidation. The PDC also contains a thiamine pyrophosphate prosthetic group at one of its active sites, which is necessary for biological activity and is involved in catalyzing oxidative decarboxylation. The PDC was recently reported to carry the majority of pyruvate entering the TCA cycle<sup>142,143</sup>.

Regulation of the PDC is crucial; a high ratio of AMP or ADP to ATP will stimulate the PDC, thus increasing pyruvate's entry rate into the TCA. In addition, the PDC is regulated by pyruvate dehydrogenase kinase (PDK-1) expression, which phosphorylates the PDC $\alpha$  subunit and inactivates the PDC. Overexpression of pyruvate dehydrogenase kinases, including PDK-1, has been linked to the oncogenic activation of AKT and HIF pathways that are deeply tied to dysregulated cancer metabolism<sup>144</sup>. PDK-1 expression can be hijacked by cancer cells and continually overexpressed to inactivate the PDC, which contributes to the Warburg-identified glycolytic alterations. Furthermore, it has been shown that knockdown of PDK-1 restores the PDC to normal activity levels and reverses the aforementioned glycolytic effects<sup>145</sup>.

PDK-1 inhibition is an attractive strategy for cancer therapy. Dichloroacetate (DCA), long used to treat patients with mitochondrial abnormalities and in topical cosmetics, is a weak pan-PDK inhibitor whose clinical trials for treatment of cancer have not shown conclusive results (NCT01386632; NCT01029925)<sup>146,147</sup>. Radicol is also well-documented as a PDK-3 inhibitor, but targeting PDK-3 alone has not been conclusively shown to effectively kill cancer cells<sup>148</sup>. However, in combination with cisplatin, an anticancer effect was seen. This combinatorial effect prompted the development of mitaplatin, a DCA-cisplatin combination with an IC<sub>50</sub> of 14.0  $\mu$ M<sup>149-151</sup>. Other small-molecule inhibitors of PDK include CPI-613, a lipoate derivative currently in phase I/II/III clinical trials (NCT01766219; NCT01835041; NCT03435289; NCT03504423; NCT03504410)<sup>152-154</sup>. A variety of other efforts are also underway, including two DCA derivatives, N-(3-iodophenyl)-2, 2-dichloroacetamide and Mito-DCA, both with published micromolar inhibition specific to PDK-1<sup>151</sup>.

### 3.4. The Tricarboxylic Acid Cycle

The enzymes of the TCA cycle, as well as the aforementioned PDC, are located in the mitochondrial matrix. The TCA cycle involves a group of reactions that combine the 2-C acetyl unit from acetyl-CoA with a 4-C oxaloacetate molecule to produce citrate, cycle through various reactions that ultimately releases two CO<sub>2</sub> molecules, three NADH, one FADH<sub>2</sub>, and one GTP, and recycle the oxaloacetate molecule for reuse. The two carbons that leave as CO<sub>2</sub> during these reactions are not the same ones that entered the cycle as acetate. In this process, reducing power is stored in the high-energy electron carriers NADH and FADH<sub>2</sub>, which will eventually be re-oxidized in the ETC to store energy as ATP.

Isocitrate is converted to citrate, which can be cleaved to yield acetyl-CoA. In reductive carboxylation conditions, glutamine provides the majority of acetyl-CoA necessary for FA synthesis, which reduces the amount of acetyl-CoA that must be derived from glucose. Oxaloacetate, which is used to produce a variety of 4-carbon intermediates, is also produced from citrate cleavage. Therefore, reductive carboxylation can be the source of an entire pool of TCA cycle intermediates<sup>13</sup>.

Isocitrate can also be converted to  $\alpha$ -ketoglutarate ( $\alpha$ -KG), and vice versa, in the mitochondria via isocitrate dehydrogenase 2 (IDH2). IDH2 mutations are extremely important in driving tumorigenesis in many types of cancer, as they result in an enzyme that readily converts  $\alpha$ -KG to oncogenic D-2-hydroxyglutarate (2-HG) (Figure 1.2). Levels of 2-HG are significantly upregulated in tumors with IDH2 mutations; 2-HG can competitively inhibit the targets of  $\alpha$ -KG, which have DNA and histone demethylase activity. Therefore, high levels of 2-HG production can cause changes in gene expression, which has been shown to impair differentiation<sup>155–158</sup>. Inhibition of mutated IDH2 (mIDH2) by AGI-6780 has been effective *in vitro* in acute myeloid leukemia (AML) cells, where 2-HG levels normalized, histone and DNA hypermethylation were reversed, and the cells differentiated and ceased proliferating<sup>157,159,160</sup>. A bromodomain-containing protein 4 (BRD4) inhibitor, JQ1, has also shown promising results *in vivo* in mice with IDH2-driven AML<sup>157</sup>. Furthermore, AG-221 (Agiros Pharmaceuticals, Inc./Celgene) has suppressed 2-HG production and induced cell differentiation in both *in situ* IDH2-mutant AML cells and *in vivo* in xenograft mouse models<sup>161</sup>. AG-221 is currently in phase I/II clinical trials targeting AML patients harboring IDH2 mutations (NCT01915498)<sup>162</sup>. Although this study is still active, the FDA recently approved AG-221 for use in treating AML (now to be sold as Idhifa). In addition, comparable dose escalation studies of AG-221 in patients with mIDH2 gliomas, other solid tumors, and angioimmunoblastic T cell lymphoma have recently completed phase I trials (NCT02273739)<sup>162</sup>. Such results further supported initiation of a phase I/II combination study looking at AG-221 with azacitidine in newly-diagnosed AML patients (NCT02677922).

A variety of other TCA cycle enzymes (i.e. succinate dehydrogenase and fumarate hydratase) and ETC components can be mutated in cancer, interfering with glutamine-derived oxaloacetate<sup>13</sup>. For example, succinate dehydrogenase (SDH), a known tumor suppressor, converts succinate to fumarate, producing FADH<sub>2</sub>. SDH mutations lead to familial paraganglioma and familial pheochromocytoma, and no subunit mutation specificity (between B, C, and D) has yet been identified despite their distinct functions in the complex<sup>18,163</sup>. Mutated SDH is inactive, resulting in a succinate buildup in the mitochondria; excess succinate effectively stabilizes HIF-1 $\alpha$  via HIF-1 $\alpha$  prolyl hydroxylase inhibition, resulting in the transcription of tumorigenic genes and hypermethylation of histones and DNA<sup>164,165</sup>. SDH gene mutations are observed frequently in several types of cancer including RCC, gastrointestinal stromal tumors, colorectal cancer, and ovarian cancer, and are associated with malignancy and poor prognosis<sup>166–172</sup>. SDHB, one of four subunits of SDH and the one with the most frequently detected mutations, has recently been shown to be sensitive to bromodomain and extra-terminal (BET) inhibitors; these include JQ1 and various chemotypes including I-BET151, I-BET762, and PFI-1 (Figure 1.3)<sup>169,173,174</sup>. However, BET inhibitors are still in the beginning stages of development and effective therapies have not yet been established.

Fumarate hydratase (FH), also a tumor suppressor, converts fumarate to malate. FH mutations lead to a buildup of fumarate, which acts as a competitive inhibitor to HIF-1 $\alpha$  prolyl hydroxylase and stabilizes HIF-1 $\alpha$ <sup>8</sup>. FH mutations have been previously reported to lead to hereditary leiomyomatosis and renal cell carcinoma (HLRCC)<sup>18</sup>. Some successful inhibitors have been published with *in vitro* validation, but as with the SDH inhibitors, development of FH inhibitors remains challenging and is still in very early stages<sup>175</sup>.

Reductive carboxylation serves as a minor source of isocitrate, citrate, and acetyl-CoA in many healthy tissues<sup>176,177</sup>. This is especially important when the pathways that normally produce such metabolites are inactivated in cancer, which is often due to hypoxic conditions or dysregulated metabolism. For example, the tumor suppressor pVHL is implicated in the oxygen-dependent degradation of HIF-1 $\alpha$  and HIF-2 $\alpha$ , preventing the expression of HIF target genes. In those cancer cells lacking VHL, regardless of the presence of oxygen, the HIF target genes are therefore expressed. HIF target genes include glucose transporters and glycolytic enzymes, whose sustained expression contributes to the cell's adaptability to hypoxic conditions. In the case of hypoxic condition, PDK1 expression is also facilitated, which inhibits PDC and thus impairs the cell's ability to produce acetyl-coA and citrate from glucose. Glutamine-dependent reductive carboxylation, therefore, provides citrate and fatty acids in cultured cancer cells lacking pVHL<sup>13</sup>.

### 3.5. The Electron Transport Chain and Oxidative Phosphorylation

Oxidative phosphorylation couples the oxidation of NADH and FADH<sub>2</sub> in the electron transport chain (ETC) to chemiosmosis, the phosphorylation of ADP to produce ATP. The ETC is a group of five electron carriers, all of which are bound to the inner mitochondrial membrane. Each member of the chain reduces the next member down the line. Three of these are large protein complexes are cytochromes, thus contain a heme group, while the other two are small mobile electron carriers bound loosely to the inner mitochondrial membrane. The energy released via the ETC's oxidation reactions is used to pump protons out of the mitochondrial matrix and into the intermembrane space. The resulting proton gradient can then provide energy to drive the otherwise unfavorable phosphorylation of ADP to ATP.

In recent years, analysis of particularly aggressive and drug-resistant cancers has shown that they rely heavily on oxidative phosphorylation rather than glycolysis for survival<sup>178</sup>. These findings oppose the traditionally accepted, and diminished, role of the mitochondria in cancer cell metabolism<sup>179</sup>. The importance of the ETC for cancer survival suggests that the current understanding of tumor metabolism is still underdeveloped and lacking in nuance, and underscores the potential effectiveness of therapies targeting oxidative phosphorylation<sup>178,179</sup>. Developing therapies targeting components of the ETC holds great potential to achieve the goal of effectively drugging all cancer types.

The ETC is organized so that the first large carrier, NADH dehydrogenase (also called complex I), receives reducing power in the form of electrons from NADH upon its oxidation to NAD<sup>+</sup>. It has also been shown that NADH dehydrogenase polymorphisms correlate with breast cancer incidence, and though further research is necessary to investigate its use as a biomarker, therapeutic inhibition is currently being pursued as a

cancer treatment strategy<sup>180,181</sup>. Great interest has been focused on the use of biguanides for NADH dehydrogenase inhibition in cancer, with metformin being the most commonly studied. Metformin, which is currently approved as an anti-diabetic drug, is known to inhibit complex I, though the entirety of its anti-cancer mechanism is yet to be understood<sup>182</sup>. With initial clinical trials producing promising results, subsequent trials are underway<sup>183</sup>. Other biguanides, such as phenformin, have also been put forth as potential cancer therapeutics, but similar knowledge gaps exist for these. Sensitivity to biguanides varies between cancers, and recent work has shed light on cancer response to biguanides; low-glucose sensitivity can help identify which cancers would respond to drugs targeting the ETC, allowing for more targeted applications of biguanides and a more informed expectation of tumor response<sup>184</sup>. In addition, NADH dehydrogenase is inhibited by the small molecules VLX600 and ME-344, which result in cell death upon treatment<sup>185-187</sup>. Clinical trials with both are currently underway, and results from initial dose escalation studies with ME-344 have been positive (NCT02806817; NCT0222363)<sup>188</sup>.

NADH dehydrogenase then passes its electrons to a carrier, called coenzyme Q or ubiquinone. Ubiquinone receives electrons from both NADH dehydrogenase as well as directly from FADH<sub>2</sub> and any NADH produced in glycolysis and arriving from the cytoplasm. Ubiquinone passes its electrons to the next large protein complex, cytochrome C reductase (complex III), which subsequently passes its electrons to cytochrome C, which passes off electrons to the last large bound protein complex, cytochrome C oxidase (complex IV). Electrons are finally passed to O<sub>2</sub>, reducing it to water, which is the end product of the ETC. Each of the three large, membrane-bound proteins in the ETC pumps protons from the matrix into the intermembrane space when electrons flow past, producing a large proton gradient primed for chemiosmosis.

Complexes III-IV have also been implicated in cancer pathogenicity. The ubiquinol-cytochrome c reductase hinge protein (UQCRH), a protein within complex III, has been shown to be downregulated in ccRCC as compared to other RCCs, raising its potential as a biomarker<sup>189</sup>. Cytochrome C plays a part as well, as recent studies have revealed that cancerous cells inhibit cytochrome C-mediated apoptosis by supplying sufficient glutathione to keep cytochrome C in a reduced and inactive state<sup>190</sup>. In addition, it has been shown that knockdown of complex IV increases cancer aggressiveness, and complex IV has specifically been implicated in esophageal tumor progression<sup>191</sup>.

Compound	Target	Clinical trial phase	Relevant cancer(s)
fasentin	GLUT1 inhibitor	NA	
STF-31536	GLUT1 inhibitor	NA	
3-bromopyruvate	HK-2 inhibitor (?)	NA	
2-deoxyglucose	HK inhibitor	phase II	prostate, lung, breast, head & neck, pancreatic, gastric
3PO	PFKFB3 inhibitor	NA	
PK-158	PFKFB3 inhibitor	NA	
LAS17	GSTP1 inhibitor	NA	
koningic acid	GSTP1 inhibitor	NA	
AT-101	LDHA inhibitor	phase II	prostate, NSCLC, lung
Dichloroacetate (DCA)	PDK-1 inhibitor	phase II	breast, NSCLC, glioma, head & neck, neoplasms
radicol	PDK-3 inhibitor	NA	
mitaplatin	PDK-3 inhibitor	NA	
CPI-613	PDK-1 inhibitor	phase III	lung, pancreatic, liver
AGI-6780	IDH2 inhibitor	NA	
N-(3-iodophenyl)-2, 2-dichloroacetamide	PDK-1 inhibitor	NA	
Mito-DCA	PDK-1 inhibitor	NA	
JQI	BET inhibitor	NA	
I-BET151	BET inhibitor	NA	
I-BET762	BET inhibitor	phase II	breast, prostate, solid tumors
PFI-1	BET inhibitor	NA	
AG-221	IDH2 inhibitor	approved	
metformin	NADH dehydrogenase inhibitor	phase III	prostate, breast, endometrial, rectal, lung, bladder, colon
phenformin	NADH dehydrogenase inhibitor	phase I	melanoma
VLX600	NADH dehydrogenase inhibitor	phase I	solid tumors
ME-344	NADH dehydrogenase inhibitor	phase I	breast, solid tumors

**TABLE 3:** Summary of glucose metabolism-related drugs with clinical status.



## 4. AMINO ACID METABOLISM

Cancer cells require lipids, proteins, and nucleic acids – the standard building blocks necessary for cellular growth and proliferation – in addition to the maintenance of cellular redox status for optimal functioning. Amino acid metabolism provides many of these required elements. Amino acids play many roles in cancer cell growth and survival, including supplying carbons to the TCA cycle and nitrogen to nucleobase synthesis, and in regulating redox balance. Much like glucose, amino acids support the energy metabolism and anabolic processes that cancer cells require. Modern cancer therapies are now taking advantage of amino acids' importance in cancer survival in order to treat the disease.

### 4.1. Glutamine

The notion that proliferating cells require glutamine was discovered by Harry Eagle in the 1950s<sup>192</sup>. Glutamine is one of the eleven nonessential amino acids (meaning it can be synthesized sufficiently endogenously) in human metabolism. In fact, glutamine is the most abundant amino acid in circulation in human plasma. However, under certain circumstances, such as rapid growth or other cellular stressors, glutamine can become *conditionally essential*, meaning that the demand for glutamine overwhelms the cell's ability to produce it. In these conditions, the cell must find other means of obtaining glutamine, such as from the diet.

Glutamine contains an amine functional group which aids in its many biological roles within the cell, including involvement in various anabolic and catabolic processes. In regards to the former, glutamine is a source of nitrogen and carbon, both of which are used in the production of macromolecules such as nucleobases, lipids, and nucleotides. Concerning the latter, glutamine is originally trafficked into cells via transporters (including SLC1A5 and SLC7A5) and then catabolized, which is called glutaminolysis; it is then converted into many biological metabolites, such as glutamate, citrate, pyruvate, lactate, aspartate, alanine, and CO<sub>2</sub>. Due to its important – often essential – role in cancer cell proliferation and survival, efforts to target glutaminolysis via small molecule inhibitors are underway (Figure 1.4)<sup>193,194</sup>.

Specific inhibition of SLC1A5, the major glutamine transporter in many cancers, has shown promise in treating cancer. Benzylserine, l- $\gamma$ -glutamyl-p-nitroanilide (GPNA), and  $\gamma$ -FBP all inhibit SLC1A5 (Table 4) and some have been used to show that upon SLC1A5 inhibition, tumor growth is suppressed in both lung cancer and melanoma<sup>195,196</sup>. The SLC7A5 transporter may also be a useful target for cancer treatment, as treatment with its inhibitor, 2-aminobicyclo(2,2,1)-heptane-2-carboxylic acid (BCH), results in restricted mTOR signaling<sup>197</sup>.

Building upon this finding, inhibitors of SLC1A5 and SLC7A5 may also show promise in certain cancer cells as indirect inhibitors of mTORC1. Glutamine flux, as regulated by SLC1A5 and SLC7A5, can regulate mTOR activation, thus exerting control over cellular growth and proliferation<sup>197</sup>. Many studies support the role of amino acids, especially those of glutamine and leucine, in activating mTORC1-dependent signaling<sup>198–203</sup>.

The first reaction in glutaminolysis is the deamination of glutamine into glutamate and ammonia by glutaminase (GLS), of which there are several human isozymes. Glutamate can then be oxidized, usually via the enzyme glutamate dehydrogenase

(GLDH), into  $\alpha$ -KG, NAD(P)H, and ammonia.  $\alpha$ -KG is then used to produce ATP and anabolic carbons, which are subsequently utilized in amino acid, nucleotide, and lipid synthesis. Glutamine itself is also utilized in nucleotide and amino acid biosynthesis, donating nitrogen to the production of purines and pyrimidines and providing for the production of hexosamines and certain other nonessential amino acids<sup>204</sup>. Therefore, glutamine plays an integral role in both macromolecule synthesis and respiration, as glutaminolysis helps regulate redox balance, mTOR signaling, apoptosis, and autophagy<sup>194,205–208</sup>.

As previously stated, glutaminolysis is critical for cancer cell proliferation and survival, and glutamine is conditionally essential in rapidly proliferating malignant cells. It has been previously shown that high concentrations of extracellular glutamine fuel cancer cell growth and survival<sup>209–211</sup>. Not surprisingly, increased amounts of glutamine are utilized in both tumor and rapidly dividing cells alike<sup>212</sup>. Mitochondrial enzymes relevant to glutamine/glutamate oxidation are also elevated in tumor cells<sup>213,214</sup>. Moreover, many cultured cancer cells depend on glutamine for cell survival, known as glutamine addiction<sup>215</sup>. For example, it has been shown that human glioma and HeLa cells die in the absence of glutamine despite the presence of excess glucose<sup>216</sup>. The resulting tumor microenvironment produced by an augmented consumption of glutamine is one in which T cell/immune cells are deprived of glutamine, depleting immune cell functions.

In addition to the aforementioned functions of glutamine in the context of cell proliferation, recent studies have revealed that it plays additional roles in regulating drivers of proliferation. For instance,  $\alpha$ -KG produced from glutamine can be used to produce citrate (via reductive carboxylation) in order to sustain lipid synthesis in cells undergoing hypoxia or mitochondrial dysfunction<sup>217,218</sup>. Metabolic labeling experiments revealed that glutamine is metabolized via an unusual mechanism involving the reversal of IDH enzyme activity. IDH typically functions as an oxidative decarboxylase; IDH3 plays this role exclusively, converting isocitrate to  $\alpha$ -KG and CO<sub>2</sub>, while the other two isoforms (IDH1 and IDH2) can function as oxidative decarboxylases (with NADP<sup>+</sup>/NADPH cofactors) or reductive carboxylases. In the case of IDH's reductive carboxylase functionality, isocitrate is produced by carboxylating  $\alpha$ -KG and converting NADPH to NADP<sup>+</sup>. As mentioned previously, isocitrate can then be used to produce citrate, whose cleavage produces acetyl-CoA.

In addition to IDH2 inhibitors previously discussed in section 3.4, mutant IDH1 (mIDH1) inhibitors are also being developed. IDH1, a cytosolic enzyme that converts isocitrate to  $\alpha$ -KG, can be mutated, subsequently converting  $\alpha$ -KG to the oncogenic 2-HG. The effect of mIDH1 ultimately interferes with regulating cellular metabolism and epigenetics, thus contributing to tumorigenesis and lack of cellular differentiation<sup>162</sup>. In addition, mIDH1 additionally is prognostically relevant for measures of overall survival in patients with glioma<sup>219</sup>. The small molecule AGI-5198 is a selective inhibitor of mIDH1 that reduces 2-HG levels and inhibits cancer cell growth in both *in vitro* and *in vivo* glioma models<sup>220</sup>. Another selective mIDH1 inhibitor, AG-120 (Agiros Pharmaceuticals, Inc.), is currently in phase I clinical trials to investigate its use in treating advanced hematologic malignancies as well as advanced solid tumors with mIDH1, including gliomas, cholangiocarcinomas, and chondrosarcomas (NCT02074839; NCT02073994)<sup>162,221</sup>. Preliminary results from ongoing phase I studies demonstrated

that AG-120, when administered as a single agent, had a favorable safety profile and produced approximately a 35% overall response rate from patients with advanced mIDH1 hematologic malignancies<sup>222</sup>. Other IDH1 inhibitors, such as BAY1436032, FT-2102, and AG-881, are in clinical development as well<sup>223–225</sup>. Phase I clinical trials are underway for all three drugs; BAY1436032 trials are currently active (NCT02746081; NCT03127735), two FT-2102 trials are currently recruiting (NCT02719574, NCT03684811), and trials for AG-881 are underway (NCT02492737; NCT02481154, NCT0334319).

Glutaminolysis does not only promote cellular proliferation, but also plays an integral role in preventing cell death. Cancer cells encounter multifarious stress signals, including levels of reactive oxygen species (ROS) much higher than those experienced by normal cells. While a slight ROS increase promotes cell proliferation and differentiation, extreme levels of ROS can negatively impact cells, resulting in oxidative damage to proteins, lipids, and nucleotides<sup>226,227</sup>. ROS balance is maintained via reducing agents such as glutathione (GSH) and NADPH, both of which are produced in part by glutaminolysis<sup>228,229</sup>. In addition, glutamine-derived fumarate is integral to the regulation of oxidative stress; fumarate increases levels of glutathione peroxidase 1 (GPx1) and activates nuclear factor erythroid 2-related factor 2 (Nrf2), which are involved in ROS scavenging and antioxidant signaling, respectively<sup>194,230,231</sup>. The roles of glutaminolysis in maintaining redox balance are diverse and integral to cancer cell survival.

Intriguingly, not all cancer cells are addicted to glutamine, and their existence has allowed researchers to probe for oncogenic mutations or alterations that could explain glutamine dependence in some cancers but not others. As alluded to earlier, studies have shown that MYC, for example, increases glutamine metabolism by upregulating the expression GLS, leading to enhanced glutamate production and eventually elevated  $\alpha$ -KG entry into the TCA cycle<sup>228</sup>. Metabolomic studies have further confirmed that MYC induction significantly impacts glutaminolysis in cancer cells<sup>232</sup>. MYC has not only been shown to induce the expression of GLS, but it has been revealed that MYC upregulates glutamine transporters as well<sup>232</sup>. Collectively, these studies indicate that MYC's induction of transcription promotes glutaminolysis in cancer cells.

Inhibiting GLS has been shown to suspend tumor growth in numerous models<sup>233–235</sup>. Impairment of tumor growth via GLS inhibition has been reported in multiple cancer models, including lymphoma and breast cancer<sup>228,235</sup>. GLS is inhibited by several small molecules, such as bis-2-[5-phenylacetamido-1, 2, 4-thiadiazol-2-yl] ethyl sulfide (BPTES), CB-839, and compound 968<sup>235–237</sup>. In particular, the orally-bioavailable inhibitor CB-839 (Calithera) was found to be a potent, selective, and reversible inhibitor of GLS in preclinical trials<sup>237,238</sup>. CB-839 allosterically inhibits the dimer-to-tetramer GLS transition, a critical step for enzyme activation<sup>236,239</sup>. CB-839 is currently being tested in multiple phase II trials, including one trial designed to study CB-839 in combination with everolimus in patients with metastatic ccRCC (NCT03163667) and another phase II clinical trial looking at CB-839 with paclitaxel in patients with TNBC (NCT03057600). Furthermore, it has been shown that CB-839 yielded positive initial clinical responses in RCC and AML (NCT02071862; NCT02071927).

In addition to GLS inhibitors, other approaches to therapeutically targeting glutaminolysis, such as focusing on GLDH, are being pursued. It has been shown that

RNAi-mediated knockdown of GLDH, which is typically upregulated in breast and lung cancer cells, and inhibition via R162, a GLDH-specific inhibitor result in significant reductions in  $\alpha$ -KG production and anabolic glutamine-dependent RNA biosynthesis as well as elevated ROS levels<sup>194</sup>. Another strategy for targeting glutaminolysis uses glutamate-dependent transaminases. Aminooxyacetate, a non-specific transaminase inhibitor, inhibited cell proliferation and overall tumor growth in multiple preclinical studies<sup>240,241</sup>.

## 4.2. Asparagine

Cancer cells require asparagine in order to synthesize DNA. Asparagine's role has been exploited therapeutically with L-asparaginase, as Elspar (Merck & Co, Inc.), Erwinase (Speywood Pharmaceuticals, Inc.), and Oncospar (Enzon Pharmaceuticals) are successful therapeutics used against pediatric acute lymphoblastic leukemia (ALL)<sup>202,242</sup>. L-asparaginase works by hydrolyzing asparagine into aspartic acid and ammonia<sup>202,242</sup>. ALL cells are unable to synthesize asparagine *de novo*, leaving the cells without any asparagine and, thus, unable to make new DNA. Interestingly, asparaginase is also able to hydrolyze glutamine to glutamic acid and ammonia, thus significantly depleting glutamine levels<sup>243,244</sup>.

Unfortunately, clinical trials looking at asparaginase treatment in adults revealed substantial toxicity, including increased rates of thrombosis<sup>245,246</sup>. Although more research is still needed to clarify the mechanism of asparaginase against childhood versus adult glutamine-addicted cancers, researchers have been working on developing less toxic forms of asparaginase for use in adult cancers. For example, asparaginase has been modified by covalently conjugating it with monomethoxypolyethylene glycol to increase its half-life and reduce immunogenicity<sup>247</sup>. Furthermore, erythrocyte-encapsulated asparaginase, currently in clinical trials, was developed by researchers to decrease toxicity and improve the drug's delivery (NCT01523782)<sup>246,248,249</sup>. Lastly, it is worth noting that asparaginase is an effective treatment for ALL through young adulthood, but the age cutoff for consideration is not yet clear<sup>246</sup>.

## 4.3. Serine

Serine serves not only as a building block for proteins, but also (along with serine and glycine) contributes carbon to the serine, glycine, one-carbon (SGOC) metabolic network<sup>250</sup>. The SGOC network plays a role in various cellular processes, including nucleotide synthesis, lipid and protein synthesis, methylation metabolism, polyamine metabolism, and redox balance<sup>251</sup>.

*De novo* serine metabolism, which is significantly elevated in some cancer cells and feeds into one-carbon metabolism, produces NADPH and glutathione<sup>252,253</sup>. It has been shown that breast cancer and colorectal cancer, among others, rely on serine for cellular proliferation and survival. In fact, increased activity of the SGOC network can further drive the advancement of these cancers, most likely due to augmented nucleotide synthesis rates<sup>250</sup>. A recent study using <sup>13</sup>C serine labeling revealed a flux of serine into nucleotides and glutathione synthesis<sup>253</sup>. Serine-fueled folate metabolism contributes substantially to NADPH production, indicating a potential function in redox balancing, which could be critical to cell proliferation<sup>252,254–257</sup>. Furthermore, *de novo*

synthesis of serine from glucose is increasingly seen in serine-deprived circumstances, which indicates the importance of serine to proliferating cancer cells<sup>258,259</sup>.

The first committed reaction in serine biosynthesis is catalyzed by 3-phosphoglycerate dehydrogenase (PHGDH), which oxidizes 3-phosphoglycerate (diverted from glycolysis) to 3-phosphohydroxypyruvate, a serine precursor<sup>260</sup>. PHGDH is upregulated in multiple cancers, including TNBC and NSCLC<sup>261</sup>. Cancer cells utilize increased PHGDH activity for proliferative benefit, as the products of its catalyzed reaction yield not only serine but are also used to replenish the TCA cycle's supply of  $\alpha$ -KG<sup>260</sup>.

Inhibition of PHGDH has been the subject of extended investigation, and multiple inhibitors, including CBR-5884, NCT-502, and NCT-503, are currently undergoing preclinical studies<sup>262,263</sup>. These inhibitors can reduce the levels of serine in cells that have overexpressed PHGDH, and PHGDH inhibition via NCT-502 or NCT-503 treatment in *in vivo* tumor xenograft studies resulted in reduced tumor growth as compared to controls<sup>264</sup>. The *in vivo* results illustrate the potential therapeutic use of developing PHGDH inhibitors for treatment of serine-addicted cancers.

#### 4.4 Tryptophan

Tryptophan is another essential amino acid and its breakdown occurs through one of two main pathways in humans, producing either NAD<sup>+</sup> or serotonin, with the former being the dominant pathway<sup>265,266</sup>. In the dominant pathway, various tryptophan catabolites, especially kynurenine, are active and block effector T cell activation and trigger T cell apoptosis. T cells are important in mediating the immune system's ability to destroy pathogens, and by reducing the number of T cells, upregulated tryptophan catabolites prevent the immune system from successfully destroying cancer cells<sup>267-270</sup>. Indoleamine (2,3)-dioxygenase (IDO), which controls the breakdown of tryptophan to later produce kynurenine, is broadly expressed in tumors, including gastrointestinal, lung, gynecological, and breast cancers<sup>271-273</sup>. In fact, it has been shown that increased IDO expression is associated with a decrease in the survival of patients with colorectal cancer, small-cell lung cancer (SCLC), and melanoma, among others<sup>274-277</sup>.

The IDO enzyme has two isoforms – IDO1 and IDO2 – with IDO1 being the predominantly expressed and more active isoform<sup>278</sup>. IDO is a cytoplasmic, monomeric, heme-containing enzyme, and its expression can suppress the body's immune responses to cancer and allow tumors to grow unchecked<sup>273</sup>. It has been previously shown that overexpression of IDO1 is sufficient to drive immune escape by mediating immunosuppression through T cells' sensitivity to tryptophan deprivation<sup>279-282</sup>. Furthermore, IDO expression decreases T cell infiltration into tumor microenvironments, promotes inflammation around tumor tissues and the surrounding microenvironment, and causes overall immune tolerance<sup>283-288</sup>. It is worth noting that some tumor and surrounding microenvironment cells even express IDO to protect themselves from the immune system<sup>273,289</sup>. Lastly, the downstream byproduct of tryptophan breakdown, kynurenine, is a native ligand for the aryl hydrocarbon receptor that, ultimately, further promotes inflammatory carcinogenesis<sup>290</sup>.

Recently, researchers have been interested in developing IDO inhibitors. It has been suggested that overexpression of IDO in tumors is one possible mechanism of tumor drug resistance against chemotherapy<sup>291</sup>. In support of the IDO hypothesis, IDO1

inhibitors have been shown to boost the effectiveness of current immunotherapies, including epacadostat (Incyte Corporation) combined with anti-PD1 and indoximod (NewLink Genetics) combined with anti-PD1<sup>270</sup>.

Epacadostat (previously INCB24360) is an orally-available tryptophan-competitive IDO1 inhibitor<sup>292</sup>. Epacadostat is currently the most advanced agent in clinical trials with promising early-phase study results, particularly in melanoma (NCT02178722). Epacadostat in combination with pembrolizumab, a PD1 inhibitor, has entered phase III clinical trials to treat advanced melanoma (NCT02752074). Similarly, epacadostat combined with nivolumab, another PD1 inhibitor, has entered clinical trials and has already shown positive results in patients with melanoma (NCT02327078). Further, epacadostat/PD1 inhibitor combination therapies have shown efficacy in other cancer types, including squamous cell carcinoma of the head and neck (SCCHN), NSCLC, urothelial cell carcinoma, and RCC (NCT02327078; NCT03085914).

Another IDO modulator, indoximod (previously D-1-methyl-tryptophan and NLG-8189), acts directly on immune cells to reverse IDO pathway-mediated suppression, most likely through de-repressing mTORC1 in T cells<sup>270,283,289,293-296</sup>. Indoximod also had early-phase clinical trial success in treating melanoma patients when used in combination with PD1 inhibitors, and recently entered phase III trials (NCT03301636).

Other IDO1 inhibitors in development include BMS-986205 (Bristol-Myers Squibb), NLG-802 (NewLink Genetics), and HTI-1090 (Atridia Pty Ltd)<sup>270,297</sup>. BMS-986205 has also shown promising early-phase results across various advanced cancers including melanoma, NSCLC, cervical, SCCHN, bladder, and other advanced solid tumors<sup>270</sup>.

Compound	Target	Clinical trial phase	Relevant cancer(s)
benzylserine	SLC1A5 inhibitor	NA	
l-y-glutamyl-p-nitroanilide (GPNA)	SLC1A5 inhibitor	NA	
y-FBP	SLC1A5 inhibitor	NA	
2-aminobicyclo(2,2,1)-heptane-2-carboxylic acid (BCH)	SLC7A5 inhibitor	NA	
BPTES	GLS inhibitor	NA	
CB-839	GLS inhibitor	phase II	colorectal, TNBC, NSCLC, ccRCC, AML
compound 968	GLS inhibitor	NA	
R162	GLDH inhibitor	NA	
aminoxyacetate	transaminase inhibitor	NA	
L-asparaginase (Elspar, Oncaspar)	asparagine hydrolase	approved pediatric/ phase II adult	
erythrocyte-encapsulated asparaginase	asparagine hydrolase	phase III	pancreatic, AML, ALL
CBR-5884	PHGDH inhibitor	NA	
NCT-502	PHGDH inhibitor	NA	
NCT-503	PHGDH inhibitor	NA	
epacadostat	IDO1 inhibitor	phase III	NSCLC, colorectal, ovarian, head and neck, peritoneal
indoximod	IDO1 inhibitor	phase III	prostate, breast, NSCLC, pancreatic, glioblastoma
BMS-986205	IDO1 inhibitor	phase III	NSCLC, head and neck, melanoma, gastric
NLG-802	IDO1 inhibitor	phase I	solid tumors
HTI-1090	IDO1 inhibitor	phase I	solid tumors

**TABLE 4:** Summary of amino acid metabolism-related drugs with clinical status.

## 5. ADDITIONAL PATHWAYS

### 5.1. One-carbon Metabolism

One-carbon metabolism is centered on the chemical reactions of folate compounds and proceeds in a cyclical nature<sup>251,298–300</sup>. Folic acid is a B vitamin, so it can only be obtained via the diet or production by the microbiome in the intestines. In cells, folic acid is reduced to produce tetrahydrofolate (THF). THF can be converted to 5,10-methylene-THF (me-THF) via serine hydroxymethyl transferase (SHMT); me-THF can be reduced to 5-methyltetrahydrofolate (mTHF) by methylenetetrahydrofolate reductase (MTHFR) or can be converted to 10-formyltetrahydrofolate. Finally, the folate cycle comes to a close when mTHF is demethylated, donating the carbon to the methionine cycle. The mTHF-sourced carbon is integrated via the methylation of homocysteine, which occurs through methionine synthase, generating methionine. Methionine is then used to produce S-adenosylmethionine (SAM) via methionine adenytransferase (MAT). The overall combination of the folate and methionine cycles is called one-carbon metabolism. In addition, the methionine pathway is connected to the trans-sulphuration pathway through homocysteine, as trans-sulphuration generates glutathione via serine metabolism, contributing greatly to redox regulation in the cell.

As established earlier, amino acids play an important role in cellular metabolism by providing carbon units involved in one-carbon metabolism. The one-carbon metabolism cycle functions to provide carbon units to other metabolic pathways such as nucleotide biosynthesis. Nucleotides are made via reactions that include those in the folate cycle, while phospholipids can be built partially via the methionine cycle. Furthermore, one-carbon metabolism is implicated in maintaining redox status<sup>251</sup>. The pathways of one-carbon metabolism exert redox control through the reduction of NADPH and the oxidation of NADP<sup>+</sup>; for example, one molecule of NADPH is consumed for each iteration of the folate cycle by the reduction of THF via MTHFR.

Interestingly, some modern cancer therapies developed in part from the idea that folate antagonists might result in reduced proliferation of malignant blood cells<sup>301,302</sup>. The usefulness of this idea has resulted in the use of folate metabolism antagonists in chemotherapy for decades<sup>303–305</sup>. Sydney Farber initially noted in 1947 that folic acid could stimulate ALL cell proliferation<sup>301</sup>. Farber and colleagues were the first to show that aminopterin, an intermediate in B vitamin synthesis and an antagonist of folate, can induce remission in children with ALL (Table 5)<sup>302,306</sup>. Still today, chemical variants of aminopterin, such as methotrexate and pemetrexed, are used as frontline treatments for numerous cancer types, including ALL, lymphomas, breast, and bladder cancer (Figure 1.5)<sup>303,307–311</sup>. These drugs inhibit dihydrofolate reductase and tetrahydrofolate reductase activity, disrupting one-carbon metabolism<sup>312,313</sup>.

Additionally, many chemotherapies target pathways downstream of one-carbon metabolism. 5-fluorouracil (5-FU), for example, is commonly used to treat a variety of cancers, including advanced colorectal cancer. 5-FU effectively impacts nucleotide metabolism because it is an analog of uracil and potently inhibits thymidine synthase<sup>314,315</sup>. 5-FU's interaction with thymidine synthase prevents the dUMP to dTMP methylation process, disrupting the folate cycle<sup>316</sup>. The thymidine synthase inhibitor capecitabine (sold as Xeloda by Genentech) is also approved for solo and combinatorial use; it is often used in tandem with docetaxel in breast cancer treatment and oxaliplatin



in colorectal cancer treatment<sup>317,318</sup>. Many other combinatorial applications are currently being tested, including capecitabine plus lapatinib in HER2-amplified breast cancer (NCT02650752). Two other nucleotide metabolism antagonists of note are gemcitabine and cytarabine, which are used to treat various cancers.<sup>319</sup> Gemcitabine, also called Gemzar (Eli Lilly), is FDA-approved to be used alone or in combination to treat pancreatic cancer, ovarian cancer, NSCLC, and metastatic breast cancer. A nucleoside analog, gemcitabine prevents deoxynucleotide formation<sup>320,321</sup>.

Other drugs are being developed to target polyamine metabolism, which includes the breakdown of ornithine and the decarboxylation of SAM, resulting in the generation of spermidine<sup>261</sup>. It has been previously established that an increase in polyamines, mainly through upregulation of polyamine-biosynthetic enzymes, correlate with increased cellular proliferation and tumorigenesis<sup>261,322–325</sup>. Furthermore, the upregulation of polyamines are associated with colon, breast, skin, and prostate cancers, among others<sup>326–329</sup>.

Ornithine decarboxylase (ODC), the enzyme involved in the rate-limiting reaction in ornithine catabolism, is important for normal cell growth and is upregulated in many cancers (including non-melanoma skin cancer, breast cancer, and prostate cancer)<sup>326,328–332</sup>. An inhibitor of ODC, 2-difluoromethyl ornithine (DFMO), also inhibits several enzymes that are competitive inhibitors of SAM decarboxylase and is currently being tested in clinical trials for patients with neuroblastoma (NCT01586260; NCT02679144; NCT01349881; NCT00003814, NCT02796261)<sup>333</sup>. Other drugs that similarly target polyamine metabolism are also entering clinical trials<sup>333</sup>.

## 5.2. The Pentose Phosphate Pathway

The pentose phosphate pathway (PPP), also called the hexose monophosphate shunt, diverts G6P from glycolysis to biosynthesize NADPH, ribose-5-phosphate (R5P), and various glycolytic intermediates. Like glycolysis, the PPP takes place in the cytosol and consists of an irreversible oxidative phase followed by a non-oxidative phase consisting of a series of reversible reactions. NADPH and R5P are produced in the oxidative phase, while the glycolytic intermediates are made in the non-oxidative phase. Overall, glucose can be shunted out of glycolysis to generate NADPH and R5P when necessary, and the glycolytic intermediates shunted back in.

The initial enzyme in the PPP is glucose-6-phosphate dehydrogenase (G6PDH), and it is the primary point of regulation for the pathway. As G6PDH's substrate, G6P, is converted to 6-phosphogluconate, its product, NADPH, acts via negative feedback to inhibit G6PDH. The conversion of 6-phosphogluconate to R5P, which is the next step of the PPP, also generates NADPH and CO<sub>2</sub>. The two successive oxidations make up the oxidative phase of the PPP, while the remaining non-oxidative reactions generate the glycolytic intermediates that can be returned to the glycolysis pathway.

Transketolase-like protein 1 (TKTL1), an enzyme associated with the non-oxidative reactions in the pathway, has been implicated in ROS sensitivity, lactate production, and tumor proliferation<sup>334,335</sup>. Increased levels of TKTL1 have been associated with invasive colon and urothelial cancers, as well as poor patient prognosis<sup>336</sup>. TKTL1 has also been shown to be overexpressed in breast cancer, although it has not been yet shown that its overexpression correlates to breast cancer patients' outcome and survival<sup>337</sup>. And while inhibited expression of TKTL1 via RNAi in

*in vitro* experiments significantly inhibits cell proliferation, successful TKTL1 inhibitors have not yet been developed<sup>338</sup>.

### 5.3. NADPH

NADPH is important in cancer metabolism, and its generation and use in cancer has been discussed throughout this review; it will be briefly considered further here. NADPH is mainly produced from the aforementioned serine-driven one-carbon metabolism and the PPP, and plays a variety of important roles in cancer pathogenesis. NADPH is necessary for reductive biosynthesis, most notably *de novo* lipid synthesis<sup>9,339</sup>. In addition, as previously mentioned, NADPH aids in the scavenging and neutralization of ROS, which are increased in most cancer types. NADPH production is associated with enhanced cancer cell survival and apoptosis suppression. Since glutathione biosynthesis requires NADPH, and glutathione protects cells from redox stress, apoptosis resistance occurs<sup>340–342</sup>. Moreover, NADPH oxidases produce hydrogen peroxide, which inhibits tyrosine phosphatases; subsequent kinase activation further promotes cellular survival as well as mitogenic signaling<sup>342</sup>.

Compound	Target	Clinical trial phase	Relevant cancer(s)
aminopterin	folate antagonist	discontinued	endometrial, leukemia
methotrexate	dihydrofolate reductase, tetrahydrofolate reductase inhibitor	approved	
pemetrexed	dihydrofolate reductase, tetrahydrofolate reductase inhibitor	approved	
5-fluorouracil (5-FU)	thymidine synthase inhibitor	approved	
capecitabine	thymidine synthase inhibitor	approved	
Gemcitabine	ribonucleotide reductase inhibitor	approved	
cytarabine	ribonucleotide reductase inhibitor	approved	
2-difluoromethyl ornithine (DFMO, eflornithine)	ornithine and SAM decarboxylase inhibitor	phase III	bladder, neoplasms, gastric, colorectal, neuroblastoma
AGI-5198	IDH1 inhibitor	NA	
AG-120	IDH1 inhibitor	phase III	cholangiocarcinoma, AML
BAY1436032	IDH1 inhibitor	phase I	neoplasms, AML
FT-2102	IDH1 inhibitor	phase I	AML
AG-881	IDH1 inhibitor	phase I	AML, glioma

**TABLE 5:** Summary of one-carbon metabolism, pentose phosphate pathway, and NADPH-related drugs with clinical status.

## 6. FATTY ACID METABOLISM

Fatty acids (FAs) provide additional substrate sources to meet the demanding needs of a proliferating cancer cell and, in fact, are essential for proliferation. FAs play important roles in synthesizing cell membranes, producing and storing energy, and cell signaling. It has been shown that a broad increase in endogenous FA synthesis is seen in numerous cancer cell types<sup>343</sup>. A cell can increase their amount of FAs by increasing biosynthesis (*de novo* lipogenesis), reducing the breakdown of FAs (fatty acid beta-oxidation, or FAO), increasing FA release from storage (lipolysis), and decreasing FA flux towards storage (re-esterification).

### 6.1. Fatty Acid Anabolism

Cancer cells rely on heightened *de novo* lipogenesis to produce the necessary FAs for proliferation, particularly at the beginning stages of the disease<sup>344–346</sup>. When tumor cells do not need to rely on increased *de novo* lipogenesis, however, they can obtain sufficient levels of FAs from their environment for growth<sup>347</sup>. For example, it has been reported that proximity to adipocytes influences malignancy and metastasis in ovarian cancers, as the adipocytes prompt metastasis to the omentum and provide cancer cells with fatty acids<sup>348</sup>. The influence of FAs in the tumor microenvironment is relevant to various cancers, including prostate, ovarian, breast, and endometrial cancers, and targeting the symbiotic relationship between adipocytes and tumor cells is thought to hold great potential as an effective treatment strategy<sup>349–351</sup>. Interest has risen in targeting the adipocyte effect for cancer therapies, and work is underway to identify effective modulators of the tumor microenvironment, such as the aforementioned metformin<sup>352</sup>. Metformin, a drug best known as a standard treatment for type 2 diabetes, has also been shown to exert anti-cancer properties, perhaps through its previously discussed interaction with ETC complex I (Figure 1.6). Metformin's attenuation of tumor growth has also been linked to its caloric-restriction-like effect; metformin activates sirtuin 1 (SIRT1) and AMPK while inhibiting AKT and mTOR. Overall, metformin's mechanism of action in cancer remains contested in the literature<sup>353–356</sup>.

In addition, interest has risen in targeting signaling lipids for cancer therapy. Platelet-activating factor (PAF) is a phospholipid signaling molecule cleaved by the PAF acetylhydrolases (PAFAHs): PAFAH1B1, PAFAH1B2, and PAFAH1B3. PAFAH1B2 and PAFAH1B3 specifically have been identified as metabolic enzymes upregulated in cancer<sup>357</sup>. Inhibiting the function of both isoforms with small molecule P11, which blocks PAFAH1B2 and PAFAH1B3 activity (Table 6), impaired cancer pathogenicity across a broad range of cancer types, including breast and ovarian cancers<sup>358</sup>.

The synthesis of FAs takes place in the cytoplasm of cells, allowing for easier regulation; enzymes required for synthesis and breakdown are separated, since FAO occurs in the mitochondria. *De novo* lipogenesis involves the repeated addition of two-carbon subunits, beginning with the acetyl-CoA produced by ATP citrate lyase (ACL). Knocking down ACL has been shown to prevent the formation of FA precursors, resulting in impaired xenograft tumor growth<sup>359–361</sup>. A small molecule inhibitor, SB-204990, brings about the same changes, but the integral cellular role of ACL's products may render ACL inhibition a poor route for selective cancer therapy<sup>360,362</sup>.

Acetyl-CoA is first activated, with the investment of ATP, in a carboxylation reaction that produces the three-carbon malonyl-CoA. The acetyl-CoA activation step is the committed reaction in FA synthesis and is facilitated by acetyl-CoA carboxylase (ACC) and regulated by AMPK, as phosphorylation of ACC renders it inactive<sup>363</sup>.

ACC is overexpressed in several tumor types, and is even maintained by several tumorigenic mutations<sup>363–365</sup>. However, its particular role in cancer cell metabolism is not fully understood and further study into the differing roles of ACC isoforms will be required to understand these effects. While some groups have shown that selective inhibition of ACC activity (via inhibitors such as sorafen A) induces apoptosis in prostate and breast cancer cells, others have shown that inactivation of ACC1 increased lung cell growth<sup>366–371</sup>. It has been shown that ACC2 can regulate FAO, whereas ACC1 cannot<sup>372</sup>. For instance, the breast cancer type 1 susceptibility protein (BRCA1), a tumor suppressor gene, can prevent the dephosphorylation of ACC, thus stimulating FA synthesis<sup>373</sup>. Also, aldo-keto reductase family 1 B10 (AKR1B10), a protein often overexpressed in NSCLC and hepatocellular carcinoma, can protect ACC from degradation, similarly stimulating FA synthesis<sup>374</sup>. ND-646, an allosteric inhibitor of ACC, was able to suppress FA synthesis in NSCLC *in vitro* and *in vivo*, resulting in markedly reduced lung tumor growth in several mouse models of NSCLC<sup>375</sup>.

To synthesize a full FA chain, FA synthase (FASN), a large enzyme with multiple catalytic domains, is the next enzyme in the pathway. Acetyl-CoA first binds the acyl carrier protein (ACP) domain, and is then shifted to another domain on the enzyme with a cysteine residue. Malonyl-CoA then binds the ACP, is subsequently condensed with the already-bound acetyl group via the decarboxylation of malonyl, and as a result the ACP domain holds a four-carbon unit. The four-carbon unit then undergoes two reductions via NADPH oxidation, and the resulting saturated unit is shifted to the domain with the cysteine residue. Another malonyl-CoA binds the ACP and the process begins again.

FASN is highly expressed in numerous cancers, rendering it an attractive target for cancer therapies<sup>357,376</sup>. Inhibiting FASN has been shown to induce cytotoxicity in cancer cells as well as re-sensitize cells that have become resistant to mainline treatment, such as breast cancer cells to Herceptin<sup>370,377–379</sup>. Initial inhibitors of FASN, including C-75, orlistat, and GSK837149A, were promising indicators of the effectiveness of targeting FASN for cancer therapy<sup>380–382</sup>. However, it has taken unexpectedly longer for these inhibitors to make their way into the clinic due to issues with toxicity and off-target effects. For example, C-75's reported other interaction with CPT1A in the hypothalamus induced hypophagia and body weight loss in mice<sup>383</sup>. The newest generation of FASN inhibitors, including TVB-2640, GSK2194069, JNJ-54302833, and IPI-9119, attempts to combat these challenges by building upon previous scaffolds after SAR research<sup>384–386</sup>. The inhibitor TVB-2640 was the first to reach clinical trials, with phase I studies in solid malignant tumors recently completed (NCT02223247)<sup>387</sup>.

Another issue plaguing the pursuit of FASN inhibitors is an uncertainty as to which cancers will be most responsive, or perhaps even resistant, to FASN inhibitor treatment. It has been previously shown that different cancers exhibit varying sensitivities to targeting FASN, unrelated to FASN expression levels<sup>388</sup>. However, the driving force behind these differences has been shown to rest on a cell's ability to

maintain DAG levels and DAG-PKC signaling amidst FASN inhibition, suggesting that FASN inhibitor resistance can be overcome by combinatorial treatment with FASN and PKC inhibitors; the cellular ability to maintain these levels can be probed by investigating the incorporation of glucose into complex lipids<sup>388</sup>. As development of FASN inhibitors advances, it will be critical to understand in which contexts they will be most effective. Results from clinical trials, such as the current phase II studies of TVB-2640, will be influential in further developments (NCT03032484, NCT03179904, NCT03808558).

Once a sixteen-carbon-long FA is synthesized, additional enzymes aid in further modification of the FA, such as the addition of functional groups and further elongation. Enzymes involved include the oxygen-consuming stearoyl-CoA desaturase (SCD), which catalyzes the rate-limiting reaction in the production of monounsaturated FA from stearoyl-CoA (mainly). SCD has been shown to be upregulated in some cancers including colon, esophageal, and liver cancer; its inhibition results in the death of cancer cells, preventing tumor growth without affecting overall body weight<sup>389–391</sup>. SCD exists in two isoforms in humans, SCD-1 and SCD-5. Inhibition of SCD-1 by the small molecule CVT-11127 was reported to impair proliferation in lung cancer cells by activating AMPK and interfering with ACC activity<sup>392,393</sup>. It has also been shown that SCD-1 is successfully inhibited by a prodrug. Cytochrome P450 (CYP450), which is overexpressed in certain cancers, can be used to metabolize prodrug molecules into irreversible SCD-1 inhibitors; the prodrug approach helps avoid toxicity to sebocytes. Reported SCD-1 prodrug inhibitor scaffolds of oxalamides and benzothiazoles are yet to be built upon<sup>394</sup>. Other attempts to inhibit SCD, such as the small molecule MK-8245, have been undertaken in the context of diabetes and are untested in cancer models<sup>395</sup>.

Before synthesized FA is bioavailable, a CoA must be appended via acyl-CoA synthetases (ACS). Of the five ACS enzymes (ACSL1, ACSL3, ACSL4, ACSL5, and ACSL6), ACSL4 and ACSL5 levels increase in colon and other cancers, and overexpression of ACSL4 in particular prevents cell apoptosis<sup>396</sup>. Triacsin C is a reported inhibitor of ACSL1, 3, and 4 and induces cell death in various cancers, but has not been clinically developed<sup>396,397</sup>. Various thiazolidinedione compounds have also been shown to bind ACSL4, but are not widely studied in the context of cancer treatment<sup>398</sup>. Further elucidation of each isoform's role specificity is necessary before targeted therapies can be developed for effective treatment.

As mentioned previously, hypoxia suppresses the production of acetyl-CoA from glucose by stimulating the expression of PDK1, which inhibits the PDC via phosphorylation. PDC inactivation impairs the cell's ability to produce glucose-derived acetyl-CoA, rendering glutamine the main acetyl-CoA source for FA synthesis. It has been reported that hypoxic cells reduce dependence on *de novo* lipogenesis altogether, which also reduces the cell's reliance on SCD1<sup>399</sup>. This phenomenon can be reproduced with RAS upregulation, rendering both hypoxic and RAS-driven cells resistant to SCD1 inhibition as a useful therapy<sup>399</sup>.

In glycolysis, when F1,6-BP is converted to DHAP, ether lipids are also produced; ether lipids are present in heightened levels in liver cancer, but this correlation is not fully understood<sup>400,401</sup>. A critical enzyme in the ether lipid synthetic pathway, alkyl-glycerone phosphate synthase (AGPS), has been shown to be upregulated in a variety of aggressive cancers such as melanoma and breast cancer<sup>402</sup>.

AGPS catalyzes the conversion of acyl-glycerone-3-phosphate into alkyl-glycerone-3-phosphate, a precursor of ether lipids. It has been shown that inactivation of AGPS results in a reduction of several oncogenic signaling lipids, impairing cancer pathogenicity<sup>402</sup>. A selective AGPS inhibitor, 1a, caused a reduction in ether lipid levels and impacted cell migration and survival, showing that AGPS is an attractive target for future therapies<sup>403</sup>.

## 6.2. Fatty Acid Oxidation

When FAs are directed for degradation, FAO cleaves two carbons at a time until acetyl-CoA remains, producing NADH and FADH<sub>2</sub> in every iteration of the cycle. Although cancer cells are often increasing lipid levels resulting in decreased FAO, there are times when cancer cells are required to increase FAO. Most often, FAO is upregulated when there is an augmented need for ATP production; cancer cells that have undergone loss of attachment (LOA) to the extracellular matrix often activate FAO to increase ATP concentration and avoid LOA-induced anoikis<sup>363,404</sup>. FAO is also required for cell survival in certain cancer types, such as some lymphomas and leukemias. Although the reason for FAO's importance is not completely clear, FAO may play a role in BAX- and BAK-dependent mitochondrial permeability transition pore formation or in the anti-apoptotic function of carnitine palmitoyl transferase 1 (CPT1)<sup>363,405-407</sup>.

Directing FAs toward FAO relies on CPT1, which converts FAs to FA carnitines outside the mitochondria<sup>408</sup>. The role of CPT1 in cancer pathogenicity is complex. Overexpression of CPT1, for example, correlates with tumor progression in many cancer types, including breast and prostate cancer, and CPT1 plays an integral role in cancer cell apoptosis<sup>372</sup>. It has been shown that BCL-2-mediated apoptosis decreases CPT1 levels, resulting in a buildup of palmitoyl-CoA and eventual cell death; CPT1 clears palmitoyl-CoA, but when inhibited, the remaining palmitoyl-CoA and other lipid species can be converted to toxic lipids such as ceramide<sup>372</sup>. Inhibition of CPT1 also increases flux through aerobic glycolysis<sup>372</sup>. While increasing CPT1-mediated FAO could be expected to impair cancer cell pathogenicity, survival is instead increased in various lymphomas and leukemias. It has also been shown that blocking FAO reduces tumor growth in certain MYC-driven breast cancers<sup>409</sup>. In addition, chemical inhibition of CPT1 can kill various cancer cells<sup>407,410</sup>. Multiple CPT1 inhibitors and derivatives are currently in development, including ST1326, ranolazine, and etomoxir<sup>372,411,412</sup>. Etomoxir showed initial promise, but has encountered some issues in the clinic due to toxicity<sup>413,414</sup>.

The specific roles of CPT1 isoforms (CPT1A, CPT1B, and CPT1C) are not yet fully understood. CPT1A, which is ubiquitously expressed, is regulated via miR-370 in liver cancer; miR-370's downregulation of CPT1A reduced FAO by 40%<sup>372</sup>. Inhibition of CPT1A also results in impaired cancer cell division in AML<sup>372</sup>. It has also been speculated that the CPT1C isoform is oncogenic, as its expression in cancer cells promotes FAO, tumor growth, and resistance to therapy<sup>415</sup>. Overall, one can speculate that an increase in FAO provides more ATP to the cell, thus providing energy for continued cancer cell growth and proliferation.

Compound	Target	Clinical trial phase	Relevant cancer(s)
P11	PAFAH1B2 and PAFAH1B3 inhibitor	NA	
ST1326	CPT1 inhibitor	NA	
etomoxir	CPT1 inhibitor	NA	
SB-204990	ACL inhibitor	NA	
ND-646	ACC inhibitor	NA	
C-75	FASN inhibitor	NA	
orlistat	FASN inhibitor	NA	
GSK837149A	FASN inhibitor	NA	
GSK2194069	FASN inhibitor	NA	
JNJ-54302833	FASN inhibitor	NA	
IPI-9119	FASN inhibitor	NA	
TVB-2640	FASN inhibitor	phase II	astrocyma, breast, colon
CVT-11127	SCD1 inhibitor	NA	
MK-8245	SCD1 inhibitor	NA	
Triacsin C	ACSL inhibitor	NA	
1a	AGPS inhibitor	NA	

**TABLE 6:** Summary of fatty acid metabolism-related drugs and clinical status.

## 7. CONCLUSION

Metabolic dysregulation is an emerging hallmark of cancer and a clear focus of research today. We also know that cancers exhibit many alterations to metabolic pathways, as mutational heterogeneity is found even between cancers classified as the same type. From well-understood oncogenes, such as KRAS and MYC, to insufficiently-understood proteins, such as ACSL3 and TKTL1, cancer's impact on the metabolic landscape is wide-ranging and still poorly understood. Working to elucidate the variety of metabolic variations in cancer will lay the groundwork for a more robust understanding of the disease and enable the development of more specific therapies with lower toxicities and lessened side effects.

Understanding each metabolic mutation's disease implications will allow for more nuanced treatments targeting specific alterations. Some of these steps toward precision medicine are already being taken, particularly in the realm of combinatorial therapy. Current efforts focus on designing a therapeutic cocktail targeting mutations specific to the cancer at hand. Synergistic treatments are prompted by the discovery of increased anti-cancer activity upon inhibition of multiple proteins (or isoforms of a protein), such as the anti-cancer effect seen by tandem MCT1 and MCT4 inhibition in colon cancer or the many examples of combinatorial therapies, including ZD1839 and anastrozole, FTI-277 and GGTI-298, and CB-839 and everolimus<sup>416-418</sup>. In addition, combinatorial therapies hold promise for those cancers notorious for developing resistance to frontline therapies. By targeting multiple mutations in the cancer, it is hoped that a lower dosage can be used and full drug resistance avoided, both of which are critical goals to meet in the effective treatment of cancer<sup>418,419</sup>.

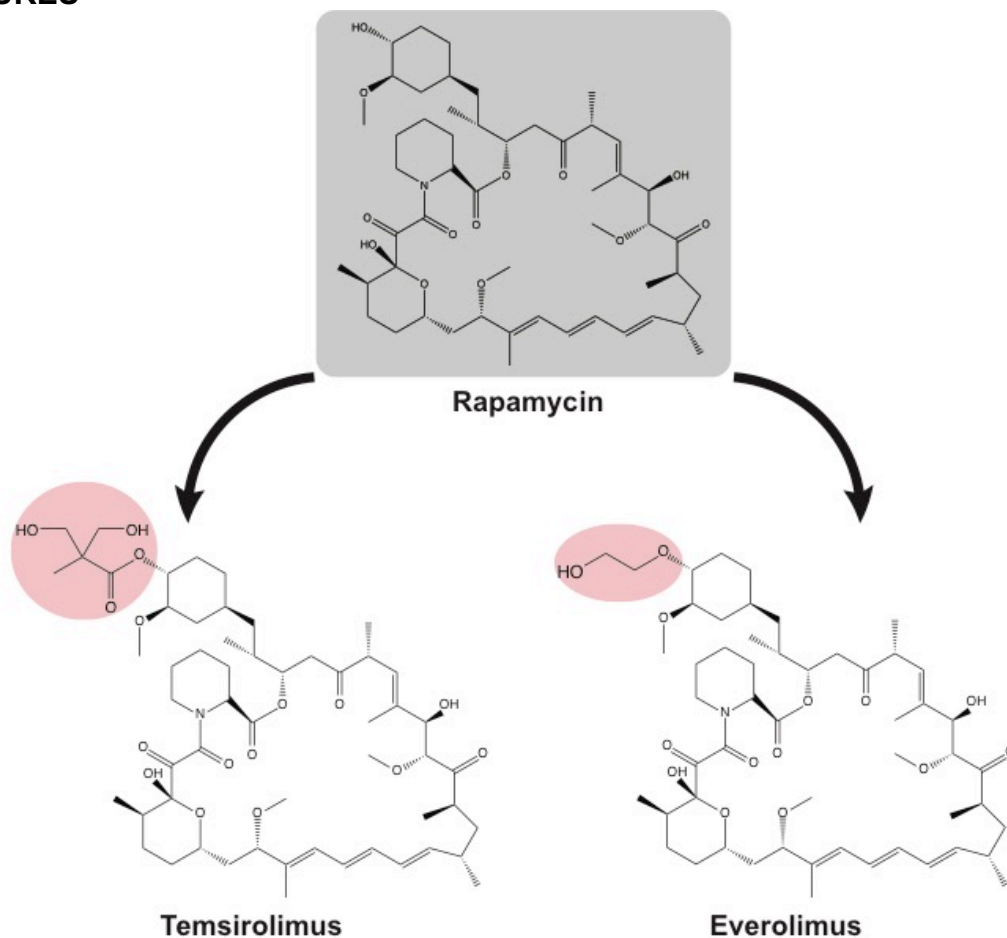
As our understanding of cancer's metabolic landscape expands, however, an increasing number of targets arise; to effectively drug each of them, it is necessary to reach for all possible strategies in drug discovery. Perhaps one of the most fruitful - yet rather underutilized - approaches is to investigate the natural compounds produced by living organisms. In previous decades, researchers lacked efficient assays for such approaches, but the -omics era has provided viable options for screening natural products and an impetus to do so<sup>420</sup>. Several natural products mentioned in this review, such as sorafenib and koniginic acid, have been integral to our understanding of particular metabolic mutations and are influencing the development of drugs for their targets. Rapamycin is also a particularly compelling example of the power of natural products, as it and several rapalogue derivatives have been approved for use in the clinic. In order to continue bringing metabolism-targeting drugs to market, investigation into natural products and their derivatives must be pursued further.

This review serves to underscore the importance of researching cancer's metabolic alterations. The mutations already identified are plentiful, and the number of metabolic drugs currently in clinical trials emphasizes the potential effectiveness of a metabolic strategy. However, we recognize that the current state of knowledge is vastly incomplete – though an enzyme may be implicated in cancer pathogenicity, such as CPT1, simply inhibiting its activity can produce a number of unanticipated physiological effects resulting in toxicity<sup>236,237</sup>. As the field continues to develop, our understanding of cancer's metabolic implications is expanding beyond the simplistic, singular cause-and-effect relationships upon which earlier, unsuccessful inhibitors were based. Though a simplistic relationship is where our exploration must begin, a more in-depth

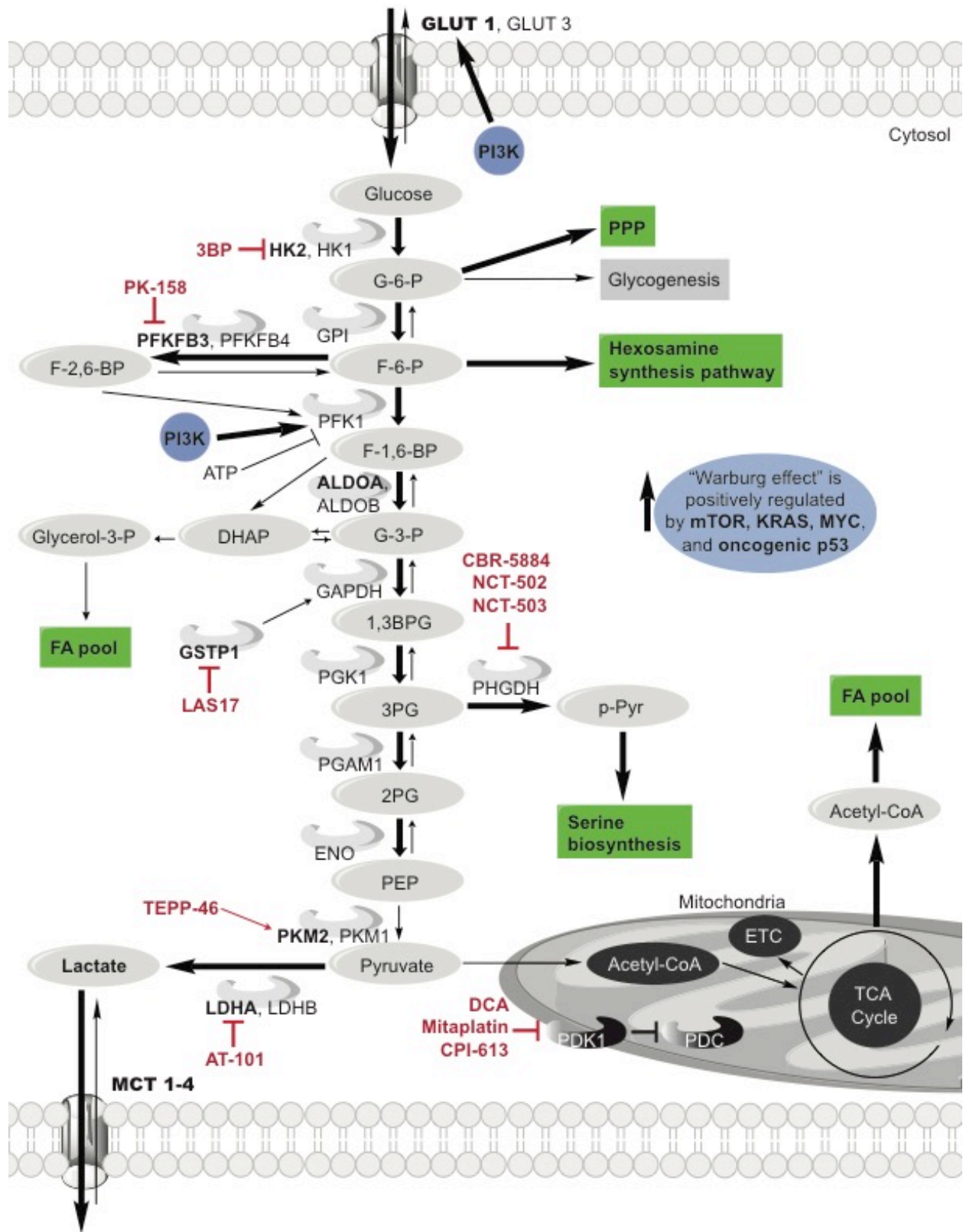


understanding will be necessary to effectively cure one of society's most rampant diseases. Innovative metabolic therapies will usher in the availability of highly specific and decreasingly toxic therapies, optimizing clinical outcomes and completely redefining cancer druggability.

## 8. FIGURES

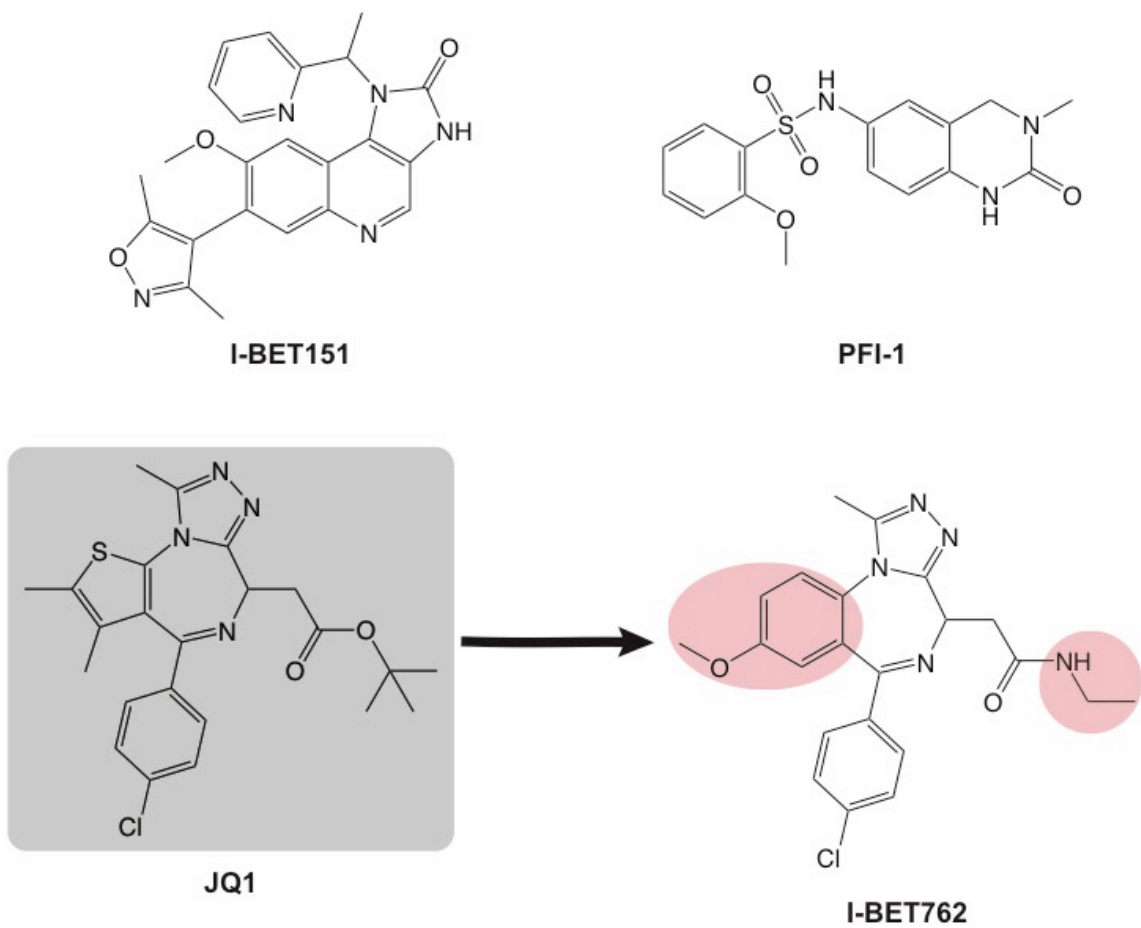


**FIGURE 1.1:** Analogs of rapamycin, or “rapalogues”, that have been developed as cancer therapies.

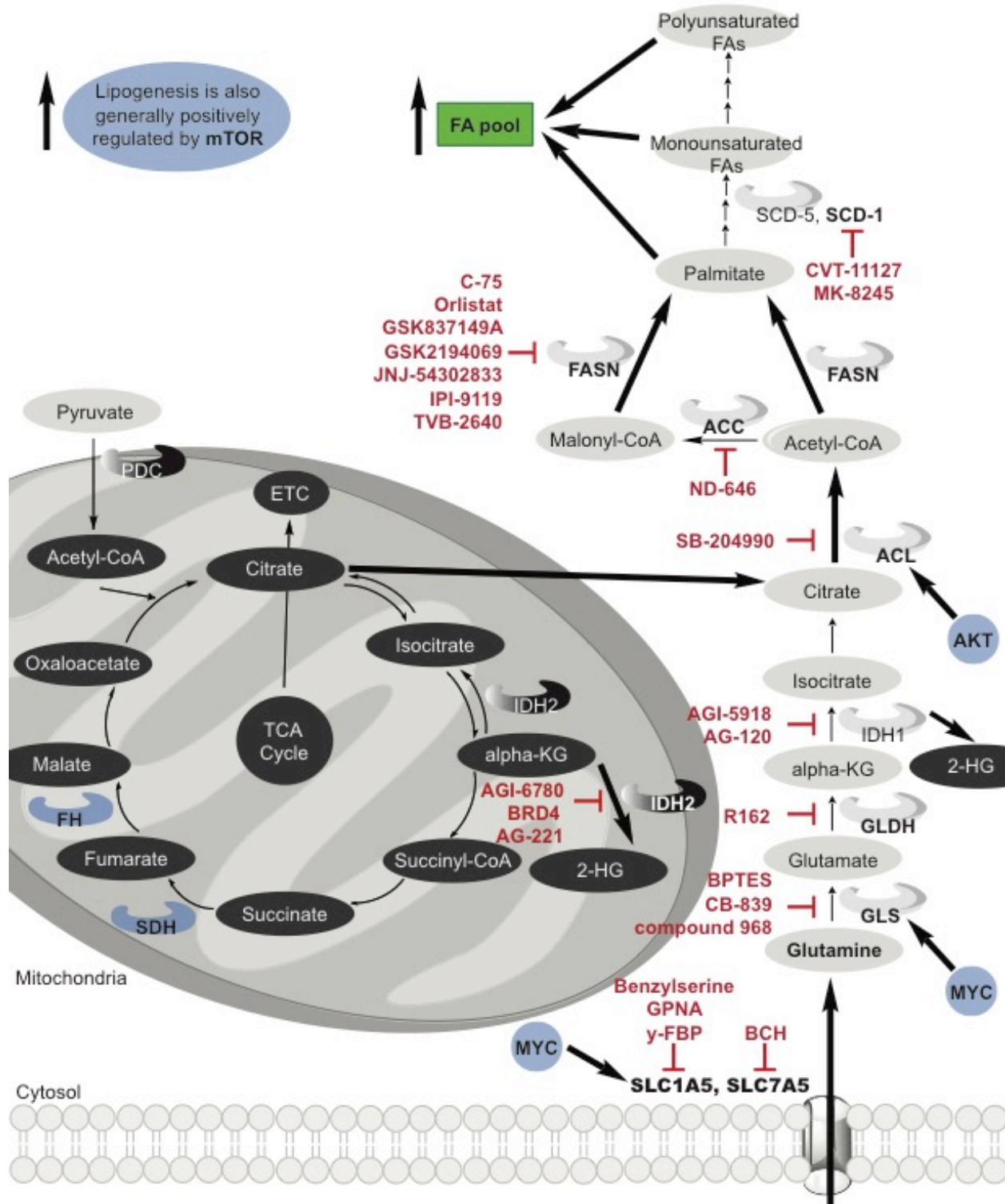


**FIGURE 1.2:** Glucose metabolism in cancer and associated dysregulations and inhibitor therapies. Glycolysis is a series of metabolic processes; it involves nine reactions, of which three are highly regulated (hexokinase (HK), phosphofruktokinase (PFK), and

pyruvate kinase (PK)). As indicated, this pathway also fuels several other pathways, including the pentose phosphate pathway (PPP) and the hexosamine synthesis pathway. Glucose metabolism also contributes to the biosynthesis of fatty acids (FAs) and serine, among others. In cancer cells, pyruvate's conversion into lactate is upregulated but can also be imported into the mitochondrial matrix to fuel the tricarboxylic acid (TCA) cycle. Thicker black arrows indicate reactions that are upregulated in cancer cells. Similarly, upregulated enzymes in cancer metabolism are indicated with bolded text. Current cancer therapies in clinic or preclinic targeting enzymes associated with glucose metabolism are shown in red. Oncogenes that upregulate glucose metabolism in cancer cells are indicated in blue. Transporters: glucose transporter (GLUT); monocarboxylate transporter (MCT). Glycolytic intermediates: glucose-6-phosphate (G-6-P), fructose-6-phosphate (F-6-P); fructose-1,6-bisphosphate (F-1,6-BP); fructose-2,6-bisphosphate (F-2,6-BP); dihydroxyacetone phosphate (DHAP); glyceraldehyde-3-phosphate (G-3-P); 1,3-bisphosphoglycerate (1,3BPG); 3-phosphoglycerate (3PG); 2-phosphoglycerate (2PG); phosphoenolpyruvate (PEP). Enzymes: glucose-6-phosphate isomerase (GPI); aldolase (ALDO); glyceraldehyde 3-phosphate dehydrogenase (GAPDH); phosphoglycerate kinase (PGK); phosphoglycerate mutase (PGAM); enolase (ENO); lactate dehydrogenase (LDH); pyruvate dehydrogenase kinase (PDK); pyruvate dehydrogenase complex (PDC). Oncogenes: phosphatidylinositol-3 kinase (PI3K); mammalian target of rapamycin (mTOR). Chemical inhibitors: 2-deoxy-glucose (2-DG); 3-bromopyruvate (3BP), koningic acid (KA); dichloroacetate (DCA).

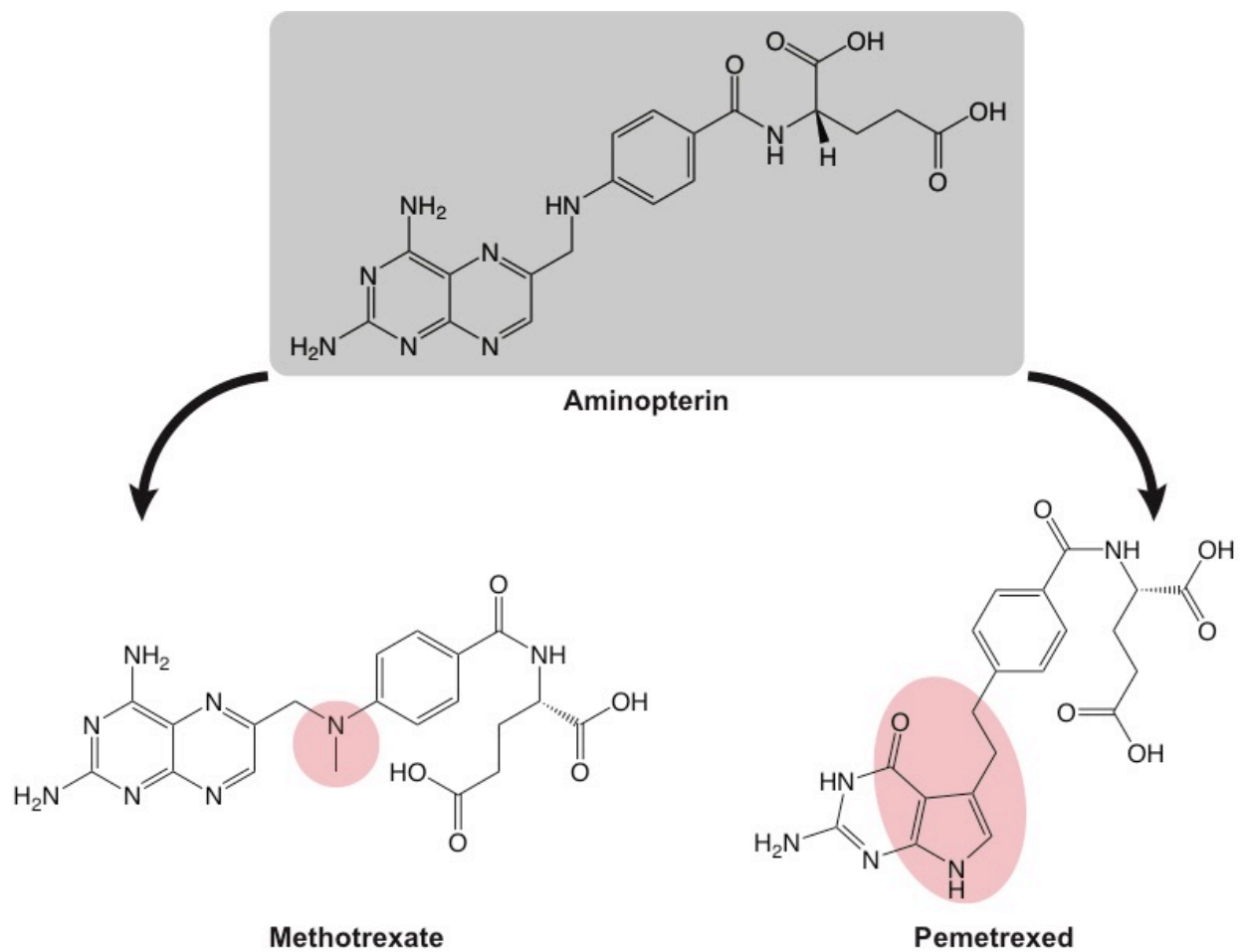


**FIGURE 1.3:** Variety of BET inhibitors that are in development, including the second-generation analog of JQ1, I-BET762.



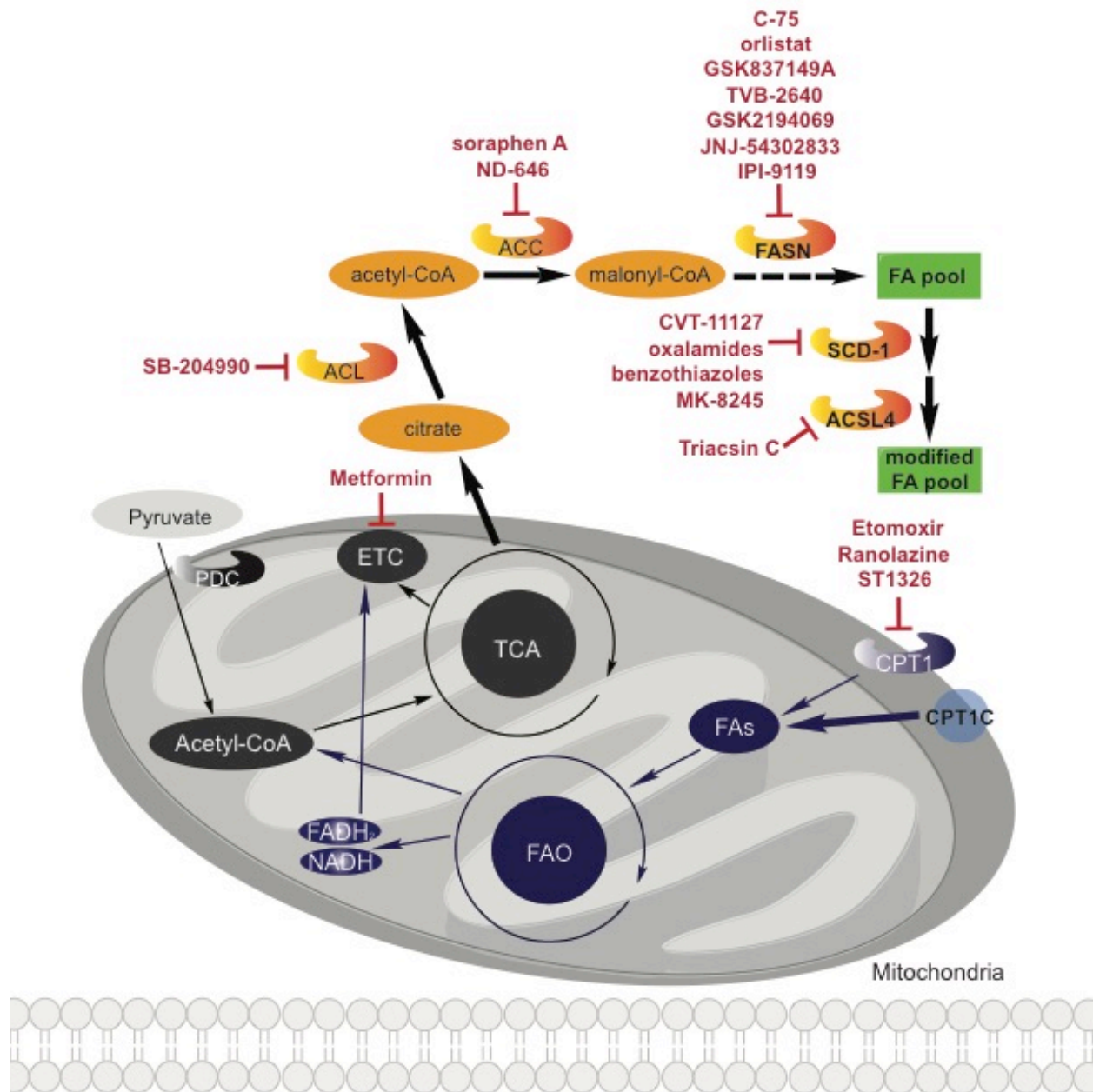
**FIGURE 1.4:** Intersection and dysregulation of the glutaminolysis pathway and the tricarboxylic acid (TCA) cycle in cancer and their associated therapies. The catabolism of glutamine is an important feature in various cancer cells, and promotes cell survival

and proliferation. Upregulation of the oncogene MYC increases both an increased uptake in glutamine into the cancer cell and an increase in glutaminolysis. Both glutaminolysis and the TCA cycle contribute to increased levels of citrate and acetyl-CoA, eventually leading to an increased fatty acid (FA) pool. Thicker black arrows indicate reactions that are upregulated in cancer cells. Similarly, upregulated enzymes are indicated with bolded text. Current cancer therapies in clinic or preclinic targeting enzymes associated with glutaminolysis, the TCA cycle, or lipogenesis are shown in red. Oncogenes that upregulate glutaminolysis, the TCA cycle, or lipogenesis in cancer cells are indicated in blue. Metabolites: alpha-ketoglutarate (alpha-KG); D-2-hydroxyglutarate (2-HG). Enzymes: glutaminase (GLS); glutamate dehydrogenase (GLDH); isocitrate dehydrogenase (IDH); ATP citrate lyase (ACL); acetyl-CoA carboxylase (ACC); fatty acid synthase (FASN); pyruvate dehydrogenase complex (PDC); fumarase (FH); succinate dehydrogenase (SDH). Oncogene: protein kinase B (AKT). Chemical inhibitors: l-glutamyl-p-nitroanilide (GPNA); 2-aminobicyclo(2,2,1)-heptane-2-carboxylic acid (BCH); bis-2-[5-phenyl- acetamido-1, 2, 4-thiadiazol-2-yl] ethyl sulfide (BPTES); bromodomain-containing protein (BRD).



**FIGURE 1.5:** Analogs of aminopterin that inhibit dihydrofolate reductase and tetrahydrofolate reductase.





**FIGURE 1.6:** Fatty acid (FA) anabolism and catabolism in cancer and relevant inhibitor therapies. While in certain cell types and survival situations cancer cells may perform FA catabolism through FA oxidation (FAO), more often cancer cells try to increase their FA pool. Lipogenesis via citrate and acetyl- CoA is the most common pathway to chemically target and, thus, inhibit FA biosynthesis. Metabolites and enzymes associated with FA anabolism, or lipogenesis, are shown in orange, while those associated with FAO are shown in dark blue. Thicker black arrows indicate reactions that are upregulated in cancer cells. Similarly, upregulated enzymes are indicated with bolded text. Current cancer therapies in clinic or preclinic targeting enzymes associated with FA metabolism are shown in red. Oncogenic CPT1C, which upregulates FAO

lipogenesis in certain cancer cells, is indicated in light blue. Enzymes: carnitine palmitoyltransferase I (CPT1); pyruvate dehydrogenase complex (PDC); ATP citrate lyase (ACL); acetyl-CoA carboxylase (ACC); fatty acid synthase (FASN); stearoyl-CoA desaturase (SCD); long-chain acyl-CoA synthetase (ACSL). Oncogene: mammalian target of rapamycin (mTOR).

**CHAPTER 2**  
Covalent Ligand Discovery against Druggable Hotspots  
Targeted by Anti-cancer Natural Products

The work in this chapter is based on the *Cell Chemical Biology* publication “Covalent ligand discovery against druggable hotspots targeted by anti-cancer natural products”<sup>421</sup> and is adapted with permission from all co-authors.

## 1. Introduction

There are countless natural products that have been isolated from microbes, plants, and other living organisms that demonstrate diverse biological action, including antibiotic, anti-inflammatory, and anti-cancer activities<sup>422</sup>. Among these natural products are agents that contain potential reactive electrophilic centers that can covalently react with nucleophilic amino acid hotspots on proteins to modulate their biological action. Examples include natural product scaffolds such as  $\beta$ -lactones and  $\beta$ -lactams, many of which show antibiotic activity through covalent modification and inhibition of the catalytic serines of transpeptidases. In addition, there are many more reactive natural products that bear other reactive moieties such as Michael acceptors, epoxides, and aldehydes, which may react with other nucleophilic side chains such as cysteines and lysines<sup>422</sup>.

However, the reactivity and direct targets of most natural products that bear reactive centers remain poorly understood. Traditional approaches for target identification of natural products entail synthesis or derivatization of the natural products so that they can be appended to enrichment handles or beads for subsequent isolation and chemoproteomic studies. Many natural products are incredibly complex to synthesize or may not necessarily have appropriate sites for derivatization, hindering the ability to develop natural product analogs for traditional chemoproteomic target identification.

Isotopic tandem orthogonal proteolysis-enabled activity-based protein profiling (isoTOP-ABPP) has arisen as a complementary chemoproteomic approach for target discovery of covalently acting small molecules. IsoTOP-ABPP uses reactivity-based chemical probes to map proteome-wide reactive, functional, and ligandable hotspots directly in complex proteomes. When used in a competitive manner, covalently acting small molecules can be competed against the binding of reactivity-based probes directly in complex proteomes to map their proteome-wide reactivity and identify targets<sup>423–426</sup>. While the disadvantages of the isoTOP-ABPP strategy include biasing oneself to profiling of sites targeted by reactivity-based probes and the indirect nature of the assay inherent to competing small molecules against probe binding, a major advantage of this method is that it enables identification of the specific amino acids targeted by covalently acting small molecules. Furthermore, this type of competitive isoTOP-ABPP strategy can be performed with the original parent molecule without having to synthesize analogs or derivatize the molecule. Several recent studies have used ABPP strategies to identify direct targets of reactive natural products such as licochalcone A, celastrol, and curcumin<sup>427–429</sup>.

The advantage of identifying the direct targets and druggable hotspots targeted by covalently acting anti-cancer natural products is that these sites can subsequently be deconvoluted to identify the specific target(s) responsible for the bioactivity; the identified targets can then be further pharmacologically interrogated with other chemical scaffolds to advance drug discovery efforts. This method contrasts with having to perform medicinal chemistry efforts on natural product scaffolds that are often synthetically challenging, with readouts based on their bioactivity rather than affinity to specific protein targets. Furthermore, identifying the nucleophilic amino acid hotspots targeted by reactive natural products enables covalent ligand discovery against these sites toward developing more potent and selective covalent inhibitors; the novel

covalent inhibitors identified may also be more synthetically accessible compared with the potentially more complex structures of natural products. Recent studies have shown that covalent ligand discovery can be used to identify selective lead ligands against unique nucleophilic druggable hotspots in proteins<sup>423,430,431</sup>.

Here, we have used the isoTOP-ABPP platform to couple target identification of a covalently acting anti-cancer natural product with covalent ligand screening to identify a lead ligand that selectively interacts with the same target of interest. For this study, we have chosen to investigate the proteome-wide reactivity and targets of the natural product withaferin A, a steroidal lactone from the Ayurvedic plant *Withania somnifera*, which has been shown to possess anti-inflammatory, anti-diabetic, and anti-cancer activity<sup>432–435</sup>.

Withaferin A bears a Michael acceptor that may react with cysteine nucleophilic hotspots in protein targets (Figure 2.1A). Previous studies have shown that withaferin A binds to functional cysteines in targets such as vimentin and nuclear factor  $\kappa$  B, and these interactions have been postulated to account for its cancer and anti-inflammatory activities, respectively<sup>436,437</sup>. However, these studies either used a derivatized version of withaferin A, which could have missed targets that did not interact with this derivatized form, or performed experiments with specific proteins. Thus, withaferin A may potentially interact with additional targets that may be responsible for its anti-cancer activity.

We have determined that withaferin A targets a particular cysteine on a regulatory subunit of the tumor suppressor protein phosphatase 2A (PP2A) to activate PP2A activity and inactivate multiple oncogenic signaling pathways, which contributes to impairments in breast cancer pathogenicity. We have also identified a significantly more synthetically tractable covalent ligand that selectively targets this same site to recapitulate the effects observed with withaferin A.

## **2. Anti-cancer Activity of Withaferin A in Breast Cancer Cells**

We first tested the anti-cancer activity of withaferin A across several breast cancer cell lines including the receptor-positive MCF7 cells and triple-negative breast cancer (TNBC) cells 231MFP and HCC38 (devoid of estrogen, progesterone, and HER2 receptors). TNBCs are highly aggressive breast cancers that show the worst prognosis and have little to no targeted therapies available<sup>438</sup>. Identifying agents and new druggable hotspots in anti-cancer targets that are capable of impairing TNBC pathogenicity would contribute significantly toward combatting breast cancer.

Consistent with previous studies, we show that withaferin A impairs serum-free cell survival and proliferation in MCF7, 231MFP, and HCC38 breast cancer cells (Figures 2.1B–D). We show that withaferin A impairs 231MFP cell proliferation in a dose-dependent manner with a 50% effective concentration (EC<sub>50</sub>) of 7.5  $\mu$ M (Figure 2.5).

## **3. Mapping Withaferin A Targets with IsoTOP-ABPP**

We next used competitive isoTOP-ABPP platforms to map the proteome-wide cysteine-reactivity of withaferin A in 231MFP breast cancer cell proteomes. While previous studies have demonstrated biological effects of withaferin A at lower concentrations<sup>436</sup>, in this study we used the minimum concentration of withaferin A (10

μM) that yielded the maximal anti-proliferative effect.

To ascertain the direct targets of withaferin A without potential confounding effects from protein expression changes, we initially performed isoTOP-ABPP studies in vitro, in which we competed withaferin A against the reactivity of a broadly cysteine-reactive iodoacetamide-alkyne (IAyne) probe in 231MFP breast cancer cell proteomes. We subsequently appended isotopically light (for vehicle-treated) or heavy (for withaferin A-treated) enrichment handles by copper-catalyzed azide-alkyne cycloaddition (CuAAC), followed by combining vehicle and withaferin A-treated proteomes in a 1:1 ratio, and enrichment and isolation of probe-modified tryptic peptides for quantitative proteomic analysis (Figure 2.2A). Out of the >3,000 total probe-modified peptides identified, we only interpreted those peptides that were present in at least two out of three biological replicates. Through this analysis, we identified C377 of PPP2R1A, a regulatory subunit of PP2A, as the primary and only target that showed a light to heavy ratio of >5 across all three biological replicates (Figure 2.2B). We also confirmed that C377 of PPP2R1A was the primary in situ target of withaferin A in 231MFP cells, showing an isotopically light to heavy ratio of 4.0 (Figure 2.5B).

Previous studies have uncovered several targets of withaferin A, including C328 on vimentin as well as several cysteines on KEAP1<sup>436,439</sup>. In our study, we identified C328 on vimentin as a site of IAyne labeling, but this site was not a target of withaferin A, as evidenced by a light to heavy ratio of 1.0 from in vitro treatment of 231MFP breast cancer cell proteomes with withaferin A (10 μM) (Table A3.1) as well as a lack of competition observed between withaferin A and IAyne labeling of pure human vimentin by gel-based ABPP (Figure 2.5C). While we did not observe IAyne-labeled KEAP1 peptides in our isoTOP-ABPP studies, we also showed no competition between withaferin A and IAyne labeling of pure human KEAP1 by gel-based ABPP studies (Figure 2.5C). These results do not negate the possibility that withaferin A may still interact with these targets under other conditions, but suggest that these proteins are likely not the primary targets of withaferin A in 231MFP breast cancer cells. We thus focused on further investigating the role of withaferin A interactions with PPP2R1A and its influence on PP2A activity and breast cancer pathogenicity.

#### **4. Withaferin A Interactions with PPP2R1A**

PP2A is a tumor suppressor that dephosphorylates and inactivates oncogenic signaling pathways such as AKT. There has been considerable interest in developing direct or indirect activators of PP2A for cancer therapy<sup>440</sup>. While our IAyne probe labeled both C377 and C390 on PPP2R1A, withaferin A specifically targets C377 but not C390 on PPP2R1A (Figure 2.2B). We confirmed this interaction as demonstrated by competition of withaferin A against IAyne labeling of pure human PPP2R1A protein using gel-based ABPP methods (Figure 2.2C). In these gel-based studies, we used a lower concentration of IAyne than our isoTOP-ABPP studies, which may explain why we observe full competition of withaferin A against IAyne labeling.

C377 sits at an interface between three subunits of the core PP2A complex based on previously solved crystal structures of the PP2A heterotrimeric holoenzyme complex (Figure 2.2D)<sup>441</sup>. We postulated that withaferin A activates PP2A activity through targeting C377 on PPP2R1A to impair 231MFP breast cancer cell proliferation. Consistent with this premise, we showed that withaferin A activated PP2A activity in a

reconstituted in vitro biochemical assay with purified human wild-type PPP2R1A protein and the regulatory and catalytic subunits PPP2R2A and PPP2CA, respectively, but not with the PPP2R1A C377A mutant protein (Figure 2.2E).

Treatment of 231MFP cells with withaferin A also reduced phosphorylated AKT levels, and this effect was rescued by co-treatment with the PP2A-selective inhibitor cantharidin (Figure 2.2F).

Further confirming that targeting of PPP2R1A is involved in withaferin A effects, PPP2R1A knockdown with short interfering RNA (siPPP2R1A) significantly attenuated the anti-proliferative effects observed with withaferin A treatment in 231MFP breast cancer cells (Figures 2.5D and 2.5E). The lack of complete attenuation of withaferin A-induced anti-proliferative effects in siPPP2R1A cells may be due to residual PPP2R1A protein expression in the knockdown cells or the contribution of additional withaferin A targets to the anti-proliferative effects. Nonetheless, our data indicate that withaferin A targeting of C377 of PPP2R1A and activation of PP2A activity is, in part, involved in the observed anti-proliferative effects of withaferin A.

## **5. Screening Cysteine-Reactive Fragment Libraries to Reveal PPP2R1A Ligands**

To identify more synthetically tractable covalent ligands against C377 of PPP2R1A, we next screened a library of cysteine-reactive small-molecule ligands in 231MFP breast cancer cells to identify any compounds that recapitulated the phenotypes of withaferin A in impairing 231MFP cell proliferation (Figures 2.3A and 2.3B; Appendix 2). The top hit that arose from this screen was the chloroacetamide DKM 2-90 (Figures 2.3B, 2.3C, and 2.4A).

We next performed competitive isoTOP-ABPP experiments to identify the targets of DKM 2-90 through competition of this lead fragment against IAYne labeling of 231MFP proteomes. While this ligand was not potent, only showing anti-proliferative effects at 100  $\mu$ M, we found that DKM 2-90 showed considerable selectivity in targeting C377 of PPP2R1A in vitro (Figure 2.4B and Table A3.3). We also confirmed DKM 2-90's selectivity through gel-based ABPP methods, showing significant competition of DKM 2-90 against IAYne labeling of pure human PPP2R1A protein with a 50% inhibitory concentration (IC<sub>50</sub>) of 10  $\mu$ M (Figure 2.4C). We also showed that other chloroacetamide ligands of similar structures do not bind to PPP2R1A, suggesting that DKM 2-90 interacts with PPP2R1A in vitro relatively specifically, despite its simple structure (Figure 2.5F). IsoTOP-ABPP analysis of DKM 2-90 treatment in 231MFP cells in situ also showed targeting of C377 of PPP2R1A with an isotopically light to heavy ratio of 5.9. However, four additional targets were also evident that showed an isotopically light to heavy ratio >5, including TXNDC17 C43, CLIC4 C35, ACAT1 C196, and SCP2 C307 (Figure 2.5G). Nonetheless, while DKM 2-90 was a very simple and non-potent covalent ligand, it showed remarkable overall selectivity, with only five total sites showing a ratio >5 out of more than 1,000 cysteines profiled (Figure 2.5G and Table A3.4).

Despite additional targets of DKM 2-90, we still observed an attenuation of DKM 2-90-mediated anti-proliferative effects in siPPP2R1A 231MFP cells compared with DKM 2-90-treated siControl cells (Figure 2.5H). We also recapitulated the reduced levels of phosphorylated AKT and cantharidin rescue with DKM 2-90 treatment in 231MFP cells (Figure 2.4D).

## 6. JNS 1-40: An Optimized Covalent Ligand Targeting C377 of PPP2R1A

While DKM 2-90 was not a potent ligand against PPP2R1A, we showed that isoTOP-ABPP could be used to identify simpler covalent ligands that hit the same druggable hotspots targeted by complex natural products such as withaferin A with decent selectivity and cell penetration.

We next sought to optimize the potency of DKM 2-90. We found that replacing the benzodioxan ring with a tetralin with JNS 1-37 dramatically reduced the potency, with an IC<sub>50</sub> value of 300  $\mu$ M (Figure 2.6A) compared with 10  $\mu$ M in DKM 2-90. Adding an N-benzyl group to DKM 2-90 with JNS 1-40 improved potency toward PPP2R1A by 16-fold, with an IC<sub>50</sub> of 630 nM (Figure 2.7A). We thus moved forward with further characterization of JNS 1-40.

Both in vitro and in situ isoTOP-ABPP analysis showed that JNS 1-40 selectively targets C377 of PPP2R1A in both 231MFP complex proteome and cells, and C377 is the only target exhibiting an isotopically light to heavy ratio >5 (Figures 2.6B and 2.7B; Tables A3.5 and A3.6). Much like withaferin A, JNS 1-40 activated PP2A activity in vitro with purified PP2A complex proteins with wild-type PPP2R1A, but not with the PPP2R1A C377A mutant protein (Figure 2.7C). Similarly, JNS 1-40 treatment in 231MFP cells significantly reduced phosphorylated AKT levels and impaired proliferation and survival (Figures 2.7D and 2.7F). The anti-proliferative effects observed with JNS 1-40 were also attenuated in siPPP2R1A 231MFP cells compared with siControl cells (Figure 2.6C).

With the improved potency and selectivity observed with JNS 1-40, we next sought to determine whether JNS 1-40 targeting of PPP2R1A could reduce breast cancer tumor growth in vivo. Daily treatment of mice with JNS 1-40 (50 mg/kg intraperitoneally) in vivo began 15 days after 231MFP tumor xenograft initiation and significantly attenuated tumor growth (Figure 2.7G). Daily treatment with JNS 1-40 for >30 days did not cause any overt toxicity or loss of body weight, suggesting that this compound is well tolerated in vivo (data not shown).

To confirm target engagement, we also performed ex vivo isoTOP-ABPP analysis of 231MFP tumor xenografts from in vivo JNS 1-40 treated mice. We demonstrated that JNS 1-40 selectively targeted C377 of PPP2R1A in vivo in 231MFP tumors, showing an isotopically light to heavy ratio of 5.7 (Figure 2.7H and Table A3.7). Collectively, our data indicated that the improved covalent ligand JNS 1-40 selectively targeted C377 of PPP2R1A to activate PP2A activity and impair breast cancer cell proliferation and in vivo tumor growth.

## 7. Conclusion

We showed here that isoTOP-ABPP platforms can be used to identify the druggable hotspots targeted by bioactive covalently acting natural products, which can in turn be pharmacologically interrogated with more synthetically tractable covalent ligands. In this study, we revealed that withaferin A targets C377 of PPP2R1A, a unique druggable hotspot within the PP2A tumor-suppressor complex, to activate PP2A activity, inhibit AKT signaling, and impair breast cancer cell proliferation. Through screening a library of fragment-based covalent ligands, we identified a much simpler covalent ligand DKM 2-90 that also targeted the same site as withaferin A. We further



optimized this hit to generate JNS 1-40, a lead covalent ligand with nanomolar potency that selectively targets C377 of PPP2R1A in vitro, in situ, and in vivo to recapitulate the effects observed with withaferin A: activating PP2A, inactivating AKT signaling, and impairing breast cancer pathogenicity.

Previous studies have identified various additional targets of withaferin A, including vimentin, KEAP1, Hsp90, and IKK  $\beta$ <sup>436,437,439,442</sup>. Withaferin A has also been shown to affect important processes such as proteostasis<sup>443</sup>. Our studies do not rule out that these and other protein targets may also play important roles in the anti-proliferative and pathogenic impairments observed with withaferin A, but instead reveal C377 of PPP2R1A as an additional target of this natural product and a unique druggable hotspot that can be targeted to activate PP2A and impair breast cancer pathogenicity.

While we and many other groups have used ABPP platforms to identify targets of covalently acting natural products, we show here that this process can be coupled with covalent ligand discovery approaches, yielding much more synthetically tractable small molecules that do not require significant synthetic or isolation efforts, and which recapitulate the effects observed with complex natural products<sup>426–430,444</sup>.

Overall, our study demonstrates the utility of using isoTOP-ABPP platforms to map the reactivity and targets of covalently acting natural products toward identifying their therapeutic mechanism of action and discovering druggable hotspots that can be interrogated by alternative pharmacological scaffolds for future drug discovery efforts.

While there are countless natural products that exhibit therapeutic activity, translating these natural products into drugs has been hindered by difficulty in synthesis and isolation of these compounds. Here, we show that isoTOP-ABPP-based chemoproteomic platforms and covalent ligand discovery approaches can be coupled to discover synthetically tractable covalent ligands that target druggable hotspots targeted by more complex covalently acting natural products. In this study, we discovered that withaferin A specifically targets C377 of PPP2R1A, a regulatory subunit within the tumor suppressor PP2A, to activate PP2A activity, inactivate AKT signaling, and impair breast cancer pathogenicity. Through covalent ligand screening and optimization, we identify a synthetically accessible small molecule that targets the same site as withaferin A and produces identical effects. Overall, our study provides an alternative strategy for translating natural products into therapeutics, by developing simpler covalent ligands that hit the same druggable hotspots targeted by natural products using chemoproteomics-enabled covalent ligand discovery platforms.

## 8. Materials and Methods

### Chemicals

Withaferin A was obtained from Sigma. IAYNE was obtained from CHESS GmbH. Heavy and light TEV-biotin tags were synthesized per previously described methods<sup>445</sup>. The synthesis for most of our cysteine-reactive ligand library has been described previously<sup>430</sup>. New ligands screened in this paper that were not previously described are in Appendix 1. All compounds in our library were confirmed to be >95 % pure. The structures of the covalent ligand library screened in this paper are all listed in Appendix 2.

### **In Vivo Animal Studies**

Animal experiments were conducted in accordance with the guidelines of the Institutional Animal Care and Use Committee of the University of California, Berkeley. Female immune-deficient SCID mice (6 weeks old) purchased from Taconic laboratories were used for tumor xenograft studies. Tumor xenograft and pharmacology studies were performed as previously described<sup>402,446</sup>.

### **Cell Culture**

The 231MFP cells were obtained from Prof. Benjamin Cravatt and were generated from explanted tumor xenografts of MDA-MB-231 cells. These cells have been previously characterized as a more aggressive variant of the MDA-MB-231 cells<sup>447,448</sup>. HCC38 and MCF7 cells were obtained from the American Type Culture Collection. 231MFP cells were cultured in L15 medium containing 10% FBS, supplemented with 1% glutamine (200 mM stock), and maintained at 37°C with 0% CO<sub>2</sub>. HCC38 and MCF7 cells were cultured in RPMI medium containing 10% FBS, supplemented with 1% glutamine (200 mM stock), and maintained at 37°C with 5% CO<sub>2</sub>. Unless otherwise specified, all cell culture materials were purchased from Gibco. Withaferin A, DKM 2-90, JNS 1-40, and all other covalent ligands were dissolved in DMSO and final DMSO concentrations in cells were 0.1%.

### **Cellular Phenotype Studies**

Cell survival and proliferation assays were performed as previously described using Hoechst 33342 dye (Invitrogen) according to manufacturer's protocol (Louie et al., 2016). Cells were seeded into 96-well plates (40,000 for survival and 20,000 for proliferation) in a volume of 150 µL and allowed to adhere overnight. Cells were treated with an additional 50 µL of media containing 1:250 dilution of 1000x compound stock in DMSO. Medium was removed from each well and 100 µL of staining solution containing 10% formalin and Hoechst 33342 dye was added to each well and incubated for 15 min in the dark at room temperature. After incubation, staining solution was removed and wells were washed with PBS before imaging. Studies with HCC38 cells were also performed as above but were seeded with 20,000 cells for survival and 10,000 cells for proliferation.

### **Western Blotting**

Antibodies to vinculin, phospho-Akt (Ser473), and Akt were obtained from Cell Signaling Technology and proteomes were blotted per recommended manufacturer's procedure. Cells were lysed in lysis buffer (containing the following: 20 mM Tris pH 7.5, 150 mM NaCl, 1 mM EDTA, 1 mM EGTA, 1% Triton X-100, 2.5 mM pyrophosphate, 50 mM NaF, 5 mM β-glycero-phosphate, 1 mM Na<sub>3</sub>VO<sub>4</sub>, 50 nM calyculin A (EMD Millipore), and protease inhibitors (Roche)). Lysate was incubated on a rotator at 4° C for 30 min, and insoluble material was removed via centrifugation at max speed for 10 min. Proteins were resolved by SDS/PAGE and transferred to nitrocellulose membranes using the iBlot system (Invitrogen). Blots were blocked with 5% nonfat milk in Tris-buffered saline containing Tween 20 (TBST) solution for 1 hour at room temperature, washed in TBST, and probed with primary antibody diluted in recommended diluent per manufacturer overnight at 4°C. Following washes with TBST, the blots were incubated in the dark with

secondary antibodies purchased from Rockland and used at 1:10 000 dilution in 5% nonfat milk in TBST at room temperature. Blots were visualized using an Odyssey Li-Cor scanner after additional washes.

### **Purification of PPP2R1A and PPP2R2A Subunits**

Wild-type mammalian expression plasmids with C-terminal FLAG tag were purchased from Origene (PPP2R1A: RC200056; PPP2R2A, MR207137). The PPP2R1A C337A mutant was generated with Agilent QuickChange Lightning site-directed mutagenesis kit according to manufacturer's instructions. HEK293T cells (ATCC CRL-11268) were grown to 60% confluency in DMEM (Corning) supplemented with 10% FBS (Corning) and 2mM L-glutamine (Life Technologies) and maintained at 37°C with 5% CO<sub>2</sub>. Immediately prior to transfection, media was replaced with DMEM + 5% FBS. Each plate was transfected with 20 µg of overexpression plasmid with 100 µg PEI (Sigma). After 48hrs cells were collected in TBS, lysed by sonication, and batch bound with anti-DYKDDDDK resin (GenScript) for 1hr. Lysate and resin was loaded onto a gravity flow column and washed, followed by elution with 250ng/µL 3xFLAG peptide (ApexBio A6001). Purity and concentration were verified by PAGE, UV/Spectroscopy, and BCA assay.

### **In Vitro PP2A Activity Assay**

Recombinant PPP2CA (40 nM, Origene TP301334) was combined with pulled-down WT or mutant PPP2R1A (50 nM) as well as PPP2R2A (50 nM) and incubated with 10 µM withaferin A, JS 1-40, or vehicle for 30 min at RT in TBS. Activity was assayed by addition of 60 µM Thr phosphopeptide (KRpTIRR, Millipore, 12-219) at 37° C for 25 min, and free phosphate was detected colorimetrically by malachite green kit (Cayman 10009325) per manufacturer's instructions.

### **PPP2R1A Knockdown Studies**

PPP2R1A was transiently knocked down with siRNA using previously described methods<sup>449</sup>. siRNA for a scrambled RNA oligonucleotide control and pooled RNA oligonucleotides targeting PPP2R1A were purchased from Dharmacon.

### **IsoTOP-ABPP**

IsoTOP-ABPP studies were done as previously reported<sup>423,430,445</sup>. Cells were lysed by probe sonication in PBS and protein concentrations were measured by BCA assay. Proteome samples diluted in PBS (4 mg of proteome per biological replicate) were treated with a covalently-acting small molecule or vehicle for 30 min at 37° C. Then, Iayne labeling (100 µM) was performed for 1 h at room temperature. CuAAC was used by sequential addition of tris(2-carboxyethyl)phosphine (1 mM, Sigma), tris[(1-benzyl-1H-1,2,3-triazol-4-yl)methyl]amine (34 µM, Sigma), copper (II) sulfate (1 mM, Sigma), and biotin-linker-azide, the linker functionalized with a TEV protease recognition sequence along with an isotopically light or heavy valine for treatment of control or treated proteome, respectively. After click reactions, proteomes were precipitated by centrifugation at 6500 x g, washed in ice-cold methanol, combined in a 1:1 control/treated ratio, washed again, then denatured and resolubilized by heating in 1.2% SDS/PBS to 80°C for 5 minutes. Insoluble components were precipitated by

centrifugation at 6500 x g and soluble proteome was diluted in 5 ml 0.2% SDS/PBS. Labeled proteins were bound to avidin-agarose beads (170  $\mu$ L resuspended beads/sample, Thermo Pierce) while rotating overnight at 4°C. Bead-linked proteins were enriched by washing three times each in PBS and water, then resuspended in 6 M urea/PBS (Sigma) and reduced in TCEP (1 mM, Sigma), alkylated with iodoacetamide (18 mM, Sigma), then washed and resuspended in 2 M urea and trypsinized overnight with 0.5  $\mu$ g/ $\mu$ L sequencing grade trypsin (Promega). Tryptic peptides were eluted off. Beads were washed three times each in PBS and water, washed in TEV buffer solution (water, TEV buffer, 100  $\mu$ M dithiothreitol) and resuspended in buffer with Ac-TEV protease and incubated overnight. Peptides were diluted in water and acidified with formic acid (1.2 M, Spectrum) and prepared for analysis.

### **MS Analysis**

Peptides from all proteomic experiments were pressure-loaded onto a 250  $\mu$ m inner diameter fused silica capillary tubing packed with 4 cm of Aqua C18 reverse-phase resin (Phenomenex # 04A-4299) which was previously equilibrated on an Agilent 600 series HPLC using gradient from 100% buffer A to 100% buffer B over 10 min, followed by a 5 min wash with 100% buffer B and a 5 min wash with 100% buffer A. The samples were then attached using a MicroTee PEEK 360  $\mu$ m fitting (Thermo Fisher Scientific #p-888) to a 13 cm laser pulled column packed with 10 cm Aqua C18 reverse-phase resin and 3 cm of strong-cation exchange resin for isoTOP-ABPP studies. Samples were analyzed using an Q Exactive Plus mass spectrometer (Thermo Fisher Scientific) using a 5-step Multidimensional Protein Identification Technology (MudPIT) program, using 0%, 25%, 50%, 80%, and 100% salt bumps of 500 mM aqueous ammonium acetate and using a gradient of 5-55% buffer B in buffer A (buffer A: 95:5 water:acetonitrile, 0.1% formic acid; buffer B 80:20 acetonitrile:water, 0.1% formic acid). Data was collected in data-dependent acquisition mode with dynamic exclusion enabled (60 s). One full MS (MS1) scan (400-1800 m/z) was followed by 15 MS2 scans (ITMS) of the nth most abundant ions. Heated capillary temperature was set to 200°C and the nanospray voltage was set to 2.75 kV.

Data was extracted in the form of MS1 and MS2 files using Raw Extractor 1.9.9.2 (Scripps Research Institute) and searched against the Uniprot human database using ProLuCID search methodology in IP2 v.3 (Integrated Proteomics Applications, Inc) (Xu et al., 2015). Cysteine residues were searched with a static modification for carboxyamino-methylation (+57.02146) and up to two differential modifications for methionine oxidation and either the light or heavy TEV tags (+464.28596 or +470.29977, respectively). Peptides were required to have at least one tryptic end and to contain the TEV modification. ProLUCID data was filtered through DTASelect to achieve a peptide false-positive rate below 1%. Only those probe-modified peptides that were evident in two out of three biological replicates were interpreted for their isotopic light to heavy ratios. MS1 peak shapes were confirmed to be of good quality for interpreted peptides. Targets of covalently-acting molecules are defined here as targets that showed >4 light to heavy ratios across all three biological replicates.

### **Gel-Based ABPP**

Gel-based ABPP methods were performed as previously described<sup>450,451</sup>. Recombinant

pure human proteins were purchased from Origene. Pure proteins (0.2  $\mu\text{g}$ ) were pre-treated with DMSO or covalently-acting small molecules for 30 min at 37° C in an incubation volume of 50  $\mu\text{L}$  PBS, and were subsequently treated with IAyne (10  $\mu\text{M}$  final concentration) for 30 min at room temperature. CuAAC was performed to append rhodamine-azide (1  $\mu\text{M}$  final concentration) onto IAyne probe-labeled proteins. The samples were separated by SDS/PAGE and scanned using a ChemiDoc MP (Bio-Rad Laboratories, Inc). Inhibition of target labeling was assessed by densitometry using ImageJ.

### **General Synthetic Methods**

Chemicals and reagents were purchased from major commercial suppliers and used without further purification. Reactions were performed under a nitrogen atmosphere unless otherwise noted. Silica gel flash column chromatography was performed using EMD or Sigma Aldrich silica gel 60 (230-400 mesh). Proton and carbon nuclear magnetic resonance ( $^1\text{H}$  NMR and  $^{13}\text{C}$  NMR) data was acquired on a Bruker AVB 400, AVQ 400, or AV 600 spectrometer at the University of California, Berkeley. High resolution mass spectrum were obtained from the QB3 mass spectrometry facility at the University of California, Berkeley using positive or negative electrospray ionization (+ESI or -ESI). Yields are reported as a single run.

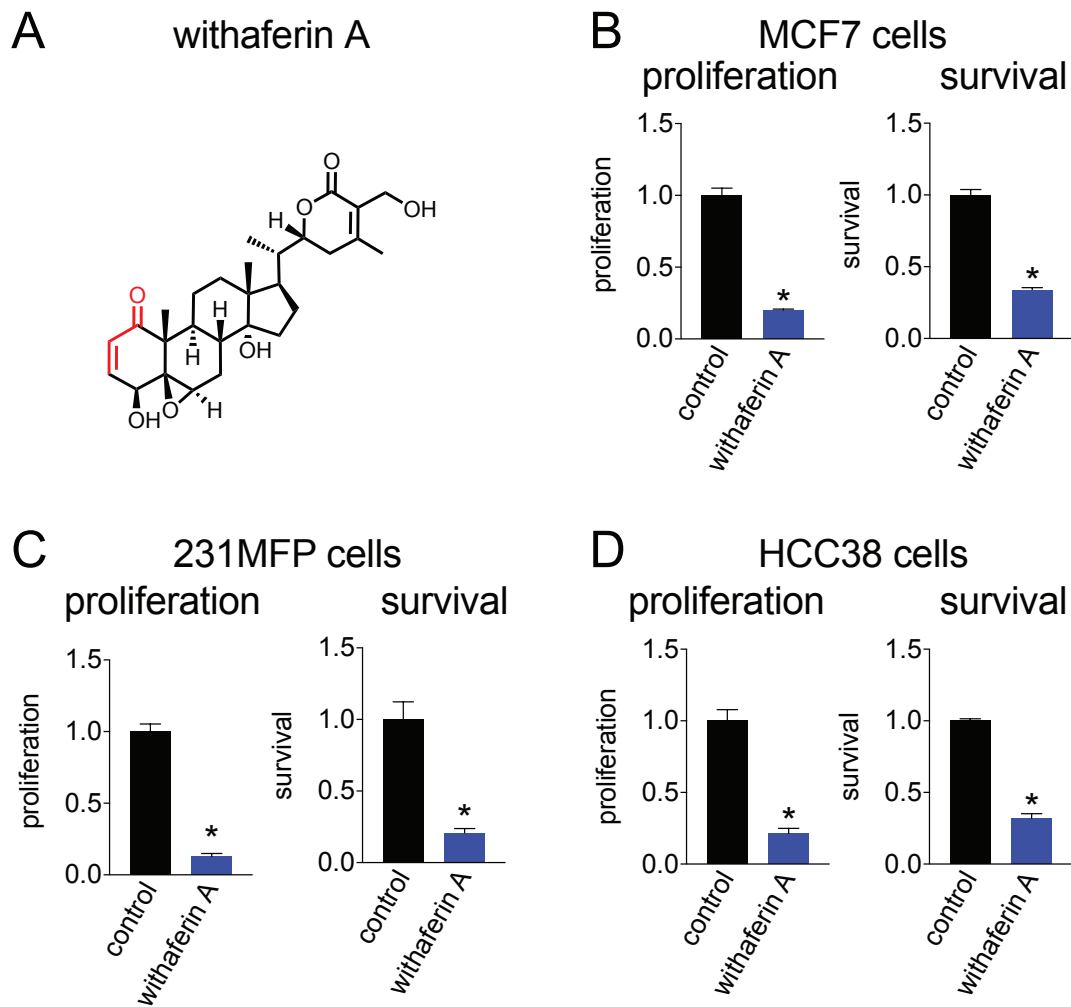
General Procedure A: The amine (1 eq.) was dissolved in DCM (5 mL/mmol) and cooled to 0°C. To the solution was added acryloyl chloride (1.2 eq.) followed by triethylamine (1.2 eq.). The solution was warmed to room temperature and stirred overnight. The solution was then washed with brine and the crude product was purified by silica gel chromatography (and recrystallization if necessary) to afford the corresponding acrylamide.

General Procedure B: The amine (1 eq.) was dissolved in DCM (5 mL/mmol) and cooled to 0°C. To the solution was added chloroacetyl chloride (1.2 eq.) followed by triethylamine (1.2 eq.). The solution was warmed to room temperature and stirred overnight. The solution was then washed with brine and the crude product was purified by silica gel chromatography (and recrystallization if necessary) to afford the corresponding chloroacetamide.

### **Quantification and Statistical Analysis**

Microsoft Excel and Graphpad Prism software were used for statistical analysis. Statistical and quantification details of experiments can be found in the figure legends. Significance was defined a  $p < 0.05$  between comparison groups.

## 9. FIGURES

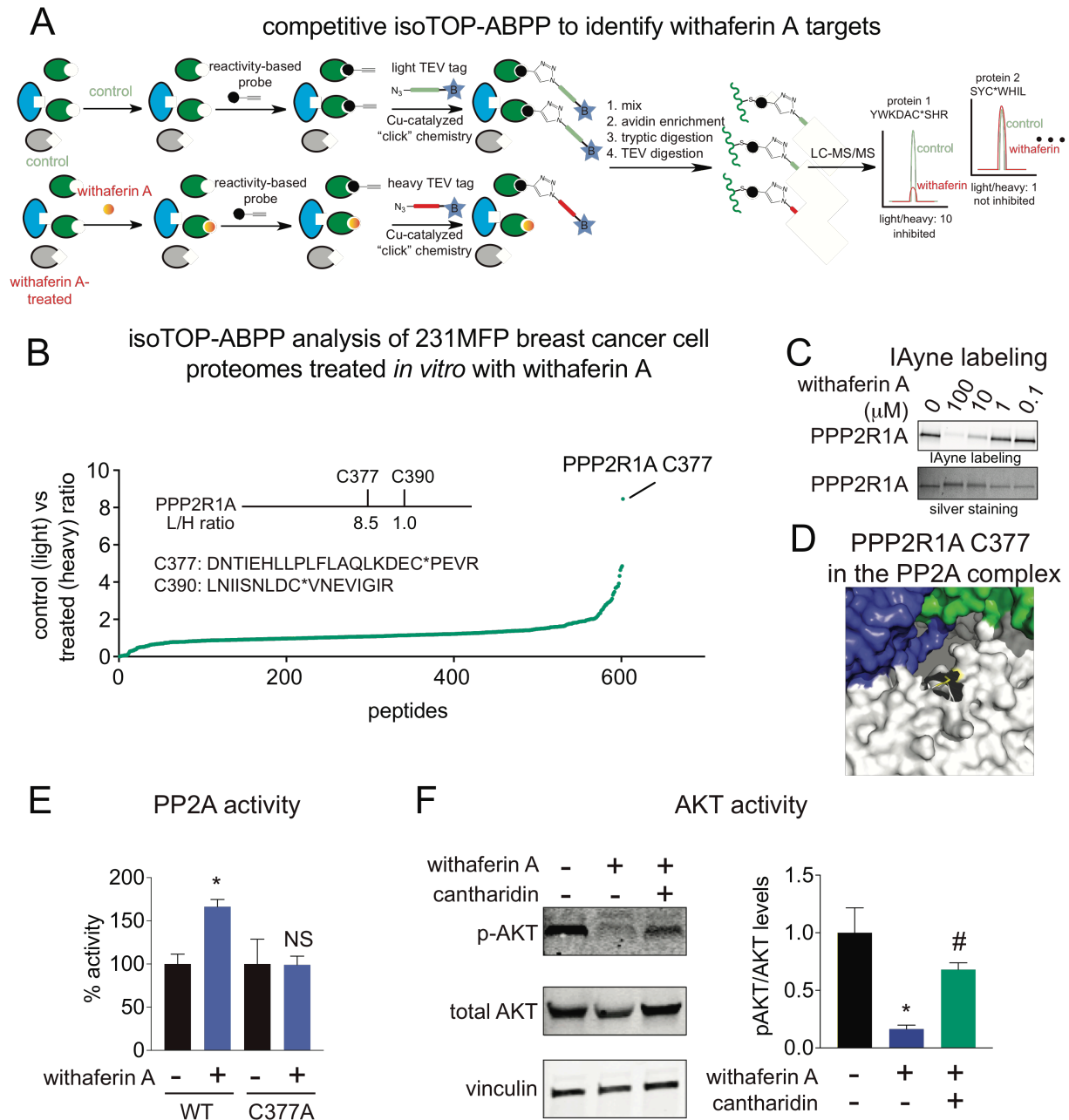


**FIGURE 2.1:** Withaferin A impairs breast cancer cell pathogenicity

**(A)** Structure of withaferin A. Reactive Michael acceptor is indicated in red.

**(B–D)** Withaferin A (10  $\mu$ M) impairs cell proliferation and serum-free cell survival after 48 hr in MCF7 (B), 231MFP (C), and HCC38 (D) cells compared with DMSO-treated controls.

Data are presented as mean  $\pm$ SEM,  $n=5$ . Significance is shown as  $*p<0.05$  compared with vehicle-treated controls.



**FIGURE 2.2:** Using isoTOP-ABPP platforms to map proteome-wide targets of withaferin A in breast cancer cells

**(A)** Competitive isoTOP-ABPP method. We mapped the cysteine reactivity of withaferin A by pre-incubating withaferin A (10 μM) for 30 min in 231MFP breast cancer cell proteomes, prior to labeling with the cysteine-reactive iodoacetamide-alkyne (IAyne) probe (100 μM, 30 min). Probe-labeled proteins were then tagged with an isotopically light (for control) or heavy (for withaferin A-treated) biotin-azide tag bearing a TEV protease recognition site by CuAAC. Control and treated proteomes were then mixed in a 1:1 ratio, probe-labeled proteins were avidin-enriched and tryptically digested, probe-labeled tryptic peptides were avidin-enriched again, released by TEV protease, and

analyzed by quantitative proteomic methods, and light to heavy peptide ratios were quantified. LC-MS/MS, liquid chromatography-tandem mass spectrometry; TEV, tobacco etch virus.

**(B)** Competitive isoTOP-ABPP analysis of withaferin A cysteine reactivity in 231MFP breast cancer cell proteomes in vitro. Light to heavy ratios of  $\sim 1$  indicate peptides that were labeled by IAYne, but not bound by withaferin A. We designate light to heavy ratios of  $>5$  as targets that were bound by withaferin A. Also shown are the peptide sequences and sites of modification of probe-modified peptides identified for PPP2R1A and the light to heavy ratios of C377 and C390 on PPP2R1A.

**(C)** Validation of PPP2R1A as a target of withaferin A. Withaferin A was pre-incubated with pure human PPP2R1A protein followed by IAYne. Probe-labeled proteins conjugated to rhodamine-azide by CuAAC and analyzed by SDS-PAGE and in-gel fluorescence. Shown above is fluorescence detection of IAYne labeling and shown below is silver staining of the gel showing PPP2R1A protein expression.

**(D)** Crystal structure of PP2A complex showing C377 of PPP2R1A (shown in white), the catalytic subunit shown in blue, and another regulatory subunit shown in green. PDB structure used is PDB: 2IAE.

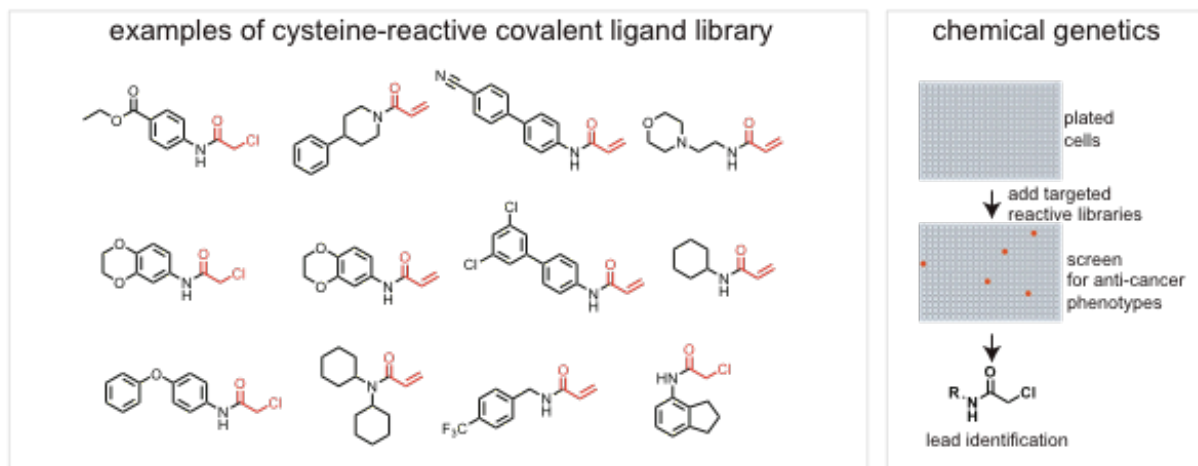
**(E)** PP2A activity assay with PP2A complex proteins PPP2R1A wild-type (WT) or C377A mutant and PPP2R2A and PPP2CA subunits measuring phosphate release from a PP2A substrate phosphopeptide. This PP2A complex was treated in vitro with DMSO or withaferin A ( $10 \mu\text{M}$ ) for 30 min prior to initiation of the assay.

**(F)** Withaferin A ( $10 \mu\text{M}$ , 4 hr) treatment significantly reduces phospho-AKT levels in 231MFP breast cancer cells and this reduction is rescued by co-treatment with cantharidin ( $10 \mu\text{M}$ , 4 hr).

Data in (B) are average ratios from  $n=3$ . Gel in (C) is a representative gel from  $n=3$ . Data in (E) and (F) are presented as mean  $\pm$ SEM,  $n=3$ . Significance is expressed as  $*p<0.05$  compared with vehicle-treated controls and  $\#p<0.05$  compared with withaferin A-treated control. NS refers to not significant compared with the vehicle-treated C377A PPP2R1A group. For withaferin A in situ isoTOP-ABPP analysis, see Figure 2.5.

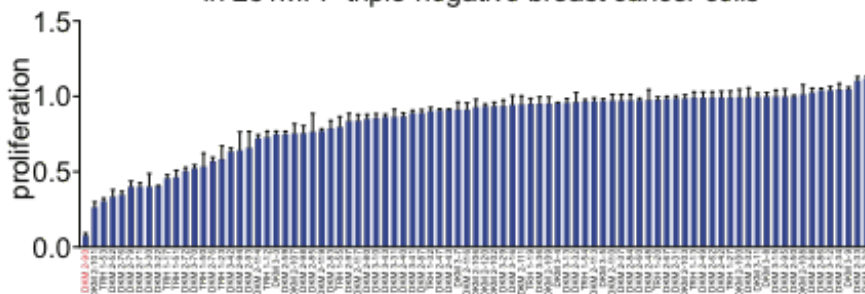


A



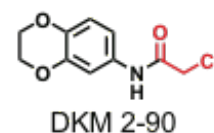
B

cysteine-reactive fragment screen  
in 231MFP triple-negative breast cancer cells

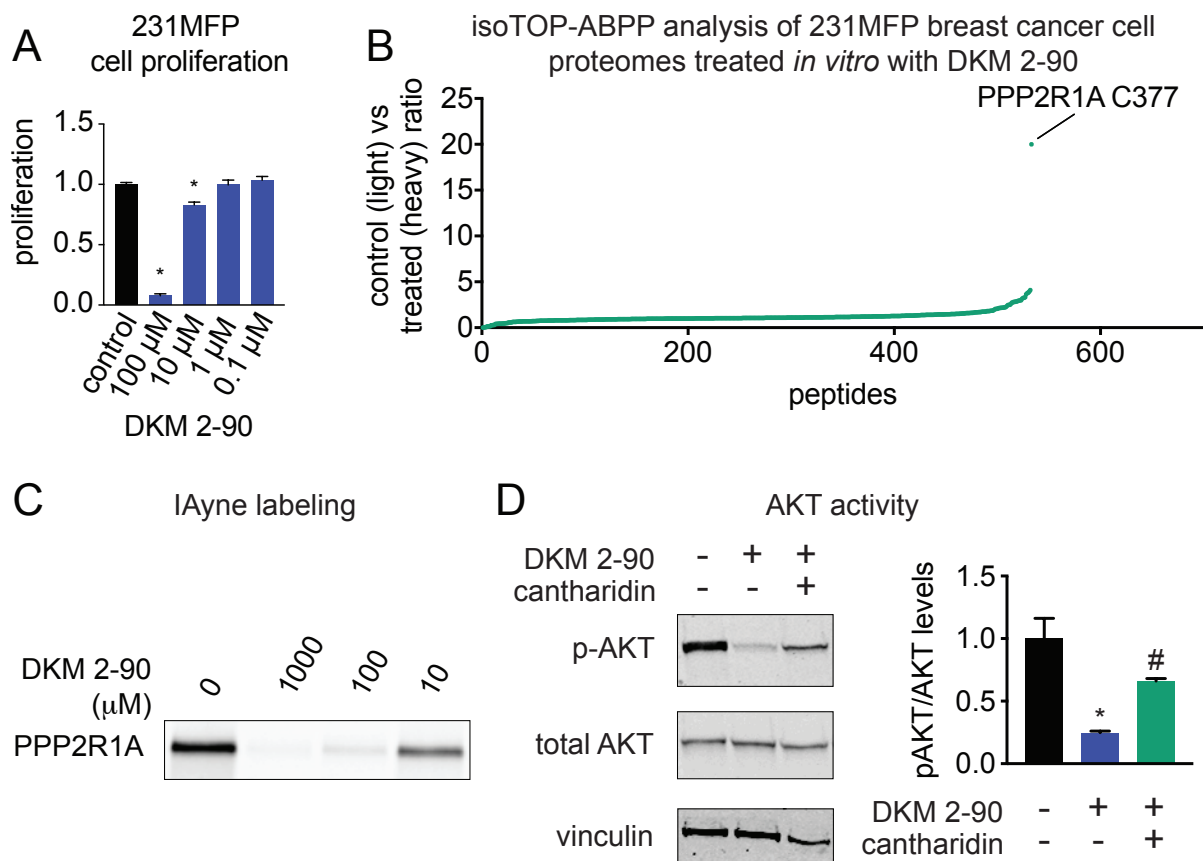


C

lead cysteine-reactive fragments



**FIGURE 2.3:** Screening of covalent ligand libraries in breast cancer cells  
**(A)** Coupled screening of a cysteine-reactive covalent ligand library in 231MFP breast cancer cells with competitive isoTOP-ABPP platforms to identify anti-cancer lead compounds, targets, and ligandable hotspots within these targets.  
**(B)** We screened a cysteine-reactive fragment library consisting of acrylamides and chloroacetamides in 231MFP breast cancer cells (100  $\mu$ M) to identify any leads that significantly impaired 231MFP breast cancer cell proliferation. Cell viability was assessed 48 hr after treatment by Hoechst staining. Data are presented as mean  $\pm$ SEM, n=3.  
**(C)** Shown is the structure of the lead covalent ligand DKM 2-90. Reactive chloroacetamide warheads are designated in red.



**FIGURE 2.4:** Target identification of DKM 2-90 using competitive isoTOP-ABPP platforms

**(A)** Dose-responsive effects of DKM 2-90 on cell proliferation in 231MFP breast cancer cells. 231MFP cells were treated with DMSO or DKM 2-90 and proliferation was assessed 48 hr after treatment by Hoechst staining.

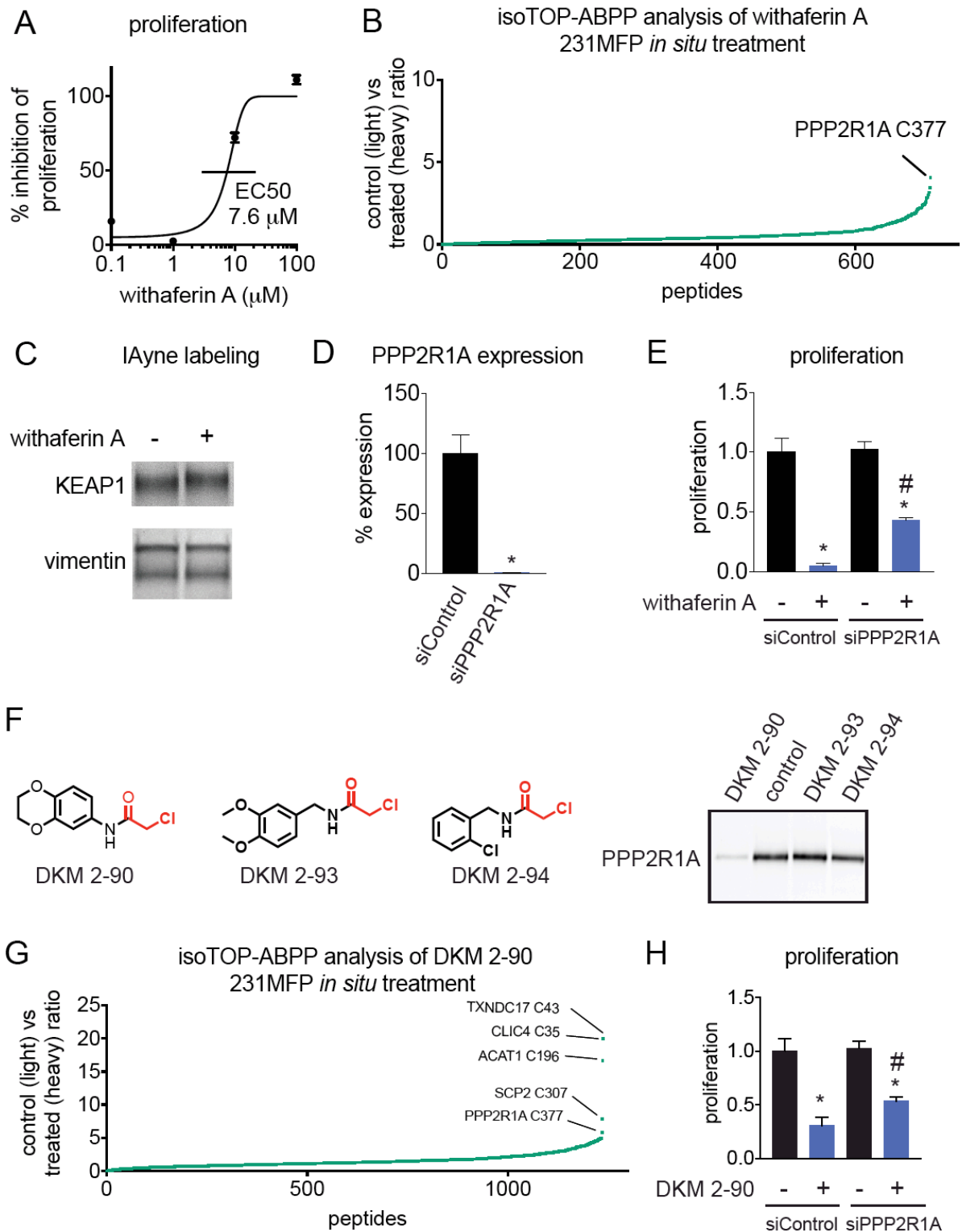
**(B)** IsoTOP-ABPP analysis of DKM 2-90 in 231MFP cell proteomes *in vitro*. 231MFP proteomes were pre-treated with DMSO or DKM 2-90 (100  $\mu$ M) for 30 min prior to labeling proteomes with IAYne (100  $\mu$ M) and subjected to the isoTOP-ABPP method. A light to heavy ratio of 1 indicates that the probe-labeled cysteine-bearing peptide was not bound by the covalent ligand, whereas a ratio  $>5$  indicates bound sites.

**(C)** Competition of DKM 2-90 against IAYne labeling of pure human PPP2R1A protein. DKM 2-90 was pre-incubated with pure PPP2R1A protein for 30 min prior to labeling with IAYne (100  $\mu$ M) for 30 min. Rhodamine-azide was appended on by copper-catalyzed azide-alkyne cycloaddition, and proteins were separated by SDS-PAGE and analyzed by in-gel fluorescence.

**(D)** Levels of total and phosphorylated AKT (p-AKT) and vinculin as a loading control in 231MFP breast cancer cells. 231MFP cells were treated with vehicle, DKM 2-90 (100  $\mu$ M), or cantharidin (10  $\mu$ M) and DKM 2-90 (100  $\mu$ M) for 5 hr. Proteins were blotted for p-AKT, total AKT, and vinculin loading control.

All data shown represent  $n=3-5$ /group. Data in (B and D) are presented as means

±SEM. Significance in (B and D) expressed as \* $p < 0.05$  compared with vehicle-treated controls. Significance in (D) expressed as # $p < 0.05$  compared with DKM 2-90-treated cells. For isoTOP-ABPP analysis of DKM 2-90 in situ, see Figure 2.5.



**FIGURE 2.5:** Investigating the interactions of withaferin A and DKM 2-90  
**(A)** Anti-proliferative dose-response of withaferin A in 231MFP cells. Cells were treated with DMSO or withaferin A for 48 h in serum-containing media and cell viability was

assessed by Hoechst staining.

**(B)** IsoTOP-ABPP analysis of withaferin A treatment in 231MFP cells. 231MFP cells were treated with DMSO or withaferin A (10  $\mu$ M) for 4 h. Proteomes were subsequently labeled *ex situ* with IAYne for 1 h and subjected to the isoTOP-ABPP method. Light to heavy ratios of probe-modified peptides are shown.

**(C)** Gel-based ABPP analysis of withaferin A competition against IAYne labeling of pure human KEAP1 and vimentin. Purified proteins were pre-treated with DMSO or withaferin A (10  $\mu$ M) for 30 min at 37°C before IAYne labeling (10  $\mu$ M) for 30 min at room temperature. Probe labeled proteins were subsequently appended to rhodamine-azide by CuAAC and analyzed by SDS/PAGE and in-gel fluorescence.

**(D)** PPP2R1A expression as assessed by qPCR. 231MFP cells were transfected with siControl or siPPP2R1A oligonucleotides and cells were harvested for qPCR analysis after 48 h.

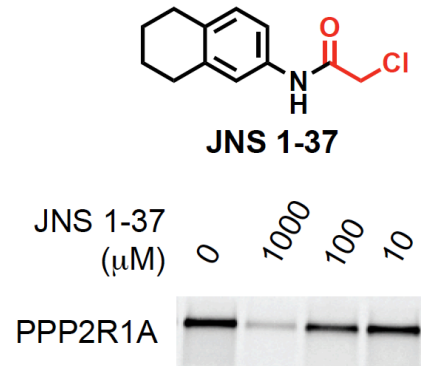
**(E)** 231MFP cell proliferation. 231MFP cells were transfected with siControl or siPPP2R1A oligonucleotides for 48 h and then cells were seeded and treated with either DMSO or withaferin A (10  $\mu$ M) for an additional 48 h and cell viability was assessed by Hoechst staining.

**(F)** Gel-based ABPP analysis of IAYne labeling of pure PPP2R1A. Purified proteins were pre-treated with DMSO or covalent ligands (100  $\mu$ M) (positive control DKM 2-90 and negative control DKM 2-93 and DKM 2-94) for 30 min at 37°C before IAYne labeling (10  $\mu$ M) for 30 min at room temperature. Probe labeled proteins were subsequently appended to rhodamine-azide by CuAAC and analyzed by SDS/PAGE and in-gel fluorescence.

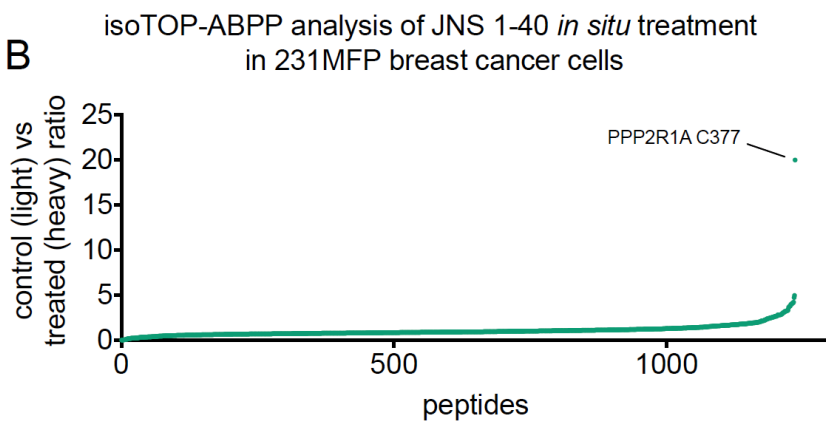
**(G)** IsoTOP-ABPP analysis of DKM 2-90 treatment in 231MFP cells. 231MFP cells were treated with DMSO or DKM 2-90 (100  $\mu$ M) for 4 h. Proteomes were subsequently labeled *ex situ* with IAYne for 1 h and subjected to the isoTOP-ABPP method. Light to heavy ratios of probe-modified peptides are shown.

**(H)** 231MFP cell proliferation. 231MFP cells were transfected with siControl or siPPP2R1A oligonucleotides for 48 h and then cells were seeded and treated with either DMSO or DKM 2-90 (100  $\mu$ M) for an additional 48 h and cell viability was assessed by Hoechst staining. Data in (A, D, E, and G) is presented as mean  $\pm$ SEM, n=3-5/group. Significance in (D, E, and G) is expressed as \*p<0.05 compared to vehicle-treated siControl cells and #p<0.05 compared to withaferin A or DKM 2-90-treated siControl cells.

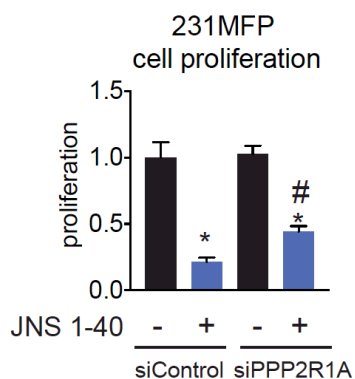
A



B



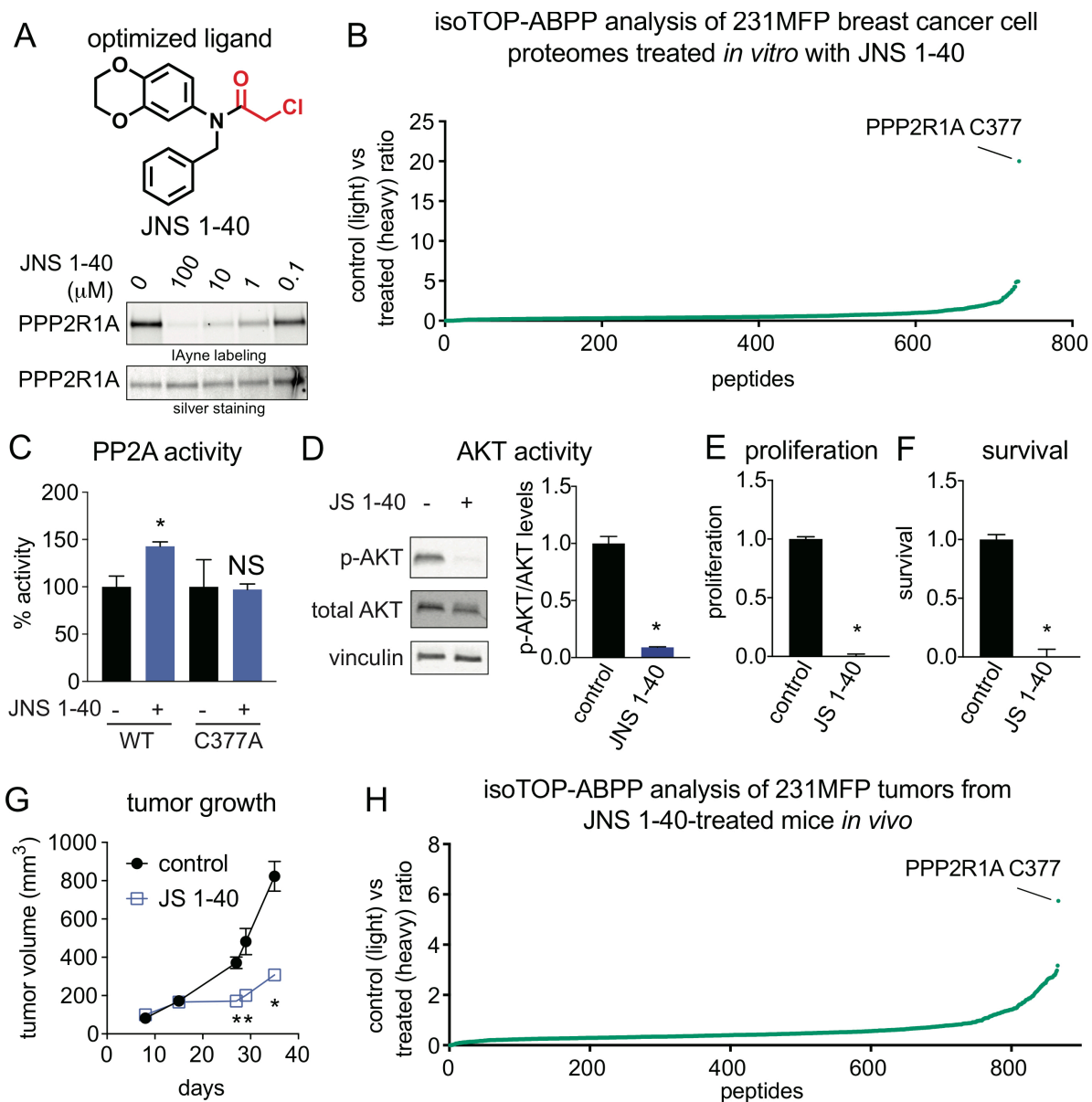
C



**FIGURE 2.6:** Characterization of DKM 2-90 analogs JNS 1-37 and JNS 1-40  
**(A)** Structure of JNS 1-37 and gel-based ABPP analysis of its potency against PPP2R1A. Reactive chloroacetamide is shown in red. Pure human PPP2R1A was pre-treated with DMSO or JNS 1-37 for 30 min at 37°C prior to IAtyne labeling for 30 min at room temperature. Probe-labeled proteins were appended to rhodamine-azide by CuAAC and analyzed by SDS/PAGE and in-gel fluorescence.  
**(B)** IsoTOP-ABPP analysis of JNS 1-40 treatment in 231MFP cells. 231MFP cells were treated with DMSO or JNS 1-40 (100  $\mu$ M) for 4 h. Proteomes were subsequently labeled

*ex situ* with I<sup>125</sup>Ayne for 1 h and subjected to the isoTOP-ABPP method. Light to heavy ratios of probe-modified peptides are shown.

**(C)** 231MFP cell proliferation. 231MFP cells were transfected with siControl or siPPP2R1A oligonucleotides for 48 h and then cells were seeded and treated with either DMSO or JNS 1-40 (100  $\mu$ M) for an additional 48 h and cell viability was assessed by Hoechst staining. Data in (C) is presented as mean  $\pm$ SEM, n=5/group. Significance in (C) is expressed as \*p<0.05 compared to vehicle-treated siControl cells and #p<0.05 compared to JNS 1-40-treated siControl cells.



**FIGURE 2.7:** Optimized covalent ligand JNS 1-40 selectively targets C377 of PPP2R1A to increase PP2A activity and impair breast cancer pathogenicity

**(A)** Structure of JNS 1-40 and gel-based ABPP analysis of its potency against PPP2R1A. Reactive chloroacetamide is shown in red. Pure human PPP2R1A was pre-treated with DMSO or JNS 1-40 for 30 min at 37°C prior to IAYne labeling for 30 min at room temperature. Probe-labeled proteins were appended to rhodamine-azide by CuAAC and analyzed by SDS-PAGE and in-gel fluorescence. Shown above is fluorescence detection of IAYne labeling and shown below is silver staining of the gel showing PPP2R1A protein expression.

**(B)** IsoTOP-ABPP analysis of JNS 1-40 treatment in 231MFP cells. 231MFP proteomes were treated *in vitro* with DMSO or JNS 1-40 (100 μM) for 30 min prior to IAYne labeling for 1 hr and subjected to the isoTOP-ABPP method. Light to heavy ratios of probe-modified peptides are shown.



**(C)** PP2A activity assay with PP2A complex proteins PPP2R1A wild-type (WT) or C377A mutant and PPP2R2A and PPP2CA subunits measuring phosphate release from a PP2A substrate phosphopeptide. This PP2A complex was treated in vitro with DMSO or JNS 1-40 (100  $\mu$ M) for 30 min prior to initiation of the assay.

**(D)** Levels of total and phosphorylated AKT (p-AKT) and vinculin as a loading control in 231MFP breast cancer cells. 231MFP cells were treated with vehicle or JNS 1-40 (100  $\mu$ M) for 75 min.

**(E and F)** JS 1-40 (100  $\mu$ M) impairs cell proliferation (E) and serum-free cell survival (F) after 48 hr in 231MFP cells.

**(G)** 231MFP tumor xenograft growth in immune-deficient SCID mice. 231MFP cells were subcutaneously injected into mice. Daily once-per-day treatment with vehicle or JNS 1-40 (50 mg/kg intraperitoneally) was initiated 15 days after tumor implantation.

**(H)** IsoTOP-ABPP analysis of 231MFP tumor xenografts from JNS 1-40-treated mice in vivo. Tumors harvested from the end of the study shown in (G) were labeled with IAYne ex vivo and subjected to the isoTOP-ABPP methodology.

Data in (C) to (G) are presented as mean  $\pm$ SEM, n=3–7/group. Data in (B) and (H) are average ratios from n=3. Significance is shown as \*p<0.05 compared with vehicle-treated controls. NS indicates not significant (p>0.05) compared with the vehicle-treated C377A PPP2R1A group. For isoTOP-ABPP analysis of JNS 1-40 in situ, see Figure 2.6.

## **CONCLUSION**

Though many proteins have been implicated in cancer pathogenicity, few have been successfully pharmacologically exploited for effective treatments. It has been shown that the knowledge that a protein is involved in disease progression is not sufficient to encourage the creation of a drug to target that protein; rather, the biochemical tools necessary to do so must first be established in order to spur on therapeutic developments<sup>452</sup>. Therefore, uncovering fundamental knowledge of the molecular mechanisms driving cancer is the essential first step in developing targeted drugs.

In chapter one, I examined the current knowledge of numerous oncogenes, tumor suppressors, and metabolic pathways relevant to cancer. Chapter one also reviewed existing pharmacological approaches that modulate these proteins and pathways and identified drugs currently in development or available clinically.

Several of the drugs discussed in chapter one impact protein and pathway functionality via covalent binding to a disease-relevant target; however, for many covalently-acting compounds, their precise mechanism of action is unknown. It is of paramount importance to decipher how each drug exerts its therapeutic effects, both to aid in the development of the drug itself as well as to add to the underlying knowledge of cancer malignancy and progression.

Chemoproteomic technologies have arisen as a powerful tool for answering these questions, enabling the proteome-wide assessment of compound reactivity directly in complex biological systems. Using chemoproteomics has facilitated the discovery of covalently-acting compounds that bind to protein binding pockets of interest, the off-targets of therapeutic compounds, and even druggable anti-cancer protein targets, unveiling novel approaches for cancer treatment.

In chapter two, I demonstrated the power of chemoproteomic platforms by using them to identify C377 on PPP2R1A as a target of covalently-acting anti-cancer natural product withaferin A, subsequently identifying an anti-cancer small molecule that also bound C377 on PPP2R1A, DKM 2-90, and developing a more selective and potent small molecule, JNS 1-40, a lead covalent ligand with nanomolar potency that selectively targets C377 of PPP2R1A *in vitro*, *in situ*, and *in vivo* to recapitulate the effects observed with withaferin A: activating PP2A, inactivating AKT signaling, and impairing triple negative breast cancer pathogenicity.

Looking forward, it is imperative to continue pursuing both basic and translational cancer research, as the development of the former compliments and encourages the latter. Basic research will help elucidate the precise structures and functions of the proteins and pathways mentioned here, enabling therapeutic targeting of proteins that will then be considered “druggable”. For those proteins whose binding pockets have been discovered, such as PPP2R1A, continual pharmacological interrogation must be pursued and the resulting compounds seen through clinical development. Research must continue to aim at identifying strategies for pharmacological manipulation in order to develop targeted cancer treatments, and applying the technologies highlighted in the second chapter will contribute greatly to this overall goal.

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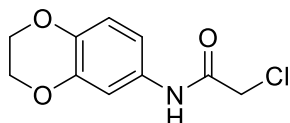
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## **APPENDICES**

## Appendix 1

Selected synthesis notes and compound characterization.



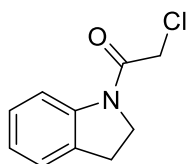
### 2-Chloro-N-(2,3-dihydrobenzo[b][1,4]dioxin-6-yl)acetamide (DKM 2-90)

Following **General Procedure B** starting from 1,4-benzodioxan-6-amine (1.51 g, 10 mmol) product was obtained after silica gel chromatography (40% ethyl acetate in hexanes) in 70% yield as an off-white solid (1.59 g).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** δ 8.11 (s, 1H), 7.18 (d, *J* = 2.4 Hz, 1H), 6.92 (dd, *J* = 2.4, 8.7 Hz, 1H), 6.83 (d, *J* = 8.7 Hz, 1H), 4.25 (s, 4H), 4.17 (s, 2H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 163.8, 143.7, 141.3, 130.4, 117.5, 114.0, 110.2, 64.5, 64.4, 43.0.

**HRMS (+ESI):** Calculated: 228.0422 (C<sub>10</sub>H<sub>11</sub>ClNO<sub>3</sub>). Observed: 228.0421.



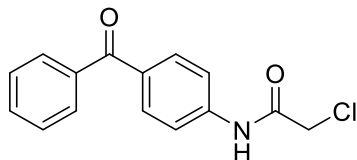
### 2-chloro-1-(indolin-1-yl)ethan-1-one (DKM 2-79)

Following **General Procedure B** starting from indoline (331 mg, 2.8 mmol) product was obtained after silica gel chromatography (0% to 20% ethyl acetate in hexanes) in 51% yield as a pale brown solid (278 mg).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** δ 8.17 (d, *J* = 8.0 Hz, 1H), 7.20-7.16 (m, 2H), 7.04 (t, *J* = 7.4 Hz, 1H), 4.09 (s, 2H), 4.05 (t, *J* = 8.4 Hz, 2H), 3.17 (t, *J* = 8.4 Hz, 2H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 164.0, 142.4, 131.3, 127.6, 124.7, 124.5, 117.1, 47.7, 43.02, 28.1.

**HRMS (+ESI):** Calculated: 196.0524 (C<sub>10</sub>H<sub>11</sub>ClNO). Observed: 196.0523.



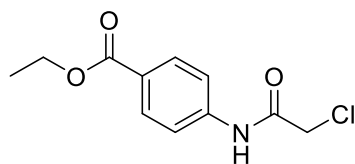
### N-(4-Benzoylphenyl)-2-chloroacetamide (DKM 3-22)

Following **General Procedure B** starting from 4-aminobenzophenone (590 mg, 3.0 mmol) product was obtained after silica gel chromatography (30% to 50% ethyl acetate in hexanes) in 83% yield as a light brown solid (679 mg).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** δ 8.48 (s, 1H), 7.85-7.83 (m, 2H), 7.78-7.76 (m, 2H), 7.71-7.68 (m, 2H), 7.61-7.57 (m, 1H), 7.50-7.46 (m, 2H), 4.22 (s, 2H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 195.7, 164.2, 140., 137.7, 134.1, 132.5, 131.7, 130.0, 128.5, 119.3, 43.0.

**HRMS (-ESI):** Calculated: 272.0484 (C<sub>15</sub>H<sub>11</sub>NO<sub>2</sub>Cl). Observed: 272.0482.



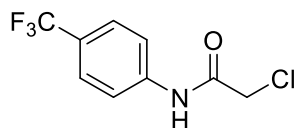
#### Ethyl 4-(2-chloroacetamido)benzoate (TRH 1-17)

Following **General Procedure B** starting from benzocaine (498 mg, 3.0 mmol) product was obtained after silica gel chromatography (2% to 20% ethyl acetate in hexanes) in 68% yield as a white solid (494 mg).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** δ 8.67 (s, 1H), 7.98 (d, *J* = 8.0 Hz, 2H), 7.62 (d, *J* = 8.0 Hz, 2H), 4.33 (q, *J* = 8.0 Hz, 2H), 4.15 (s, 2H), 1.34 (t, *J* = 6.0 Hz, 3H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 166.1, 164.5, 141.0, 130.7, 126.7, 119.3, 61.1, 43.0, 14.3.

**HRMS (-ESI):** Calculated: 240.0433 (C<sub>11</sub>H<sub>11</sub>NO<sub>3</sub>Cl). Observed: 240.0430.



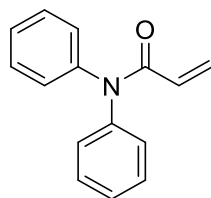
#### 2-Chloro-N-(4-(trifluoromethyl)phenyl)acetamide (TRH 1-51)

Following **General Procedure B** starting from 4-(trifluoromethyl)aniline (346 mg, 2.0 mmol) product was obtained after silica gel chromatography (10% to 30% ethyl acetate in hexanes) in 61% yield as a white solid (309 mg).

**<sup>1</sup>H NMR (400 MHz, MeOD):** δ 7.77 (d, *J* = 8.3 Hz, 2H), 7.61 (d, *J* = 8.3 Hz, 2H), 4.20 (s, 2H).

**<sup>13</sup>C NMR (100 MHz, MeOD):** δ 167.7, 162.4, 142.9, 127.14, 127.10, 127.06, 127.02, 124.3, 120.9, 44.0.

**HRMS (-ESI):** Calculated: 236.0095 (C<sub>9</sub>H<sub>6</sub>NOCIF<sub>3</sub>). Observed: 236.0094.



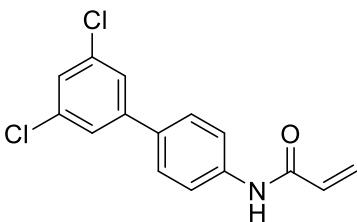
#### N,N-diphenylacrylamide (DKM 3-70)

A solution of diphenylamine (347 mg, 2.1 mmol) in DCM (10 mL) was cooled to 0 °C. To the solution was added acryloyl chloride (222 mg, 2.5 mmol) followed by triethylamine (279 mg, 2.8 mmol). The solution was allowed to warm to room temperature and stirred overnight. The solution was washed with brine and citric acid and the crude product was purified via silica gel chromatography (20% to 60% ethyl acetate in hexanes) to afford the product in 24% yield as a dark yellow oil (112 mg).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** δ 7.43-7.28 (m, 10H), 6.52 (dd, *J* = 2.0, 16.8 Hz, 1H), 6.25 (dd, *J* = 10.2, 16.8 Hz, 1H), 5.67 (dd, *J* = 1.8, 10.2 Hz, 1H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 165.8, 142.6, 129.7, 129.3, 128.5, 127.0.

**HRMS (+ESI):** Calculated: 246.0889 (C<sub>15</sub>H<sub>13</sub>NONa). Observed: 246.0887.



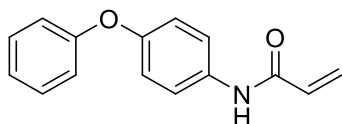
### N-(3',5'-dichloro-[1,1'-biphenyl]-4-yl)acrylamide (DKM 3-3)

Following **General Procedure A** starting from 4-amino-3,5-dichlorobiphenyl (717 mg, 3.0 mmol), product was obtained after silica gel chromatography (20% to 45% ethyl acetate in hexanes) and recrystallization from toluene in 23% yield as a white solid (203 mg).

**<sup>1</sup>H NMR (600MHz, MeOD):**  $\delta$  7.77 (d,  $J$  = 8.6 Hz, 2H), 7.59 (d,  $J$  = 8.6 Hz, 2H), 7.56 (d,  $J$  = 1.7 Hz, 2H), 7.37 (t,  $J$  = 1.7 Hz, 1H), 6.46 (dd,  $J$  = 9.9, 17.0 Hz, 1H), 6.39 (dd,  $J$  = 1.7, 17.0 Hz, 1H), 5.80 (dd,  $J$  = 1.7, 9.9 Hz, 1H).

**<sup>13</sup>C NMR (150MHz, MeOD):**  $\delta$  166.2, 145.2, 140.4, 136.5, 135.2, 132.4, 128.5, 128.0, 127.7, 126.2, 121.7.

**HRMS (-ESI):** Calculated: 290.0145 (C<sub>15</sub>H<sub>10</sub>NOCl<sub>2</sub>). Observed: 290.0143.



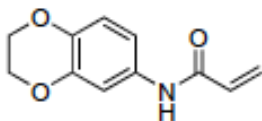
### N-(4-phenoxyphenyl)acrylamide (DKM 2-119)

Following **General Procedure A** starting from 4-phenoxyaniline (571 mg, 3.1 mmol), product was obtained after silica gel chromatography (10% to 30% ethyl acetate in hexanes) in 69% yield as a white solid (512 mg).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):**  $\delta$  8.17 (s, 1H), 7.55 (d,  $J$  = 8.9 Hz, 2H), 7.33-7.29 (m, 2H), 7.08 (t,  $J$  = 7.4 Hz, 1H), 6.98-6.94 (m, 4H), 6.42 (dd,  $J$  = 1.4, 16.9 Hz, 1H), 6.31 (dd,  $J$  = 10.0, 16.9 Hz, 1H), 5.73 (dd,  $J$  = 1.4, 10.0 Hz, 1H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):**  $\delta$  16.0, 157.5, 153.8, 13.4, 131.2, 129., 12.8, 123.3, 122.1, 119.6, 118.6.

**HRMS (+ESI):** Calculated: 240.1019 (C<sub>15</sub>H<sub>14</sub>NO<sub>2</sub>). Observed: 240.1015.



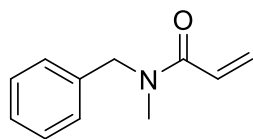
### N-(2,3-dihydrobenzo[b][1,4]dioxin-6-yl)acrylamide (DKM 2-87)

Following **General Procedure A** starting from 1,4-benzodioxan-6-amine (462 mg, 3.1 mmol), product was obtained after silica gel chromatography (40% ethyl acetate in hexanes) in 38% yield as a light yellow solid (239 mg).

**<sup>1</sup>H NMR (400MHz, (CD<sub>3</sub>)<sub>2</sub>SO):**  $\delta$  9.97 (s, 1H), 7.33 (d,  $J$  = 2.4 Hz, 1H), 7.03 (dd,  $J$  = 2.4, 8.7 Hz, 1H), 6.79 (d,  $J$  = 8.7 Hz, 1H), 6.38 (dd,  $J$  = 10.0, 17.0, 1H), 6.22 (dd,  $J$  = 2.1, 17.0 Hz, 1H), 5.71 (dd,  $J$  = 2.1, 10.0 Hz, 1H), 4.23-4.18 (m, 4H).

**<sup>13</sup>C NMR (100MHz, (CD<sub>3</sub>)<sub>2</sub>SO):** δ 162.7, 142.9, 139.5, 132.7, 131.9, 126.4, 116.8, 112.5, 108.4, 64.2, 63.9.

**HRMS (+ESI):** Calculated: 206.0812 (C<sub>11</sub>H<sub>12</sub>NO<sub>3</sub>). Observed: 206.0807.



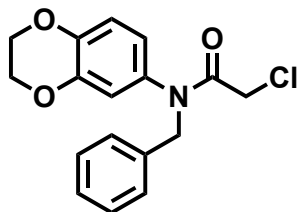
### **N-((tetrahydrofuran-2-yl)methyl)acrylamide (DKM 3-15)**

Following **General Procedure A** starting from tetrahydrofurfurylamine (294 mg, 2.9 mmol), product was obtained after silica gel chromatography (20% to 70% ethyl acetate in hexanes) in 55% yield as a pale yellow oil (246 mg).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** 6.48 (s, 1H), 6.20 (dd, *J* = 1.7, 17.0 Hz, 1H), 6.07 (dd, *J* = 10.1, 17.0 Hz, 1H), 5.54 (dd, *J* = 1.7, 10.1 Hz, 1H), 3.96-3.90 (m, 1H), 3.80-3.75 (m, 1H), 3.70-3.64 (m, 1H), 3.58-3.52 (m, 1H), 3.17-3.11 (m, 1H), 1.95-1.87 (m, 1H), 1.86-1.78 (m, 2H), 1.53-1.44 (m, 1H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 165.7, 130.8, 126.3, 77.7, 68.0, 43.2, 28.7, 25.7.

**HRMS (+ESI):** Calculated: 156.1019 (C<sub>8</sub>H<sub>14</sub>NO<sub>2</sub>). Observed: 156.1017.



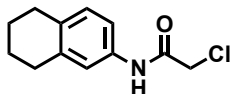
### **N-benzyl-2-chloro-N-(2,3-dihydrobenzo[b][1,4]dioxin-6-yl)acetamide (JNS 1-40)**

A solution of DKM 2-90 (1 g, 4.39 mmol) and sodium hydride (0.7 g 60% dispersion in mineral oil, 17.56 mmol, 4 eq.) in THF (50 mL) was allowed to stir at 0 °C for 15 min, after which benzyl bromide (2.1 mL, 17.56 mmol, 4 eq.) was added. After 3 hr at 0 °C, the reaction was quenched with NaHCO<sub>3</sub> and diluted with EtOAc for extraction. The organic layer was subsequently washed with brine and dried over MgSO<sub>4</sub>. The crude product was purified by silica gel chromatography (30% ethyl acetate in hexanes) to obtain the desired product in 55% yield as an off-white solid (770 mg).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** δ 7.26 (m, 5H), 6.79 (d, *J* = 8.6 Hz, 1H), 6.56 (d, 2.5 Hz, 1H), 6.45 (dd, *J* = 8.5 Hz, 2.5 Hz, 1H), 4.84 (s, 2H), 4.25 (s, 4H), 3.90 (s, 2H).

**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 166.4, 144.0, 143.9, 136.7, 134.0, 129.0, 128.5, 127.7, 121.31, 118.0, 117.1, 64.3, 53.8, 42.2.

**HRMS (+ESI):** Calculated: 318.0891 (C<sub>17</sub>H<sub>17</sub>ClNO<sub>3</sub>). Observed: 318.0898.



### **2-Chloro-N-(5,6,7,8-tetrahydronaphthalen-2-yl)acetamide (JNS 1-37)**

Following **General Procedure B** starting from 1,2,3,4-tetrahydronaphthalen-2-amine (1.472 g, 10.0 mmol) product was obtained after silica gel chromatography (30% ethyl acetate in hexanes) in 98% yield as an off-white solid (2.2 g).

**<sup>1</sup>H NMR (400MHz, CDCl<sub>3</sub>):** δ 8.17 (s, 1H), 7.23 (m, 2H), 7.03 (d, *J* = 8.1 Hz, 1H), 4.12



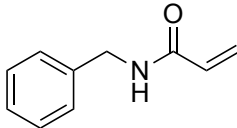
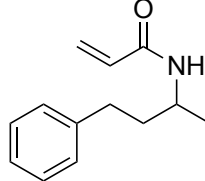
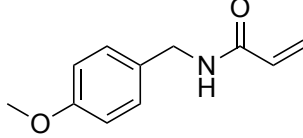
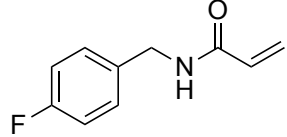
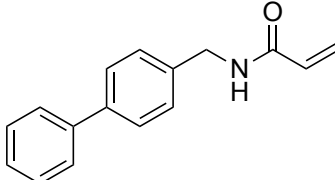
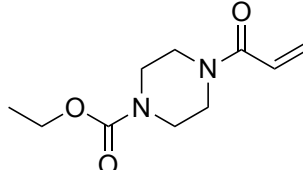
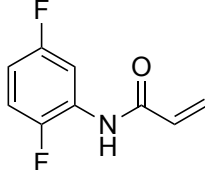
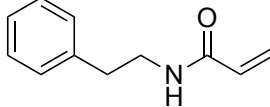
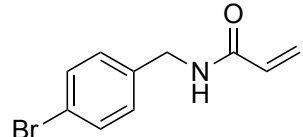
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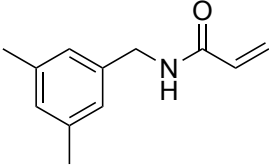
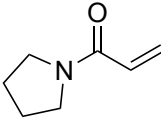
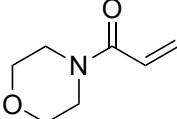
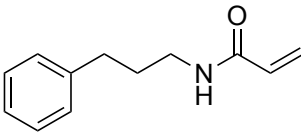
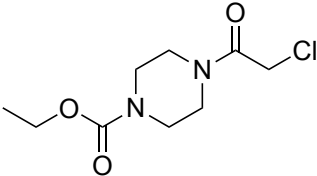
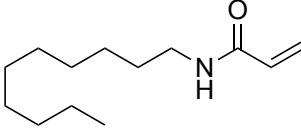
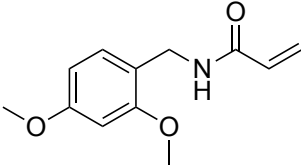
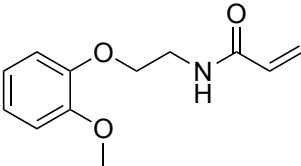
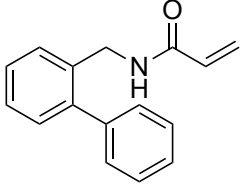
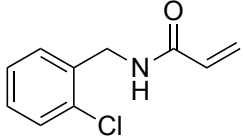
**<sup>13</sup>C NMR (100MHz, CDCl<sub>3</sub>):** δ 170.9, 163.8, 137.8, 134.3, 134.0, 129.4, 120.6, 117.6, 60.2, 53.4, 42.9, 30.7, 29.4, 28.8, 23.0, 20.8, 14.1.

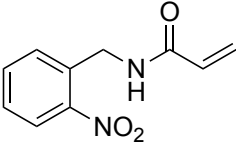
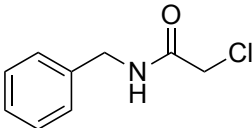
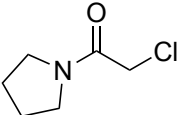
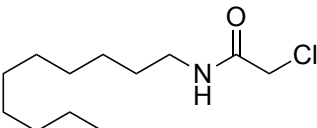
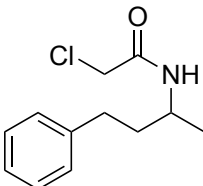
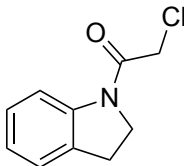
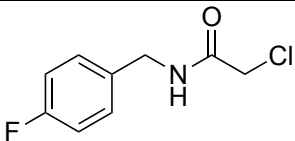
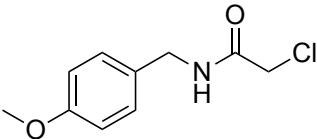
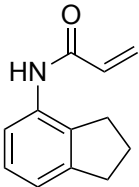
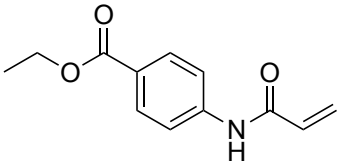
**HRMS (+ESI):** Calculated: 224.0837(C<sub>12</sub>H<sub>15</sub>ClNO). Observed: 224.0835.

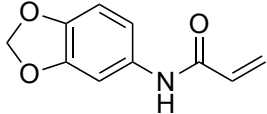
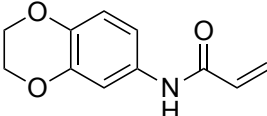
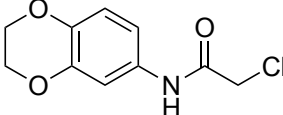
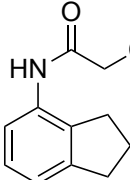
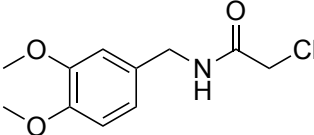
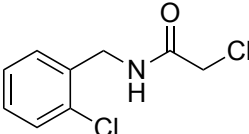
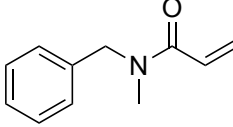
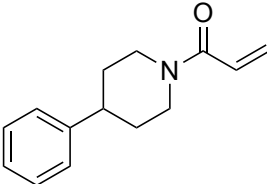
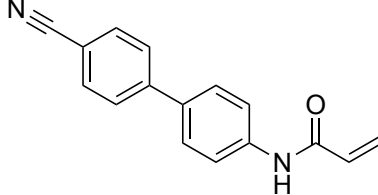
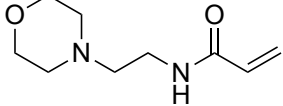
## Appendix 2

Structures of cysteine-reactive covalent ligand library screened in 231MFP cells as referenced in section 2.5.

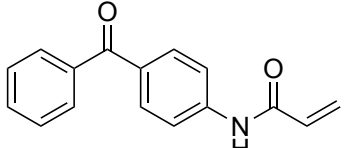
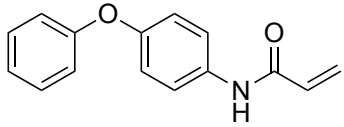
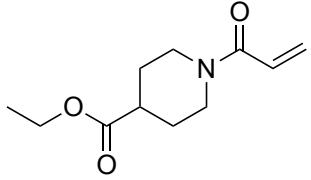
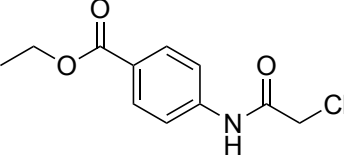
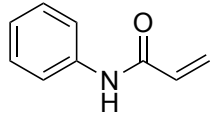
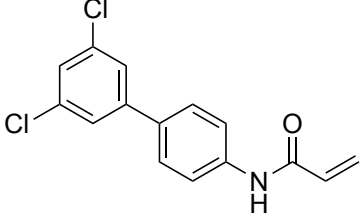
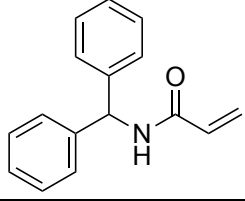
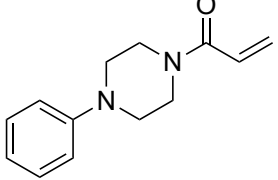
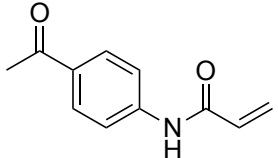
Compound name	Compound structure
DKM 2-31	
DKM 2-32	
DKM 2-33	
DKM 2-34	
DKM 2-37	
DKM 2-39	
DKM 2-40	
DKM 2-42	
DKM 2-43	

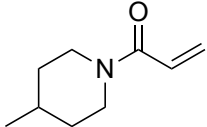
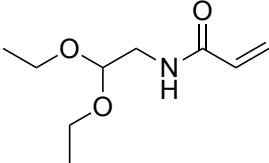
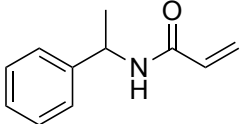
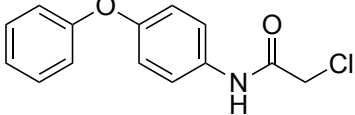
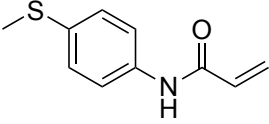
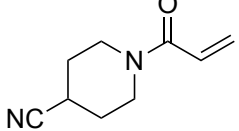
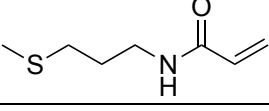
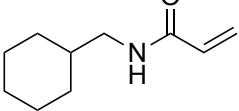
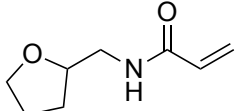
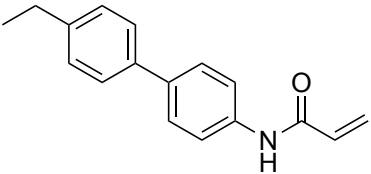
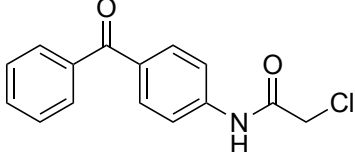
DKM 2-47	
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DKM 2-49	
DKM 2-50	
DKM 2-52	
TRH 1-12	
TRH 1-13	
DKM 2-58	
DKM 2-59	
DKM 2-60	

DKM 2-62	
DKM 2-67	
DKM 2-71	
DKM 2-72	
DKM 2-76	
DKM 2-79	
DKM 2-80	
DKM 2-83	
DKM 2-84	
DKM 2-85	

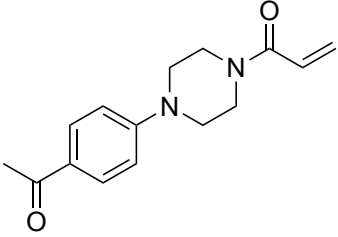
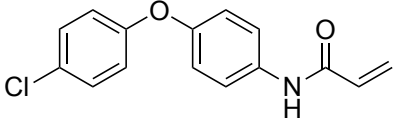
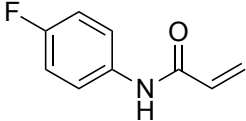
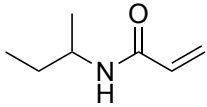
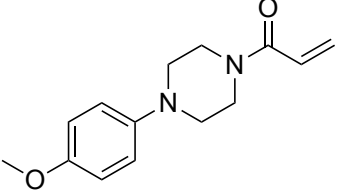
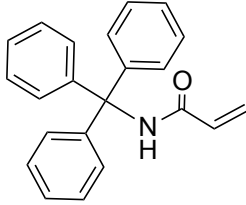
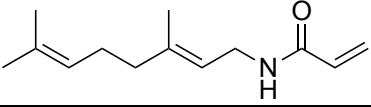
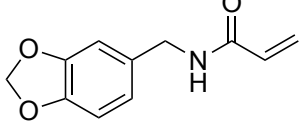
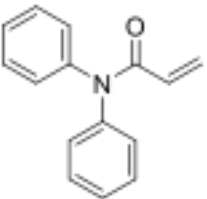
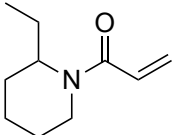
DKM 2-86	
DKM 2-87	
DKM 2-90	
DKM 2-91	
DKM 2-93	
DKM 2-94	
DKM 2-95	 (Two rotamers in equal amounts)
DKM 2-97	
DKM 2-98	
DKM 2-100	

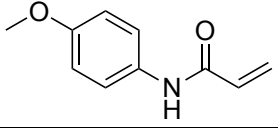
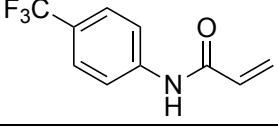
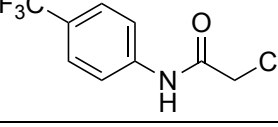
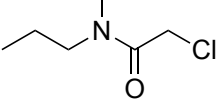
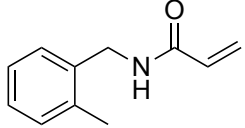
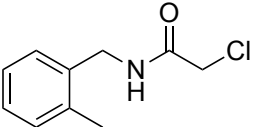
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DKM 2-109	
DKM 2-110	
DKM 2-111	
DKM 2-113	
DKM 2-114	
DKM 2-116	

DKM 2-117	
DKM 2-119	
DKM 2-120	
TRH 1-17	
TRH 1-19	
DKM 3-3	
DKM 3-4	
DKM 3-5	
DKM 3-7	

DKM 3-8	
DKM 3-9	
TRH 1-20	
TRH 1-23	
DKM 3-10	
DKM 3-11	
DKM 3-12	
DKM 3-13	
DKM 3-15	
DKM 3-16	
DKM 3-22	



DKM 3-29	
DKM 3-30	
DKM 3-31	
DKM 3-32	
DKM 3-36	
DKM 3-41	
DKM 3-42	
DKM 3-43	
DKM 3-70	
TRH 1-27	

TRH 1-32	
TRH 1-50	
TRH 1-51	
TRH 1-53	
TRH 1-54	
TRH 1-55	

### Appendix 3

IsoTOP-ABPP analysis of withaferin A and DKM 2-90 targets in 231MFP breast cancer proteomes. We mapped the cysteine-reactivity of withaferin A and DKM 2-90 by pre-incubating withaferin A (10  $\mu$ M) or DKM 2-90 (100  $\mu$ M) for 30 min in 231MFP breast cancer cell proteomes, prior to labeling with the cysteine-reactive iodoacetamide-alkyne (IAyne) probe (100  $\mu$ M, 30 min). Probe labeled proteins were then tagged with an isotopically light (for control) or heavy (for withaferin A- or DKM 2-90-treated) biotin-azide tag bearing a TEV protease recognition site by copper-catalyzed azide-alkyne cycloaddition. Control and treated proteomes were then mixed in a 1:1 ratio, probe labeled proteins were avidin-enriched and tryptically digested, probe-labeled tryptic peptides were avidin-enriched again, and released by TEV protease and analyzed by quantitative proteomic methods and light to heavy peptide ratios were quantified.

Competitive isoTOP-ABPP analysis of withaferin A and DKM 2-90 cysteine-reactivity in 231MFP breast cancer cell proteomes. Light to heavy ratios of  $\sim$ 1 indicate peptides that were labeled by IAyne, but not bound by withaferin A or DKM 2-90. We designate light to heavy ratios of  $>10$  as targets that were bound by withaferin A or DKM 2-90. Tabs 1 and 3 shows average light versus heavy ratios from those probe-modified peptides found in at least 2 out of 3 biological replicates.

Tables A1-A7. IsoTOP-ABPP analysis of withaferin A (10  $\mu$ M), DKM 2-90 (100  $\mu$ M), JNS 1-40 (100  $\mu$ M) treatment in vitro in 231MFP proteomes or in situ in 231MFP cells, or 231MFP tumors from JNS 1-40 daily in vivo treatment in mice. For in vitro experiments, DMSO or compounds were pre-treated for 30 min prior to labeling with IAyne. For in situ experiments, cells were treated with DMSO or compounds for 4 hours and cell proteomes were subsequently labeled with IAyne. For in vivo study in Table A7, tumors were taken from the study shown in Fig. 2.7G.

**Table A3.1**IsoTOP-ABPP analysis of withaferin A (10  $\mu$ M) in vitro in 231MFP proteomes.

Peptide	Modified residue	Average area ratio	Uniprot ID	Protein
DNTIEHLLPLFLAQLKDEC*PEVR	C377	8.457838102	P30153	P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
GQIIC*NLGDNLGSDLPNTLQIFLER	C598	4.860106203	Q86VP6	Q86VP6 Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 #
AVQDLC*GWR	C428	4.781393219	Q9P258	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 #
EMQNLSFQDC*YSSK	C111	4.647784856	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
TIIP LISQC*TPK	C212;C105	4.33049671	P40926 G3XAL0	P40926 Malate dehydrogenase# mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 # G3XAL0 Malate dehydrogenase OS=Homo sapiens GN=MDH2 PE=1 SV=1 #
C*LLIHPNPESALNEEAGR	C118;C147	3.921239818	Q16763 K7EPJ1	Q16763 Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=2 # K7EPJ1 Ubiquitin-conjugating enzyme E2 S (Fragment) OS=Homo sapiens GN=UBE2S PE=1 SV=1 #
IIP TLEEGLQLPSPTATSQLPLESDAVEC*LNYQHVK	C132;C132	3.777590173	P61978 P61978	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK #
QHC*AYTIAK	C166	3.74843352	Q6YN16	Q6YN16 Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 #
YLAEVAC*GDDR	C134	3.702387295	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #
HVGQAGVQMGNAC*WELYCLEHGIQPDGQMPSDK	C20	3.678285	P68366	P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
ITWDELAASGLPSC*DAAVNL AGENILNPLR	C52;C78	3.47581	Q9NRG7 Q9NRG7	Q9NRG7-2 Isoform 2 of Epimerase family protein SDR39U1 OS=Homo sapiens GN=SDR39U1 # Q9NRG7 Epimerase family protein SDR39U1 OS=Homo sapiens GN=SDR39U1 PE=1 SV=2 #
YSNSALGHVNC*TIK	C282;C1101;C301	3.412980828	Q9NQC3 Q9NQC3 Q9NQC3	Q9NQC3-2 Isoform 2 of Reticulon-4 OS=Homo sapiens GN=RTN4 # Q9NQC3 Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2 # Q9NQC3-5 Isoform 5 of Reticulon-4 OS=Homo sapiens GN=RTN4 #
NMITGTSQADC*AVLIVAAGV GEFEAGISK	C111;C111	3.315065841	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
IISDNLYC*K	C205	3.113861612	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #
TFVPAMTAIHGPPITAPVVC*TR	C620;M646 C660;M580 C549;M606 C594	3.023916154	Q96RN5 Q96RN5 Q96RN5 G3V1P5	Q96RN5-3 Isoform 3 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 # Q96RN5-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 # Q96RN5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=2 # G3V1P5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=1 #

VVTAGAIIPFLAPGQSLPDSL MQFGGATPWTPLSAC*GEPS GTR	C403;M354 C368 C403;M389	2.984595	Q9BUK6 Q9BUK6 Q9BUK6 Q9BUK6	Q9BUK6 Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 PE=1 SV=1 # Q9BUK6-2 Isoform 2 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 # Q9BUK6-3 Isoform 3 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 # Q9BUK6-7 Isoform 7 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 # G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 # I3L139 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=1 # Q9HA64 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 # P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 # P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 # P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 # E9PCY7 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # F8WBS6 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=1 # O43175 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 # Q5SZU1 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 # O00233-2 Isoform p27-S of 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 # O00233 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 # J3KN29 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H7X1 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H5V4 26S proteasome non-ATPase regulatory subunit 9 (Fragment) OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5GX23 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # Q00325-2 Isoform B of Phosphate carrier protein# mitochondrial OS=Homo sapiens GN=SLC25A3 #
C*LHNFLTDGVP AEGAFTEDF QGLR	C316;C268	2.937845873	G3V1A6 P57764	
QIPAITC*IQSQWR	C781	2.914757047	P46940	
ATGHSGGGC*ISQGR	C24;C24	2.886311523	I3L139 Q9HA64	
EAVFPFQPGSVAEVC*ITFDQ ANLTVK	C89	2.847177483	P09382	
EIEQKYDC*GEEILITVLSAMT EEAAVAIK	C159;C129	2.776138173	P63241 P63241	
DLNYC*FSGMSDHR	C267	2.773661832	P31943 G8JLB6 P55795 E9PCY7	
C*PEALFQPSFLGMESCGIHE TTFNSIMK	C257	2.695232205	P60709	
LAEQC*GGLQGFLIFRSFGGG TGSGFTSLLMER	C96	2.628856873	A6NHL2 A6NHL2	
ISDTGSAGLMLVEFFAPC*SIP AGFE	C56	2.54503	F8WBS6	
NAGNC*LSPAVIVGLLK	C369;C335	2.516485807	O43175 Q5SZU1	
GIGMNEPLVDC*EGYPR	C59;M52 C59	2.465708333	O00233 O00233 J3KN29 F5H7X1 F5H5V4 F5GX23	
AVEEYSC*EFGSAK	C56	2.335794004	Q00325	

FVVDVDKNIDINDVTPNC*R	C112;C104	2.320345	P62195 P62195	P62195 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 # P62195-2 Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 #
VVFIKPTC*PYCR	C23	2.265212	P35754	P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 # O15446-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP # O15446 DNA- directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP PE=1 SV=1 #
FC*AFGGNPPVTGPR	C152;C150	2.18712	O15446 O15446	O15446-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP # O15446 DNA- directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP PE=1 SV=1 #
IC*DQWDALGSLTHSR	C499	2.145285977	O43707	O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # C9J8E1 MAP kinase-activated protein kinase 3 (Fragment) OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 # Q16644 MAP kinase-activated protein kinase 3 OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 #
KETTQNALQTPC*YTPYYVAP EVLGPEK	C203;C203	2.091076667	C9J8E1 Q16644	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B # Q12923-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-4 Isoform 4 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-3 Isoform 3 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923 Tyrosine- protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2 #
SLC*NLEESITSAGRDDLESF QLEISGFLK	C63;C63	2.068788271	Q52LJ0 Q52LJ0	Q12923-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-4 Isoform 4 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-3 Isoform 3 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923 Tyrosine- protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2 #
KSQTGILLGVC*SK	C798;C798;C79 8;C798	2.036276412	Q12923 Q12923 Q12923 Q12923	Q12923-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-4 Isoform 4 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-3 Isoform 3 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923 Tyrosine- protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2 #
EC*ISHVGGQAGVQIGNACWE LYCLEHGIQPDGQMPSDK	C4;C4;C4;C74;C 4	2.023105	Q13748 P68363 Q9BQE3 F5H5D3 Q71U36	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P36776-3 Isoform 3 of Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 # K7EKE6 Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=1 # P36776 Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 # P36776-2 Isoform 2 of Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 # K7EJE8 Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=1 #
ILC*FYGPPGVGK	C324;C406;C52 0;C456;C390	2.02052579	P36776 K7EKE6 P36776 P36776 K7EJE8	P36776-3 Isoform 3 of Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 # K7EKE6 Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=1 # P36776 Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 # P36776-2 Isoform 2 of Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 # K7EJE8 Lon protease homolog# mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=1 #
VAC*IGAWHPAR	C253	2.01685	P39023	P39023 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 # Q9P2J5-2 Isoform 2 of Leucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=LARS # Q9P2J5 Leucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 # P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #
NFEATLGWLQEAC*SR	C519;C573	2.015873234	Q9P2J5 Q9P2J5	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #
GLGTDEDSLIEIC*SR	C151;C133	2.013363592	P07355 P07355	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #
VIEINPYLLGTMAGGAADC*S FWER	C111	1.98632	P28074	P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #

SNIIIFC*DEVMLLLENLGNVHR	C689	1.985565	Q14974 Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
ASC*LYGQLPK	C48	1.972258419	P09211	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 #
IYFGSNIPNMFVDSSC*ALK	C310	1.955515608	O75477	O75477 Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 #
WGTIMEVENTHC*EFAYLR	C367;C524;C419;C512;C531;C280;C513;C307	1.949429706	Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8	Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-8 Isoform 8 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-4 Isoform 4 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-9 Isoform 9 of Septin-9 OS=Homo sapiens GN=SEPT9 #
YDLLFMPPSFPFGGMENPCLTFVTPC*LLAGDR	C311	1.90667	Q9H4A4	Q9H4A4 Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 #
LQHINPLLPAC*LNK	C325;C152;C325	1.901935	Q9BTE3 Q9BTE3 Q9BTE3	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 # Q9BTE3-3 Isoform 3 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP # Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP #
GVLFVPGAFTPGC*SK	C100;C48;C100	1.896698259	P30044 P30044 P30044	P30044 Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 # P30044-2 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 # P30044-3 Isoform 3 of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 #
ILATGANVILTTGGIDDMC*LK	C296 C296;M295	1.896565	E7ERF2 P17987	E7ERF2 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
VEYPIMYSTDPENGHIFNC*IQ R	C56 C70;M43 C56;M57	1.887503535	Q5VV87 Q5VV89 O14880	Q5VV87 Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1 # Q5VV89 Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1 # O14880 Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1 #
HPLTQELKEC*EGIVPVPLAE K	C105	1.884917435	P82932	P82932 28S ribosomal protein S6# mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 #
YSDVEVPASVTGYSFASDGD SGTC*SPLR	C430;C430;C136;C430;C430;C430;C430;C430;C430	1.880581412	P35611 P35611 H0Y9H2 P35611 E7ENY0 P35611 E7EV99 P35611 P35611	P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-5 Isoform 5 of Alpha-adducin OS=Homo sapiens GN=ADD1 # H0Y9H2 Alpha-adducin (Fragment) OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 # E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 # E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 #

					Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EUV4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # H3BVG0 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=1 # Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 # Q8N1F7-2 Isoform 2 of Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 # H3BPA9 Nuclear pore complex protein Nup93 (Fragment) OS=Homo sapiens GN=NUP93 PE=1 SV=7 # P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 # A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G # Q709C8-3 Isoform 3 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C # Q709C8-4 Isoform 4 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C # Q709C8 Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1 # Q709C8-2 Isoform 2 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C # P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 #
LQGINC*GPDFTPSFANLGR	C662;C622;C575;C662;C575;C466;C622;C498;C669;C498;C466	1.872296622	Q04637 Q04637 E9PGM1 Q04637 Q04637 E7EUV4 Q04637 Q04637 E7EX73 Q04637		
LNQVC*FDDDDGTSSPQDR	C422;C422;C299;C215	1.867201022	H3BVG0 Q8N1F7 Q8N1F7 H3BPA9		
ENFDEVVNDADIILVEFYAPWCGHC*KK	C209	1.840875	P13667		
QYPWGVAEVENGEHC*DFTILR	C279;C280;C280;C260	1.828383647	Q16181 Q16181 E7EPK1 E7ES33		
AVASQLDC*NFLK	C207;C193	1.821501745	A0A087X2I1 P62333		
WFLTC*INQPQFR	C194;C244	1.819321717	P26641 P26641		
LDC*NIEIQNIAIELTKPQYLSMIDLLESVDYMVRR	C279	1.817489806	Q709C8 Q709C8 Q709C8 Q709C8		
NC*GC*LGASPNLEQLQEENLK	C34 C32	1.804730896	P54136		



NFNYHILSPC*DLSNYTDLAM STVK	C461	1.802415249	G5E9W3 Q9UKF6	G5E9W3 Cleavage and polyadenylation specific factor 3# 73kDa# isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # J3QR12 Tether-containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 # J3QL04 Tether-containing UBX domain for GLUT4 (Fragment) OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 # Q9BZE9-2 Isoform 2 of Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 # Q9BZE9-4 Isoform 4 of Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 # J3KRG1 Tether-containing UBX domain for GLUT4 (Fragment) OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 # Q9BZE9-3 Isoform 3 of Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 # Q9BZE9 Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 # J3QRW3 Tether-containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 # F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 # C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 # P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 # P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # Q15398-1 Isoform 2 of Disks large-associated protein 5 OS=Homo sapiens GN=DLGAP5 # G3V4E5 Disks large-associated protein 5 (Fragment) OS=Homo sapiens GN=DLGAP5 PE=1 SV=1 # Q15398-3 Isoform 3 of Disks large-associated protein 5 OS=Homo sapiens GN=DLGAP5 # Q15398 Disks large-associated protein 5 OS=Homo sapiens GN=DLGAP5 PE=1 SV=2 #
LQDSFC*SGQTLWELLSHFP QIR	C32;C106;C109; C32;C90;C32;C109;C109	1.769451603	J3QR12 J3QL04 Q9BZE9 Q9BZE9 J3KRG1 Q9BZE9 Q9BZE9 J3QRW3	
IIPGFMC*QGGDFTR	C62 C62;M61	1.765198643	F8WE65 C9J5S7 P62937	
CPEALFQPSFLGMESC*GIHE TTFNSIMK	C272;C272	1.763953676	P63261 P60709	
YRPDMPC*FLLSNQNAVK	C48;C129;C129; C129	1.756617231	Q15398 G3V4E5 Q15398 Q15398	

VFAEC*NDESFWFR	C38;C38;C38;C38; C38;C38;C38; C38;C38;C38;C38; 8	1.755145	D6R918 Q9NX40 D6RIT9 D6RG39 D6RBC5 D6RA54 Q9NX40 Q9NX40 D6RC55 Q9NX40 D6RDI5	D6R918 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIA1 PE=1 SV=1 # Q9NX40-2 Isoform 2 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIA1 # D6RIT9 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIA1 PE=1 SV=1 # D6RG39 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIA1 PE=1 SV=1 # D6RBC5 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIA1 PE=1 SV=1 # D6RA54 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIA1 PE=1 SV=1 # Q9NX40-4 Isoform 4 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIA1 # Q9NX40 OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIA1 PE=1 SV=1 # D6RC55 OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIA1 PE=1 SV=1 # Q9NX40-3 Isoform 3 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIA1 # D6RDI5 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIA1 PE=1 SV=1 #
FMC*AQLPNPVLDSISIIDTPGI LSGEK	C152;M137 C138;M151 C152	1.727661474	A0A024R5 71 Q9H4M9 C9JC03	A0A024R571 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=1 # Q9H4M9 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 # C9JC03 EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=1 SV=1 #
VLPMNTGVEAGETAC*K	C150	1.721658021	P04181	P04181 Ornithine aminotransferase# mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 #
SSPGLSDTIFC*R	C27	1.696895479	Q9H8M7	Q9H8M7 Protein FAM188A OS=Homo sapiens GN=FAM188A PE=1 SV=1 #
AFAFVTFADDQIAQSLC*GED LIIK	C244;C244;C244; 4;C244;C244	1.655685432	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
DGTVLC*ELINALYPEGQAPV KK	C63;C84;C63	1.644001427	P37802 P37802 X6RJP6	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
NDITAWQEC*VNN SMAQLEH QAVR	C106	1.63093928	O75934	O75934 Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 #
IC*DQWDNLGALTQK	C480;C480;C480; 0;C480	1.628433575	P12814 P12814 P12814 P12814	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-3 Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-4 Isoform 4 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 #
VLSSSGSEAAVPSVC*FLVPP PNQEAQEA VTR	C992	1.627936667	Q15149	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 #

LMAVTEYIPPKPAIHPSC*LPS PPSPQEEIGLIR	C64;C74	1.618975	Q7Z7H8 Q7Z7H8	Q7Z7H8 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 # Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 #
SC*NGPVLVGSPQGGVDIEE VAASNPELIFK	C162;C162;C54; C162	1.618443353	Q96I99 E9PDQ8 H0Y852 Q96I99	Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # H0Y852 Succinyl- CoA ligase [GDP-forming] subunit beta# mitochondrial (Fragment) OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
AVC*MLSNTTAAIEAWAR	C376;C310;C40 0;C376;C376;C3 76	1.615200961	P68363 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9NY65- 2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
NEC*DPALALLSDYVLHNSNT MR	C459	1.606066	Q13200	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 #
LALFNPDVC*WDR	C44	1.602485874	O00483	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 #
GLC*AIAQAESLR	C97	1.600606106	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #
VQPQWSPAGTQPC*R	C27;C40;C27;C1 10	1.600571876	P49589 B4DKY1 P49589 P49589	P49589-2 Isoform 2 of Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS # B4DKY1 Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=1 # P49589 Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=3 # P49589-3 Isoform 3 of Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS #
LNLSC*IHSPVVNELMR	C106	1.595753333	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #
VQYPQSQAC*K	C633	1.590738889	Q14204	Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 #
GISC*MNTTLESSEPFK	C242	1.588687099	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 #
SGQGAFGNMC*R	C96	1.585439266	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
LYYFQYPC*YQEGLR	C130	1.580209227	Q9NRW3	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 #
GVLMYGPPGC*GK	C179;C210	1.573175496	P43686 P43686	P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 #
HGFC*GIPITDTGR	C140	1.571034989	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
TVEIC*PFSFDSR	C572;C536	1.542985491	Q9ULW0 Q9ULW0	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 # Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 #

SPVPLTPPGC*VALDTR	C173;C198	1.542198937	Q567V2 Q567V2	Q567V2-2 Isoform 2 of Mpv17-like protein 2 OS=Homo sapiens GN=MPV17L2 # Q567V2 Mpv17-like protein 2 OS=Homo sapiens GN=MPV17L2 PE=1 SV=2 #
C*PIQLNEGVSFQDLDTAK	C179	1.538069561	A6NDU8	A6NDU8 UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 # P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
VFIMDNC*EELIPEYLNfir	C496;M371 C374	1.527595437	P07900 P07900	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 # P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 # Q8N9T8 Protein KRI1 homolog OS=Homo sapiens GN=KRI1 PE=1 SV=3 # P68133 Actin# alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 # P68032 Actin# alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 # D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # P51665 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2 # Q56VL3 OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 # Q56VL3-2 Isoform 2 of OCIA domain- containing protein 2 OS=Homo sapiens GN=OCIAD2 # J3KPI9 OCIA domain- containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 # D6RD77 OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 # F5H6Q1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # F5H3F0 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # J3KR44 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 # Q96FW1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 # O60610-3 Isoform 3 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # O60610-2 Isoform 2 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # A0A140T8Z0 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # A0A0G2JH68 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # H9KV28 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 # O60610 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 # P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
SLHDALC*VLAQTVK	C395	1.52675852	P78371	
SYIEGYVPSQADVAVFEAVSS PPPADLC*HALR	C50	1.514358381	P24534	
LLGPTVMLGGC*EFSR	C667	1.51311	Q8N9T8	
LC*YVALDFENEMATAASSSS LEK	C219	1.50772047	P68133 P68032	
WC*NVQSTQDEFEELTMSQK	C59	1.507520686	D6RCP9 P27707 D6RFG8	
YC*PNSVLVIIDVKPK	C116	1.505275	P51665	
QSLLC*PK	C27;C27;C27;C2 7	1.50335217	Q56VL3 Q56VL3 J3KPI9 D6RD77	
QEPLGSDSEGVNC*LAYDEAI MAQQDR	C23	1.497422937	F5H6Q1 F5H3F0 J3KR44 Q96FW1	
AGC*AVTSLASELTK	C1218;C1203;C 1218;C1227;C11 83;C1227	1.491256706	O60610 O60610 A0A140T8 Z0 A0A0G2J H68 H9KV28 O60610	
KC*STPEEIK	C6;C23	1.4907915	P60981 P60981	

LHDAIVEVVC*LLR	C483;C470;C470; 0;C470;C470;C483; 83;C483;C470	1.483306593	O00429 O00429 O00429 O00429 O00429 G8JLD5 O00429	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 # O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 # O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L #
VGVDYEGGGC*R	C727;C680	1.481087104	Q02809 Q02809	Q02809-2 Isoform 2 of Procollagen-lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 # Q02809 Procollagen-lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 # Q9NZD2 Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=3 # F5GZ49 Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=1 # F5H0U5 Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=1 #
QIETGPFLEAVSHLPPFFDC*L GSPVFTPIK	C36;C36;C36	1.47934	Q9NZD2 F5GZ49 F5H0U5	Q9NZD2 Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=3 # F5GZ49 Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=1 # F5H0U5 Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=1 #
GIDQC*IPLFVEAALER	C757	1.462965917	O95373	O95373 Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 #
ELDSLNNC*LG DAGILQLVES VR	C409	1.459878147	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
YIYDQC*PAVAGYGPIEQLPD YNR	C453	1.454328725	P31930	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 #
SC*SGVEFSTSGSSNTDTGK VTGTLETK	C47;C47	1.438875183	Q5JSD2 P45880	Q5JSD2 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=7 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
GEAYNLFEHNC*NTFSNEVA QFLTGR	C108	1.43744818	Q6ICB0	Q6ICB0 Desumoylating isopeptidase 1 OS=Homo sapiens GN=DESI1 PE=1 SV=1 #
C*MQLTDFILK	C54	1.425380746	E7EPB3 P50914	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 #
LTALDYHNPAGFNC*KDETEF R	C19	1.417926445	Q9Y224	Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 #
QNSDFLC*QMDLLQEFYETTL EALKDAK	C130	1.41548954	P61201	P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 #
HELQANC*YEEVKDR	C177;C122;C139	1.413830353	E9PK25 G3V1A4 P23528	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 #
LC*PLKDEPWPPIHPWEPGSF R	C105;C93;C78;C78	1.412257588	E7ETU7 H0Y9G6 E9PF06 P09001	E7ETU7 39S ribosomal protein L3# mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # H0Y9G6 39S ribosomal protein L3# mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # E9PF06 39S ribosomal protein L3# mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # P09001 39S ribosomal protein L3# mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 #

HC*SQVDSVR	C112;C112;C112	1.411954431	Q14247 Q14247 Q14247	Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN # Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 # Q14247-2 Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN #
YAYLNVVGMVGSIDNDFC*GT DMTIGTDSALHR	C179	1.411532821	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
SSSSSSASAAAAAASSSA SC*SR	C100	1.411454959	Q07065	Q07065 Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 #
LC*PNSTGAEIR	C377	1.4045	P35998	P35998 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 #
TTC*SSGSALGPGAGAAQPS ASPLEGLLDLSYPR	C12;C12;C12	1.400136224	Q96FZ5 F8WDZ3 Q96FZ5	Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=2 SV=1 # F8WDZ3 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 # Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 #
YLEC*SALTQR	C157;C157;C176	1.396367915	P60763 P63000 P63000	P60763 Ras-related C3 botulinum toxin substrate 3 OS=Homo sapiens GN=RAC3 PE=1 SV=1 # P63000 Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1 # P63000-2 Isoform B of Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 #
C*VYTYIQEFYR	C415;C288;C948;C892	1.395647392	B5MCI0 A0A096LNK9 K9 A0A087WVP4 P53814	B5MCI0 Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=1 # A0A096LNK9 Smoothelin (Fragment) OS=Homo sapiens GN=SMTN PE=1 SV=1 # A0A087WVP4 Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=1 # P53814-5 Isoform B2 of Smoothelin OS=Homo sapiens GN=SMTN #
VLDALFPCVQGGTTAIPGAFG C*GK	C221;C254	1.395525363	P38606 P38606	P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A # P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 #
LNCQVIGASVDSHFC*HLAWV NTPK	C83;C83	1.392437476	Q06830 A0A0A0MSI0 SI0	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 # A0A0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 #
VGSFC*LSEAGAGSDFSALK	C73;C175	1.392359639	P45954 P45954	P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB # P45954 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 #
VVVAENFDEIVNENKDVLI FYAPWC*GHCK	C406	1.388010772	P30101	P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 #
KGAGNPQASTLALQSNITQC* LLGQPWPLNEAQVQASVVK	C1298;C1221;C1260;C1334;C1298;C1222;C1299;C1261;C1260	1.386301144	E7ETY2 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 J3KQ96	E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 # Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-6 Isoform 6 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 # Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 # J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 #

QYPWGVVQVENENHC*DFVK	C260;C293;C293;C293;C268;C293;C278;C270;C278;C268;C268	1.383069602	D6RDU5 Q9P0V9 Q9P0V9 E7EW69 D6RGI3 B5ME97 Q9NVA2 Q9P0V9 E7EX04 Q9NVA2 D6RER5	D6RDU5 Septin-11 (Fragment) OS=Homo sapiens GN=SEPT11 PE=1 SV=1 # Q9P0V9-2 Isoform 2 of Septin-10 OS=Homo sapiens GN=SEPT10 # Q9P0V9 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EW69 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 # D6RGI3 Septin 11# isoform CRA_b OS=Homo sapiens GN=SEPT11 PE=1 SV=1 # B5ME97 Septin 10# isoform CRA_c OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # Q9NVA2-2 Isoform 2 of Septin-11 OS=Homo sapiens GN=SEPT11 # Q9P0V9-3 Isoform 3 of Septin-10 OS=Homo sapiens GN=SEPT10 # E7EX04 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 # Q9NVA2 Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 # D6RER5 Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=1 #
MC*LFAGFQR	C575 C594;M574	1.383066341	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
NAFAC*FDEEATGTIQEDYLR	C108;C114;C109	1.382301159	P19105 J3QRS3 O14950	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 # J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 # O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 #
LGTDESC*FNMILATR	C363;C341	1.380726374	P20073 P20073	P20073 Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 # P20073-2 Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7 #
APPTAC*YAGAAPAPSQVK	C248;C50;C225	1.377742273	P17676 P17676 P17676	P17676 CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB PE=1 SV=2 # P17676-3 Isoform 3 of CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB # P17676-2 Isoform 2 of CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB #
FTSC*VAFFNILNELNDYAGQR	C69;C69;C69;C69;C69;C69	1.375379243	Q5T0N5 S4R347 Q5T0N5 Q5T0N5 Q5T0N5 Q5T0N5	Q5T0N5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=1 # Q5T0N5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=3 # Q5T0N5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L #
KAQC*PIVER	C66;C87;C66	1.374996055	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
NTLANSC*GTGIR	C393;C416	1.372126201	Q96BF6 Q96RE7	Q96BF6 Nucleus accumbens-associated protein 2 OS=Homo sapiens GN=NACC2 PE=1 SV=1 # Q96RE7 Nucleus accumbens-associated protein 1 OS=Homo sapiens GN=NACC1 PE=1 SV=1 #
VNSDC*DSVLPSNFFLLGGNIFDPLNLNLSLLDDEEVS	C177	1.37174	Q7L2J0	Q7L2J0 7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1 #

LQFHDVAGDIFHQQC*K	C415;C385;C43 1	1.370637189	P11413 P11413 P11413	P11413-3 Isoform 3 of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD # P11413 Glucose-6-phosphate 1- dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 # P11413-2 Isoform Long of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 # P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 # Q02338 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 # E9PCG9 D- beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=1 # Q9BXJ9 N-alpha-acetyltransferase 15# NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 # P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 # P60604-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 # P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 # Q9Y2Q3-3 Isoform 3 of Glutathione S- transferase kappa 1 OS=Homo sapiens GN=GSTK1 # Q9Y2Q3 Glutathione S- transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3 # Q9Y2Q3-4 Isoform 4 of Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 # Q9Y2Q3-2 Isoform 2 of Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 # E9PEX6 Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=1 SV=1 # P09622 Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 # P09622-2 Isoform 2 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD # P09622-3 Isoform 3 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD # O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 # E2QRB3 Pyrroline-5-carboxylate reductase 1# isoform CRA_c OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322 Pyrroline- 5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # Q96C36 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 #
IMDSC*DELIPEYLNfir	C366	1.368775527	P08238	
AAVEEGIVLGGGC*ALLR	C442	1.36568507	P10809	
METYC*SSGSTDTSPVIDAVT HALTATTPYTR	C201 C288;M197	1.365028547	Q02338 E9PCG9	
LFNTAVC*ESK	C721	1.35810659	Q9BXJ9	
C*PFTGNVSIR	C60	1.35659822	P62280	
VC*ISILHAPGDDPMGYESSA ER	C61;C89	1.349257832	P60604 P60604	
ETTEAAC*R	C164;C176;C13 3;C232	1.344690531	Q9Y2Q3 Q9Y2Q3 Q9Y2Q3 Q9Y2Q3	
VLGAHILGPGAGEMVNEAAL ALEYGASC*EDIAR	C454;C477;C37 8;C429	1.337608413	E9PEX6 P09622 P09622 P09622	
ATFHTPFSLGQSPEGC*SSY TFPK	C247;C252;C28 2	1.337079835	O75521 A0A0C4D GA2 O75521	
LLINAVEASC*IR	C231;C262;C26 2;C289;C262	1.335918119	E2QRB3 P32322 P32322 P32322 Q96C36	



AYHEQLSVAEITNAC*FEPAN QMVK	C280	1.335497777	P68366 P68363 Q71U36 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # Q9UJW0 Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1 # Q9UJW0-2 Isoform 2 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # Q9UJW0-3 Isoform 3 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 #
LLQPDFQPVC*ASQLYPR	C258;C201;C265	1.335072425	Q9UJW0 Q9UJW0 Q9UJW0	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
LMWLFGC*PLLLDDVAR	C66	1.334992828	O15067	P49411 Elongation factor Tu# mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 #
GEETPVIVGSALC*ALEGRDP ELGLK	C222	1.328916417	P49411	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-3 Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-4 Isoform 4 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 #
MVSDINNAWGC*LEQVEKGY EEWLLNEIR	C370;M360 C370	1.326274788	P12814 P12814 P12814 P12814	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 #
LTWHSC*PEDEAQ	C177	1.319138895	Q13185	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #
AGAIAPC*EVTVPAQNTGLGP EK	C119	1.318346505	P05388	O95197-3 Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3 #
SCSSSC*AVHDLIFWR	C46	1.317828893	O95197	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
AITIAGVPQSVTEC*VK	C158	1.315240605	Q15365	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # Q96RS6-2 Isoform 2 of NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 #
DSAQC*AAIAER	C376;C347	1.3146	Q96RS6 Q96RS6	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 # A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q15185-3 Isoform 3 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 #
VIEINPYLLGTMSGC*AADCQ YWER	C116;C120;C120	1.313267422	P28062 X5D2R7 P28062	P37235 Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3 # F5H4Z3 Proteasome inhibitor PI31 subunit (Fragment) OS=Homo sapiens GN=PSMF1 PE=1 SV=2 # Q5QPM7 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 # Q92530 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 #
LTFSC*LGGSDNFK	C44;C40;C40;C40	1.312746264	A0A087WYT3 Q15185 Q15185 Q15185	P52657 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 # A0A0B4J1Z5 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 #
LLQC*DPSSASQF	C185	1.309206636	P37235	
QPPWC*DPLGPFVVGEDLD PFGPR	C11;C185;C185	1.307057003	F5H4Z3 Q5QPM7 Q92530	
FC*DNVWTFVLNDVEFR	C68;C33	1.30566822	P52657 A0A0B4J1Z5	

LDNWLNELEYC*TR	C139;C110;C223;C86	1.301939785	Q9NP72 Q9NP72 H0Y6T8 A0A087X163	Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # H0Y6T8 Ras-related protein Rab-18 (Fragment) OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 #
FHADSVK	C25	1.301669312	Q9BW61	Q9BW61 DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1 #
ENFDEVNDADIILVEFYAPW C*GHCK	C206	1.298544207	P13667	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 #
AGIDGESIGNC*PFSQR	C191;C32;C32	1.290757004	Q9NZA1 Q9NZA1 Q9NZA1	Q9NZA1 Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3 # Q9NZA1-3 Isoform 3 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 # Q9NZA1-2 Isoform 1 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 #
C*EFQDAYVLLSEK	C237	1.285527027	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
VIIVQAC*R	C173;C258;C245;C328;C257;C258;C315;C202;C211	1.282448014	P51878 P49662 P51878 P51878 P51878 P49662 P51878 P49662 A0A087WZP8	P51878-3 Isoform 3 of Caspase-5 OS=Homo sapiens GN=CASP5 # P49662-4 Isoform 4 of Caspase-4 OS=Homo sapiens GN=CASP4 # P51878-6 Isoform 6 of Caspase-5 OS=Homo sapiens GN=CASP5 # P51878-5 Isoform 5 of Caspase-5 OS=Homo sapiens GN=CASP5 # P51878-2 Isoform 2 of Caspase-5 OS=Homo sapiens GN=CASP5 # P49662 Caspase-4 OS=Homo sapiens GN=CASP4 PE=1 SV=1 # P51878 Caspase-5 OS=Homo sapiens GN=CASP5 PE=1 SV=3 # P49662-2 Isoform 2 of Caspase-4 OS=Homo sapiens GN=CASP4 # A0A087WZP8 Caspase OS=Homo sapiens GN=CASP4 PE=1 SV=1 #
LEGDLTGPSVDVEVPDVELE C*PDAK	C2162	1.28088174	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
EMFPYEASTPTGISASC*R	C323;M348 C254 C363;M239	1.277802115	G5E972 P42167 P42167	G5E972 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 # P42167 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 # P42167-2 Isoform Gamma of Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO #
DCIGGC*SDLVSLQQSGELLT R	C83	1.275924646	P35754	P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
LC*DFGISGQLVDSIAK	C257;C246	1.271709269	P45985 P45985	P45985-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens GN=MAP2K4 # P45985 Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens GN=MAP2K4 PE=1 SV=1 #
AVC*MLSNTTAVAEAWAR	C376	1.271004195	Q9BQE3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
MGIGLGSENAAGPC*NWDEA DIGPWAK	C498 C498;M485 C516;M485	1.26972	Q9UNF1 Q5H909 Q9UNF1	Q9UNF1 Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2 # Q5H909 Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2 # Q9UNF1-2 Isoform 2 of Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 #
VTDGALVVVDCVSGVC*VQT ETVLR	C136	1.267042905	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
LGEVWGLC*K	C92	1.266381518	P25398	P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 #

STPYEC*GFDPMSPAR	C39	1.266288293	P03897	P03897 NADH-ubiquinone oxidoreductase chain 3 OS=Homo sapiens GN=MT-ND3 PE=1 SV=1 #
WLSDEC*TNAAVFNFLSR	C345;C350;C380	1.266109813	O75521 A0A0C4DGA2 O75521	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 #
CEHC*DCLQGFLTHSLGGG TGSGMGTLISK	C127	1.26388	Q9BUF5	Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
PMC*VESFSDYPPLGR	C411;C390	1.262232342	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
SYC*NDQSTGDIK	C106	1.259072267	P00492	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
LFTESC*SISPK	C68;C68;C68	1.258923355	C9JXQ7 Q9Y6I9 C9JHH5	C9JXQ7 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 # Q9Y6I9 Testis-expressed sequence 264 protein OS=Homo sapiens GN=TEX264 PE=1 SV=1 # C9JHH5 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 #
HYLDQLNHILGILGSPSQEDL NC*IINLK	C254	1.252136667	P28482	P28482 Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3 #
FLENTPSSLNIEDIEDLFLSLAQ YYC*SK	C283;C146;C283	1.251647238	Q9NUY8 E9PGE5 Q9NUY8	Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 # E9PGE5 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=1 # Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 #
HLNEIDL FHC*IDPNDSK	C62;C58;C58	1.248535177	A0A087WYT3 Q15185 Q15185	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 #
MVYSTC*SLNPIEDEAVIASLL EK	C85;M316 C321;M281 C286	1.247485334	Q08J23 Q08J23 Q08J23	Q08J23 tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 # Q08J23 tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 # Q08J23-2 Isoform 2 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 #
IAILTC*PFEPKPK	C232;C215;C253	1.246798483	E9PCA1 B7ZAR1 P48643	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 #
SQSPAASDC*SSSSSASLPS SGR	C179;C121	1.244518179	O95817 C9JFK9	O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 # C9JFK9 BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=1 SV=1 #
VVMALGDYMGASC*HACIGG TNVR	C131	1.244412162	P60842	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
PCSRAITPEC*VVGWSR	C242	1.243633425	Q96MC9	Q96MC9 Uncharacterized protein C1orf147 OS=Homo sapiens GN=C1orf147 PE=2 SV=2 #
VC*NFLASQVPPFSR	C214	1.242134074	Q99714	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 #

GISEFIVMAADAEPLEILHLPL LC*EDKNVPYVVR	C73 C77;M56	1.239985919	B1AHD1 P55769	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 # P68036 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 # P68036-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 # P68036-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 # Q9BRJ7 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # W4VSQ8 Nudix (Nucleoside diphosphate linked moiety X)-type motif 16-like 1# isoform CRA_b OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # K7EIN2 Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # Q9BRJ7-2 Isoform 2 of Protein syndesmos OS=Homo sapiens GN=NUDT16L1 # K7ENA3 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # Q9NS25 Sperm protein associated with the nucleus on the X chromosome B1 OS=Homo sapiens GN=SPANXB1 PE=2 SV=2 # Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 # Q01518 Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 # Q01518-2 Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 # P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 # Q14203-5 Isoform 5 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-4 Isoform 4 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-2 Isoform p135 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-6 Isoform 6 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-3 Isoform 3 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203 Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3 # E7EX90 Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=1 # P50991 T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 # O95273 Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 PE=1 SV=2 # O95273-3 Isoform 3 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 # O95273-2 Isoform 2 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 # O95273-4 Isoform 4 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 # H3BPR2 Nucleoside diphosphate kinase OS=Homo sapiens GN=NME3 PE=1 SV=1 # Q13232 Nucleoside diphosphate kinase 3 OS=Homo sapiens GN=NME3 PE=1 SV=2 #
GQVC*LPVISAENWKPATK	C86;C54;C144	1.239644193	P68036 P68036 P68036	
VLGLGLGC*LR	C88;C88;C75;C88;C88	1.234701416	Q9BRJ7 W4VSQ8 K7EIN2 Q9BRJ7 K7ENA3	
SVPC*ESNEANEANEANK	C16	1.232171805	Q9NS25	
FQLTDC*QIYEVLSVIR	C143;C179	1.23212058	Q16555 Q16555	
ALLVTASQC*QQPAENK	C93;C92	1.229416944	Q01518 Q01518	
GSDC*GIVNVNIPTSGAEIGG AFGGEK	C450;C478	1.229297155	P49419 P49419	
VTFC*AAGFGQR	C1113;C1227;C1118;C1245;C1210;C1252;C1230	1.227680001	Q14203 Q14203 Q14203 Q14203 Q14203 E7EX90	
AQDIEAGDGTTSVVIAGSLLD SC*TK	C120	1.223633049	P50991	
DQVAQLDDIVDISDEISPSVD DLALSIYPPMC*HLTVR	C172 C172;M299 C300;M171	1.22269	O95273 O95273 O95273 O95273	
ADELLC*WEDSAGHWLYE	C74;C158	1.219948101	H3BPR2 Q13232	

TDVNKIEEFLEEVLC*PPK	C100	1.217726191	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
HTGPGILSMANAGPNTNGSQ FFIC*TAK	C115;C115;C115	1.213422236	F8WE65 C9J5S7 P62937	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 # C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 # P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #
LLSNMMC*QYR	C156;C160;C160	1.213304835	P28062 X5D2R7 P28062	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 # H3BUD0 E3 ubiquitin-protein ligase CHIP (Fragment) OS=Homo sapiens GN=STUB1 PE=1 SV=2 # H3BS86 E3 ubiquitin-protein ligase CHIP (Fragment) OS=Homo sapiens GN=STUB1 PE=1 SV=7 # Q9UNE7 E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2 # Q9UNE7-2 Isoform 2 of E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 # H3BTA3 E3 ubiquitin-protein ligase CHIP (Fragment) OS=Homo sapiens GN=STUB1 PE=1 SV=1 #
AQQAC*IEAK	C105;C180;C199; C127;C66	1.213085	H3BUD0 H3BS86 Q9UNE7 Q9UNE7 H3BTA3	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 # P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK # P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 # P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK #
VC*TLAIIDPGDSDIIR	C92;C92	1.211201197	P62888 E5RI99	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
TGC*TFPEKPDFH	C318;C353;C336	1.208980484	P55263 P55263 P55263	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
EEFASTC*PDDEEIELAYEQV AK	C223	1.206176032	O00299	Q01813 ATP-dependent 6- phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 # Q9BV86 N-terminal Xaa-Pro-Lys N- methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #
NMMAAC*DPR	C303;C303;C303; C650;C303;C303; C285;C303	1.206104951	A0A0B4J269 Q9BVA1 P04350 Q5JP53 Q9BUF5	Q01813 ATP-dependent 6- phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 # Q9BV86 N-terminal Xaa-Pro-Lys N- methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #
NESC*SENYTTDFIYQLYSEE GK	C641	1.206025169	Q01813	Q01813 ATP-dependent 6- phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 # Q9BV86 N-terminal Xaa-Pro-Lys N- methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #
EENVGLHQTLTDLNQLNLC*I	C283;C109;C247	1.205682215	P67936 K7EPB9 P67936	Q9BV86 N-terminal Xaa-Pro-Lys N- methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #
IIC*SAGLSLLAERQENLPDEI YHVYSFALR	C195;C107	1.205064814	Q9BV86 S4R338	Q9BV86 N-terminal Xaa-Pro-Lys N- methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #

MPC*QLHQVIVAR	C640;C562	1.204969433	P17655 P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P17655-2 Isoform 2 of Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 # P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 # P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 #
LQDAFSSIGQSC*HLDLPQIAV VGGQSAGK	C27;C27;C27;C27; 7;C27	1.204956378	P50570 P50570 P50570 P50570 P50570	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
LEGDLTGPSVGVPEVDVELE C*PDAK	C1900	1.203880903	Q09666	P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 # P63208 S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # A0A087WSZ2 Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=1 # Q08043 Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # P12814-3 Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-4 Isoform 4 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 # Q7Z7H8 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 # Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 #
QYDADLEQILIQWITTQC*R	C38;C59;C38	1.202048166	P37802 P37802 X6RJP6	
EDPTVSALLTSEKDWQGFLE LYLQNSPEAC*DYGL	C237	1.200582835	P78417	
GLLDVTC*K	C120	1.197816575	P63208	
YMACC*LLYR	C316;C316;C28 3;C316;C323;C3 16	1.197055422	P68363 Q9BQE3 A6NHL2 Q71U36 A6NHL2 P68366	
C*QLEINFNTLQTK	C389;C346;C33 2;C332;C351;C3 32;C332	1.19509	A0A087W SZ2 Q08043 P12814 P12814 O43707 P12814 P12814	
TDVLVLSC*DLITDVALHEVVD LFR	C106;C106;C10 6	1.192657476	Q9NR50 Q9NR50 Q9NR50	
TVPFLPLLGGC*IDDTILSR	C180;C190	1.190951831	Q7Z7H8 Q7Z7H8	
NDPPEAAGFTAQVILNHPG QISAGYAPVLD*HTAHIACK	C363;M314 C342	1.188315838	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 # P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 #
KITAFVPNDGC*LNFIENDEV LVAGFGR	C90	1.188095784	P62266	

EALEAESAWC*YLYGTGSVA GVYLPGSR	C3652;C3670;C3662;C3821;C3684;C3711;C3688;C3684	1.186636444	Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
SIQFVDWC*PTGFK	C332;C347;C347	1.18573921	P68366 P68363 P68366	Q8WW01 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # Q8WW01-2 Isoform 2 of tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 # HOYCV5 tRNA-splicing endonuclease subunit Sen15 (Fragment) OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # E9PPN1 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # F2Z3M0 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 #
GDSEPTPGC*SGLGPGGVR	C13;C13;C12;C13;C13	1.184719488	Q8WW01 Q8WW01 HOYCV5 E9PPN1 F2Z3M0	F1T011 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 # J3KNL6 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 # P36959 GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 # P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 # P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # A5A3E0 POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 # A0A0A0MSX9 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # P41252 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 # O75369 Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 # O75369-9 Isoform 9 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-3 Isoform 3 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-8 Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB #
ANNNAAVAP TTC*PLQPV TDP FAFSR	C46;C46	1.18421789	F1T011 J3KNL6	
VGVGPGSVC*TTR	C186	1.181854575	P36959	
AEPQC* TSLAWSADGQTLF AGYTDNLVR	C286	1.181602762	P63244	
EGIC*ALGGTSELSSSEG TQHS YSEEEKYAFVNWINK	C104	1.180560153	P13797	
C*PEALFQPSFLGMESC*GIH ETTFNSIMK	C272 C272;C257 C257	1.178639449	P63261 P60709	
LC*YVALDFEQEMATVASSSS LEK	C917	1.178585256	A5A3E0	
ISEVFDC*WFESGSM PYAQV HYPFENKR	C526;C526	1.178316	A0A0A0MSX9 SX9 P41252	
SSTETC*YSAIPK	C2501;C2490;C2477;C2460;C2532;C2436	1.17806397	O75369 O75369 O75369 O75369 O75369	

YVFNLAELAEALVPMYVGIPE C*IK	C416 C295;M165 C357;M287 C173;M408	1.176615	Q12982 Q12982 H7C096 J3KN59	Q12982-2 Isoform 2 of BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 # Q12982 BCL2/adenovirus E1B 19 kDa protein- interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # H7C096 BCL2/adenovirus E1B 19 kDa protein- interacting protein 2 (Fragment) OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # J3KN59 BCL2/adenovirus E1B 19 kDa protein- interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 #
SYILTQGPLPNTC*GHFWEMV WEQK	C92	1.1750825	P18031	P18031 Tyrosine-protein phosphatase non- receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 # O60828-2 Isoform 2 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828 Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # O60828-3 Isoform 3 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # C9JQA1 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # O60828-7 Isoform 7 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828-6 Isoform 6 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828-4 Isoform 4 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # H0YLV5 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # Q9P2T1 GMP reductase 2 OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNJ6 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNH0 GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMPR2 PE=1 SV=7 # Q9P2T1-2 Isoform 2 of GMP reductase 2 OS=Homo sapiens GN=GMPR2 # H0YMB3 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # F8WAN9 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # A0A087WWM4 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YLB8 GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNS9 GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMPR2 PE=1 SV=7 # Q9P2T1-3 Isoform 3 of GMP reductase 2 OS=Homo sapiens GN=GMPR2 # I3L0K2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # I3L3M7 Thioredoxin domain- containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # A0A0U1RQF0 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=1 # P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 # P17858 ATP-dependent 6- phosphofructokinase# liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 #
VFDPSC*GLPYWNADTDLV SWLSPHDPNSVVTK	C60;C60;C60;C6 0;C60;C60;C60	1.173864836	O60828 O60828 O60828 C9JQA1 O60828 O60828 O60828	
VGIGPGSVC*TTR	C171;C186;C20 4;C229;C204;C1 53;C187;C186;C 46;C32;C158	1.173324585	H0YLV5 Q9P2T1 H0YNJ6 H0YNH0 Q9P2T1 H0YMB3 F8WAN9 A0A087W WM4 H0YLB8 H0YNS9 Q9P2T1	
SWC*PDCVQAEPVVR	C43;C43;C43	1.172016488	I3L0K2 I3L3M7 Q9BRA2	
AINC*ATSGVGLVNCLR	C1448;C1446	1.17118937	P49327 A0A0U1R QF0	
SNELGDVGVHC*VLQGLQTP SCK	C75	1.170668663	P13489	
C*HDYYTTEFLYNLYSSEGK	C630	1.168132754	P17858	



SSSSVTTSETQPC*TPSSSDY SDLQR	C334;C103	1.165828607	P50552 K7EM16	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 # K7EM16 Vasodilator-stimulated phosphoprotein (Fragment) OS=Homo sapiens GN=VASP PE=1 SV=1 # P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # E5RIE1 Lymphokine-activated killer T-cell- originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=1 # Q96KB5 Lymphokine- activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 # Q96KB5-2 Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK # E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9UI10-3 Isoform 3 of Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 # Q9UI10-2 Isoform 2 of Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 # A0A087WTA5 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9UI10 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDICFR	C201;C201;C20 1;C201;C183;C2 01	1.163850352	P07437 P68371 Q9BVA1 P04350 Q5JP53 Q9BUF5	
SVLC*STPTINIPASPFMQK	C22	1.162796667	E5RIE1 Q96KB5 Q96KB5	
LLNLVYDVTPELVDLVITELG MIPC*SSVPVLLR	C508;M526 C509 C506;M506 C529;M503 C530;M505	1.161708576	E7ERK9 Q9UI10 Q9UI10 A0A087W TA5 Q9UI10	
GMYGIENEVFLSLPC*ILNAR	C294	1.160331766	P07195	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 #
YKWC*EYGLTFTEK	C76	1.160276464	P45880	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
EKLC*YVALDFEQEMATAASS SSLEK	C917	1.15651056	Q6S8J3	Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 # Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #
VWNLANC*K	C182	1.155351857	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
C*SSFMAPPVTDLGELR	C127	1.154478359	P36551	P36551 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 #
AC*QSIYPLHDFVFR	C164;C201;C18 1	1.152399817	D6RAT0 P61247 D6RG13	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 # Q96AG4 Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 #
ATILDLSC*NK	C48	1.150873605	Q96AG4	
YADLTEDQLPSC*ESLKDTIA R	C153	1.149705743	P18669	P18669 Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 #

VPLDVAC*AR	C3126;C3144;C3136;C3295;C3158;C3185;C3162;C3158	1.1473127	Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
EGDVAAC*YANPSLAQEELG WTAALGLDR	C307	1.146479648	Q14376	Q14376 UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 #
FQSAAGALQEASEAYLVGLF EDTNLC*AIHAK	C111;C111	1.141751301	K7EK07 P84243	K7EK07 Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1 # P84243 Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 #
NC*PHVVVGTGPR	C164	1.141516646	O00148	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 #
C*IPALDSLTPANEDQK	C447	1.141403968	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
HSMNPFC*EIAVEEAVR	C42	1.140428233	M0QY67	M0QY67 Electron transfer flavoprotein subunit beta (Fragment) OS=Homo sapiens GN=ETFB PE=1 SV=1 #
GC*LLYGPPGTGK	C184;C170	1.139000104	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
TFVGTPC*WMAPEVMEQVR	C237	1.138580919	Q9UEW8 O95747 C9JIG9 Q9UEW8	Q9UEW8 STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens GN=STK39 PE=1 SV=3 # O95747 Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 # C9JIG9 Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 # Q9UEW8-2 Isoform 2 of STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens GN=STK39 #
EC*SNPSNLELYTQAILDMT YFEENKLVDEDFPEDSSSQK	C57	1.137495	A6NDU8	A6NDU8 UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 # G3V267 Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=1 # A0A0C4DFM0 Glutathione transferase zeta 1 (Maleylacetoacetate isomerase)# isoform CRA_c OS=Homo sapiens GN=GSTZ1 PE=1 SV=1 # G3V4T6 Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=1 # G3V5T0 Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=1 #
LLVLEAFQVSHPC*R	C178;C205;C206;C191	1.137340827	G3V267 A0A0C4D FM0 G3V4T6 G3V5T0	
C*GVPDVAQFVLTEGNPR	C92	1.137307383	P03956	P03956 Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3 # A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 # Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL #
SDVC*TPGGTTIYGLHALEQG GLR	C247;C235;C215	1.136922226	A0A0A0M QS1 Q53H96 Q53H96	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417-3 Isoform 3 of Calponin-3 OS=Homo sapiens GN=CNN3 # Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 #
C*ASQAGMTAYGTR	C132;C127;C173;C132	1.134950282	E9PDU6 Q15417 Q15417 Q15417	

SQSVSVSGPGPGPGPGLC*P GPNVLLNQNPAPQPQH LAR	C222	1.134832114	Q9H0L4	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 #
GYDFC*QVLQWFAER	C175;C175	1.13400867	Q9H223 A0A087W UA5	Q9H223 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 # A0A087WUA5 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 # Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q9UI30- 2 Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 #
IC*PVEFNPNFVAR	C33;C33;C33	1.132328011	Q9UI30 Q9UI30 F5GX77	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 # Q9Y679-2 Isoform Short of Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 # Q9Y679-3 Isoform 3 of Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 # Q9Y679 Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 PE=1 SV=1 # E7EWX8 Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=1 # Q99685-2 Isoform 2 of Monoglyceride lipase OS=Homo sapiens GN=MGLL # H7C599 Monoglyceride lipase (Fragment) OS=Homo sapiens GN=MGLL PE=1 SV=1 # A0A0C4DFN3 Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=1 # H7C4E0 Monoglyceride lipase (Fragment) OS=Homo sapiens GN=MGLL PE=1 SV=1 # Q99685 Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=2 # A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
WTQTLSELDLAVPFC*VNFR	C188	1.131981658	Q9Y266	Q9Y679 Q9Y679 Q9Y679
TGC*VDLTITNLEGA VAFMP EDITK	C325;C325;C39 1	1.12918324	Q9Y679 Q9Y679 Q9Y679	E7EWX8 Q99685 H7C599 A0A0C4D FN3 H7C4E0 Q99685
VC*FGIQLLNAVSR	C182;C188;C10 2;C218;C114;C2 08	1.123954427	A0A0C4D FN3 H7C4E0 Q99685	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 # Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 # Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanylyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1- phosphate guanylyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # M0QXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 # P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 # P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC # Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
DHQPC*IIFMDEIDAIGGR	C242;C228	1.123551213	A0A087X2 I1 P62333	
NWYVQPSC*ATSGDGLY EGL TWLTSNYKS RPLNPLASGQGTSEENT FY S WLEGLC*VEK	C155 C241	1.122397728 1.114471801	P62330 Q96HE7	
GPFVEAEVDPVDLEC*P DAK	C1833	1.112992121	Q09666	
VQENSAYIC*SR	C585	1.111671077	Q9Y3T9	
LC*SGPGIVGNLVDPSAR	C245;C245	1.111640378	Q9Y5P6 Q9Y5P6	
VLC*ELADLQDKEVGDG TTSV VIAAELLK	C76	1.111468672	P17987	
QMFEPVSC*TFTYLLGDR	C34 C34;M28	1.109457376	O95571 M0QXB5	
LPITVLNGAPGFINLC* DALNA WQLVK	C241;C240	1.105008167	P31939 P31939	
EGTDSQGIQQLVSNISAC* Q VIAEAVR	C29	1.104921546	Q99832	

TDC*SPIQFESAWALTNIASG TSEQTK	C133	1.101212207	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
NVC*TEAGMFAIR	C361;C347	1.100496667	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
VVMALGDYMGASCHAC*IGG TNVR	C134	1.099875307	P60842	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
TVDSQGPTPVC*TPTFLER	C237;C46;C132	1.098992069	Q9BYG3 H7BZL0 C9J808	Q9BYG3 H7BZL0 C9J808 domain-interacting nucleolar phosphoprotein (Fragment) OS=Homo sapiens GN=NIFK PE=1 SV=1 # C9J808 MKI67 FHA domain-interacting nucleolar phosphoprotein (Fragment) OS=Homo sapiens GN=NIFK PE=1 SV=7 #
TATAVAHC*K	C25;C8;C25;C25 ;C25	1.098025515	M0R3H0 M0R1M5 M0R210 Q6IPX4 P62249	M0R3H0 M0R1M5 M0R210 Q6IPX4 P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 # M0R210 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 # Q6IPX4 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 # P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 #
AFQYVETHGEVC*PANWTPD SPTIKPSAASK	C229;C211	1.097597437	P30048 P30048	P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 # P30048-2 Isoform 2 of Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 #
EPFDLGEPEQSNGGFPC*TT APK	C213;C277;C22 9	1.095599167	Q99961 Q99961 Q99961	Q99961-3 Isoform 3 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 # Q99961 Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 # Q99961-2 Isoform 2 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 #
TGQATVASGIPAGWMGLDC* GPRESSKK	C288;C316	1.09375181	P00558 P00558	P00558-2 Isoform 2 of Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 # P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
VVGC*SCVVVK	C106	1.093388076	P25398	P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 #
TDETYCIDNEALYDIC*FR	C211;C211;C55 8;C211;C211;C1 93;C211	1.092454895	Q13509 P68371 A0A0B4J2 69 Q9BVA1 P04350 Q5JP53 Q9BUF5	Q13509 P68371 A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
GFEVVMTEPIDEYC*VQQLK	C394;C521	1.091303038	Q58FF7 P08238	Q58FF7 Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1 # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
TIGGGDSFTTFFC*ETGAGK	C39;C54	1.090967895	P68366 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #

LGGSLIVAFEGC*PV	C146;C163	1.090316674	P60981 P60981	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
VTDDLVC*LVIYK	C48	1.087677049	P49458	P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 #
TVGVQGDC*R	C523	1.086464988	P49915	P49915 GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 #
DLC*FSPGLMEASHVVNDVN EAVQLVFR	C392;C362	1.085377984	Q9BXW7 Q9BXW7	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 # Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 #
SC*PSFSASSEGTR	C9;C9	1.084293121	P27707 D6RFG8	P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
NNQESDC*VSK	C297;C33	1.08247662	A6NDG6 H3BV17	A6NDG6 Glycerol-3-phosphate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 # H3BV17 Glycerol-3-phosphate phosphatase (Fragment) OS=Homo sapiens GN=PGP PE=1 SV=1 #
VIGIEC*SSISDYAVK	C73;C119;C101; C109;C95;C91	1.082184177	E9PKG1 H7C211 Q99873 Q99873 Q99873	E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # H7C211 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 # Q99873-2 Isoform 2 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
GEVPC*TVTSASPLEEATLSE LK	C141	1.081718919	P48047	P48047 ATP synthase subunit O# mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 #
TDFQQGC*AK	C170;C170	1.081572828	O95571 M0QXB5	O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # M0QXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 #



IAVHC*TVR	C72;C70;C71	1.071035	P62913 Q5VVC8 P62913	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 # Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 # P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 #
YWLC*AATGPSIK	C249	1.069436905	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 # P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 # P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
LC*VQNSPQEAR	C150;C150;C150;C150;C141	1.06854961	P33240 P33240 E7EWR4 E9PID8 A0A0A0MT56	Q9NVG8-2 Isoform 2 of TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 # Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
ELSFSGIPC*EGGLR	C36;C36	1.068297751	Q9NVG8 Q9NVG8	Q1MX18 Protein inscuteable homolog OS=Homo sapiens GN=INSC PE=1 SV=1 # Q1MX18-4 Isoform 4 of Protein inscuteable homolog OS=Homo sapiens GN=INSC # A0A0A0MSI1 Protein inscuteable homolog OS=Homo sapiens GN=INSC PE=4 SV=1 # Q1MX18-6 Isoform 6 of Protein inscuteable homolog OS=Homo sapiens GN=INSC # Q1MX18-5 Isoform 5 of Protein inscuteable homolog OS=Homo sapiens GN=INSC # Q1MX18-2 Isoform 2 of Protein inscuteable homolog OS=Homo sapiens GN=INSC # H0YEB6 Sjogren syndrome/scleroderma autoantigen 1 (Fragment) OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # O60232 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # G3V1B8 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 #
SMKAC*VSETLSMLGQHFGQLLELALTR	C215;C168;C168;C168;C168	1.066931333	Q1MX18 Q1MX18 A0A0A0MSI1 SI1 Q1MX18 Q1MX18 Q1MX18	P14868 Aspartate--tRNA ligase# cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 # Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 # C9JX21 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # C9JNR4 Transforming protein RhoA (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 #
AAQGPPAPAVPPNTDVMAC*TQTALLQK	C146;C152;C115	1.066000539	H0YEB6 O60232 G3V1B8	O75940 Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 #
LQSGIC*HLFR	C203	1.065779583	P14868	
HFC*PNVPIILVGNKK	C107;C107;C107;C107;C107	1.065274116	Q5JR08 C9JX21 C9JNR4 P61586 P08134 E9PQH6	
VGVGTC*GIADKPMYQDTSK	C214	1.064921927	O75940	

ELEVLLMC*NK	C91;C109;C91	1.062932782	P62910 F8W727 D3YTB1	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
NDPPMEAAGFTAQVILNHPG QISAGYAPVLDCHTAHIAC*K	C370;C349	1.062847143	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
HDDSSDNFC*EADDIQSPEAE YVDLLLNER	C166	1.062027928	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 #
VAC*ITEQVLTLVNKR	C477	1.060724201	P04843	P04843 Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 #
ADPDGPEAQAEAC*SGER	C18;C18;C18;C18	1.060430647	D6RCB9 D6RC52 Q9NX24 J3QSY4	D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # D6RC52 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 # J3QSY4 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 #
C*IPYAVLLEALALR	C110;C110;C110;C110;C110	1.058940939	F5H248 Q9UBW8 F5H4U8 F5GYF7 F5H7C6	F5H248 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # Q9UBW8 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5H4U8 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5GYF7 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=7 # F5H7C6 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 #
NIC*FTVWDVGGQDK	C62	1.056269308	P84085	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 #
LLDLVQQSC*NYK	C34;C30	1.054839465	B1AHD1 P55769	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #
NIC*FTVWDVGGQDR	C62	1.05017776	P18085	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 #
C*FLAQPVTLLDIYTHWQQTS ELGR	C38;C38;C38;C38;C38;C38;C38;C38;C38;C38	1.049729032	E7ETY2 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 J3KQ96	E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 # Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 # J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 #



					A0A140T9H3 HLA class I histocompatibility antigen# B-46 alpha chain (Fragment) OS=Homo sapiens GN=HLA-B PE=1 SV=1 # Q04826 HLA class I histocompatibility antigen# B-40 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30481 HLA class I histocompatibility antigen# B-44 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # A0A140T951 HLA class I histocompatibility antigen# B-46 alpha chain (Fragment) OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P18465 HLA class I histocompatibility antigen# B-57 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # A0A140T9A9 HLA class I histocompatibility antigen# B-46 alpha chain (Fragment) OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30460 HLA class I histocompatibility antigen# B-8 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30461 HLA class I histocompatibility antigen# B-13 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P03989 HLA class I histocompatibility antigen# B-27 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=2 # P30480 HLA class I histocompatibility antigen# B-42 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30485 HLA class I histocompatibility antigen# B-47 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30479 HLA class I histocompatibility antigen# B-41 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
GGSYSQAAC*SDSAQGSVDVSLTA	C228;C349;C349;C228;C349;C228;C349;C349;C349	1.047460041	A0A140T9H3 Q04826 P30481 A0A140T951 P18465 A0A140T9A9 P30460 P30461 P03989 P30480 P30485 P30479		
YFNPTGAHASGC*IGEDPQGI PNNLMPYVSQVAIGR QVQSLTC*EVDALKGTNESLERR	C196 C328	1.047332694 1.046794387	Q14376 P08670	Q14376 UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 # P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 # J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 # Q07020 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 # O14933 Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens GN=UBE2L6 PE=1 SV=4 # O14933-2 Isoform 2 of Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens GN=UBE2L6 # E9PKV2 39S ribosomal protein L17# mitochondrial (Fragment) OS=Homo sapiens GN=MRPL17 PE=1 SV=1 # Q9NRX2 39S ribosomal protein L17# mitochondrial OS=Homo sapiens GN=MRPL17 PE=1 SV=1 #	
GC*GTVLLSGPR	C136;C134;C134	1.044599186	J3QQ67 G3V203 Q07020		
TC*QVLEALNVLVNRPNIR	C102;C36	1.04420309	O14933 O14933		
GNC*LPPLPLPR	C106;C129	1.042281283	E9PKV2 Q9NRX2		
IDC*FSEVPTSVFGEK	C158;C384;C125	1.042160952	H0YDU4 O00567 H0Y653	H0YDU4 Nucleolar protein 56 (Fragment) OS=Homo sapiens GN=NOP56 PE=1 SV=1 # O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # H0Y653 Nucleolar protein 56 (Fragment) OS=Homo sapiens GN=NOP56 PE=1 SV=1 # P21980 Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 #	
VVSGMVNC*NDDQGVLGR	C230	1.041311813	P21980	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 #	
SSGEIVYC*GQVFEK	C64	1.040739502	Q02543		

GLIAAIC*AGPTALLAHEIGFG SK	C106;C86;C67	1.040500999	Q99497 K7ELW0 K7EN27	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 # K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 # K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 #
LWNTLGVC*K	C138;C138	1.038584995	D6RHH4 P63244	D6RHH4 Receptor of-activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=1 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
VPAFEGDDGFC*VFESNAIAY YVSNEELR	C68;C118	1.037885377	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G # Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=7 # C9JX21 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # P62745 Rho-related GTP-binding protein RhoB OS=Homo sapiens GN=RHOB PE=1 SV=1 # C9JNR4 Transforming protein RhoA (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOA PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 #
TC*LLIVFSK	C20;C20;C20;C20; C20;C20;C20	1.03767	Q5JR08 C9JX21 P62745 C9JNR4 P61586 P08134 E9PQH6	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # P43487 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # C9JJ34 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # F6WQW2 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # P43487-2 Isoform 2 of Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 # Q14232 Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=1 SV=1 # P26583 High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 # Q5T7C4 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=1 # B2RPK0 Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 # D6R9A6 High mobility group protein B2 (Fragment) OS=Homo sapiens GN=HMGB2 PE=1 SV=1 # P09429 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 # C9JWF7 SRSF protein kinase 2 (Fragment) OS=Homo sapiens GN=SRPK2 PE=1 SV=1 # P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 # Q96IJ6 Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 # Q96IJ6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA #
TIAEC*LADELINAAK	C172;C193;C172 2	1.035835564	P46782 M0R0R2 M0R0F0	
AWVWNTHADFADEC*PKPEL LAIR	C132;C132;C209; C132	1.033648729	P43487 C9JJ34 F6WQW2 P43487	
ALC*HLNVPVTVLDAAVGYI MEK	C169	1.033544235	Q14232	
MSSYAFFVQTC*R	C23;M13 C23	1.033153408	P26583 Q5T7C4 B2RPK0 D6R9A6 P09429	
EERWC*ETR	C21	1.031790817	C9JWF7	
FIC*TTSIAIQNR	C20	1.03145628	P53396	
LLPAITILGC*R	C389;C442	1.029692844	Q96IJ6 Q96IJ6	



NWYIQATC*ATSGDGLYEGL DWLSNQLR	C159	1.016953808	P84077	P84077 ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2 #
C*ELSSSVQTDINLPYLTMDS SGPK	C317	1.016677722	P38646	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 #
APELLGC*K	C177;C177	1.016452296	P24941 G3V5T9	P24941 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2 # G3V5T9 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=1 #
QGEYGLASIC*NGGGGASAM LIQK	C413	1.013262786	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
ADDTFEALC*IEPFSSPELPD VMKPDQSGSSANEQAVQ	C111	1.012629487	I3L0M9 Q15370 B8ZZU8	I3L0M9 Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # Q15370 Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # B8ZZU8 Transcription elongation factor B (SIII)# polypeptide 2 (18kDa# elongin B)# isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 #
HVLALTGC*GPGR	C51	1.010629603	Q9BTY7	Q9BTY7 Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1 #
GC*TATLGNFAK	C229	1.009763296	P15880	P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 #
WHLC*PTLYESR	C264;C263;C22 2	1.004292561	Q9H3H3 Q9H3H3 Q9H3H3	Q9H3H3-3 Isoform 3 of UPF0696 protein C11orf68 OS=Homo sapiens GN=C11orf68 # Q9H3H3-2 Isoform 2 of UPF0696 protein C11orf68 OS=Homo sapiens GN=C11orf68 # Q9H3H3 UPF0696 protein C11orf68 OS=Homo sapiens GN=C11orf68 PE=1 SV=2 #
YIELFLNSC*PK	C420;C449;C41 3;C314;C476	1.004227493	F5H5I6 HOYAK1 HOY8R1 Q12849 Q12849	F5H5I6 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=2 # HOYAK1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 # HOY8R1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 # Q12849-5 Isoform 2 of G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 # Q12849 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=3 #
NFPAIGGTGPTSDTGWGC*M LR	C74	1.001073333	Q9Y4P1	Q9Y4P1 Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B PE=1 SV=2 # P32321 Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1 SV=2 #
IVGIGYNGMPNGC*SDDVLP WR	C71 C60;M67	1.000233128	P32321 P32321	P32321-2 Isoform 2 of Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
TIQFVDWC*PTGFK	C347;C281;C37 1;C347;C347	1.000052128	Q9BQE3 Q9NY65 C9J2C0 Q71U36 Q9NY65	Q15084-2 Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-4 Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-5 Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 # Q15084-3 Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 #
EVIQSDSLWLVEFYAPWC*G HCQR	C107;C60;C103; C55;C52	0.999869972	Q15084 Q15084 Q15084 Q15084 Q15084	

LNIISNLDC*VNEVIGIR	C390	0.999285443	P30153	P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
PMC*IPPSYADLGK	C13;C13	0.999059259	A0A0A0MR02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
ATVAPEDVSEVIFGHVLAAGC *GQNPVR	C65	0.998107697	Q9BWD1	Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 #
GSQMGTVQPIPC*LLSMPTR	C531 C531;M551 C559;M523	0.997	Q9NZB2 Q9NZB2 Q9NZB2	Q9NZB2-4 Isoform D of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 #
AAAENLPVPAELPIEDLC*SLT SQSLPIELTSVVPESTEDILLK	C65;C65	0.996615	Q96JB2 Q96JB2	Q96JB2-2 Isoform 2 of Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 # Q96JB2 Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3 #
NMSVHLSPC*FR	C116	0.996323991	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
LMSSLPNFC*GIFNHLER	C35;C35;C21;C35; 5;C35;C35;C35	0.99512771	Q96PU8 Q96PU8 H0YFB7 Q96PU8 Q96PU8 Q96PU8	Q96PU8-8 Isoform 5 of Protein quaking OS=Homo sapiens GN=QKI # Q96PU8-3 Isoform 2 of Protein quaking OS=Homo sapiens GN=QKI # H0YFB7 Protein quaking (Fragment) OS=Homo sapiens GN=QKI PE=1 SV=1 # Q96PU8-9 Isoform 6 of Protein quaking OS=Homo sapiens GN=QKI # Q96PU8-5 Isoform 3 of Protein quaking OS=Homo sapiens GN=QKI # Q96PU8 Protein quaking OS=Homo sapiens GN=QKI PE=1 SV=1 # Q96PU8-6 Isoform 4 of Protein quaking OS=Homo sapiens GN=QKI #
LTNTYCLVAIGGSENFYSVFE GELSDTIPVVHASIAGC*R	C56	0.993923659	P56537	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 #
ISLGLPVGAVINC*ADNTGAK	C28	0.993007409	P62829	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 #
IISNASC*TTNCLAPLAK	C152	0.989529009	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
AFDTAGNGYC*R	C223	0.986439331	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #

				F8VYE8 Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=1 SV=1 # P62136-2 Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA # P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 # E9PMD7 Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CA PE=1 SV=1 # P36873 Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1 # P36873-2 Isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC # F8W0W8 Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=1 SV=1 # Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 #
GNHEC*ASINR	C127;C138;C126;C127;C127;C127;C127;C136	0.986327185	F8VYE8 P62136 P62140 P62136 E9PMD7 P36873 P36873 F8W0W8	
C*ALSSPSLAFTPIIK	C120;C238;C255	0.9856404	Q8NFH5 Q8NFH5 Q8NFH5	
FQSSAVMALQEASEAYLVGL FEDTNLC*AIHAK	C111	0.985611924	Q71DI3	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 # Q5TH30 NDRG family member 3# isoform CRA_c OS=Homo sapiens GN=NDRG3 PE=1 SV=1 # F8WBF9 Protein NDRG3 OS=Homo sapiens GN=NDRG3 PE=1 SV=1 # Q9UGV2-3 Isoform 3 of Protein NDRG3 OS=Homo sapiens GN=NDRG3 # Q9UGV2-2 Isoform 2 of Protein NDRG3 OS=Homo sapiens GN=NDRG3 # Q9UGV2 Protein NDRG3 OS=Homo sapiens GN=NDRG3 PE=1 SV=2 # Q9NX47 E3 ubiquitin-protein ligase MARCH5 OS=Homo sapiens GN=MARCH5 PE=1 SV=1 #
FALNHPELVEGLVLINVDPC*A K	C166;C71;C77;C154;C166	0.982953143	Q5TH30 F8WBF9 Q9UGV2 Q9UGV2 Q9UGV2	
LQILNSIFPGIGC*PVPR	C188	0.981245771	Q9NX47	
YC*FPNYVGRPK	C34;C34	0.98032	P42025 P61163	P42025 Beta-actin OS=Homo sapiens GN=ACTR1B PE=1 SV=1 # P61163 Alpha-actinin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 #
AHVVPC*FDASK	C1157;C1130;C1130;C1157	0.97899459	P21333 A0A087WY3 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # A0A087WY3 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
VMTIPYQPMPASSPVIC*AGG QDR	C194	0.978518596	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 # K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 # Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 #
SGEEDFESLASQFSDC*SSAK	C40;C113;C113	0.977755378	K7EN45 K7EMU7 Q13526	
IPGGIIEDSC*VLR	C168;C213	0.977035176	B4DUR8 P49368	B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 # P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 #
KLDTNSDGLDFSEFLNLIGG LAMAC*HDSFLK	C91	0.975982974	P31949	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 #

ATDYPC*LLILDQPNEFETLR	C145	0.975963779	Q9NVG8	Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
ADHQPLTEASYVNLPTIALC* NTDSPLR	C153;C148;C148	0.975330796	A0A0C4D G17 C9J9K3 P08865	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #
EIITLQLGQC*GNQIGFEFWK	C13;C13	0.973888651	P23258 Q9NRH3	P23258 Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2 # Q9NRH3 Tubulin gamma-2 chain OS=Homo sapiens GN=TUBG2 PE=2 SV=1 # Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOPE PE=1 SV=7 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOPE PE=1 SV=1 # E9PQH6 Rho- related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOPE PE=1 SV=1 #
ISAFGYLEC*SAK	C159;C159;C159	0.973065699	Q5JR08 P08134 E9PQH6	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOPE PE=1 SV=7 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOPE PE=1 SV=1 # E9PQH6 Rho- related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOPE PE=1 SV=1 #
LLAPDC*EIIQEVGK	C215	0.970345372	Q9NQT5	Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 # P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 # F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 # P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN # P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN #
TSSVSNPQDSVSGSPC*SR	C108;C106;C108; C108	0.969225483	P49023 F5GZ78 P49023 P49023	P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 # F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 # P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN # P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN #
YLEC*SALQQDGVKEVFAEAV R	C157	0.968378518	P84095	P84095 Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOPE PE=1 SV=1 # A0A087WX29 TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA- binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # K7EJM5 TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # K7EN94 TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens GN=TARDBP PE=1 SV=6 # K7EJ99 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A0A0MSV7 TAR DNA- binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
NPVSQC*MR	C50;C50;C50;C50; C50;C50;C50; C50;C50;C50	0.968048971	A0A087W X29 A0A087X2 60 B1AKP7 A0A087W YY0 K7EJM5 Q13148 K7EN94 K7EJ99 G3V162 A0A0A0M SV7	A0A087WX29 TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA- binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # K7EJM5 TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # K7EN94 TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens GN=TARDBP PE=1 SV=6 # K7EJ99 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A0A0MSV7 TAR DNA- binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
FSPNSSNPIIVSC*GWDK	C168;C168	0.965892694	D6RHH4 P63244	D6RHH4 Receptor of-activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=1 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
GC*EVVVSGK	C134	0.965087799	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 # O95340 Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2 # O95340-2 Isoform B of Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 #
IHESAGLPFFEIVDAPLNIC*E SR	C155;C155	0.964672468	O95340 O95340	O95340 Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2 # O95340-2 Isoform B of Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 #

EEQVISLGPQVAEGENVFGV C*HIFASFNDTFVHVTDLSGK	C31;C31	0.964575096	P62263 E5RH77	P62263 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 # E5RH77 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=1 #
QAVLGAGLPSTPC*TTINK	C119	0.963963376	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
NWMSQLQANAYC*ENPDIVLI GNK	C123	0.96175909	O00194	O00194 Ras-related protein Rab-27B OS=Homo sapiens GN=RAB27B PE=1 SV=4 #
IHMGC*AENTAK	C196	0.96146642	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
NSFYMGTC*QDEPEQLDDW NR	C1891;C1893;C1907;C771	0.960655	A0A087WY61 Q14980 Q14980 Q14980	A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 #
YINENLIVNTDELGRDC*LINA AK	C147	0.96009474	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
NQSFC*PTVNLDKLWTLVSE QTR	C70;C70;C13	0.959832623	P46776 E9PLL6 E9PJD9	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 # E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 # E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 #
QEC*GEPALPSASEEQVAQD TEEVFR	C14;C14;C14	0.957649923	A0A0A0MRG8 Q16611 Q16611	A0A0A0MRG8 Bcl-2 homologous antagonist/killer OS=Homo sapiens GN=BAK1 PE=1 SV=1 # Q16611-2 Isoform 2 of Bcl-2 homologous antagonist/killer OS=Homo sapiens GN=BAK1 # Q16611 Bcl-2 homologous antagonist/killer OS=Homo sapiens GN=BAK1 PE=1 SV=1 #
VPTANVSVDLTC*R	C247	0.955406883	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
SPWLAGNELTVADVVLWSVL QQIGGC*SVTVPANVQR	C222	0.955290747	F8W950	F8W950 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=1 #
AC*YLSINPQKDELETEDEK	C222	0.953843636	P61163	P61163 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 #
TFDLYANVRPC*VSIEGYK	C49;C127	0.952630819	P50213 P50213	P50213-2 Isoform 2 of Isocitrate dehydrogenase [NAD] subunit alpha# mitochondrial OS=Homo sapiens GN=IDH3A # P50213 Isocitrate dehydrogenase [NAD] subunit alpha# mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 #
VC*NYGLTFTQK	C66;C65	0.949420467	Q9Y277 Q9Y277	Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 # Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #
ALNALC*DGLIDELNQALK	C62	0.948834873	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
ALVDGPC*TQVR	C42;C42	0.948826546	E7EPB3 P50914	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 #



LTTPTYGDLNHLVSATMSGV TTC*LR	C239;C239;C239; 9;C239;C221	0.947947052	P07437 P68371 Q9BVA1 P04350 Q5JP53	P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 # P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB # F5GZQ3 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=1 #
FNNWGGSLSLGHPFGATGC* R	C435;C413;C42 0	0.94727573	P55084 P55084 F5GZQ3	P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 # P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB # F5GZQ3 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=1 #
FC*IWTESAFR	C250	0.946669804	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 # Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 #
DLTTAGAVTQC*YR	C109	0.94658369	Q02543	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 #
LREC*LPLIIFLR	C41	0.944816359	P62701	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 #
AYHEQLTVAEITNAC*FEPAN QMVK	C295	0.943147302	Q9BQE3 F5H5D3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 #
DHEKDAFEHIVTQFSSVPVSV VSDSYDIYNAC*EK	C287	0.94274	P43490	P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 # P25705 ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 # P25705-3 Isoform 3 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 # P25705-2 Isoform 2 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 #
YTIVVSATASDAAPLQYLAPY SGC*SMGEYFR	C294;C272;C24 4	0.936141349	P25705 P25705 P25705	P25705 ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 # P25705-3 Isoform 3 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 # P25705-2 Isoform 2 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 #
EGYTSFWNDC*ISSGLR	C84	0.934886958	Q9H4A6	Q9H4A6 Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 # Q9Y3D2 Methionine-R-sulfoxide reductase B2# mitochondrial OS=Homo sapiens GN=MSRB2 PE=1 SV=2 #
YC*SGTGWPSFSEAHGTSGS DESHTGILR	C105	0.93441	Q9Y3D2	Q9Y3D2 Methionine-R-sulfoxide reductase B2# mitochondrial OS=Homo sapiens GN=MSRB2 PE=1 SV=2 #
AYGGS MC*AK	C83	0.934328631	P49207	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 # P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
VDLNSNGFIC*DYELHELK	C33	0.933739653	P13797	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
FDPTQFQDC*IIQGLTETGTDL EAVAK	C35;C67;C39	0.933034845	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain- containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain- containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
VIGSGC*NLDSAR	C192;C164;C16 3	0.93290274	P00338 P07195 P00338	P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #

VTEDENDIEIPSEDDGTVL LSTVTAQFPGAC*GLR	C39;C39;C39;C3 9;C39	0.930966736	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
LDINLLDNVNC*LYHGEGAQ QR	C34	0.930318701	O14980	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 #
VNQAIWLLC*TGAR	C155;C176;C15 5	0.92819417	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
IINDNATYC*R	C211	0.927559207	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
LNISFPATGC*QK	C12	0.927208482	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
C*HTPPLYR	C22	0.926006995	Q02543	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 #
AAAPAPEEEMDEC*EQALAA EPK	C316 C266;M313	0.92457842	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1- gamma OS=Homo sapiens GN=EEF1G #
DVQIGDIVTVGEC*RPLSK	C131	0.923807142	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
ATC*APQHGAPGPGPADASK	C2535;C2211;C 2516;C2543	0.922258827	P21333 A0A087W WY3 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # A0A087WWY3 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
GTPEQPQC*GFSNAVQILR	C67	0.921291975	Q86SX6	Q86SX6 Glutaredoxin-related protein 5# mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 #
EGGVQLLLTIVDTPGFGDAVD NSNC*WQPVYIDYIDSK	C125;C126;C12 6;C106	0.920134267	Q16181 Q16181 E7EPK1 E7ES33	Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 #
IGAAIQEELGYNC*QTGGVIAE ILR	C112	0.91913871	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
RPYGVLLIAGYDDMGPHIFQ TC*PSANYFDCR	C148 C154;M140	0.918814559	P25786 P25786	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 # P25786 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 #

				P10316 HLA class I histocompatibility antigen# A-69 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=2 # P30493 HLA class I histocompatibility antigen# B-55 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P01892 HLA class I histocompatibility antigen# A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # A0A140T913 HLA class I histocompatibility antigen# A-3 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # A0A140T951 HLA class I histocompatibility antigen# B-46 alpha chain (Fragment) OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30460 HLA class I histocompatibility antigen# B-8 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P01891 HLA class I histocompatibility antigen# A-68 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=4 # P18463 HLA class I histocompatibility antigen# B-37 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30480 HLA class I histocompatibility antigen# B-42 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # A0A140T9J9 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q29963 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # A0A140T912 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P30508 HLA class I histocompatibility antigen# Cw-12 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # Q07000 HLA class I histocompatibility antigen# Cw-15 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q29960 HLA class I histocompatibility antigen# Cw-16 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q29940 HLA class I histocompatibility antigen# B-59 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # A0A140T910 HLA class I histocompatibility antigen# A-3 alpha chain (Fragment) OS=Homo sapiens GN=HLA-A PE=1 SV=1 # Q29960-2 Isoform 2 of HLA class I histocompatibility antigen# Cw-16 alpha chain OS=Homo sapiens GN=HLA-C # P30492 HLA class I histocompatibility antigen# B-54 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # A0A140T9X5 HLA class I histocompatibility antigen# A-3 alpha chain (Fragment) OS=Homo sapiens GN=HLA-A PE=1 SV=1 # P30479 HLA class I histocompatibility antigen# B-41 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 #
				P10316 P30493 P01892 A0A140T913 A0A140T951 P30460 P01891 P18463 P30480 A0A140T9J9 Q29963 A0A140T912 P30508 Q07000 Q29960 Q29940 A0A140T910 Q29960-2 P30492 A0A140T9X5 P30479  G5E9C7 Q02750 Q02750-2 P36507
	C188;C188;C188;C61;C188;C188;C188;C188;C188;C188;C188;C188;C188;C188;C188		0.918608008	
AYLEGTG*VEWLR				
LC*DFGVSGQLIDSMANSFVG TR	C114	0.918056546		

VQEAPIDEHWIIEC*NDGVFQR	C91;C91	0.917835092	Q14353 Q14353	Q14353-2 Isoform 2 of Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT # Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 #
LADQC*TGLQGFLVFHSFGG GTGSGFTSLLMER	C129	0.9155211	P68363 Q9BQE3 Q71U36	P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 #
GC*WDSIHVVEVQEK	C147;C147;C176;C135;C173	0.912732991	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d # OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a # OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AH87 Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=1 SV=1 # P30536 Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 #
APPWVPAMGFTLAPSLGC*F VGSR	C19;M9 C19	0.909307852	B1AH87 P30536	I3L1Z2 Fragile X mental retardation syndrome-related protein 2 (Fragment) OS=Homo sapiens GN=FXR2 PE=1 SV=1 # P51116 Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 #
GDFYVIEYAAC*DATYNEIVTL ER	C66;C109	0.908786986	I3L1Z2 P51116	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # P61225 Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1 #
LLLC*GGAPLSATTQR	C450	0.908646387	O95573	Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 #
ALAEWSC*PFMETSAK	C140	0.908095	P61225	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 #
YAGLSTC*FR	C300;C300	0.907419302	Q5T5C7 P49591	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 # Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 #
MYGISLC*QAILDETKGDYEK	C324	0.906317141	P04083	Q00325-2 Isoform B of Phosphate carrier protein# mitochondrial OS=Homo sapiens GN=SLC25A3 #
PGHLQEGFGC*VVTNRFDQL FDDESDPFEVLK	C11;C11;C11;C11	0.903387669	Q8NC51 Q8NC51 Q8NC51 Q8NC51	P12955-2 Isoform 2 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
YYALCGFGGVLSC*GLTHTAV VPLDLVK	C75	0.903024471	Q00325	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
IEEDVVVTDSGIELLTC*VPR	C426;C467	0.90285441	P12955 P12955	
SYC*AEIAHNVSSK	C96;C114;C96	0.902833986	P62910 F8W727 D3YTB1	

LIDFLEC*GK	C234;C234	0.901701316	P17844 J3KTA4	P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # J3KTA4 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 #
TIC*AILENYQTEK	C460;C438	0.899197674	Q5T5C7 P49591	Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 #
DDVFLSVPK*ILGQNGISDLVK	C322;C293	0.898590025	P00338 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
YGIIC*MEDLIHEIYTVGKR	C186	0.897868821	P18124	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 #
AFC*GFEDPR	C4494	0.895385232	Q15149	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 #
EITSLDTENIDEILNADVALV NFYADWC*R	C58	0.894085379	Q9BS26	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 #
C*TPACISFGPK	C34;C34	0.892736393	A0A087W YC1 P34932	A0A087WYC1 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=1 # P34932 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 #
EITAISSVPC*QLLESVLQEL K	C645;C704	0.891557074	O75694 O75694	O75694-2 Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 # O75694 Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 #
LVSSPCC*IVTSTYGWTANME R	C590	0.889782466	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
LC*YVALDFEQEMAMVASSS SLEK	C880	0.889709957	P0CG39	P0CG39 POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 #
QTISNAC*GTIGLIHAIANNKD K	C95;C59;C95	0.889424559	P15374 A0A087W TB8	P15374 Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 # A0A087WTB8 Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=UCHL3 PE=1 SV=1 #
ENVNVEEMFNC*ITELVLR	C147;C163	0.886345414	F5H157 Q15286	contaminant_UBIQUITIN10 no description# F5H157 Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=1 SV=1 # Q15286 Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 #
QLFALSC*TAEQGVLPDDL GVIR	C96;C60;C112;C 75;C112;C96	0.886257802	P04899 P04899 P04899 P04899 P04899	P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
DNLTWTSDSAGEEC*DAAE GAEN	C237	0.88495719	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #
ITSC*IFQLLQEAGIK	C63	0.884421004	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
SDLYEVIQSTLDGLLC*TSLPV WLENHTALTVMASK	C322	0.884402442	P22102	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 #

SGTIC*SSELPGAFAEAAAGFHL NEHLYNMIIRR	C122;C190;C14 1;C190	0.884118616	U3KQE2 A0A0C4D GQ5 A0A075B7 C0 P04632	U3KQE2 Calpain small subunit 1 (Fragment) OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # A0A0C4DQG5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # A0A075B7C0 Calpain small subunit 1 (Fragment) OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #
VLTC*TDLEQGPFFLDLFENA QPTESEKEIYNQVNVVLK	C10	0.883168345	Q9NUQ9	Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 # Q7Z7H8 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 # Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 #
LPSLPLVQGELVGGGLTC*LTA QTHSLLQHQPQLTLLDQYI R	C213;C223	0.877771124	Q7Z7H8 Q7Z7H8	H7CON4 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 # Q15637-6 Isoform 6 of Splicing factor 1 OS=Homo sapiens GN=SF1 # H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 #
YAC*GLWGLSPASR	C26;C457;C175	0.877647678	H7C0N4 Q15637 H7C561	P07858 Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 # P19404 NADH dehydrogenase [ubiquinone] flavoprotein 2# mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2 # E7EPT4 NADH dehydrogenase [ubiquinone] flavoprotein 2# mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=1 # Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 # Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 #
IC*EPGYSPTYK	C211	0.876662204	P07858	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
FSC*EPAGGLTSLTEPPKGGP FGVQAGL	C225;C228	0.876266837	P19404 E7EPT4	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 # P31153 S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 #
TSC*GSPNYAAPEVISGR	C185;C200	0.875380102	Q13131 Q13131	O76003 Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 # Q9BT17 Mitochondrial ribosome-associated GTPase 1 OS=Homo sapiens GN=MTG1 PE=1 SV=2 # Q9BT17-2 Isoform 2 of Mitochondrial ribosome-associated GTPase 1 OS=Homo sapiens GN=MTG1 # E7EVK2 Mitochondrial ribosome-associated GTPase 1 OS=Homo sapiens GN=MTG1 PE=1 SV=1 # Q96E39 RNA binding motif protein# X-linked- like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 #
AGSDGESIGNC*PFSQR	C35	0.873047038	Q9Y696	P62191 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 # P62191-2 Isoform 2 of 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 #
LGMLSPEGTC*K	C212	0.872989321	P49327	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 #
TWYVQATC*ATQGTGLYDGL DWLSHELK	C159	0.872419432	P84085	
TC*NVLVALEQQSPDIAQGVH LDR	C104	0.872153333	P31153	
AYSSWPTYPLQYVSGELIGG LDIIKELEASEELDTIC*PK	C229	0.871845538	O76003	
ENFPLC*GR	C23;C23;C23	0.868627892	Q9BT17 Q9BT17 E7EVK2	
SDLYSSC*DR	C338	0.867204958	Q96E39	
AIC*TEAGLMALR	C399;C326	0.865003913	P62191 P62191	
TAFQEALDAAGDKLVVDF ATWC*GPKC	C32	0.863394599	P10599	

YC*VRPNSGIIDPGSTVTVSV MLQPFYDYPNEK	C60;C60	0.863242302	Q9P0L0 Q9P0L0	Q9P0L0 Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 # Q9P0L0-2 Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA #
LVAFC*PFASSQVALENANAV SEGVVHEDLR	C52	0.861190669	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
LEKPNEGYLEFFVDC*SASAT PEFEGR	C85	0.859509258	Q15024	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 #
YGAVDLLLALLAVPDMSSLAC *GYLR	C223	0.858863779	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
TDLLDSESQSGVFLPELDE PEYC*NAQNTALWELHALR	C683	0.855597499	Q8WTT2	Q8WTT2 Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1 SV=1 #
VVNEINIEDLC*LTK	C92	0.855104739	Q8N5K1	Q8N5K1 CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 #
QVLMGPYPNPTDC*PEVGFFD VLGNDR	C129	0.85392667	Q9H3P7	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 #
NC*LTNFHGMDLTR	C59;C96;C76	0.852146834	D6RAT0 P61247 D6RG13	D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 # P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 #
STFFNVLTSQASAENFPFC* TIDPNESRVPVDER	C75;C55	0.844149333	J3KQ32 Q9NTK5	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 #
AILFSQPLQITDTQQGC*IAPV ELR	C716	0.840386878	Q8NBF2	Q8NBF2 NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 #
VTEAPC*YPGAPSTEASGQT GPQEPTSAR	C523	0.837297811	P40222	P40222 Alpha-taxilin OS=Homo sapiens GN=TXLNA PE=1 SV=3 #
NSQWVPTLPNSSHHLDAVPC *STTINR	C147;C138;C138	0.836703056	Q12824 Q12824 G5E975	Q12824 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 PE=1 SV=2 # Q12824-2 Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 # G5E975 SWI/SNF related# matrix associated# actin dependent regulator of chromatin# subfamily b# member 1# isoform CRA_c OS=Homo sapiens GN=SMARCB1 PE=1 SV=1 #
FAC*HSASLTVR	C56;C145	0.833774427	Q15233 Q15233	Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 #
TYDPSGDSTLPTC*SK	C439	0.833142059	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #
VDEFPLC*GHMVSDEYEQLS SEALEAAR	C49;C49	0.832306617	X1WI28 P27635	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 #
QVLVAPGNAGTAC*SEK	C41	0.830551304	P22102	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 #
AC*LIFDFEIDAIGGAR	C270	0.829890863	P35998	P35998 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 #

INEIVYFLPFC*HSELIQLVNK	C572;C527;C542;C577	0.828199988	Q9H078 Q9H078 Q9H078 H0YGM0	Q9H078 Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1 # Q9H078-4 Isoform 4 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-2 Isoform 2 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # H0YGM0 Caseinolytic peptidase B protein homolog (Fragment) OS=Homo sapiens GN=CLPB PE=1 SV=1 #
TWYVQATC*ATQGTGLYEGL DWLSNELSKR	C159	0.827224841	P18085	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 #
WNTDNTLGTEIAIEDQIC*QGL K	C103	0.825299642	P45880	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDIC*FR	C211;C183 C211;C201 C193;C201 C211 C201	0.822284932	P68371 Q9BVA1 P04350 Q5JP53 Q9BUF5	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
AETSDVANAVLDGADC*IMLS GETAK	C401;C370	0.820735354	P30613 P30613	P30613 Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR PE=1 SV=2 # P30613-2 Isoform L-type of Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR #
NLSDLIDLVPSLC*EDLLSSVD QPLK	C36;C36;C65;C24;C62	0.814987228	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
C*DNFTSSWR	C317;C207	0.809119405	Q15149 Q15149	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC #
VVVVDDLLATGGTMNAAC*EL LGR	C140;C113	0.808349205	P07741 H3BQZ9	P07741 Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 # H3BQZ9 Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=1 #
NLSFFLTPPC*AR	C492;C492;C494	0.808343843	P42224 P42224 J3KPM9	P42224 Isoform Beta of Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 # P42224 Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 # J3KPM9 Signal transducer and activator of transcription OS=Homo sapiens GN=STAT1 PE=1 SV=1 #
FLSQIESDC*LALLQVR	C794	0.801541167	P52789	P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
EYVEGEVTELTTPC*ETENPM GGYGK	C141	0.79254793	Q9Y265	Q9Y265 RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 #
VAASC*GAIQYIPTELDQVR	C134	0.790648067	Q7L2H7	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #



				J3KRX5 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621-2 Isoform 2 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 # J3QLC8 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=1 # A0A087WXM6 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # A0A0A0MRF8 Protein RPL17-C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 # A0A0A6YYL6 Protein RPL17-C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 # P18621 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 # J3QQT2 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621-3 Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 #
INPYMSSPC*HIEMILTEK	C144 C144;M102 C144;M140 C134;M140 C106;M140 C106;M130	0.789367758	J3KRX5 P18621 J3QLC8 A0A087WXM6 A0A0A0MRF8 A0A0A6YYL6 P18621 J3QQT2 P18621	
NYLPAINGIVFLVDC*ADHSR	C59;C102	0.788228228	Q9NR31 Q9NR31	Q9NR31-2 Isoform 2 of GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A # Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 #
NC*IVLIDSTPYRQWYESHYA LPLGR	C100	0.786708929	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #
AVAILC*NHQR	C630	0.786545356	P11387	P11387 DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 #
FSPEFVDFTAQC*LR	C310;C276;C305	0.785096512	P46734 P46734 P46734	P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 # P46734-2 Isoform 1 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 # P46734 Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 #
QPAIMPQSYGLEDGSC*SYK	C413;C472	0.784749696	M0QXS5 P14866	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
DAANC*WTSLLESEYAADPW VQDQMQR	C99	0.7846025	Q8WVJ2	Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 #
SDITKLEVDIVNAANSSLLG GGVDGC*IHR	C186	0.783703424	Q9BQ69	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #
LESLQSMEMAHSGSLRDEL C*LDFPCDSPEK	C386;C183;C321;C270	0.782054011	Q9NX95 B3KRD1 Q9NX95 Q9NX95	Q9NX95-4 Isoform 4 of Syntabulin OS=Homo sapiens GN=SYBU # B3KRD1 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-2 Isoform 2 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95-5 Isoform 5 of Syntabulin OS=Homo sapiens GN=SYBU #
C*IADVVSFLFITVMDK	C128	0.780899815	Q9UK41	Q9UK41 Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1 #
SGRYEAAFPFLSPC*GR	C90;C143;C98	0.780226186	Q6P1X6 H0YF29 Q6P1X6	Q6P1X6-2 Isoform 2 of UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 # H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 # Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 #
LC*PGGQLPFLLYGTEVHTDT NK	C59	0.779657281	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
FGVIC*LEDLIEIAFP GK	C184	0.778932962	Q6DKI1	Q6DKI1 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 #

ALDLSSC*K	C508;C437;C461;C60	0.77637	P31948 P31948 P31948 H0YGI8	P31948-2 Isoform 2 of Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 # P31948-3 Isoform 3 of Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 # P31948 Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 # H0YGI8 Stress-induced-phosphoprotein 1 (Fragment) OS=Homo sapiens GN=STIP1 PE=1 SV=1 # M0QYS1 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=1 SV=2 # Q9Y6B6 GTP-binding protein SAR1b OS=Homo sapiens GN=SAR1B PE=1 SV=1 # D6R9R5 GTP-binding protein SAR1b (Fragment) OS=Homo sapiens GN=SAR1B PE=1 SV=7 # D6RDB2 GTP-binding protein SAR1b OS=Homo sapiens GN=SAR1B PE=1 SV=1 # Q9H029 GTP-binding protein SAR1b OS=Homo sapiens GN=DKFZp434B2017 PE=1 SV=1 # D6RD69 GTP-binding protein SAR1b (Fragment) OS=Homo sapiens GN=SAR1B PE=1 SV=1 # P02545-5 Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-4 Isoform 4 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 # Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU # Q5JS54-3 Isoform 3 of Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 # Q5JS54 Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 PE=2 SV=2 # Q5JS54-2 Isoform 2 of Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 # D6RB92 Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 PE=1 SV=1 # P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 # Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 # Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 # O14684 Prostaglandin E synthase OS=Homo sapiens GN=PTGES PE=1 SV=2 # F8WBU3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # F8WCL3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # C9JNL5 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=8 # Q96I15-2 Isoform 2 of Selenocysteine lyase OS=Homo sapiens GN=SCLY # H7C2M1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=1 # H7C4A1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=7 # A0A0A0MQU4 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # Q96I15 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=4 #
C*EGINISGNFYR	C37	0.772623645	M0QYS1	
NYLPAINGIVFLVDC*ADHER	C102;C34;C102;C34;C102	0.771238873	Q9Y6B6 D6R9R5 D6RDB2 Q9H029 D6RD69	
AQNTWGC*GNSLR	C423;C410;C522	0.752972546	P02545 P02545 P02545	
GNFTLPEVAEC*FDEITYVEL QKEEAQK	C648;C629	0.747671154	Q00839 Q00839	
NLAVAMC*SR	C55;C55;C55;C55	0.745775	Q5JS54 Q5JS54 Q5JS54 D6RB92	
DIDFLKEEEHDC*FLEEIMTK	C173	0.741849892	P12268	
GTLTLC*PYHSDR	C779;C649	0.741152236	Q13200 Q13200	
SVTYTLAQLPC*ASMALQILW EAAR	C137	0.73562	O14684	
DAPAPAASQPSGC*GK	C22;C22;C30;C22;C13;C23;C30;C22	0.729686754	F8WBU3 F8WCL3 C9JNL5 Q96I15 H7C2M1 H7C4A1 A0A0A0MQU4 QU4 Q96I15	

C*AGPTPEAELQALAR	C52	0.705397844	Q15050	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 #
C*TGGEVGATSALAPK	C17	0.70474242	P30050	P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 #
AAC*LESAQEPAGAWGNK	C53;C53;C53;C53;C53;C53;C53;C53;C53;C53;C53	0.703866437	C9JT62 C9JES8 C9JBS3 C9JEJ8 C9JK79 C9JHZ8 C9JZ1 C9JZ18 A0A0U1RVI6 A0A024R4E5 C9J5E5 C9JHS7 C9JHN6	C9JT62 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JEJ8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JBS3 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JEJ8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JK79 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JHZ8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JZ1 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JZ18 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # A0A0U1RVI6 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # A0A024R4E5 High density lipoprotein binding protein (Vigilin)# isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1 # C9J5E5 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JHS7 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JHN6 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 #
GNIPAESYFFIDILLDIRDEI AGC*IEK	C211;C274;C211	0.701307271	K7EJR3 P48556 R4GMR5	K7EJR3 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=7 # P48556 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2 # R4GMR5 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=1 #
IQFNDLQSLLC*ATLQNVLR	C585;C440	0.698910826	Q14974 Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
LVSSPC*CIVTSTYGWTANMER	C589	0.684250054	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
ERESLNASIVDAINQAADC*W GIR	C167	0.683240542	Q9UJZ1	Q9UJZ1 Stomatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 #
STLTDSLVC*K	C41	0.68008245	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
SVNSLDGLASVLYPGC*DTLD KVFTYAK	C85	0.677575563	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 #
TNHIGHTGYLNTVTVSPDGSL C*ASGGK	C207;C207	0.667237222	D6RHH4 P63244	D6RHH4 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=1 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
STC*SLTPALAAHFSENLIK	C553;C450;C508;C401	0.665727332	Q9BTA9 Q9BTA9 Q9BTA9 A0A0A0MRT2	Q9BTA9 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=3 # Q9BTA9-5 Isoform 4 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC # Q9BTA9-2 Isoform 2 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC # A0A0A0MRT2 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=1 #
DEFTNTC*PSDKEVEIAYSDV AK	C234	0.655595	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #

IIDLEEAEDIQEIIVLSQ C*DSSYVTK	C77;C77;C77;C7 7	0.650801207	B4E0Y9 Q9P289 Q8NBY1 Q9P289	B4E0Y9 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 # Q9P289-3 Isoform 3 of Serine/threonine- protein kinase 26 OS=Homo sapiens GN=STK26 # Q8NBY1 Serine/threonine- protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 # Q9P289 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=2 # P51114-2 Isoform 2 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # B4DXZ6 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # P51114 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3 #
GEFYVIEYAAC*DATYNEIVTF ER	C99;C86;C99	0.650543688	P51114 B4DXZ6 P51114	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 # P30044 Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 # P30044-2 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 # P30044-3 Isoform 3 of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 # O43684 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 # J3QT28 Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=1 SV=1 # O43684-2 Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 #
NC*NDFQYESK	C112	0.635948598	Q04917	P30566 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 # P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 # O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 #
ALNVEPDGTGLTC*SLAPNIIS QL	C204;C152;C16 0	0.634680319	P30044 P30044 P30044	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
TPC*NAGTFSQPEK	C129;C129;C12 9	0.625596995	O43684 J3QT28 O43684	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 # P14625 Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 #
IC*LAEAFLTADTILNTLQNISE GLVVYPK	C340	0.593270173	P30566	
GPC*IIYNEDNGIIK	C208	0.590991186	P36578	
FMTPIQDNPSGWGPC*AVP EQFR	C19 C19;M5	0.567508308	O15371 O15371 O15371	
C*SGVMEFSTSGHAYTDTGK	C36	0.567409864	Q9Y277	
IAVYSC*PFDGMITETK	C244	0.556125224	P50990	
LEFSIYPAPQVSTAVVEPYNSI LTHTTLEHSDC*AFMVDNEA IYD	C185	0.535746053	P68366 P68363 Q9BQE3 F5H5D3 Q71U36 P68366	
ETYQSVYNWQYVHCLFLWC* R	C416	0.521690837	Q9Y3T9	
LTESPC*ALVASQYGWSGNM ER	C645	0.521592792	P14625	

NDAPEEAGEGC*VAAILGETE VQQFLR	C57;C57	0.515453948	Q96DC7 Q96DC7	Q96DC7 Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 PE=1 SV=2 # Q96DC7-2 Isoform 2 of Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 #
EGGQYGLVAAC*AAGGQGH AMIVEAYPK	C458;C436	0.51329003	P55084 P55084	P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 # P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB #
IC*PVETLVEEAIQCAEK	C213	0.509775714	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 # Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 #
TDVC*VFAAQEDLETMQAFA QVFNK	C96	0.504907639	Q7L1Q6 Q7L1Q6 Q7L1Q6	P15170-2 Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 # P15170-3 Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 # O15533-2 Isoform 2 of Tapasin OS=Homo sapiens GN=TAPBP # A0A0G2JH37 Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 # O15533-3 Isoform 3 of Tapasin OS=Homo sapiens GN=TAPBP # O15533 Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 # A0A0G2JKZ1 Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 # Q6P1N7 TAPBP protein OS=Homo sapiens GN=TAPBP PE=1 SV=1 # A2AB90 Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 # A0A0A0MSV9 Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 # C9JA35 Tapasin (Fragment) OS=Homo sapiens GN=TAPBP PE=1 SV=1 # Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #
EQSDFC*PWYIGLPFIPYLDNL PNFNR	C413;C414	0.487598559	P15170 P15170	
WASGLTPAQNC*PR	C115;C115;C115; C115;C115;C115; C115;C115;C115; C58	0.47958126	O15533 A0A0G2JH37 O15533 O15533 A0A0G2JKZ1 KZ1 Q6P1N7 A2AB90 A0A0A0MSV9 SV9 C9JA35	
LLYEALVDC*K	C175	0.471484451	Q7L2H7	
MAC*GLVASNLNLKPGECLR	C3	0.406442469	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 #
SVANVIQQAGC*PVPEYIK	C536	0.378615746	Q9Y2R4	Q9Y2R4 Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3 #

				H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
LC*EPEVLNSLEETYSPPFR	C177;C261;C261;C106;C224;C261;C261;C227;C261;C261;C242	0.377323634	H0YJA2 Q6PJT7 Q6PJT7 G3V5I6 Q6PJT7 G3V256 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7	OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
MLSC*AGADR	C105;M102 C105	0.334442372	Q96L21 P27635	Q96L21 60S ribosomal protein L10-like OS=Homo sapiens GN=RPL10L PE=1 SV=3 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 # A0A087X1Z3 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1 # Q9UL46 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 #
C*GFLPGNEK	C106;C91	0.333696787	A0A087X1 Z3 Q9UL46	H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # H0YN73 40S ribosomal protein S17 (Fragment) OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 #
VC*EEIAIPSK	C35;C35;C34;C35	0.309545418	H0YN88 A0A075B7 16 H0YN73 P08708	P06703 Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 # P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 # P34897-3 Isoform 3 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # P51811 Membrane transport protein XK OS=Homo sapiens GN=XK PE=1 SV=5 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
MAC*PLDQAIGLLVAIFHK	C3	0.306920554	P06703	G3V1V0 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # G3V1Y7 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660-2 Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 # P60660 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 # F8W1R7 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 #
GLELIASENFC*SR	C80;C59	0.292615	P34897 P34897	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
MWQALTLFSLPC*ALVQLT LLFVHRDLR	C48	0.281358785	P51811	
HLYTLDDGGDIINALC*FSPNR	C240	0.201556802	P63244	
MC*DFTEDQTAEFK	C2 C2;M1	0.130697019	G3V1V0 G3V1Y7 P60660 P60660 F8W1R7	
LPACVVDC*GTGYTK	C12	0.082601425	P61158	

C*GEYGENFNHC*SPLNTYEL IHTGEMSYR	C333 C337 C343;C327	0.074891127	Q9UJU3 Q9UJU3	Q9UJU3 Zinc finger protein 112 OS=Homo sapiens GN=ZNF112 PE=2 SV=2 # Q9UJU3-2 Isoform 2 of Zinc finger protein 112 OS=Homo sapiens GN=ZNF112 #
VILITPTPLC*ETAWEEQC*I	C137 C125 C145;C24 C32;C117	0.070647841	Q2TAA2 Q2TAA2 H7C5G1	Q2TAA2 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 # Q2TAA2-2 Isoform 2 of Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 # H7C5G1 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 #
ECENCDC*LQGFQLTHSLGG GTGSGMGTLLISK	C129;C476	0.070121704	Q13509 A0A0B4J2 69	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 #
KQC*QLQTAIAEAEQR	C383	0.061171189	Q5XKE5	Q5XKE5 Keratin# type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 #
C*VEKHNGYLCDC*TNSPYEG PFCK	C984 C973	0.045121336	Q8WYK1	Q8WYK1 Contactin-associated protein-like 5 OS=Homo sapiens GN=CNTNAP5 PE=2 SV=1 #
ECENC*DCLQGFQLTHSLGG GTGSGMGTLLISK	C127;C474	0.044347652	Q13509 A0A0B4J2 69	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 #
KEC*ENCDC*LQGFQLTHSLG GGTSGMGTLLISK	C124;C471	0.032081264	Q13509 A0A0B4J2 69	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 #
VGLGIC*YDMR	C153	0.029159381	Q9NQR4	Q9NQR4 Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 #
FFAFWGQDINNLTTPLEC*GR ESR	C635;C735	0.001	A8MT40 Q8NCN5	A8MT40 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # Q8NCN5 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 #

**Table A3.2**IsoTOP-ABPP analysis of withaferin A (10  $\mu$ M) in situ in 231MFP proteomes.

Peptide	Modified residue	Average area ratio	Uniprot ID	Protein
DNTIEHLLPLFLAQLKDEC*PE VR	C377	4.045132742	P30153	P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
AYHEQLSVAEITSSC*FEPNS QMVK	C229;C319;C29 5	3.451953646	Q9NY65 C9J2C0 Q9NY65	Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
VAC*AEEWQESR	C87	3.170238465	O75663	O75663 TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 #
FTSC*VAFFNILNELNDYAGQ R	C69;C69;C69;C6 9;C69;C69	3.01293261	Q5T0N5 S4R347 Q5T0N5 Q5T0N5 Q5T0N5 Q5T0N5	Q5T0N5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L PE=1 SV=1 # Q5T0N5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L # Q5T0N5 Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L PE=1 SV=3 # Q5T0N5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L # Q5T0N5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L #
LGAEAAAGAVDDGGC*SRGG GAGEK	C55	2.850411423	O95935	O95935 T-box transcription factor TBX18 OS=Homo sapiens GN=TBX18 PE=1 SV=3 # E7EMD6 A-kinase anchor protein 10# mitochondrial OS=Homo sapiens GN=AKAP10 PE=1 SV=3 # O43572 A-kinase anchor protein 10# mitochondrial OS=Homo sapiens GN=AKAP10 PE=1 SV=2 #
SC*LDYQTQETK	C110;C110	2.828953297	E7EMD6 O43572	Q15019-2 Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2 # Q15019 Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 # Q15019-3 Isoform 3 of Septin-2 OS=Homo sapiens GN=SEPT2 #
LTVVDTPGYGDAINC*R	C146;C111;C12 1	2.609087036	Q15019 Q15019 Q15019	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
VDDEILGFISEATPLGGIQAAS TESC*NQQLDLALCR	C561	2.585030395	P42166	P31749 RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2 # P31751 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 # P31749-2 Isoform 2 of RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 # Q9Y243-2 Isoform 2 of RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 # Q9Y243 RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 PE=1 SV=1 #
C*SGIGDNPGSETAAPR	C2675	2.4085	P50851	P50851 Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4 #
DLSYC*LSGMYDHR	C267	2.407	P52597	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 #



DLNYC*FSGMSDHR	C267	2.35337	P31943 G8JLB6	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 #
YDSYESC*DSR	C128	2.349399564	Q9ULX6	Q9ULX6 A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3 #
TDGFGIDTC*R	C144	2.235994547	P04632	P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # O43184 Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 PE=1 SV=3 # O43184-3 Isoform 3 of Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 #
NCHC*EAHWAPPFC*DKFGF GGSTDSGPIR	C687;C675 C678 C684;C678 C684	2.228855348	O43184 O43184 O43184 O43184	O43184 metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 # O43184-2 Isoform 2 of Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 # O43184-4 Isoform 4 of Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 #
MSVIEEGDC*KR	C437	2.221235	P11216	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 #
GC*STVLSPEGSAQFAAQIFG LSNHLVWSK	C374	2.205384066	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
LYYFQYPC*YQEGLR	C130	2.173728903	Q9NRW3	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 #
NGLQSC*PIKEDSFLQR	C1058	2.165451938	P00533	P00533 Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 #
YIYDQC*PAVAGYGPIELPD YNR	C453	2.095183539	P31930	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 #
YSTGSDSASFPHHTPSMC*LN PDLEGPPLAAYTIQQYAIPQ PDLTK	C217 C217;M212 C213;M216	1.989557035	Q15366 Q15366 Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
SGIQPLC*PER	C341	1.979870609	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
EFRATLEC*HPLTMTDPIEEH R	C245;C191	1.92799	Q99661 Q99661	Q99661 Kinesin-like protein KIF2C OS=Homo sapiens GN=KIF2C PE=1 SV=2 # Q99661-2 Isoform 2 of Kinesin-like protein KIF2C OS=Homo sapiens GN=KIF2C #
VNQAIWLLC*TGAR	C155;C176;C15 5	1.905337954	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
SATMSGVTTC*LR	C239;M233 C239;M215 C221	1.858202207	Q13885 P68371 A6NNZ2 Q9BVA1 P04350 Q5JP53	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
TVFAEHISDEC*K	C114	1.856952429	P39023	P39023 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 #

IGAAIQEELGYNC*QTGGVIAE ILR	C112	1.840505908	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
PEEAC*SFILSADFPALVVK	C134	1.82983	P22102	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 #
GMENLLEVQVPEDVEQQLQQ LDC*R	C368	1.799263416	Q9BTY7	Q9BTY7 Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1 #
FEIINAIYEPTEEEC*EWKPDE EDEISELK	C91	1.747415383	B7Z9C2	B7Z9C2 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 #
GLNPLNAYSDLAEFLETEC*Y QTPFNK	C343	1.746557923	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
VAAASGHC*GAFSGSDSSR	C947;C919	1.739149103	Q9NZB2 Q9NZB2	Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 #
VMTIPYQPMPASSPVIC*AGG QDR	C194	1.737380395	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
SCYYLPC*FVTSKNECLWTD MLSNFGYPGYQSK	C155	1.71174354	P35625	P35625 Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2 #
YSDVEVPASVTGYSFASDGD SGTC*SPLR	C430;C430;C430; 0;C430;C430;C430; 30;C430;C430	1.670371361	P35611 P35611 P35611 E7ENY0 P35611 E7EV99 P35611 P35611	P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-5 Isoform 5 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 # E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 # E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 #
SQQAAQSADVSLNPC*NTPQ KIFTTPLTPSQYYSGSK	C142	1.668251158	P49454	P49454 Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2 #
SCYDLSC*HAR	C471	1.60686072	P41250	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 #
NNQESDC*VSK	C297	1.553768357	A6NDG6	A6NDG6 Glycerol-3-phosphate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 #
HAELIASTFVDQC*K	C283;C219	1.55214742	Q9UBB4 Q9UBB4	Q9UBB4 Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1 # Q9UBB4-2 Isoform 2 of Ataxin-10 OS=Homo sapiens GN=ATXN10 #
LNNLIC*DESDVKDLAFK	C362	1.530196667	Q96EB1	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 #
IPDWC*SLNNPPEMMFDVG K	C388	1.528749986	Q9NZ32	Q9NZ32 Actin-related protein 10 OS=Homo sapiens GN=ACTR10 PE=1 SV=1 #
LGC*NITISEDITPR	C38;C38	1.509807566	Q96FJ0 Q96FJ0	Q96FJ0 AMSH-like protease OS=Homo sapiens GN=STAMBPL1 PE=1 SV=2 # Q96FJ0-2 Isoform 2 of AMSH-like protease OS=Homo sapiens GN=STAMBPL1 #
VSC*LGVTDDGMAVATGSWD SFLK	C317;C317	1.494816866	P62879 P62873	P62879 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 # P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 #
DIC*NDVLSLLEK	C94	1.461958188	P63104	P63104 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 #
DASALLDPMEC*TDTAEERQ	C287 C287;M285	1.457710428	Q9BTE3 Q9BTE3	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 # Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP #

VC*ENIPIVLCGNK	C112;C130;C129;C108	1.456871729	P62826 J3KQE5 B5MDF5 F5H018	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 # J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 # B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 # F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 #
ENFDEVVNDADIILVEFYAPWC*GHCK	C206	1.427598003	P13667	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 # Q6P9B6 TLD domain-containing protein 1 OS=Homo sapiens GN=TLDC1 PE=1 SV=2 # H3BUB0 TLD domain-containing protein 1 (Fragment) OS=Homo sapiens GN=TLDC1 PE=1 SV=1 # H3BM75 TLD domain-containing protein 1 OS=Homo sapiens GN=TLDC1 PE=1 SV=1 #
SFC*SQFLPEEQAEIDQLFDA LSSDKNSPNVSSK	C13;C13;C13	1.425263004	Q6P9B6 H3BUB0 H3BM75	P48506 Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 # E1CEI4 Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=1 # P09914 Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 # P09914-2 Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 #
GGNAVVDGC*GK	C501;C463	1.381583205	P48506 E1CEI4	P09914 Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 # P09914-2 Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 #
MEC*PEIDCEEGWALLK	C138;M105 C107	1.374826823	P09914 P09914	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 # Q8TC07-3 Isoform 3 of TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 # Q8TC07-2 Isoform 2 of TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 # Q8TC07 TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 PE=1 SV=2 #
SVVC*QESDLPDELLYGR	C187	1.373759941	Q9NS86	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
NDSPTQIPVSSDVC*R	C677;C669;C686	1.356918787	Q8TC07 Q8TC07 Q8TC07	O14929 Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1 # Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 # H3BQH0 Calponin-2 (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=2 # Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # Q99439-2 Isoform 2 of Calponin-2 OS=Homo sapiens GN=CNN2 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # H3BVI6 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X1X5 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #
EVFSSC*SSEVVLSGDDEEYQR	C108	1.352671012	Q09666	
SC*TPSPDQISHR	C272;C272	1.347035739	C9J6P4 Q7Z2W4	
VDENFDC*VEADDVEGK	C101	1.333775114	O14929	
IISDNLYC*K	C205	1.332715795	Q9Y2X3	
C*ASQSGMTAYGTR	C73;C175;C136; C196;C132;C112	1.288066641	H3BQH0 Q99439 Q99439 B4DUT8 H3BVI6 A0A087X1 X5	

TTSSANNPNLMYQDEC*DR	C586;M502 C507;M579 C507;M581 C584;M500 C505	1.284095	Q92841 H3BLZ8 Q92841 Q92841 Q92841	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 # Q92841-2 Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 # Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 # P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 # B0QYD3 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 # Q9UH17 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 # P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 # O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 # O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O14556 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 # K7EP73 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific (Fragment) OS=Homo sapiens GN=GAPDHS PE=1 SV=1 # O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # P49189 4-trimethylaminobutylaldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 #
SC*SGVEFSTSGSNTDTGK VTGTLETK	C47;C47	1.274127028	A0A0A0MR02 P45880	
SC*GSSTPDEFPTDIPGTK	C105	1.270874365	P41091	
NLLC*GFYGR	C247;C247	1.245943301	B0QYD3 Q9UH17	
VIEINPYLLGTMSGC*AADCQ YWER	C116;C120;C120	1.227949656	P28062 X5D2R7 P28062	
NSFYMGTC*QDEPEQLDDWNR	C1893;M1904 C771 C1907;M768	1.222586906	Q14980 Q14980 Q14980	
LHDAIVEVWTC*LLR	C483;C470;C470; 0;C470;C470;C483; C483;C470	1.213150242	O00429 O00429 O00429 O00429 O00429 G8JLD5 O00429	
YNPGSMNIVSNASC*TTNCLA PLAK	C156 C224;M148	1.2054579	O14556 K7EP73	
NTPLC*DSFVFR	C429	1.16269152	O95573	
GALMANFLTQQQVC*CNGTR	C288	1.161636677	P49189	

HC*SQVDSVR	C112;C112;C112	1.159810875	Q14247 Q14247 Q14247	Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN # Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 # Q14247-2 Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN #
LESLQSMEMAHSGSLRDEL C*LDFPCDSPEK	C259;C386;C388; C389;C183;C321; C394;C270	1.157812221	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	B7Z4D2 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-4 Isoform 4 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95-3 Isoform 3 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=2 # B3KRD1 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-2 Isoform 2 of Syntabulin OS=Homo sapiens GN=SYBU # A0A0C4DG86 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-5 Isoform 5 of Syntabulin OS=Homo sapiens GN=SYBU #
HGFC*GIPITDGR	C140	1.140393761	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
ELEVLLMC*NK	C91;C109;C91	1.128422911	P62910 F8W727 D3YTB1	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
KAC*GDSTLTQITAGLDPVGR	C25	1.12115342	P62879	P62879 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 #
FQSSAVMALQEACEAYLVGL FEDTNLC*A	C111	1.098616144	P68431	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 #
AQILVLTYPILIGNYGIPPEMD EFGLC*K	C73	1.093895317	P27708	P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
LVIVGDGAC*GK	C16;C16;C16	1.073883265	C9JX21 C9JNR4 P61586	C9JX21 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # C9JNR4 Transforming protein RhoA (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 #
VGVGTC*GIADKPMYQYQDT SK	C214	1.069938624	O75940	O75940 Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 #
IIDLEEADEIEDIQQEITVLSQ C*DSPYVTK	C77;C77;C89	1.069631575	Q9Y6E0 B4DR80 Q9Y6E0	Q9Y6E0-2 Isoform A of Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 # B4DR80 Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 # Q9Y6E0 Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 #
VSLDPELEEALTSASDTELC* DLAAILGMHNLITNTK	C132	1.066706191	Q9NYL9	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 #
FQLTDC*QIYEVLSVIR	C143;C179	1.056862602	Q16555 Q16555	Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
LC*VQNSPQEAR	C150;C150;C150; C150;C141	1.033422251	P33240 P33240 E7EWR4 E9PID8 A0A0A0M T56	P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 # P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #



TVGVQGDC*R	C523	0.942243247	P49915	P49915 GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 #
MAGIFDVNTC*YGSPQSPQLIR	C467;C468;C468;C428;C353	0.939950943	Q9BTX1 Q9BTX1 Q9BTX1 Q9BTX1 Q9BTX1	Q9BTX1-2 Isoform 2 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 # Q9BTX1 Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 PE=1 SV=2 # Q9BTX1-4 Isoform 4 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 # Q9BTX1-5 Isoform 5 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 # Q9BTX1-6 Isoform 6 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 #
LSLLEEYGCC*K	C573	0.93793748	P53350	P53350 Serine/threonine-protein kinase PLK1 OS=Homo sapiens GN=PLK1 PE=1 SV=1 #
TTPVDLC*LLEESVGSLEGSR	C1499	0.92974468	Q9UKK3	Q9UKK3 Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3 #
FTLDC*THPVEDGIMDAANFEQFLQER	C25	0.92147	P35268	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 #
GLC*AIAQAESLR	C97	0.920737697	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #
TDICQGALGDC*WLLAAIASLT LNEEILAR	C105	0.91948111	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
QC*TGLQGFLVFHSFGGGTG SGFTSLLMER	C129;C129;C129	0.911581286	Q9BQE3 Q71U36 P68366	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
LPLC*SLPGEPEGNGPDQQLQR	C75	0.911572434	Q96GX2	Q96GX2 Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 #
RVDDFEAGAAAGAAPGEEDLC*AAFNVICDNVVK	C98	0.902537261	Q13158	Q13158 FAS-associated death domain protein OS=Homo sapiens GN=FADD PE=1 SV=1 #
FQSAAGALQEASEAYLVGLF EDTNLC*A	C111;C111	0.897859559	K7EK07 P84243	K7EK07 Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1 # P84243 Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 #
LSLEPLPC*YQLELDAVAEV K	C32	0.89515824	Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 #
TDFQQGC*AK	C170	0.88336877	O95571	O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 #
ISEVFDK*WFEESGSMYPYQV HYPFENKR	C526	0.877392557	A0A0A0M SX9 P41252	A0A0A0MSX9 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # P41252 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 #
INQMVC*NSDR	C853	0.857946108	P06400	P06400 Retinoblastoma-associated protein OS=Homo sapiens GN=RB1 PE=1 SV=2 #
AAC*LESAQEPAGAWGNK	C53;C53;C53;C53;C53;C53;C53;C53;C53	0.85707	C9JT62 C9JES8 C9JK79 C9JHZ8 C9JIZ1 C9JZI8 A0A024R4 E5 C9J5E5 C9JHS7	C9JT62 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JES8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JHZ8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JIZ1 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JZI8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # A0A024R4E5 High density lipoprotein binding protein (Vigilin)# isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1 # C9J5E5 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 # C9JHS7 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 #

TDVC*VFAAQEDLETMQAFA QVFNK	C96	0.856237625	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # A9UHW6-3 Isoform 3 of MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD # J3KSB8 MIF4G domain containing isoform 4 OS=Homo sapiens GN=MIF4GD PE=1 SV=1 # J3QRZ6 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=7 # A9UHW6-2 Isoform 2 of MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD # A9UHW6 MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD PE=1 SV=1 # P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 # P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A # P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 # Q5BIX2 Chromosome 18 open reading frame 25# isoform CRA_a OS=Homo sapiens GN=ARKL1 PE=1 SV=1 # Q96B23-2 Isoform 2 of Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 # A0A087WVF1 Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=1 # K7EQH1 Uncharacterized protein C18orf25 (Fragment) OS=Homo sapiens GN=C18orf25 PE=1 SV=1 # Q96B23 Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=2 # Q16576-2 Isoform 2 of Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 # Q16576 Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 # Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 # P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 # Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 # Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 # P36959 GMP reductase 1 OS=Homo sapiens GN=GMPT PE=1 SV=1 # P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 #
VANVIVDHSLQDC*VFSK	C90;C49;C49;C83;C49	0.848571018	A9UHW6 J3KSB8 J3QRZ6 A9UHW6 A9UHW6	
YDC*GEEILITVLSAMTEEA AIAK	C159	0.847429638	P63241 P63241	
VLDALFPCVQGGTTAIPGAFG C*GK	C221;C254	0.815872075	P38606 P38606	
DGVADSTVISSMPC*LLMELR	C57	0.80984	Q5BIX2 Q96B23 A0A087WVF1 VF1 K7EQH1 Q96B23	
VHIPNDDAQFDASHC*DSDK GEFGGFGSVTGK	C141;C97	0.807377706	Q16576 Q16576	
FFACAPNYSYAALCEC*LR	C513	0.801086561	Q96RS6	
DVLIEFYAPWCGHC*K	C558;C409	0.797455	P13667 P30101	
AFVNPFPDYEEAAGALLASG AAEETGC*VRPPATTDEPLP FHQDGK	C49	0.79525253	Q9NS86	
DSAQC*AAIAER	C376	0.79452781	Q96RS6	
GSQMGTVQPIPC*LLSMPTR	C531 C559;M523	0.790326765	Q9NZB2 Q9NZB2	
VGVGPGSVCTTR	C186	0.786617838	P36959	
VVVAENFDEIVNENKDV LIEFYAPWC*GHCK	C406	0.785782507	P30101	



				O00233-2 Isoform p27-S of 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 # O00233 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 #
GIGMNEPLVDC*EGYPR	C59;M52 C59	0.783775132	O00233 O00233 J3KN29 F5H7X1 F5H5V4 F5GX23	J3KN29 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H7X1 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H5V4 26S proteasome non-ATPase regulatory subunit 9 (Fragment) OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5GX23 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 #
NCAVSC*AGEK	C141;C141	0.778658469	Q15813 Q15813	Q15813 Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 # Q15813-2 Isoform 2 of Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE #
TAIHTAAMDMLGGPGIESQC* R	C218	0.768570348	Q6YN16	Q6YN16 Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 #
LQGINC*GPDFTPSFANLGR	C662;C622;C575;C466;C622;C498;C669;C498;C466	0.766965351	Q04637 Q04637 E9PGM1 Q04637 Q04637 E7EJU4 Q04637 Q04637 E7EX73 Q04637	Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EJU4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 #
SC*GHQTSASSLK	C377	0.766829979	Q9HB90	Q9HB90 Ras-related GTP-binding protein C OS=Homo sapiens GN=RRAGC PE=1 SV=1 #
GVLLYGPPGC*GK	C137	0.764393441	Q8NBU5	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 #
FC*NIMGSSNGVDQEHFSNV VK	C150	0.762191273	Q9NYL9	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 #
NDITAWQEC*VNNSMAQLEH QAVR	C106	0.760448487	O75934	O75934 Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 #
AHSNPDFLPVDNC*LQSVLG QR	C703;C798	0.754668734	Q5VSL9 Q5VSL9	Q5VSL9-2 Isoform 2 of Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 # Q5VSL9 Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 PE=1 SV=1 #

DC*GGAAQLAGPAAEADPLGR	C8;C8;C8;C8;C8;C8;C8	0.7513982	Q9Y508 A0A096LNV3 A0A096LNT1 A0A096LP02 Q9Y508 A0A096LNN8 A0A096LPF9	Q9Y508 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNV3 E3 ubiquitin-protein ligase RNF114 (Fragment) OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNT1 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 # A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 #
VCHKLGDLLCC*ETCSAVYHLECVK	C405;C405;C405;C405;C266	0.7497	Q12830 F5GXF5 Q12830 Q12830 E7ETD6	Q12830-4 Isoform 4 of Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF # F5GXF5 Nucleosome-remodeling factor subunit BPTF (Fragment) OS=Homo sapiens GN=BPTF PE=1 SV=2 # Q12830-2 Isoform 2 of Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF # Q12830 Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3 # E7ETD6 Nucleosome-remodeling factor subunit BPTF (Fragment) OS=Homo sapiens GN=BPTF PE=1 SV=3 #
LTPGC*EAEAETEAIFFVQQFTDMEHNR	C2359	0.744371422	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
DSGAASEQATAAPNPC*SSSR	C671;C696	0.743680729	Q9BU23 Q9BU23	Q9BU23-2 Isoform 2 of Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 # Q9BU23 Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 PE=1 SV=2 #
ECISIHVGQAGVQIGNAC*WE LYCLEHQIPDGMPSDK	C20	0.742230994	Q13748 Q9BQE3 Q71U36	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 #
FQSSAVMALQEASEAYLVGL FEDTNLC*A	C111	0.739932936	Q71DI3	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 #
AQNTWGC*GNSLR	C410;C423;C148;C522;C522	0.738786104	P02545 P02545 A0A0C4DGC5 P02545 P02545	P02545-4 Isoform 4 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-5 Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA # A0A0C4DGC5 Prelamin-A/C (Fragment) OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545-3 Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA #
WLSDEC*TNAAVNFSLR	C345;C350;C380	0.737850822	O75521 A0A0C4DGA2 O75521	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 #
VILALGDYMGATCHAC*IGGT NVR	C135 C135;M128 C136;M128	0.734527535	Q14240 Q14240 E7EQG2	Q14240-2 Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 # Q14240 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2 # E7EQG2 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=1 #

VTQNLPMKEGC*TEVSLLR	C308	0.733301052	Q1KMD3	Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #
NVTQIEPFC*LETDRR	C630;C594	0.73264344	Q9ULW0 Q9ULW0	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 # Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 # Q9UJW0 Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1 #
LLQPDFQPVC*ASQLYPR	C258;C201;C265	0.731041426	Q9UJW0 Q9UJW0 Q9UJW0	Q9UJW0-2 Isoform 2 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # Q9UJW0-3 Isoform 3 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 #
SCSSSC*AVHDLIFWR	C46	0.723292975	O95197	O95197-3 Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3 #
LLSNMMC*QYR	C156;C160;C160	0.719676667	P28062 X5D2R7 P28062	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 #
LDINLLDNVNC*LYHGEGAQQR	C34	0.714218727	O14980	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 #
GEASEDLC*EMALDPELLLLR DDGEEEFAGAK	C644	0.714196488	Q8N163 Q8N163	Q8N163 Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2 # Q8N163-2 Isoform 2 of Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 #
ELETVC*NDVLSLLDK	C97	0.71406	Q04917	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 #
AAQLC*GAGMAAVVDK	C838;C834;C822;C833	0.71237	P19367 P19367 P19367 P19367	P19367-3 Isoform 3 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367 Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 # P19367-4 Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367-2 Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1 #
TTC*MSSQGSDEQIKR	C22;C22;C22;C22	0.712269092	Q9P0V9 Q9P0V9 E7EW69 B5ME97	Q9P0V9-2 Isoform 2 of Septin-10 OS=Homo sapiens GN=SEPT10 # Q9P0V9 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EW69 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 # B5ME97 Septin 10# isoform CRA_c OS=Homo sapiens GN=SEPT10 PE=1 SV=2 #
LMGLLSDPELGAAAADGFSLL MSDC*TDVLTR	C869;M825 C848	0.706208681	Q96T76 Q96T76	Q96T76-8 Isoform 5 of MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 # Q96T76 MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 #
LGTLAPFC*CPWEQLTQDWE SR	C705	0.704536351	Q99575	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 #
AVQDLC*GWR	C428	0.700260762	Q9P258	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 #
GPTKEELC*K	C466;C453	0.700010487	Q96TA1 Q96TA1	Q96TA1 Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 # Q96TA1-2 Isoform 2 of Niban-like protein 1 OS=Homo sapiens GN=FAM129B #
HEFSVDMTC*GGCAEAVSR	C12	0.695440273	O00244	O00244 Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 #
C*ASQAGMTAYGTR	C173	0.690833754	Q15417	Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 #
VVSGMVNC*NDDQGVLGR	C230	0.686876952	P21980	P21980 Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 #

TIQFVDWC*PTGFK	C347;C281;C37 1;C347;C347	0.685213432	Q9BQE3 Q9NY65 C9J2C0 Q71U36 Q9NY65	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
ADEASELAC*PTPK	C2202	0.684074761	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
SC*PSFSASSEGTR	C9;C9	0.683600163	P27707 D6RFG8	P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
TGC*TFPEKPDFH	C353;C336	0.681441347	P55263 P55263	P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 # P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK #
GDSEPTPGC*SGLGPGGVR	C13;C13;C12;C1 3;C13	0.67924564	Q8WW01 Q8WW01 HOYCV5 E9PPN1 F2Z3M0	Q8WW01 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # Q8WW01-2 Isoform 2 of tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 # HOYCV5 tRNA-splicing endonuclease subunit Sen15 (Fragment) OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # E9PPN1 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # F2Z3M0 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 #
ISDLEIC*ADEFPGSSATYR	C35;C106;C171; C106;C171	0.675243203	Q96IZ6 A0A087W W35 Q6P1Q9 Q6P1Q9 Q96IZ6	Q96IZ6-2 Isoform 2 of Methyltransferase-like protein 2A OS=Homo sapiens GN=METTL2A # A0A087WW35 Methyltransferase-like protein 2A OS=Homo sapiens GN=METTL2A PE=1 SV=1 # Q6P1Q9 Methyltransferase-like protein 2B OS=Homo sapiens GN=METTL2B PE=1 SV=3 # Q6P1Q9-2 Isoform 2 of Methyltransferase-like protein 2B OS=Homo sapiens GN=METTL2B # Q96IZ6 Methyltransferase-like protein 2A OS=Homo sapiens GN=METTL2A PE=1 SV=5 #
IIVPFVTC*GDLSSYSDSR	C238;C236	0.67470992	Q9UET6 Q9UET6	Q9UET6 Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens GN=FTSJ1 PE=1 SV=2 # Q9UET6-2 Isoform 2 of Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens GN=FTSJ1 #
FSFQC*PGR	C285;C346;C37 7	0.668120029	Q13418 Q13418 A0A0A0M TH3	Q13418-2 Isoform 2 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK # Q13418 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 # A0A0A0MTH3 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1 #
TC*NVLVALEQQSPDIAQGVH LDR	C104	0.662189393	P31153	P31153 S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 #
VGESNLNNGDEPTQC*SR	C570;C549	0.657499194	Q96T76 Q96T76	Q96T76-8 Isoform 5 of MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 # Q96T76 MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 #
FFFVGC*NK	C238	0.656087461	Q96QR8	Q96QR8 Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3 #

KLDTNSDGQLDFSEFLNLIGG LAMAC*HDSFLK	C91	0.654358907	P31949	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 #
VNSDC*DSVLPNFFLLGGNIF DPLNLSLLDDEEVS	C177	0.653818878	Q7L2J0	Q7L2J0 7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1 #
VMAEANHFIDLSQIPC*NGK	C620	0.653195838	O15294	O15294 UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3 #
AAAENLPVPAELPIEDLC*SLT SQSLPIELTSVVPESTEDILLK	C65	0.650973333	Q96JB2	Q96JB2 Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3 #
APVPSTC*SSTFPEELSPPSH QAK	C160;C160;C16 0;C160;C160;C1 60;C160;C160	0.648692882	A0A087W Y61 Q14980 Q14980 Q14980 F5H6Y5 F5H4J1 Q14980 Q14980	A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980-3 Isoform Numa-m of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # F5H6Y5 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # F5H4J1 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=7 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980-4 Isoform Numa-s of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 #
NSNVDSYLESYQSC*PR	C767;C645	0.64571132	C9J6P4 Q7Z2W4	C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
IIDINYYVPEAC*LSNKR	C492	0.642134604	P23921	P23921 Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 #
AVSTGVQAGIPMPC*FTTALS FYDGYR	C409 C422;M407	0.637865	P52209 P52209	P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6- phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
LSEAAC*EEDSASEGLGELF LDGLSTENPHGAR	C238	0.637307308	O95801	O95801 Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 # E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 #
HELQANC*YEEVKDR	C177;C122;C13 9	0.636030902	E9PK25 G3V1A4 P23528	Q96EF6 F-box only protein 17 OS=Homo sapiens GN=FBXO17 PE=1 SV=1 # Q9NQ88 Fructose-2#6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 # A0A0U1RQD1 Chromosome 12 open reading frame 5# isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 #
NLIFNSC*GEQGFRGWEVEH GGNGWAIEK	C114	0.627719128	Q96EF6	P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 # P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 #
EADQKEQFSQGSNSNC*LET SLAEIFPLGK	C161;C102	0.626185166	Q9NQ88 A0A0U1R QD1	Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
NC*DKGQSFFIDAPDSPATLA YR	C266;C277	0.626110471	P53384 P53384	O76031 ATP-dependent Clp protease ATP- binding subunit clpX-like# mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2 #
SLDDSQC*GITYK	C282	0.62332778	Q9NVG8	
NAVIPQYQALFMSDKC*ELNV TEDALK	C538	0.623094443	O76031	

FVVDVDKNIDINDVTPNC*R	C112;C104	0.622721986	P62195 P62195	P62195 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 # P62195-2 Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 #
NEC*DPALALLSDYVLHNSNT MR	C459	0.621163333	Q13200	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 #
VQILPEC*VLPSTMSAVQLES LNK	C188;C184;C18 7	0.620698194	Q96SW2 J3QT87 Q96SW2	Q96SW2 Protein cereblon OS=Homo sapiens GN=CRBN PE=1 SV=1 # J3QT87 Protein cereblon (Fragment) OS=Homo sapiens GN=CRBN PE=1 SV=1 # Q96SW2-2 Isoform 2 of Protein cereblon OS=Homo sapiens GN=CRBN #
LC*DFGISGQLVDSIAK	C257;C246	0.618496598	P45985 P45985	P45985-2 Isoform 2 of Dual specificity mitogen-activated protein kinase 4 OS=Homo sapiens GN=MAP2K4 # P45985 Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens GN=MAP2K4 PE=1 SV=1 #
SGLTPNDIDVIELHDC*FSTNE LLTYEALGLCPEGQGATLVDR	C307;C307	0.618390538	E9PLD1 P22307	E9PLD1 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=1 # P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 #
FHADSVK	C25	0.613218076	Q9BW61	Q9BW61 DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1 #
FIC*EQDHNFLR	C658;C614	0.612656727	Q92598 Q92598	Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 #
NC*LTNFHGMDLTR	C96	0.610409256	P61247	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 #
HSFYVAC*AMLLDGGITVPS FHEC*QINR	C355;C339 C355 C339	0.60916491	H7C1Q4 A6NK06	H7C1Q4 Protein ACOD1 OS=Homo sapiens GN=ACOD1 PE=4 SV=1 # A6NK06 Cis- aconitate decarboxylase OS=Homo sapiens GN=IRG1 PE=1 SV=1 #
SQTIYEIIDNSQGFYVC*PVEP QNR	C291	0.606406164	Q9Y617	Q9Y617 Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 #
LC*YVALDFENEMATAASSSS LEK	C219	0.606383968	P68032	P68032 Actin# alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 #
LEDVENLGC*R	C329;C329	0.604660465	Q9UJX3 Q9UJX3	Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 #
IEEDVVVTDSGIELLTC*VPR	C403;C467	0.602513529	P12955 P12955	P12955-3 Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa- Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
GAEPETGSAVSAAQC*QVGP TR	C90;C69	0.596709707	E7ERK9 Q9U110	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9U110 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
LGEVWGLC*K	C92	0.583404544	P25398	P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 #
EGIC*ALGGTSELSSSEGTQHS YSEEEKYAFVNWINK	C104	0.581312759	P13797	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
AVC*MLSNTTAVAEAWAR	C376	0.576160778	Q9BQE3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
SSGGFVWAC*K	C308	0.576140184	P48735	P48735 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 #
RPTEIC*ADPQFIIGGATR	C82	0.573600392	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
NAGNC*LSPAVIVGLLK	C369;C335	0.573062074	O43175 Q5SZU1	O43175 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 # Q5SZU1 D-3- phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 #

EQNYC*ESR	C160	0.571789272	Q7L5D6	Q7L5D6 Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1 # F8VWV8 3'(2')#5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens GN=BPNT1 PE=1 SV=2 # O95861-4 Isoform 4 of 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 # A6NF51 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=2 # O95861
TC*ATDLQTK	C42;C42;C42;C42;C42;C42	0.570662612	F8VWV8 O95861 A6NF51 O95861 F8VZG4 O95861 F8W1J0	OS=Homo sapiens GN=BPNT1 PE=1 SV=1 # F8VZG4 3'(2')#5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens GN=BPNT1 PE=1 SV=1 # O95861-2 Isoform 2 of 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 # F8W1J0 3'(2')#5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens GN=BPNT1 PE=1 SV=1 # A0A087WYB4 Stomatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 # Q9UJZ1 Stomatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 #
ESLNASIVDAINQAADC*WGIR	C121;C167	0.569777364	A0A087WYB4 Q9UJZ1	Q9H4L5-2 Isoform 1b of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5-3 Isoform 1c of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5 Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1 # Q9H4L5-4 Isoform 1d of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 #
QNLFQTGSNVSFSC*GGETR	C203;C203;C203;C203	0.567224995	Q9H4L5 Q9H4L5 Q9H4L5 Q9H4L5	Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 # E9PGE5 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=1 # Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 #
FLENTPSSLNIEDIEDLFLSLAQ YYC*SK	C283;C146;C283	0.56649424	Q9NUY8 E9PGE5 Q9NUY8	Q96DC7 Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 PE=1 SV=2 # A0A087WT20 DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13 PE=1 SV=1 # Q9NV06 DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13 PE=1 SV=2 #
NDAPEEAGEGC*VAAILGETE VQQFLR	C57	0.56610536	Q96DC7	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
FNPIETFLLGSC*ASDR	C367;C215	0.563870387	A0A087WT20 Q9NV06	O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB # P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
VWNLANC*K	C182	0.560903026	P63244	P55884 Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 # P55884-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B # P01769 Ig heavy chain V-III region GA OS=Homo sapiens PE=1 SV=1 #
SSTETC*YSAIPK	C2477;C2436	0.559654933	O75369 O75369	
RVFIMDNC*EELIPEYLNfir	C496;M371 C374	0.558198595	P07900 P07900	
FSHQGVQLIDFSPC*ER	C384;C384;	0.557974738	P55884 P55884 P01769	

LNQVC*FDDDDGTSSPQDR	C422;C422	0.55789403	H3BVG0 Q8N1F7	H3BVG0 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=1 # Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 #
GLDYEGGGC*R	C691	0.552648955	O60568	O60568 Procollagen-lysine#2-oxoglutarate 5- dioxxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 #
SDPLC*VLLQDVGGGSWAEL GR	C35;C30	0.552565372	B0QZ18 Q99829	B0QZ18 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # Q99829 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 #
SYC*NDQSTGDIK	C106	0.552536804	P00492	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
GC*WDSIHVVEVQEK	C147;C147;C17 6;C135;C173	0.551560645	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
C*KETPYSEEDFQHLQK	C104	0.54639311	Q9H081	Q9H081 Protein MIS12 homolog OS=Homo sapiens GN=MIS12 PE=1 SV=1 #
ENFSLDWC*K	C117	0.545707772	P23919	P23919 Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 #
FPEELTQTFMSC*NLITGMFQ R	C389 C339;M387	0.543993506	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1- gamma OS=Homo sapiens GN=EEF1G # P45984-2 Isoform Alpha-1 of Mitogen- activated protein kinase 9 OS=Homo sapiens GN=MAPK9 # P45984-4 Isoform Beta-2 of Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 # P45984 Mitogen- activated protein kinase 9 OS=Homo sapiens GN=MAPK9 PE=1 SV=2 # J3KKNK1 Mitogen- activated protein kinase OS=Homo sapiens GN=MAPK9 PE=1 SV=1 # P45984-3 Isoform Beta-1 of Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 #
TAC*TNFMTPYVVTR	C177;C177;C17 7;C177;C177	0.541913591	P45984 P45984 P45984 J3KKNK1 P45984	O94804 Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1 # Q86XX4-2 Isoform 2 of Extracellular matrix protein FRAS1 OS=Homo sapiens GN=FRAS1 # Q86XX4 Extracellular matrix protein FRAS1 OS=Homo sapiens GN=FRAS1 PE=1 SV=2 # Q86XX4-5 Isoform 5 of Extracellular matrix protein FRAS1 OS=Homo sapiens GN=FRAS1 # O00743 Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1 # O00743-3 Isoform 3 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C # O00743-2 Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C #
LSEEAEC*PNPSTPSK	C947	0.541493281	O94804	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #
DPLHVLRDGGC*ESSCGK	C543;C543;C54 3	0.541007811	Q86XX4 Q86XX4 Q86XX4	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
GAFC*DLVWSDPEDVDTWAI SPR	C192;C229;C17 0	0.539134646	O00743 O00743 O00743	
INQVFHGSC*ITEGNELTK	C1904	0.538753831	P78527	
LEIC*NLTPDTLTSPTYK	C341	0.538733436	P17655	



AYHEQLSVAEITNAC*FEPAN QMVK	C295	0.536336099	Q71U36 P68366	Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
SWC*PDCVQAEPVVR	C43	0.533233971	Q9BRA2	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 #
C*PNLTYLNLSGNK	C87;C39	0.53232	Q9BTT0 Q9BTT0	Q9BTT0 Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1 # Q9BTT0-3 Isoform 3 of Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E #
VGLGIC*YDMR	C153	0.530980294	Q9NQR4	Q9NQR4 Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 #
KC*STPEEIK	C6;C23	0.530183753	P60981 P60981	P60981-2 Isoform 2 of Dextrin OS=Homo sapiens GN=DSTN # P60981 Dextrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
IKSGEEDFESLASQFSDC*SS AK	C113	0.529384574	Q13526	Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 #
VQPQWSPAGTQPC*R	C110	0.524722863	P49589	P49589-3 Isoform 3 of Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS #
DVC*EAMEYLESKQFLHR	C540;C506;C506 6	0.520194371	Q06187 U3NG26 Q06187	Q06187-2 Isoform BTK-C of Tyrosine-protein kinase BTK OS=Homo sapiens GN=BTK # U3NG26 Tyrosine-protein kinase OS=Homo sapiens GN=BTK PE=1 SV=1 # Q06187 Tyrosine-protein kinase BTK OS=Homo sapiens GN=BTK PE=1 SV=3 #
KENQWC*EEK	C160	0.520194297	P63208	P63208 S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2 #
SPWLAGNELTVADVVLWSVL QQIGGC*SVTVPANVQR	C291	0.518925324	Q13155	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 #
VWNNSSTVNAVVPAPPVC*D VAR	C558	0.518778545	Q96EN8	Q96EN8 Molybdenum cofactor sulfurylase OS=Homo sapiens GN=MOCOS PE=1 SV=2 #
SWVFDSYSLTGPSVC*ELVR	C118;C154;C92; C78;C154	0.51830135	Q8NB37 Q8NB37 H0YF25 H0YE25 Q8NB37	Q8NB37-3 Isoform 3 of Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 # Q8NB37 Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # H0YF25 Parkinson disease 7 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # H0YE25 Parkinson disease 7 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # Q8NB37-2 Isoform 2 of Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 #
LECVEPNC*R	C77;C77;C113;C 77;C77	0.517549172	P83881 Q969Q0 J3KQN4 H7BZ11 H0Y5B4	P83881 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 # Q969Q0 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 # J3KQN4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=1 # H7BZ11 Protein RPL36A-HNRNPH2 OS=Homo sapiens GN=RPL36A-HNRNPH2 PE=3 SV=2 # H0Y5B4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=2 #
LPTDLTAC*DNR	C111	0.515689	Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDC1 PE=1 SV=2 #

ARDC*LIPMGITSEVAER	C177	0.513842644	P09110 C9JDE9	P09110 3-ketoacyl-CoA thiolase# peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 # C9JDE9 3-ketoacyl-CoA thiolase# peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=1 #
HPSIIFIDELDALC*PK	C459	0.511506064	Q8NB90	Q8NB90 Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3 # A0A0A0MR02 Voltage-dependent anion- selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 # H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 # O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 # O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 #
VC*EDLDTSVNLAWTSGTNC TR	C210;C210	0.510244529	A0A0A0M R02 P45880	
VC*EEIAIPSKK	C35;C35;C35	0.510036042	H0YN88 A0A075B7 16 P08708	
C*YVQPQWVFDVSVNAR	C391;C386	0.50966773	O00541 O00541	
NC*GCLGASPNLEQLQEENL K	C32	0.507719271	P54136	P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 #
VLLSICSLLC*DPNPDDPLVPE IAR	C111;C111	0.506807901	P61077 P61077	
C*EFQDAYVLLSEK	C237	0.505364641	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 # P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 # P53396-2 Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY # Q99757 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 # F8WDN2 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 # P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 # Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 # P29279 Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2 # P29279-2 Isoform 2 of Connective tissue growth factor OS=Homo sapiens GN=CTGF # O00487 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 # P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
FIC*TTSAIQNR	C20;C20	0.502357951	P53396 P53396	
VVNSETPVVDFHAQWC*GP CK	C90;C90	0.497242727	Q99757 F8WDN2	
VADSSPFALELLISDDCFVLD NGLC*GK	C275;C290	0.495351082	P40121 P40121	
VQENSAYIC*SR	C585	0.494207339	Q9Y3T9	
LPSPDC*PFPR	C148;C148	0.489628543	P29279 P29279	
SWMEGLTLQDYSEHC*K	C238	0.48396	O00487	
VSDTVVEPYNATLSVHQLVE NTDETYCIDNEALYDIC*FR	C211;C211;C21 1;C211;C211	0.48029841	P07437 P68371 Q9BVA1 P04350 Q9BUF5	

FDPTQFQDC*IIQGLTETGTDL EAVAK	C35;C67;C39	0.479558012	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q15084-2 Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-4 Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-5 Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 # Q15084-3 Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 #
DVIELTDDSFKNVLDSEDEVW MVEFYAPWC*GHCK	C238;M182 C187 C242;M187 C195;M230 C190;M179	0.478411337	Q15084 Q15084 Q15084 Q15084 Q15084	Q86TX2 Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 # A0A087X0W7 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # P49753-2 Isoform 2 of Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 # P49753 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 # A0A087WT95 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # A0A0J9YWB6 RNA polymerase II subunit A C-terminal domain phosphatase (Fragment) OS=Homo sapiens GN=CTDP1 PE=1 SV=1 # A0A0J9YWJ4 RNA polymerase II subunit A C-terminal domain phosphatase (Fragment) OS=Homo sapiens GN=CTDP1 PE=1 SV=1 # K7EJD2 RNA polymerase II subunit A C-terminal domain phosphatase (Fragment) OS=Homo sapiens GN=CTDP1 PE=1 SV=1 # Q9Y5B0-4 Isoform 4 of RNA polymerase II subunit A C-terminal domain phosphatase OS=Homo sapiens GN=CTDP1 # Q9Y5B0 RNA polymerase II subunit A C-terminal domain phosphatase OS=Homo sapiens GN=CTDP1 PE=1 SV=3 #
SEFYANEAC*K	C339;C339;C219; C401;C381	0.478236667	Q86TX2 A0A087X0 W7 P49753 P49753 A0A087W T95	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
LEGC*SHPVVMKGLCAEC*G QDLTQLQSK	C59;C46 C59;C114 C127;C114 C127;C46 C114 C127	0.478169088	A0A0J9Y WB6 A0A0J9Y WJ4 K7EJD2 Q9Y5B0 Q9Y5B0	Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 #
YMAC*CLLYR	C315 C315;M320 C322;M313 C282;M313 C315;M280	0.477615303	Q9BQE3 A6NHL2 Q71U36 A6NHL2 P68366	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # Q9UNA3 Alpha-1#4-N-acetylglucosaminyltransferase OS=Homo sapiens GN=A4GNT PE=2 SV=1 #
C*YLTMTQALEAR	C1888	0.477276714	Q14204	Q13325 Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 PE=1 SV=1 #
DEYSIDNEALYDIC*FR	C211	0.476542719	Q13885	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 #
SSC*LFCLPSFK	C29	0.476105023	Q9UNA3	
IDPENAEFLTALC*ELR	C476	0.47332831	Q13325	
NIC*FTVWDVGGQDK	C62	0.466917384	P84085	

ENFDEVVNDADIIILVEFYAPW CGHC*K	C209	0.46597068	P13667	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # A0A075B736 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=1 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 # Q5SQY0 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 # Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 # Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine- protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
NMMAAC*DPR	C266;M228 C231;M266 C303;M647 C303 C303;M282 C269;M300 C285;M300 C303;M300 C650;M263	0.46591953	Q13509 P68371 Q13885 A0A0B4J2 69 A0A075B7 36 Q13509 Q5SQY0 Q9BVA1 A6NNZ2 Q3ZCM7 P04350 Q5JP53 Q9BUF5	
EENVGLHQTLTDLQTLNELNC*I	C283;C109;C24 7	0.46528992	P67936 K7EPB9 P67936	
QGFWEFETLQQQEC*K	C259;C259	0.46459	Q06124 Q06124	
LNPVATC*AGK	C878	0.462817301	Q8TD19	Q8TD19 Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2 # Q8NBF2 NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 #
AILFSQPLQITDTQQGC*IAPV ELR	C716	0.461523929	Q8NBF2	
NIC*FTVWDVGGQDR	C62	0.461023049	P18085	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 # Q99590 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 # A0A0A0MTP7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 # Q99590-2 Isoform 2 of Protein SCAF11 OS=Homo sapiens GN=SCAF11 # F8VXG7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 #
VGSSSES*EQDLPLVGE EGEVK	C478;C418;C16 3;C286	0.460827843	Q99590 A0A0A0M TP7 Q99590 F8VXG7	
TAFQEALDAAGDKLVVDF ATWC*GPKK	C32	0.460218264	P10599	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 # B3KVZ3 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 # Q9H3R5 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 # Q02750 Dual specificity mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 #
AGGPPQVAGAQAAC*SEDR	C35;C35	0.45732126	B3KVZ3 Q9H3R5	
ELELMFGC*QVEGDAAETPP RPR	C251 C277;M248	0.455763132	Q02750 Q02750	

YMACC*LLYR	C316;M280 C316;M320 C316 C323;M313 C283;M313	0.451676596	Q9BQE3 A6NHL2 Q71U36 A6NHL2 P68366	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
SVPTTQC*LDNSK	C226;C226	0.451255	A0A087WV66 P46013	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 #
MYGISLC*QAILDETKGDYEK	C324	0.451155543	P04083	Q5R363 SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 # Q96SB4-3 Isoform 1 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 # H3BLV9 SRSF protein kinase 1 (Fragment) OS=Homo sapiens GN=SRPK1 PE=1 SV=1 # Q96SB4 SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 # Q96SB4-4 Isoform 3 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 #
AEIPC*EDEQEHEHNGPLDNK	C626;C626;C471;C455;C439	0.447461194	Q5R363 Q96SB4 H3BLV9 Q96SB4 Q96SB4	contaminant_INT-STD1 BSA # P22692-2 Isoform 2 of Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 # P22692 Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2 #
MPC*TEDYLSLILNR	C471	0.44240888		Q02809-2 Isoform 2 of Procollagen-lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 # Q02809 Procollagen-lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 #
THEDLYIIPINC*DR	C104;C204	0.441481782	P22692 P22692	P30041 Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 #
VGVDYEGGGC*R	C727;C680	0.441232077	Q02809 Q02809	Q8N5K1 CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 #
DFTPVC*TTELGR	C47	0.44073249	P30041	Q2NL82 Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 #
VVNEINIEDLC*LTK	C92	0.440225	Q8N5K1	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 #
DTGTVHLNELGNTQNFMLLC*PR	C126	0.439350462	Q2NL82	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
LEKPNEGYLEFFVDC*SASATPEFEGR	C85	0.436475333	Q15024	P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
VVMALGDYMGASCHAC*IGGTNVR	C134	0.43634639	P60842	O75874 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 #
VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDIC*FR	C211;C201 C211 C201	0.436005079	P07437 P68371 Q9BVA1 P04350 Q9BUF5	
SEGGFIWAC*K	C269	0.435662733	O75874	

AENGLLMTPC*YTANFVAPEV LKR	C559;M561 C584;M556 C579;M572 C575 C564;M576	0.435654723	Q15418 Q15418 E9PGT3 P51812 Q15418	Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 # P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 # Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 # Q96IJ6 Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 # Q96IJ6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA # P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 # E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # H7C2I1 Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 # Q99873-2 Isoform 2 of Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 # Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP # P23258 Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2 # P49321-2 Isoform 2 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321-3 Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 # P52272 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 # P52272-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM # A0A087X0X3 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=1 # Q86U90 YrdC domain-containing protein# mitochondrial OS=Homo sapiens GN=YRDC PE=1 SV=1 # P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
SIQFVDWC*PTGFK	C347;C347	0.435615218	P68363 P68366	
C*MPTFQFFK	C73	0.435610469	P10599	
LLPAITILGC*R	C389;C442	0.434303444	Q96IJ6 Q96IJ6	
DVLKEEGVSFLINTFEGGGC* GQPSGILAQPTLLYLRL	C1229	0.429998753	P78527	
VIGIEC*SSISDYAVK	C73;C119;C101; C109;C95;C91	0.429895609	E9PKG1 H7C2I1 Q99873 Q99873 Q99873 Q99873	
FTVNLSGC*PR	C396;C394	0.427899934	Q9BTE3 Q9BTE3	
LTQNADC*VVLDNTALNR	C201	0.427743888	P23258	
KPTDGASSSNC*VDISHLVR	C369;C710;C70 8	0.427187184	P49321 P49321 P49321	
GC*GVVKFESPEVAER	C694;C655;C69 4	0.426125332	P52272 P52272 A0A087X0 X3	
AGAVVAVPTDTLYGLACAAS C*SAALR	C99	0.425256667	Q86U90	
AFDTAGNGYC*R	C223	0.424624411	P49327	

FMTPVIQDNPSGWGPC*AVP EQFR	C19 C19;M5	0.423976418	O15371 O15371 O15371	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 # Q9BXJ9 N-alpha-acetyltransferase 15# Nata auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 # P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
VAC*ITEQVLTLVNR	C477	0.421340209	P04843	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
LFNTAVC*ESK	C721	0.421232817	Q9BXJ9	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
IHMGC*AENTAK	C196	0.41957042	P24752	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 #
C*ELLYEGPPDDEAAMGIK	C369	0.418384456	P13639	P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
VDLNSNGFIC*DYELHELFK	C33	0.415658901	P13797	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 # Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL #
AAAPAPEEEMDEC*EQALAA EPK	C316 C266;M313	0.41537935	P26641 P26641	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
SDVC*TPGGTTIYGLHALEQG GLR	C247;C235;C21 5	0.414985447	A0A0A0M QS1 Q53H96 Q53H96	P60604-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 # P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 #
VTDGALVVVDCVSGVC*VQT ETVLR	C136	0.414667375	P13639	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
VC*ISILHAPGDDPMGYESSA ER	C61	0.413884675	P60604 P60604	Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C #
YAYLNVVGMVGSIDNDFC*GT DMTIGTDSALHR	C179	0.413717727	Q01813	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 #
KC*DLISIPK	C426;C420;C47 3	0.413598237	Q9ULV4 Q9ULV4 Q9ULV4	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 #
AYGSMC*AK	C83	0.41159	P49207	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
ASC*LYGQLPK	C48	0.411554811	P09211	P11586 C-1-tetrahydrofolate synthase# cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 # A0A087WVM4 Monofunctional C1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # Q6UB35 Monofunctional C1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # B7ZM99 MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 #
AGSDGESIGNC*PFSQR	C35	0.407908873	Q9Y696	Q5VTE0 Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
QGFGNLPIC*MAK	C863;C841;C90 6;C907	0.405838666	P11586 A0A087W VM4 Q6UB35 B7ZM99	
SGDAAIVDMVPGKPMC*VES FSDYPPLGR	C411;C390	0.405350071	Q5VTE0 P68104	

IGC*LLSGGLDSSLVAATLLK	C234;C255	0.404073726	P08243 P08243	P08243-2 Isoform 2 of Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS # P08243 Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4 #
LC*SGPGIVGNVLVDPSAR	C245;C245	0.403478924	Q9Y5P6 Q9Y5P6	Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 #
SDITKLEVDIVNAANSSLLGG GGVDGC*IHR	C186	0.401571582	Q9BQ69	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #
MLSC*AGADR	C105;C105	0.40094	Q96L21 P27635	Q96L21 60S ribosomal protein L10-like OS=Homo sapiens GN=RPL10L PE=1 SV=3 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 #
DLAVVTQSAEAPAEEDLLGP NC*YYDK	C310;C310;C230	0.400420555	Q9BX40 Q9BX40 Q5TBP9	Q9BX40 Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B PE=1 SV=1 # Q9BX40-2 Isoform 2 of Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B # Q5TBP9 Protein LSM14 homolog B (Fragment) OS=Homo sapiens GN=LSM14B PE=1 SV=1 #
WNDNC*PSWNTIDPEER	C301	0.399574952	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
C*PEALFQPSFLGMESCGIHE TTFNSIMK	C257	0.39652793	P63261 P60709	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #
VLQNMEQC*QK	C365;C366	0.393139407	J3KND1 Q96ER3	J3KND1 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=1 # Q96ER3 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=2 #
EKHEEFCVPMVMVPATVSNN VPGSDFSIGADTALNTITDTC* DR	C563	0.393116288	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
MTVDESGQLISC*SMDDTV	C382	0.392346604	O75083	O75083 WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 #
C*SLPAEEDSVLEK	C652;C635	0.392155	E7EVA0 P27816	E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 #
DIEDTLSGIQTAGC*GSTFFR	C144	0.39162	Q8IYU8	Q8IYU8 Calcium uptake protein 2# mitochondrial OS=Homo sapiens GN=MICU2 PE=1 SV=2 #
DLPTSPVDLVINCLDC*PENVF LR	C413	0.391073877	Q96F86	Q96F86 Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1 #
AYHEQLTVAEITNAC*FEPAN QMVK	C295	0.390283074	Q9BQE3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
YLAEVAC*GDDRK	C134	0.390095652	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #
AC*DLPAAVHFPDTER	C181;C181;C153;C123;C181	0.389830905	A0A087W XU3 A0FGR8 A0FGR8 H7BXI1 A0FGR8	A0A087WXU3 Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8 Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8-2 Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 # H7BXI1 Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8-6 Isoform 6 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 #



PFC*EDLDQWLSEDDNHVAAI HC*KAGK	C90 C297;C71 C109;C105 C278 C297;C90 C124;C278	0.388167247	P60484 P60484 P60484 A0A0U1R R63 A0A087W T17	P60484-2 Isoform alpha of Phosphatidylinositol 3#4#5-trisphosphate 3- phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN # P60484-3 Isoform 3 of Phosphatidylinositol 3#4#5-trisphosphate 3- phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN # P60484 Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual- specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # A0A0U1RR63 Phosphatidylinositol 3#4#5- trisphosphate 3-phosphatase and dual- specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # A0A087WT17 Phosphatidylinositol 3#4#5- trisphosphate 3-phosphatase and dual- specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # Q9UL25 Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3 # P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
VLLGEGC*VGK	C29	0.388106312	Q9UL25	Q9Y693 Lipoma HMGIC fusion partner OS=Homo sapiens GN=LHFP PE=2 SV=1 #
ELDLSNNC*LGDAGILQLVES VR	C409	0.387517994	P13489	
QTC*GYTSGQFDLQK*EIGW AAYCTGAGATAAMLLCTWLA CFSGK	C152 C164	0.387240328	Q9Y693	
AHVVPC*FDASK	C1157;C1130;C 1157	0.385083131	P21333 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
VAAALENTHLLEVVNQC*LSA R	C158	0.384119559	Q9Y3D0	Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 #
IGFPETEEEELEEIASNSDC*I FPSAPDVK	C353;C340	0.381575277	Q9Y3F4 Q9Y3F4	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP # Q9Y3F4 Serine- threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 #
VEPC*SLTPGYTK	C219	0.3809571	Q96EB1	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # H0YCZ6 Transcriptional enhancer factor TEF- 1 (Fragment) OS=Homo sapiens GN=TEAD1 PE=1 SV=2 # H0YEJ9 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=1 # P28347 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=2 # P28347-2 Isoform 2 of Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 # H0YE88 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=1 #
MSDSADKPIDNDAEGVWSPD IEQSFQEALAIYPPC*GR	C53 C53;M4 C53;M19 C38;M19 C144;M19	0.380515	H0YCZ6 H0YEJ9 P28347 P28347 H0YE88	
HPSAVTAC*NLDLENLVTDSN R	C325	0.38044057	Q9Y678	Q9Y678 Coatamer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 #
ANC*IDSTASAEAVFASEVK	C268	0.378459697	P22087	P22087 rRNA 2'-O-methyltransferase fibrillar OS=Homo sapiens GN=FBL PE=1 SV=2 # O00159-3 Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C # O00159 Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 # F5H6E2 Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=1 # O00159-2 Isoform 2 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C #
C*PENAFFLDHVR	C783;C802;C77 8;C767	0.375795	O00159 O00159 F5H6E2 O00159	

MALDALLQEIALSEPQLC*EVL QVAGPDR	C38;M21 C38	0.375181712	C9J6P4 Q7Z2W4	C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
KYEDIC*PSTHNMDVPSNIK	C103;C73	0.374915293	P63241 P63241	P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 #
ATDYPC*LLILDQPNEFETLR	C145;C145	0.374816629	Q9NVG8 Q9NVG8	Q9NVG8-2 Isoform 2 of TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 # Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
QPAIMPGQSYGLEDSGC*SY KDFSESER	C472	0.37479087	P14866	P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
IC*DQWDALGSLTHSR	C499	0.374182259	O43707	O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 #
VDSAC*GMER	C275;C317;C33 3	0.373806014	O95671 O95671 O95671	O95671-3 Isoform 3 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL # O95671-2 Isoform 2 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL # O95671 N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3 #
DVQIGDIVTVGEC*RPLSK	C131	0.373431123	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
FC*DNVWTFVLNDVEFR	C68;C33	0.372701814	P52657 A0A0B4J1 Z5	P52657 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 # A0A0B4J1Z5 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 #
RQDSDLVQC*GVTSPSSAEA TGK	C261	0.369500779	Q9HC52	Q9HC52 Chromobox protein homolog 8 OS=Homo sapiens GN=CBX8 PE=1 SV=3 #
SLC*NLEESITSAGRDDLESF QLEISGFLK	C63	0.369244535	Q52LJ0	Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #
APPPSLTDC*IGTVDSR	C20;C20	0.369163361	Q9NZZ3 Q9NZZ3	Q9NZZ3 Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1 # Q9NZZ3-2 Isoform 2 of Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 #
QNSDFLC*QMDLLQEFYETTL EALKDAK	C130	0.368870846	P61201	P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 #
ALANVNIGSLIC*NVGAGGPA PAAGAAPAGGPAPSTAAAPA EEK	C36;C61	0.368831207	P05386 P05386	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 # P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 #
DHQPC*IIFMDEIDAIGGR	C242	0.367738345	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
VGSFC*LSEAGAGSDSFALK	C73;C175	0.366697008	P45954 P45954	P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB # P45954 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 #
SASLDNGGC*ALTTFSVLEGE K	C92	0.363993013	P35610	P35610 Sterol O-acyltransferase 1 OS=Homo sapiens GN=SOAT1 PE=1 SV=3 #
FQYEC*GNYSGAAYLYFFR	C141	0.362223784	P60228	P60228 Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 #
LTEGC*SFR	C77	0.361890091	P42677	P42677 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 #

NFNHYHILSPC*DLSNYTDLAM STVK	C461;C498	0.360969595	G5E9W3 Q9UKF6	G5E9W3 Cleavage and polyadenylation specific factor 3# 73kDa# isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 #
TVPFC*STFAAFFTR	C386	0.360030665	P29401	P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 #
SQEATEAAPSC*VGDMADTP R	C84	0.357431666	Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8	Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 #
IC*DPYAWLEDPDSEQTK	C25	0.356181906	P48147	P48147 Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 #
VLTC*TDLEQGNFFLDFENA QPTESEK	C10	0.355485551	Q9NUQ9	Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 #
EAVFPFQPGSVAEVC*ITFDQ ANLTVK	C89	0.354912654	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 #
LEFSIYPAPQVSTAVVEPYNSI LTTHTTLEHSDC*AFMVDNEA IYD	C200;C200;C20 0	0.354398155	Q9BQE3 Q71U36 P68366	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
NC*LNPQFSK	C54	0.353445826	O75131	O75131 Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 #
TATAVAHC*K	C25	0.352951447	P62249	P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 #
TIGGGDDSFRTFFC*ETGAGK	C54	0.352711652	P68366	P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
LTALDYHNPAGFNC*KDETEF R	C19	0.351978389	Q9Y224	Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 #
LIDFLEC*GK	C234;C234	0.350329985	P17844 J3KTA4	P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # J3KTA4 Probable ATP- dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 #
ANNNAAVAP TTC*PLQPV TDP FAFSR	C46;C46	0.350090468	F1T0I1 J3KNL6	F1T0I1 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 # J3KNL6 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 #
SGQGAFGNMC*R	C96	0.348789177	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
C*PFTGNVSIR	C60	0.348501069	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
THEAEIVEGENHTYC*IR	C2191;C2172;C 2199	0.34778021	P21333 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
IAVYSC*PFDGMITETK	C225	0.346894057	P50990 P50990	P50990-2 Isoform 2 of T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 # P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 # C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 #
VELC*SFSGYK	C6;C6;C6	0.346733374	C9JNW5 C9JXB8 P83731	C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 #
HTGCC*GDNDPIDVCEIGSK	C114	0.34645	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 #

LDNWLNELEYC*TR	C139;C110;C86	0.344040706	Q9NP72 Q9NP72 A0A087X1 63	Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
VIGSGC*NLDSAR	C192;C164;C16 3	0.343443639	P00338 P07195 P00338	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 # Q9BY32-3 Isoform 3 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA # Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 # Q9BY32-2 Isoform 2 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA #
IISNASC*TTNCLAPLAK	C152	0.341475415	P04406	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P82932 28S ribosomal protein S6# mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 #
GC*QDFGWPCFQPDGYEQ TYAEMPK	C105	0.339692001	Q9BY32 Q9BY32 Q9BY32	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 # Q96EY8 Cob(I)yrinic acid a#c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # S4R3P5 Cob(I)yrinic acid a#c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
AEQSDVANAVLDGADC*IMLS GETAK	C358	0.339559655	P14618 P14618	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 # Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 #
EC*EGIVPVPLAEK	C105	0.338300156	P82932	Q15691 Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3 #
AINC*ATSGVVGLVNCLR	C1448	0.335944472	P49327	
MAC*GLVASNLNLKPGECLR	C3	0.335766509	P09382	
IQCTLQDVGSALATPC*SSAR	C132;C80	0.33418554	Q96EY8 S4R3P5	
GC*LLYGPPGTGK	C184;C170	0.333463983	A0A087X2 I1 P62333	
PGHLQEGFGC*VVTNRFDQL FDDESDPFEVLK	C11;C11;C11;C1 1	0.333045988	Q8NC51 Q8NC51 Q8NC51 Q8NC51	
NIELIC*QENEGENDPVLQR	C228	0.330078817	Q15691	

					H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
LC*EPEVLNSLEETYSPPFR	C177;C261;C261;C106;C224;C261;C261;C227;C261;C261;C242	0.329958818		H0YJA2 Q6PJT7 Q6PJT7 G3V5I6 Q6PJT7 G3V256 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7	
TWYVQATC*ATQGTGLYEGLDWLSNELSK	C159	0.329821214	P18085	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 # Q6P1L8 39S ribosomal protein L14# mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 #	
ALIVGHC*MPGPRMTPR	C90	0.329715	Q6P1L8	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 # P53396-2 Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY #	
KPASFMTSIC*DER	C845;C835	0.328806223	P53396 P53396	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #	
AFC*GFEDPR	C4325;C4343;C4335;C4494;C4357;C4384;C4361;C4357	0.32787006		Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #	
LVPATQC*GSLIGK	C109	0.327736232	Q15365	P31150 Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 #	
TDDYLDQPC*LETVNR	C202	0.327575	P31150	Q15785 Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2 #	
YSELLC*SNLESATYSNR	C222	0.327526129	Q15785	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 #	
SMVSPVPSPTGTISVPNSC*P ASPR	C254	0.325958607	P85037	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 #	
TLQNTMVNLGLQNAC*DEAIY QLGLDLEEEIEEDAGLGNG GLGR	C109	0.325865844	P11216	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #	
VAASC*GAIQYIPTELDQVRK	C134	0.325715434	Q7L2H7	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 #	
STFFNVLTNQSASAENFFPC* TIDPNESR	C75;C55	0.325136373	J3KQ32 Q9NTK5		

LC*DFGVSGQLIDSMANSFVG TR	C114;C207;C18 1;C211	0.325047552	G5E9C7 Q02750 Q02750 P36507	G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 #
GTPEQPQC*GFSNAVQILR	C67	0.324386168	Q86SX6	Q86SX6 Glutaredoxin-related protein 5# mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 #
C*TGGEVGATSALAPK	C17	0.321604808	P30050	P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 #
DIDFLKEEEHDC*FLEEIMTK	C173	0.321430944	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
VTEPSAPC*QALVSIQDLQAT FHGIR	C795	0.318796603	Q9UPN7	Q9UPN7 Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5 #
TDVNKIEEFLEEVLC*PPK	C100	0.318562251	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
YIETSELC*GGAR	C374;C361;C36 1;C361;C361;C3 74;C374;C361	0.317867405	O00429 O00429 O00429 O00429 O00429 G8JLD5 O00429	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 # O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 # O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L #
LEGDLTGPVSGVEVPDVELE C*PDAK	C1900	0.315222686	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
SVHYC*PATK	C158;C148;C19 3	0.315034315	J3KQ69 P25205 P25205	J3KQ69 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=2 # P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 # P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 #
IKADPDGPEAQAEAC*SGER	C18	0.31481162	Q9NX24	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 #
QEPLGSDSEGVNC*LAYDEAI MAQQDR	C23	0.313636297	F5H6Q1 J3KR44 Q96FW1	F5H6Q1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # J3KR44 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 # Q96FW1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 #
AHEILPNLVCC*SAK	C130;C149	0.309934839	P50990 P50990	P50990-2 Isoform 2 of T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 # P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
DAANC*WTSLLSESEYAADPW VQDQMQR	C99	0.30897917	Q8WVJ2	Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 #
EDPTVSALLTSEKDWQGFLE LYLQNSPEAC*DYGL	C237	0.308936911	P78417	P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #

QMFEPVSC*TFTYLLGDR	C34 C34;M28	0.307617104	O95571 MOQXB5	O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # M0QXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 #
TDSPSC*EYSR	C419	0.305774175	Q9HAV4	Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 #
FC*EDIGVEPENIIMLVLAWK	C74	0.303877807	Q9BTE7	Q9BTE7 DCN1-like protein 5 OS=Homo sapiens GN=DCUN1D5 PE=1 SV=1 #
ETVYC*LNDDDETEVLKEDIQ GFR	C296	0.303024611	P13010	P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 #
VTEDENDEPIEPSDDGTVLL STVTAQFPGAC*GLR	C39;C39;C39;C3 9;C39	0.302893266	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
EVYEGETELTPC*ETENPMG GYGK	C141	0.302824325	Q9Y265	Q9Y265 RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 # Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 #
C*TPSVISFGSK	C34;C34	0.302138834	Q92598 Q92598	Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 # B4DXW1 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=1 # P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
FLGPEIFFHPEFANPDFTQPIS EVDVEVIQNC*PIDVR	C256;C307	0.301659726	B4DXW1 P61158	A0A087X0W8 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206-2 Isoform 2 of Transcription factor p65 OS=Homo sapiens GN=RELA # E9PKH5 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # Q2TAM5 RELA protein OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=2 #
DGFYEAELC*PDR	C105;C92;C116; C105;C105	0.29947042	A0A087X0 W8 Q04206 E9PKH5 Q2TAM5 Q04206	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 # A0A087WV01 Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
GTSQADC*AVLIVAAGVGEFE AGISKNGQTR	C111;C111;C11 1	0.29931058	P68104 Q05639 A0A087W V01	Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # Q9BYK1 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # P63220 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # P17858 ATP-dependent 6- phosphofructokinase# liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 # Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 # Q9Y277 Voltage- dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 # A1L0T0 Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 #
AAVEEGIVLGGGC*ALLR	C442	0.297573918	P10809	
TYAIC*GAIR	C56;C56;C56	0.296452881	Q8WVC2 Q9BYK1 P63220	
TYSHLNIAGLVGSIDNDFC*GT DMTIGTDSALHR	C170	0.296373433	P17858	
VC*NYGLTFTQK	C66;C65	0.2958409	Q9Y277 Q9Y277	
EQVPSLGSNVAC*GLAYTDY HK	C568	0.294462595	A1L0T0	

YGDLDSSLISFGPC*QTPTLG FCVER	C217;C217;C217 7;C217	0.292877958	O95985 O95985 O95985 C9JEI7	O95985-3 Isoform 3 of DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B # O95985 DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B PE=1 SV=1 # O95985-2 Isoform 2 of DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B # C9JEI7 DNA topoisomerase (Fragment) OS=Homo sapiens GN=TOP3B PE=1 SV=1 # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 # P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 # P52788 Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 # P52788-2 Isoform 2 of Spermine synthase OS=Homo sapiens GN=SMS # P28066 Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 # P28066-2 Isoform 2 of Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 # A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # A6NHK2 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P62304 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 # Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 # P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
PMC*IPPSYADLGK	C13;C13	0.292738265	A0A0A0M R02 P45880	
C*AGNEDIITLR	C81	0.292448817	P12004	
YFTQGNC*VNLTEALSLYEEQ LGR	C318;C265	0.292020141	P52788 P52788	
GPQLFHMDPSGTFVQC*DAR	C165;C107	0.291497206	P28066 P28066	
HLNEIDL FHC*IDPNDSK	C62;C58;C58	0.291378462	A0A087W YT3 Q15185 Q15185	
IEGC*IIGFDEYMNVLDDAEEI HSK	C6	0.290044108	A6NHK2 P62304	
NLSIDLIDLVPSLC*EDLLSSVD QLK	C36;C36;C65;C2 4;C62	0.28962329	P47756 P47756 B1AK88 B1AK87 B1AK85	
AFAFVTFADDQIAQSLC*GED LIK	C244;C244;C24 4;C244;C244	0.286381243	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	
VFIMDSC*DELIPEYLN FIR	C366	0.285289592	P08238	
LISPNLGVVFFNAC*EAASR	C316;C342	0.284777907	Q66K74 Q66K74	
QAVLGAGLP ISTPC*TTINK	C119	0.284755389	P24752	



EITSLDTENIDEILNNADVALV NFYADWC*R	C58	0.284133652	Q9BS26	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 #
VPAFEGDDGFC*VFESNAIAY YVSNEELR	C68;C118	0.284013406	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1- gamma OS=Homo sapiens GN=EEF1G #
FC*DNSSAIQGK	C270	0.282794244	O15067	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
LNIIINLDC*VNEVIGIR	C402;C402;C39 0	0.282437652	P30154 P30154 P30153	P30154 Serine/threonine- protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B # P30154 Serine/threonine- protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
NCGC*LGASPNLEQLQEENL K	C34	0.282134893	P54136	P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 # Q13596 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3 # Q13596-3 Isoform 3 of Sorting nexin-1 OS=Homo sapiens GN=SNX1 # H0YK42 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=1 # Q13596-2 Isoform 1A of Sorting nexin-1 OS=Homo sapiens GN=SNX1 #
LQVEVC*EEQR	C318;C318;C10 0;C253	0.281922327	Q13596 Q13596 H0YK42 Q13596	P29317 Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2 # P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 # Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 # Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 # O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 # Q15233-2 Isoform 2 of Non-POU domain- containing octamer-binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 # Q9NUQ6-4 Isoform 4 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L # Q9NUQ6 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 # Q9NUQ6-3 Isoform 3 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L #
FTTEIHPSV*VTR	C612	0.280655	P29317	P29317 Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2 #
YGIIC*MEDLIHEIYTVGK	C186	0.279224085	P18124	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 #
NNAFPC*QVNIK	C712	0.278725	Q9NQW6	Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 #
WTQTLSELDLAVPFC*VNFR	C188	0.278642663	Q9Y266	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 #
IINDNATYC*R	C211	0.277931085	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
TDC*SPIQFESAWALTNIASGT SEQTK	C133	0.27757656	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
C*SEGSFLLTTFPRPVTVEPM DQLDDEEGLPEK	C119	0.277212662	Q15233 Q15233	Q15233-2 Isoform 2 of Non-POU domain- containing octamer-binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 # Q9NUQ6-4 Isoform 4 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L # Q9NUQ6 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 # Q9NUQ6-3 Isoform 3 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L #
SDGLQWSAEQPC*NPSKPK	C193;C185;C21 5	0.275625474	Q9NUQ6 Q9NUQ6 Q9NUQ6	SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 # Q9NUQ6-3 Isoform 3 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L #
YADLTEDQLPSC*ESLKDTIAR	C153	0.273591682	P18669	P18669 Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 #
SGDAAIVEMVPGKPMC*VESF SQYPLGR	C411	0.272901364	Q05639	Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
C*FIVGADNVGSK	C27;C27	0.272532384	F8VWS0 P05388	F8VWS0 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB #
HSMNPFC*EIAVEEAVR	C42;M129 C133	0.272162451	P38117 P38117	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB #

AVLFC*LSEDKK	C77;C22;C39	0.270152616	E9PK25 G3V1A4 P23528	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 #
IWC*FGPDGTGPNILTDITK	C651	0.268628712	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
HPSAVTAC*NLDLENLITDSNR	C325	0.268367296	Q9UBF2	Q9UBF2 Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 #
STLTDSLVC*K	C41	0.266050368	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
VQTDAFVSNELDDPDDLQCK	C486;C465	0.265524069	E7ERK9 Q9UI10	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9UI10 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
AAAPAPVSEAVC*R	C456;C491;C367;C450;C394;C290;C131;C454;C336;C373;C469;C151;C166;C160;C131;C395;C408;C394;C123;C472;C408;C386	0.265454754	P20810 P20810 P20810 P20810 E7EVY3 P20810 E7EQA0 A0A0C4D GB5 E9PDE4 E9PCH5 P20810 HOYD33 HOY9H6 HOY7F0 A0A0A0M R45 P20810 P20810 B7Z574 E7EQ12 P20810 E7ES10 P20810	P20810-5 Isoform 5 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-3 Isoform 3 of Calpastatin OS=Homo sapiens GN=CAST # E7EQA0 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PDE4 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PCH5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # HOYD33 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # HOY9H6 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # HOY7F0 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0A0MR45 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-2 Isoform 2 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E7EQ12 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # E7ES10 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST # P21980 Protein-glutamine gamma- glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 #
SEGTYC*CGPVPVR	C370	0.263679257	P21980	P21980 Protein-glutamine gamma- glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 #
GVLLYGPPGC*SK	C672	0.262938958	Q8NB90	Q8NB90 Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3 #
EGTSSQGIPQLVSNISAC*QVIAEAVR	C29	0.262021466	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
NAFAC*FDEEATGTIQEDYLR	C108;C114;C109	0.261968055	P19105 J3QRS3 O14950	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 # J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 # O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 #

SEHGPISTFFPESGQPEC*LK	C295;C324;C247;C323	0.261925342	Q96ME7 Q96ME7 Q96ME7 G3XAG1	Q96ME7-3 Isoform 3 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # Q96ME7 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=2 # Q96ME7-2 Isoform 2 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # G3XAG1 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=1 #
GVLMYGPPGC*GK	C179;C210	0.260807578	P43686 P43686	P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 # I3L0M9 Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # Q15370
ADDTFEALC*IEPFSSPELPD VMKPQDSGSSANEQAVQ	C111	0.260661248	I3L0M9 Q15370 B8ZZU8	I3L0M9 Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # B8ZZU8 Transcription elongation factor B (SIII)# polypeptide 2 (18kDa# elongin B)# isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 #
VIEINPYLLGTMAGGAADC*SF WER	C111	0.25962507	P28074	P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #
LC*PGGQLPFLLYGTEVHTDT NK	C59	0.25809133	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
IC*PVETLVEEAIQCAEK	C213	0.257878823	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
C*SDSDGLAPPQHILIR	C182;C182;C182;C143;C182;C143;C143;C143	0.257506368	P04637 J3KP33 P04637 P04637 A0A0U1RQC9 P04637 P04637	P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 #
HTEVPTGTC*PVDPFEAQWA ALENK	C611;C467;C600	0.25552198	P49757 G3V3Z8 P49757	P49757 Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=2 # G3V3Z8 Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=1 # P49757-3 Isoform 3 of Protein numb homolog OS=Homo sapiens GN=NUMB #
SGVIVLPC*GAGK	C342	0.250963633	P19447	P19447 TFIIH basal transcription factor complex helicase XPB subunit OS=Homo sapiens GN=ERCC3 PE=1 SV=1 #
SLHDALC*VLAQTVK	C395	0.250140939	P78371	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 #
EC*LPLIIFLR	C41	0.24929693	P62701	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 #
SQSPAASDC*SSSSSSASLPS SGR	C179;C121	0.249284434	O95817 C9JFK9	O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 # C9JFK9 BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=1 SV=1 #
LEGDLTGPSVDVEVPDVELE C*PDAK	C2162	0.246955124	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #

VDSTTC*LFPVEEK	C246;C264	0.246001593	Q06210 Q06210	Q06210-2 Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 # Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 #
VHVDC*MTSQK	C1455	0.245251419	P27708	P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 # P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 #
VAHALAEGLGVIAC*IGEK	C127;C45;C164	0.244877874	P60174 P60174 P60174	P60174-4 Isoform 4 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 #



KAC*ADATLSQITNNIDPVGR	C25	0.243685619	P62873	P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 #
VRPSTGNSASTPQSQC*LPS EIEVK	C131;C131	0.24329341	Q9UJX3 Q9UJX3	Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 #
GFEVVMTEPIDEYC*VQQLK	C521	0.242715644	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
GTLTLC*PYHSDR	C779	0.242582617	Q13200	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 #
ADTSQEIC*SPR	C1010;C1027;C1027;C66	0.242427935	P52948 P52948 P52948 H7C3P6	P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
IIPGFMC*QGGDFTR	C62	0.242345905	P62937	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #
GTEAGQVGEPIPTGEAGPS C*SSASDKLPR	C241	0.241641891	O15355	O15355 Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 #
SLDLFNC*EITNLEDYR	C123;C75	0.239279689	Q9BTT0 Q9BTT0	Q9BTT0 Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1 # Q9BTT0-3 Isoform 3 of Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E #
ITAFVPNDGC*LNFIENDEVL VAGFGR	C90	0.238350534	P62266	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 #
LC*YVALDFEQEMATAASSSS LEK	C217	0.237402069	P63261 P60709 Q6S8J3	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 #
DLQPFPTC*QALVYR	C404	0.236662933	Q14137	Q14137 Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 #
LC*PNSTGAEIR	C240;C377	0.236246641	P35998 P35998	P35998-2 Isoform 2 of 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 # P35998 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 #
MLPTYVC*ATPDGTEKGDFLA LDLGGTNFR	C517	0.235980704	P52789	P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
VCEDLDTSVNLAWTSGTNC* TR	C242;C227;C227	0.235311408	P45880 A0A0A0MR02 P45880	P45880-1 Isoform 1 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
EEEE*HFYAGGQVYPGEASR	C51	0.234617475	Q13162	Q13162 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 #
LNISFPATGC*QK	C12	0.234022476	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
GEELSC*EER	C38	0.233447868	P31947	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 #
GYWASLDASTQTTHELTIPNN LIGC*IIGR	C293	0.233365	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #

QLFALSC*TAEQGVLPDDL GVIR	C96;C60;C112;C 75;C112;C96	0.232704949	P04899 P04899 P04899 P04899 P04899 P04899	P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # H0YN14 Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=1 # Q8TEX9 Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2 # Q8TEX9-2 Isoform 2 of Importin-4 OS=Homo sapiens GN=IPO4 #
APAALPALC*DLLASAADPQIR	C42;C42;C42	0.231870853	H0YN14 Q8TEX9 Q8TEX9	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
EEFASTC*PDDEEIELAYEQV AK	C223	0.231735942	O00299	O14523-2 Isoform 2 of C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L # O14523 C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3 #
SSSC*GDTELLGQATLPVGS SRPLSR	C359;C359	0.231643589	O14523 O14523	P27816-6 Isoform 6 of Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 # E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 # H3BVG0 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=1 # Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 # Q8N1F7-2 Isoform 2 of Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 #
MAYQEYPNSQNWPEDTNFC* FQPEQVVDPIQTDPFK	C126;M125 C126 C143;M108	0.231333153	P27816 E7EVA0 P27816	E9PLD1 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=1 # P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 # P26639 Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 # P26639-2 Isoform 2 of Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS #
SSGQSAQLLSHEPGDPPC*L R	C522;C522;C39 9	0.230396298	H3BVG0 Q8N1F7 Q8N1F7	Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 #
ALADAQIPYSAVDQACVGYVF GDSTC*GQR	C71;C71	0.230247757	E9PLD1 P22307	P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 #
DQELYFFHELSPGSC*FFLPK	C343;C376	0.230194469	P26639 P26639	P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 # Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 #
KLLAPDC*EIIQEVGK	C215	0.229492214	Q9NQT5	
AFQYVETHGEVC*PANWTPD SPTIKPSPAASK	C229	0.229217301	P30048	
GTVLLADNVIC*PGAPDFLAH VR	C223	0.228659067	P21964	
NC*NDFQYESK	C112	0.228371434	Q04917	

					P06753-5 Isoform 5 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 #
					P06753-7 Isoform 7 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 #
				P06753	J3KN67 Tropomyosin alpha-3 chain
				P06753	OS=Homo sapiens GN=TPM3 PE=1 SV=1 #
C*TKEEHLCTQR	C226;C136;C263;C226;C205;C201;C210	0.228079639	P06753 J3KN67 P06753 A0A087W WU8 Q5VU61 Q5HYB6		P06753-2 Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 #
					A0A087WWU8 Tropomyosin alpha-3 chain
					OS=Homo sapiens GN=TPM3 PE=1 SV=1 #
					Q5VU61 Tropomyosin alpha-3 chain
					OS=Homo sapiens GN=TPM3 PE=1 SV=2 #
					Q5HYB6 Epididymis luminal protein 189
					OS=Homo sapiens GN=DKFZp686J1372
					PE=1 SV=1 #
TC*FETFPDK	C326	0.226978449	P11216		P11216 Glycogen phosphorylase# brain form
					OS=Homo sapiens GN=PYGB PE=1 SV=5 #
VLC*ELADLQDKEVGDGTTSV VIAAELLK	C76;C76	0.225780777	E7ERF2 P17987		E7ERF2 T-complex protein 1 subunit alpha
					OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
					P17987 T-complex protein 1 subunit alpha
					OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
					A0A087X1Z3 Proteasome activator complex
					subunit 2 OS=Homo sapiens GN=PSME2
C*GFLPGNEK	C106;C91	0.224394301	A0A087X1 Z3 Q9UL46		PE=1 SV=1 # Q9UL46 Proteasome activator
					complex subunit 2 OS=Homo sapiens
					GN=PSME2 PE=1 SV=4 #
					Q9Y697-3 Isoform 3 of Cysteine desulfurase#
					mitochondrial OS=Homo sapiens GN=NFS1 #
					H0YGN5 Uncharacterized protein (Fragment)
					OS=Homo sapiens PE=4 SV=1 # Q9Y697-2
DVALSSGSAC*TSASLEPSYV LR	C330;C41;C321; C381;C20	0.220913123	Q9Y697 H0YGN5 Q9Y697 Q9Y697 H7C0I5		Isoform Cytoplasmic of Cysteine desulfurase#
					mitochondrial OS=Homo sapiens GN=NFS1 #
					Q9Y697 Cysteine desulfurase# mitochondrial
					OS=Homo sapiens GN=NFS1 PE=1 SV=3 #
					H7C0I5 Uncharacterized protein (Fragment)
					OS=Homo sapiens PE=4 SV=1 #
GIDQC*IPLFVEAALER	C757	0.220595	O95373		O95373 Importin-7 OS=Homo sapiens
					GN=IPO7 PE=1 SV=1 #
GMYGIENEVFLSLPC*ILNAR	C294	0.220477273	P07195		P07195 L-lactate dehydrogenase B chain
					OS=Homo sapiens GN=LDHB PE=1 SV=2 #
DTC*YSPKPSVYLSTPSSASK	C540	0.220062348	Q9Y5K6		Q9Y5K6 CD2-associated protein OS=Homo
					sapiens GN=CD2AP PE=1 SV=1 #
YGAVDLLALLAVPDMSSLAC *GYLR	C223	0.218272471	P52292		P52292 Importin subunit alpha-1 OS=Homo
					sapiens GN=KPNA2 PE=1 SV=1 #
ADIDVSGPKVDVEC*PDVNIIE GPEGK	C2806	0.21806224	Q09666		Q09666 Neuroblast differentiation-associated
					protein AHNAK OS=Homo sapiens
					GN=AHNAK PE=1 SV=2 #
C*HDYYTTEFLYNLYSSEGK	C630	0.217391239	P17858		P17858 ATP-dependent 6-
					phosphofructokinase# liver type OS=Homo
					sapiens GN=PFKL PE=1 SV=6 #
EYTAC*ELMNIYK	C195	0.214904636	Q9NSD9		Q9NSD9 Phenylalanine--tRNA ligase beta
					subunit OS=Homo sapiens GN=FARSB PE=1
					SV=3 #
					G5E972 Lamina-associated polypeptide 2#
					isoforms beta/gamma OS=Homo sapiens
EMFPYEASTPTGISASC*R	C323;M348 C363	0.212852083	G5E972 P42167		GN=TMPO PE=1 SV=1 # P42167 Lamina-
					associated polypeptide 2# isoforms
					beta/gamma OS=Homo sapiens GN=TMPO
					PE=1 SV=2 #
ALNALC*DGLIDELNQALK	C62	0.20964954	P30084		P30084 Enoyl-CoA hydratase# mitochondrial
					OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
					Q16555-2 Isoform 2 of Dihydropyrimidinase-
					related protein 2 OS=Homo sapiens
GLYDGPVC*EVSVTPK	C468;C504	0.207550093	Q16555 Q16555		GN=DPYSL2 # Q16555 Dihydropyrimidinase-
					related protein 2 OS=Homo sapiens
					GN=DPYSL2 PE=1 SV=1 #



LQDAFSSIGQSC*HLDLPQIAV VGGQSAGK	C27;C27;C27;C27 7	0.206778731	P50570 P50570 P50570 P50570	P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 # P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 #
C*GETAFIAPQCEMIPIEWVC R	C81	0.206596341	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 # Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
SC*NGPVLVGSPQGGVDIEEV AASNPELIFK	C162;C162;C162 2	0.206398197	Q96I99 E9PDQ8 Q96I99	O43684 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 # J3QT28 Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=1 SV=1 # O43684-2 Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 #
TPC*NAGTFSQPEK	C129;C129;C129 9	0.203254822	O43684 J3QT28 O43684	P55265-5 Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265-4 Isoform 4 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265 Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 #
NAEFLTC*NIPTSNASNNMVT TEK	C97	0.20257	P55265 P55265 P55265	P31946-2 Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB # P31946 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 # Q8NF37 Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 #
EKIEAELQDIC*NDVLELLDK	C94;C96	0.201793953	P31946 P31946	P12236 ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 # P12235 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 # P05141 ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 #
LPADTC*LLEFAR	C330	0.200920899	Q8NF37	Q6IBS0 Twinfilin-2 OS=Homo sapiens GN=TWTF2 PE=1 SV=2 # E2QRB3 Pyrroline-5-carboxylate reductase 1# isoform CRA_c OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322 Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # A0A087WTV6 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 #
YFAGNLAGGAAGATSLC*FV YPLDFAR	C129;C129;C129 9	0.200863885	P12236 P12235 P05141	P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # J3KR12 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 # Q96C36 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 # J3QKT4 Pyrroline-5-carboxylate reductase (Fragment) OS=Homo sapiens GN=PYCR1 PE=1 SV=1 #
HLSSC*AAPAPLTAER	C141	0.200520374	Q6IBS0	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 #
EC*PSDECGAGVFMASHFDR	C121	0.198893624	P62979	

AGEGTYALDSESC*MEK	C272	0.19584	O00541 O00541 B5MCF9	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 # O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 # B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 #
HFVLDEC*DK	C197	0.195486816	O00148	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 #
TGQATVASGIPAGWMGLDC* GPSSKK	C316	0.194425	P00558	P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
IIQFQATPC*PK	C300;C313;C298; C278;C299	0.192803962	Q06330 Q06330 Q06330 Q06330 Q06330	Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 # Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ #
YKWC*EYGLTFTEK	C76;C76	0.191547577	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
GPFVEAEVDPVDLEC*PDAK	C1833	0.191533641	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
AC*QEIQEALLESLR	C247	0.191421503	P24385	P24385 G1/S-specific cyclin-D1 OS=Homo sapiens GN=CCND1 PE=1 SV=1 #
YTIVVSATASDAAPLQYLAPY SGC*SMGEYFR	C294	0.190712136	P25705 P25705 P25705	P25705 ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 # P25705-3 Isoform 3 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 # P25705-2 Isoform 2 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 #
ISGADINSIC*QESGMLAVR	C348	0.190589239	P43686 P43686	P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 #
ISLGLPVGAVINC*ADNTGAK	C28;C28	0.187598497	P62829 J3KT29	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 # J3KT29 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 #
AVASQLDC*NFLK	C207;C193	0.186706795	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
IQFNDLQSLLC*ATLQNVLR	C585;C440	0.186398923	Q14974 Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
ADIIHAC*DIVEDAAIAYGYNNI QMTLPK	C362	0.186026667	Q9NSD9	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 #
GQNGDDSSAGGDFPPPAEV EPTPEAELLAQPC*HDSEASK	C122	0.18442408	O94992	O94992 Protein HEXIM1 OS=Homo sapiens GN=HEXIM1 PE=1 SV=1 #

AATMSAVEAATC*R	C278;M258 C266	0.18346072	A0A0A0M QS1 Q53H96	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 #
LVSSPCC*IVTSTYGWTANMER	C590	0.183258457	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
IDC*FSEVPTSVFGEK	C384	0.183079563	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
IC*DGVQFGAGIR	C457	0.181964843	Q9Y512	Q9Y512 Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3 #
FQSFGLMESCC*GIHETTFNSIMK	C272;C272	0.181875	P63261 P60709	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #
IIAIANYVC*R	C525;C637;C581;C581	0.18087575	Q16666 Q16666 Q16666 Q16666	Q16666 Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16 PE=1 SV=3 # Q16666-2 Isoform 2 of Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16 # Q16666-6 Isoform 4 of Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16 #
VLVTTNVC*AR	C361;C392;C393	0.179422261	I3L0H8 Q9NUU7 F6QDS0	I3L0H8 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 # Q9NUU7 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 # F6QDS0 HCG2043426# isoform CRA_b OS=Homo sapiens GN=hCG_2043426 PE=1 SV=1 # P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB
EGGQYGLVAAC*AAGGQGHAMIVEAYPK	C458;C436	0.179312912	P55084 P55084	P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB #
GLYGIKDDVFLSVPC*ILGQNGISDLVK	C322;C293	0.177610684	P00338 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
DEFTNTC*PSDKEVEIAYS DVAK	C234	0.175958544	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
ELEAVC*QDVLSLLDNYLIK	C97	0.174925479	P61981	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 #
YAIC*SALAASALPALVMSK	C125	0.1748768	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
LTESPC*ALVASQYGWSGNMER	C645	0.174378046	P14625	P14625 Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 #
VEQNSEPC*AGSSSESDLQTVFK	C184;C260	0.17376575	E9PCJ7 Q8N806	E9PCJ7 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 # Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 #
VVHC*QPLDLK	C161;C138	0.17015056	A0A0C4D FS6 Q9C004	A0A0C4DFS6 Protein sprouty homolog 4 OS=Homo sapiens GN=SPRY4 PE=1 SV=1 # Q9C004 Protein sprouty homolog 4 OS=Homo sapiens GN=SPRY4 PE=1 SV=2 #
ETGANLAIC*QWGFDEANHL LLQNNLPAVR	C281;C264;C302	0.170133298	E9PCA1 B7ZAR1 P48643	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 #
ASVFGGSC*FQK	C276	0.167894385	O60701	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 #

YLLQYQEPIPC*EQLVTALCDI K	C107;C76;C107; C107	0.167749305	H0YL69 H0YN18 P25789 H0YMZ1	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
LVAFC*PFASSQVALENANAV SEGVVHEDLR	C52	0.167653646	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
NESC*SENYTTDFIYQLYSEE GK	C641	0.166785158	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFBK PE=1 SV=2 #
LLNLVYDVTPELVDLVITELG MIPC*SSVPVLR	C530;M506 C509	0.1639493	E7ERK9 Q9U110	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9U110 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
LLDRDAC*DTVR	C247;C204	0.163762386	Q9NZL4 Q9NZL4	Q9NZL4-3 Isoform 3 of Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 # Q9NZL4 Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 PE=1 SV=1 #
AKVDEFPLC*GHMVSDEYEQ LSSEALEAAR	C49	0.162040261	P27635	P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 #
TPTKPSLNNQLVSVDC*K	C991	0.161334656	Q9NZV1	Q9NZV1 Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1 #
RPLNPLASGQGTSEENTFY WLEGLC*VEK	C241	0.161032951	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 #
TVDSQGPTPVC*TPTFLER	C237	0.157837531	Q9BYG3	Q9BYG3 MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 #
C*ELSSSVQTDINLPYLTMDS SGPK	C317	0.157280206	P38646	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 #
GDLENAFLNLVQC*IQNKPLY FADR	C280;C262	0.155792224	P07355 P07355	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 #
VTDDLVC*LVIYK	C48	0.155503522	P49458	P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 #
SNELGDVGVHC*VLQGLQTP SCK	C75	0.154551261	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
GNHEC*ASINR	C138;C126;C12 7	0.153702824	P62136 P62140 P62136	P62136 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 #
YNFFTGC*PK	C364	0.152690137	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
AEVLISTVGPEDC*VVPFLTRP K	C38	0.15030737	P56192	P56192 Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 #
TTEEQVQASTPC*PR	C108	0.14958397	Q14137	Q14137 Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 #
HDDSSDNFC*EADDIQSPEAE YVDLLLNER	C166	0.1464459	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 #
YVDIAIPC*NNK	C168;C163;C16 3	0.146239121	A0A0C4D G17 C9J9K3 P08865	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #
WC*NVQSTQDEFEELTMSQK	C59	0.145150982	P27707 D6RFG8	P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #

NQSFC*PTVNLDKLWTLVSEQ TR	C70	0.142598452	P46776	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 #
EGLLLWC*QR	C211;C154;C15 4;C173;C154	0.142491202	A0A087W SZ2 P12814 P12814 O43707 P12814	A0A087WSZ2 Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=1 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # P12814-3 Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # Q99700 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=2 # Q99700-2 Isoform 2 of Ataxin-2 OS=Homo sapiens GN=ATXN2 # Q99700-5 Isoform 5 of Ataxin-2 OS=Homo sapiens GN=ATXN2 # Q99700-4 Isoform 4 of Ataxin-2 OS=Homo sapiens GN=ATXN2 # F8WB06 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # F8VQP2 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # V9GY86 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # F8W0B5 Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=3 # F8WB05 Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=2 # H0YH87 Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # O75821 Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 # P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 #
RGPEVTSQGVQTSSPAC*K	C892;C892;C60 3;C892;C627;C6 27;C732;C270;C 31;C813	0.141409575	Q99700 Q99700 Q99700 Q99700 F8WB06 F8VQP2 V9GY86 F8W0B5 F8WB05 H0YH87	# Q99700-5 Isoform 5 of Ataxin-2 OS=Homo sapiens GN=ATXN2 # Q99700-4 Isoform 4 of Ataxin-2 OS=Homo sapiens GN=ATXN2 # F8WB06 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # F8VQP2 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # V9GY86 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # F8W0B5 Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=3 # F8WB05 Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=2 # H0YH87 Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # O75821 Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 # P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 #
EDLNC*QEEEDPMNK	C139	0.139876345	O75821	O75821 Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 # P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 #
TC*PVQLWVDSTPPPGTR	C141;C141;C14 1;C102;C141;C1 02;C102;C102	0.139048417	P04637 J3KP33 P04637 P04637 P04637 A0A0U1R QC9 P04637 P04637	P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 #
AC*YLSINPQKDETELEK	C222	0.137520422	P61163	P61163 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 # C9JRY4 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=1 # Q96IW7 Vesicle-trafficking protein SEC22a OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JDJ8 Vesicle- trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JNZ0 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=8 # Q14353-2 Isoform 2 of Guanidinoacetate N- methyltransferase OS=Homo sapiens GN=GAMT # Q14353 Guanidinoacetate N- methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 # Q8N490-3 Isoform 3 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490-4 Isoform 4 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490 Probable hydrolase PNKD OS=Homo sapiens GN=PNKD PE=1 SV=2 #
TNTAVRPYC*FIEFDNFIQR	C111;C111;C11 1;C111	0.137492166	C9JRY4 Q96IW7 C9JDJ8 C9JNZ0	C9JRY4 Vesicle- trafficking protein SEC22a OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JDJ8 Vesicle- trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JNZ0 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=8 # Q14353-2 Isoform 2 of Guanidinoacetate N- methyltransferase OS=Homo sapiens GN=GAMT # Q14353 Guanidinoacetate N- methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 # Q8N490-3 Isoform 3 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490-4 Isoform 4 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490 Probable hydrolase PNKD OS=Homo sapiens GN=PNKD PE=1 SV=2 #
VQEAPIDEHWIIEC*NDGVFQ R	C91;C91	0.136573437	Q14353 Q14353	Q14353 Guanidinoacetate N- methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 # Q8N490-3 Isoform 3 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490-4 Isoform 4 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490 Probable hydrolase PNKD OS=Homo sapiens GN=PNKD PE=1 SV=2 #
THC*LALQEALGPGPGPTGD DDYSR	C323;C287;C34 7	0.135426106	Q8N490 Q8N490 Q8N490	Q8N490 Probable hydrolase PNKD OS=Homo sapiens GN=PNKD PE=1 SV=2 #

VPTANVSVVLDLC*R	C247	0.135049575	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
IHEGC*EEPATHNALAK	C874;C870;C870	0.132552836	A0A087WVQ6 Q00610 Q00610	A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #
FSFCC*SPEPEAEAEAAAGPG PCER	C27;C27;C27	0.130865072	E7EMC7 E3W990 Q13501	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # E3W990 Sequestosome-1 (Fragment) OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
LDVGNFSWGSEC*CTR	C71	0.129245479	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #
PSYSSFTQGDWSWGEGEVDE EEGC*DQVAR	C48	0.128056694	Q8N6S5	Q8N6S5 ADP-ribosylation factor-like protein 6-interacting protein 6 OS=Homo sapiens GN=ARL6IP6 PE=1 SV=1 #
ATVAPEDVSEVIFGHVLAAGC *GQNPVR	C65;C94	0.127103982	Q9BWD1 Q9BWD1	Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # Q9BWD1-2 Isoform 2 of Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 #
GSDC*GIVNVNIPTSGAEIGGA FGGEK	C450;C478	0.126928132	P49419 P49419	P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 #
LAPILC*DGTATFVDLVPGR	C568	0.126708691	O43264	O43264 Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 #
APELLGC*K	C177;C177	0.125094856	P24941 G3V5T9	P24941 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2 # G3V5T9 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=1 #
YSEEANNLIEEC*EQAER	C131	0.123852992	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2
GNFTLPEVAEC*FDEITYVELQ KEEAQK	C648;C629	0.123815334	Q00839 Q00839	Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
TC*ETGEPMEAESGDSSEG PAQVYLPGR	C11	0.122178413	Q9BQ67	Q9BQ67 Glutamate-rich WD repeat-containing protein 1 OS=Homo sapiens GN=GRWD1 PE=1 SV=1 #
SSSQPSSCC*SDPSKPGGNV EGATQSLAEQMR	C290	0.120077841	E7EMC7 Q13501	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
IISNASC*TTNC*LAP	C152 C156	0.119398484	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
VGLPIGQGGFGC*IYLADMNS SESVGSDAPCVVK	C50	0.117915899	Q99986	Q99986 Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 # Q06210-2 Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 # Q06210
GYDSAGVGFDDGNDKDWEA NAC*K	C55;C55	0.117161906	Q06210 Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 #
LALFNPDVC*WDRNNPEPWN K	C44	0.117141107	O00483	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 #

VC*NFLASQVPFPSR	C205;C214	0.115950351	Q99714 Q99714	Q99714-2 Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 # Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 #
EITAISSVPC*QLLESVLQEL K	C645;C704	0.11507686	O75694 O75694	O75694-2 Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 # O75694 Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 #
FSPNSSNPIIVSC*GWDK	C168	0.114746689	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
ITSC*IFQLLQEAGIK	C63	0.1137407	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
LVPASQC*GSLIGK	C109;C109;C109; 9;C109	0.112986939	Q15366 Q15366 Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
MC*DLVSDFDGFSER	C182	0.112775	P30520	P30520 Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3 #
NC*IVLIDSTPYR	C100	0.112481702	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #
IMKDLQDC*R	C62	0.11142	P60903	P60903 Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2 #
HLYTLGGDIINALC*FSPNR	C240	0.110640284	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
TSGNVEDDLIIFPDDC*EFK	C80	0.110176763	Q16186	Q16186 Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 #
ALANSLAC*QGK	C339;C393	0.109164104	P04075 P04075	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA #
STGVVNIPAAEC*LDEYEDDE AGQKER	C173;C119	0.107094778	Q96IZ0 H0Y116	Q96IZ0 PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 # H0Y116 PRKC apoptosis WT1 regulator protein (Fragment) OS=Homo sapiens GN=PAWR PE=1 SV=1 #
LLDLVQQSC*NYK	C34;C30	0.106291492	B1AHD1 P55769	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #
LPLMEC*VQMTQDVQK	C360	0.104572083	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
YAEYFLRPMLQYVC*DNSPEV R	C933;C915	0.103169824	O00410 O00410	O00410-3 Isoform 3 of Importin-5 OS=Homo sapiens GN=IPO5 # O00410 Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 #
VC*TLAIIDPGDSDIIR	C92;C92	0.10270883	P62888 E5RI99	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #
LWNTLGVC*K	C138	0.102362923	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #

				H0YLV5 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # Q9P2T1 GMP reductase 2 OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YJ6 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNH0 GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMPR2 PE=1 SV=7 # Q9P2T1-2 Isoform 2 of GMP reductase 2 OS=Homo sapiens GN=GMPR2 # H0YMB3 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # F8WAN9 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # A0A087WWM4 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YLB8 GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNS9 GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMPR2 PE=1 SV=7 # Q9P2T1-3 Isoform 3 of GMP reductase 2 OS=Homo sapiens GN=GMPR2 # Q14699 Raftlin OS=Homo sapiens GN=RFTN1 PE=1 SV=4 # P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 # P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSC2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 # O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # E3W990 Sequestosome-1 (Fragment) OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q9UI30- 2 Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q8NBS9 Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2 # O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 # A0A0A0MR02 Voltage-dependent anion- selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
VGIGPGSVC*TTR	C171;C186;C204; C229;C204;C153; C187;C186;C46; C32;C158	0.10142416	H0YLV5 Q9P2T1 H0YJ6 H0YNH0 Q9P2T1 H0YMB3 F8WAN9 A0A087WWM4 H0YLB8 H0YNS9 Q9P2T1	
GDHASLENEKPGTGDVC*SA PAGR	C211	0.09624554	Q14699	
GC*TATLGNFAK	C229	0.09601412	P15880	
GLGTDEDSLIEIC*SR	C151;C133	0.095553202	P07355 P07355	
LQEALDAEMLEDEAGGGGAG PGGAC*K	C57 C57;M41	0.092742826	H3BQZ7 Q1KMD3	
ISSINSISALC*EATGADVVEV ATAIGMDQR	C241	0.08920822	O60701	
FSFC*CSPEPEAEAEAAAGPG PCER	C26;C26;C26	0.089114255	E7EMC7 E3W990 Q13501	
KAVVVC*PK	C607	0.088414418	Q00839	
AGAIAPC*EVTVPAQNTGLGP EK	C119	0.086966039	P05388	
IC*PVEFNPNFVAR	C33;C33;C33	0.086304983	Q9UI30 Q9UI30 F5GX77	
VDC*TAHSDVCSAQGVR	C121	0.084086035	Q8NBS9	
LLLC*GGAPLSATTQR	C450	0.083248732	O95573	
ERPTPSLNNNC*TTSEDSLVL YNR	C744	0.081961165	P07814	
WNTDNTLGTEIAIEDQIC*QGL K	C103;C103	0.081707717	A0A0A0MR02 R02 P45880	



EGTQASEGYFSQSQEEFFAQ SEELC*AK	C615;C659;C613	0.080709685	Q16643 Q16643 Q16643	Q16643-2 Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643-3 Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643 Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 #
LLSALC*PEEPPVHSSAQIVSK	C334;C334;C334	0.079735202	Q9NR50 Q9NR50 Q9NR50	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 #
MSYPQFGYPYSSAPQFLMAT NSLSTC*C*ESGGR	C26;C26 C26	0.079106814	D6RAS8 P78413 D6RC00 P78413	D6RAS8 Iroquois-class homeodomain protein IRX-4 (Fragment) OS=Homo sapiens GN=IRX4 PE=1 SV=1 # P78413 Iroquois-class homeodomain protein IRX-4 OS=Homo sapiens GN=IRX4 PE=1 SV=2 # D6RC00 Iroquois-class homeodomain protein IRX-4 OS=Homo sapiens GN=IRX4 PE=1 SV=1 # P78413-2 Isoform 2 of Iroquois-class homeodomain protein IRX-4 OS=Homo sapiens GN=IRX4 #
IAAESSENVDC*PENPK	C588;C644;C620	0.077545154	Q32MZ4 Q32MZ4 Q32MZ4	Q32MZ4-3 Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # Q32MZ4 Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 # Q32MZ4-2 Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 #
SSSVTTSETQPC*TPSSSDY SDLQR	C334;C103	0.075298727	P50552 K7EM16	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 # K7EM16 Vasodilator-stimulated phosphoprotein (Fragment) OS=Homo sapiens GN=VASP PE=1 SV=1 #
HAC*VPVDFEEVHVSSNADE EDIR	C81	0.075133322	P51553	P51553 Isocitrate dehydrogenase [NAD] subunit gamma# mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 #
YSLADQTSQDQSPLPPCTPT PPC*AEMR	C569	0.074624068	Q06124 Q06124	Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
ALVDGPC*TQVR	C42;C42	0.073348729	E7EPB3 P50914	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 #
HEC*QANGPEDLNR	C118;C135	0.07315966	P60981 P60981	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
EALAEASAWC*YLYGTGSVA GVYLPGSR	C3652;C3670;C3662;C3821;C3684;C3707;C3711;C3688;C3684	0.07313324	Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
TDDYLDQPC*YETINR	C202	0.072977772	P50395	P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 #

KEC*ENCDCLOQGFQLTHSLG GGTGSGMGTLISK	C124	0.07263	Q13509 A0A0B4J2 69 Q13509	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 #
NHLLPDIVTC*VQSSR	C184	0.07019255	Q9BSD7	Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 #
RGPC*IIYNEDNGIIK	C208	0.06860766	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
QVQSLTC*EVDALK	C328	0.068596799	P08670	P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 #
LNLPINIIGLAPLC*ENMPSGK	C335	0.067755047	P28838 P28838	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 #
AHTVLAASC*AR	C104	0.067438309	Q8WUY1	Q8WUY1 Protein THEM6 OS=Homo sapiens GN=THEM6 PE=1 SV=2 #
KGDEC*ELLGHSK	C290	0.064904875	P49411	P49411 Elongation factor Tu# mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 #
YWLC*AATGPSIK	C249	0.062727651	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
IC*LAEAFLTADTILNTLQNISE GLVVYPK	C340	0.06145621	P30566	P30566 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 #
ICDEC*NYGSYQGR	C49	0.061448271	Q7RTV0	Q7RTV0 PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1 #
TVLCGTC*GQPADK	C479;C492;C18 7;C591;C561	0.060422636	P02545 P02545 A0A0C4D GC5 P02545 P02545	P02545-4 Isoform 4 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-5 Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA # A0A0C4DGC5 Prelamin-A/C (Fragment) OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545-3 Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA #
YINENLIVNTDELGRDC*LINA AK	C147;C147	0.060376162	E7ERF2 P17987	E7ERF2 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
LNEDMAC*SVAGITSDANVLT NELR	C43;M72 C74;M72 C74;M41 C74	0.0596617	H0YL69 H0YN18 P25789 H0YMZ1	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
YEAAPFLSPC*GR	C143;C98	0.059410232	H0YF29 Q6P1X6	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 # Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 #
SDLYSSC*DR	C338	0.057356721	Q96E39	Q96E39 RNA binding motif protein# X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 #
AVMALQEAC*EAYLVGLFEDT NLCAIHAK	C97	0.056834597	P68431	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 #
VWC*PLGPQGLEGLVSR	C800	0.05614897	Q2VPB7	Q2VPB7 AP-5 complex subunit beta-1 OS=Homo sapiens GN=AP5B1 PE=1 SV=4 # A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 #
ADHQPLTEASYVNLPTIALC*N TDSPLR	C153;C148;C14 8	0.055820232	A0A0C4D G17 C9J9K3 P08865	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #

YTVQDESHSEWVSC*VR	C153	0.054934669	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
NTGIIC*TIGPASR	C49	0.053374735	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
SYIEGYVPSQADVAVFEAVSS PPPADLC*HALR	C50;C50;C50	0.052358019	P24534 F2Z2G2 C9JZW3	P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 # F2Z2G2 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 # C9JZW3 Elongation factor 1-beta (Fragment) OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 #
QVLMGPYNPDTC*PEVGFFD VLGNDR	C129 ;M121	0.052041339	P01616 Q9H3P7	P01616 Ig kappa chain V-II region MIL OS=Homo sapiens PE=1 SV=1 # Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 #
GHSSDSNPAIC*R	C31	0.050611937	Q5JTH9	Q5JTH9 RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 #
ELEASEELDTIC*PK	C229	0.048950649	O76003	O76003 Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 #
VAAAASC*LSQK	C314;C314	0.040769038	O95067 H1UBN3	O95067 G2/mitotic-specific cyclin-B2 OS=Homo sapiens GN=CCNB2 PE=1 SV=1 # H1UBN3 Cyclin B2 OS=Homo sapiens GN=CCNB2V PE=1 SV=1 #
KFLDGNELTLADC*N	C178	0.033053299	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
VSLEEIYSGC*TK	C79;C79;C79;C79; C175;C112;C179;C79	0.031884114	P25685 M0R080 M0QZD0 M0R1D6 Q9UDY4 M0QXK0 P25685 M0QYT3	P25685-2 Isoform 2 of DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 # M0R080 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # M0QZD0 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # M0R1D6 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # Q9UDY4 DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1 # M0QXK0 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # P25685 DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 # M0QYT3 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 #
QMEKDETVSDC*SPHIANIGR	C206;C206;C235; C194;C232	0.031213568	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #

				Q9HCF6-6 Isoform 6 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-5 Isoform 5 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-2 Isoform 2 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-11 Isoform 11 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-3 Isoform 3 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # E9PBI7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # A2A3F3 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # Q9HCF6 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=2 SV=4 # Q9HCF6-7 Isoform 7 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F4 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # G5E9G1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # H7BYP1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=2 # Q9HCF6-4 Isoform 4 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # Q9HCF6-8 Isoform 8 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 #
AAFPGGLGDKVEDLTCC*HPER	C1594;C1584;C1582;C1609;C1594;C1454;C1441;C1607;C1597;C1444;C1441;C1431;C1572;C1586;C1554	0.027156816	Q9HCF6 Q9HCF6 Q9HCF6 Q9HCF6 E9PBI7 A2A3F3 Q9HCF6 Q9HCF6 A2A3F4 G5E9G1 H7BYP1 Q9HCF6 A2A3F7 Q9HCF6	000622 Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # P15927-3 Isoform 3 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 # P15927-2 Isoform 2 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 # P15927 Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1 # Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9P0U3 Sentrin-specific protease 1 OS=Homo sapiens GN=SEN1 PE=1 SV=2 # P63167 Dynein light chain 1# cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
IYQNGESFQPNC*K	C117	0.02686038	O00622	
AITIAGVPQSVTEC*VK	C158	0.0231925	Q15365	
AC*PRPEGLNFQDLK	C307;C227;C219	0.021221557	P15927 P15927 P15927	
SC*SGVEFSTSGHAYTDTGK	C36	0.019963407	Q9Y277	
ECENCDC*LQGFQLTHSLGGGTGSGMGTLLISK	C129	0.015579474	Q13509 A0A0B4J269	
SQEIPQQMNGSDC*GMFACKYADCITK	C603	0.015540608	Q9P0U3	
NADMSEEMQQDSVEC*ATQALEK	C24	0.011583941	P63167	
AEPPQC*TSLAWSADGQTLFAGYTDNLVR	C286	0.008479728	P63244	

VLHDAQQC*R	C608	0.007569016	A1L0T0	A1L0T0 Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 #
NTPSFLIAC*NK	C179;C68	0.0064	Q9Y5M8 H7C4H2	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 # H7C4H2 Signal recognition particle receptor subunit beta (Fragment) OS=Homo sapiens GN=SRPRB PE=1 SV=1 #
KNEPPLTC*PYSLK	C295	0.005331041	Q9UGP8	Q9UGP8 Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2 # H3BU60 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # H3BUH3 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # B7ZAR9 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=1 # Q8NCN5-2 Isoform 2 of Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR # H3BV59 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # A8MT40 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # Q8NCN5 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # M0R3D6 60S ribosomal protein L18a (Fragment) OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R117 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R1A7 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 # O94901-9 Isoform 9 of SUN domain- containing protein 1 OS=Homo sapiens GN=SUN1 # E9PHI4 SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=1 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
FFAFWGQDINNLTPLEC*GR ESR	C93;C118;C93;C 80;C93;C635;C7 35	0.001525794	H3BU60 H3BUH3 B7ZAR9 Q8NCN5 H3BV59 A8MT40 Q8NCN5	
DLTTAGAVTQC*YR	C80;C109;C80;C 109	0.001	M0R3D6 M0R117 M0R1A7 Q02543	
LATTAC*TLGDGEAVGADSGT SSAVSLK	C63;C63	0.001	O94901 E9PHI4	
DNTIEHLLPLFLAQLKDEC*PE VR	C377	4.045132742	P30153	

**Table A3.3**IsoTOP-ABPP analysis of DKM 2-90 (100  $\mu$ M) in vitro in 231MFP proteomes.

Peptide	Modified residue	Average area ratio	Uniprot ID	Protein
DNTIEHLLPLFLAQLKDEC*PEVR	C198;C377	34.48272141	B3KQV6 P30153	B3KQV6 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=1 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
MGVEAVIALLEATPDTPAC*V VSLNGN	C343	4.0979675	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
LYYFQYPC*YQEGLR	C130	3.95484614	Q9NRW3	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 #
NC*PHVVVGTGPR	C164	3.814803826	O00148	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 #
LNLSC*IHSPVVNELMR	C106	3.780813333	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #
GLIAAIC*AGPTALLAHEIGFG SK	C106;C67	3.654402274	Q99497 K7EN27	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 # K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 #
VQVSDPESTVAVAFPTPTIPHC *SMATLIGLSIK	C55	3.326649545	J3KS95 Q9Y3D0 H3BNV7	J3KS95 Mitotic spindle-associated MMXD complex subunit MIP18 (Fragment) OS=Homo sapiens GN=FAM96B PE=1 SV=1 # Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 # H3BNV7 Mitotic spindle-associated MMXD complex subunit MIP18 (Fragment) OS=Homo sapiens GN=FAM96B PE=1 SV=1 #
LSLQNC*CLTGAGCGVLSSTL R	C95	3.268075	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
SWC*PDCVQAEPVVR	C43;C43;C43	3.232767544	I3L0K2 I3L3M7 Q9BRA2	I3L0K2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # I3L3M7 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 #
TVVNISSLC*ALQPFK	C159	3.166650015	P35270	P35270 Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1 #
SGLTPNDIDVIELHDC*FSTNE LLTYEALGLCPEGQGATLVDR	C307	2.980157573	P22307	P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCEP2 PE=1 SV=2 #
LAEQC*GGLQGFLIFRSFGGG TGSGFTSLLMER	C96	2.978357685	A6NHL2 A6NHL2	A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 #

YVAAAFPSAC*GK	C172;C318;C306;C172;C306	2.951697774	B4DW73 H0YM31 Q16822 H0YML5 A0A0A0M574	B4DW73 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 # H0YM31 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=2 # Q16822-2 Isoform 2 of Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 # H0YML5 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 # A0A0A0MS74 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 #
AVASQLDC*NFLK	C207;C193	2.927369682	A0A087X2I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
LLPAITILGC*R	C389;C442	2.859447496	Q96IJ6 Q96IJ6	Q96IJ6 Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 # Q96IJ6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA # P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 #
ISGADINSIC*QESGMLAVR	C348	2.84767525	P43686 P43686	D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # D6RC52 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 # J3QSY4 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 #
GPEAQAEAC*SGER	C18;C18;C18;C18	2.823046663	D6RCB9 D6RC52 Q9NX24 J3QSY4	Q5VTE0 Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 # P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
NMITGTSQADC*AVLIVAAGV GEFEAGISK	C111;M102 C111	2.815664186	Q5VTE0 P68104 Q05639 P68104	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # Q8N2G8-3 Isoform 3 of GH3 domain-containing protein OS=Homo sapiens GN=GHDC # Q8N2G8 GH3 domain-containing protein OS=Homo sapiens GN=GHDC PE=1 SV=2 #
VTDGALVVVDCVSGVC*VQT ETVLR	C136	2.759168845	P13639	Q96GX2 Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 #
AALAAC*PSSPFPAMPR	C463;C502	2.73967	Q8N2G8 Q8N2G8	P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAP2K3 # P46734 Dual specificity mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 #
LPLC*SLPGEPEGNGPDQQLQ R	C75	2.561339898	Q96GX2	Q86YT6 E3 ubiquitin-protein ligase MIB1 OS=Homo sapiens GN=MIB1 PE=1 SV=1 #
ISC*MSKPPAPNPTPPR	C34;C29	2.494461562	P46734 P46734	
RPDVDVNGQC*AGHTAMQAA SQNGHVDILK	C462	2.484887129	Q86YT6	

RAC*SETLAESR	C431;C367;C29; C11;C315;C4;C3 15	2.4495	A8K0R7 H0YM94 H0YM06 H0YKI3 A8K0R7 H0YNU6 A8K0R7	A8K0R7-5 Isoform 3 of Zinc finger protein 839 OS=Homo sapiens GN=ZNF839 # H0YM94 Zinc finger protein 839 (Fragment) OS=Homo sapiens GN=ZNF839 PE=1 SV=1 # H0YM06 Zinc finger protein 839 (Fragment) OS=Homo sapiens GN=ZNF839 PE=1 SV=1 # H0YKI3 Zinc finger protein 839 (Fragment) OS=Homo sapiens GN=ZNF839 PE=1 SV=1 # A8K0R7 Zinc finger protein 839 OS=Homo sapiens GN=ZNF839 PE=2 SV=1 # H0YNU6 Zinc finger protein 839 (Fragment) OS=Homo sapiens GN=ZNF839 PE=1 SV=1 # A8K0R7-2 Isoform 2 of Zinc finger protein 839 OS=Homo sapiens GN=ZNF839 #
VLDALFPCVQGGTTAIPGAFG C*GK	C221;C254	2.311718327	P38606 P38606	P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A # P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 #
SCSSC*AVHDLIFWR	C46	2.241474497	O95197	O95197-3 Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3 #
LFNTAVC*ESK	C721	2.222497114	Q9BXJ9	Q9BXJ9 N-alpha-acetyltransferase 15# Nata auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
HLNEIDLHC*IDPNDSK	C62;C58;C58;C5 8	2.188743142	A0A087W YT3 Q15185 Q15185 Q15185	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q15185-3 Isoform 3 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 #
NSNVDSYLESLYQSC*PR	C106;C767;C64 5	2.180087107	Q7Z2W4 C9J6P4 Q7Z2W4	Q7Z2W4-4 Isoform 4 of Zinc finger CCCH- type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 # C9J6P4 Zinc finger CCCH- type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
AC*QSIYPLHDFVFR	C164;C164;C20 1;C181	2.168413742	D6RB09 D6RAT0 P61247 D6RG13	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 # P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 #
YSYVC*PDLVK	C235	2.148538724	P61158	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
TVPFC*STFAAFFTR	C394;C386	2.142872977	P29401 P29401	P29401-2 Isoform 2 of Transketolase OS=Homo sapiens GN=TKT # P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 #
APELLGC*K	C177;C177	2.112569431	P24941 G3V5T9	P24941 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2 # G3V5T9 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=1 #



AVC*MLSNTTAAIEAWAR	C361;C376;C310;C400;C376;C376;C376	2.059954106	P68366 P68363 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
HGFC*GIPITDGR	C140	2.047201967	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 # Q5QPE7 Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens GN=MGME1 PE=1 SV=1 # Q5QPE8 Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens GN=MGME1 PE=1 SV=1 # Q9BQP7 Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens GN=MGME1 PE=1 SV=1 #
GVAQTPGSVEEDALLC*GPVSK	C79;C79;C79	2.03893	Q5QPE7 Q5QPE8 Q9BQP7	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 # Q6PKG0-3 Isoform 2 of La-related protein 1 OS=Homo sapiens GN=LARP1 # Q6PKG0 La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 # Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 # P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK # P04818-2 Isoform 2 of Thymidylate synthase OS=Homo sapiens GN=TYMS # P04818 Thymidylate synthase OS=Homo sapiens GN=TYMS PE=1 SV=3 # P04818-3 Isoform 3 of Thymidylate synthase OS=Homo sapiens GN=TYMS # Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 # Q9BSH4 Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1 # Q9UBQ7 Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 # U3KQ56 Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 # E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # P48643-2 Isoform 2 of T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 # P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # E7ENZ3 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 #
ASC*LYGQLPK	C48	1.957153569	P09211	
TASISSPSEGTPTVGSYGC*TPQSLPK	C787;C864	1.869151258	Q6PKG0 Q6PKG0	
IISDNLYC*K	C205	1.858325382	Q9Y2X3	
IIPLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK	C132;C132	1.845733081	P61978 P61978	
DLPLMALPPCHALC*QFYVVNSELSCQLYQR	C199;M107 C116 C165;M190	1.825601752	P04818 P04818 P04818	
AGSDGESIGNC*PFSQR	C35	1.811199984	Q9Y696	
LDSLGLC*SVSCALEFIPNSK	C252	1.802808435	Q9BSH4	
QPRPEAAEFQAEFVSTPELAAQSDFIVVAC*SLTPATEGLCNK	C216;C216	1.801169435	Q9UBQ7 U3KQ56	
IAILTC*PFEPKPK	C232;C215;C160;C253;C198	1.772101565	E9PCA1 B7ZAR1 P48643 P48643 E7ENZ3	

C*IADVVSFLFITVMDK	C111	1.752585329	E9PM90 Q9UK41 Q9UK41 E9PQR7	E9PM90 Vacuolar protein sorting-associated protein 28 homolog (Fragment) OS=Homo sapiens GN=VPS28 PE=1 SV=1 # Q9UK41 Q9UK41 Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1 # Q9UK41-2 Isoform 2 of E9PQR7 Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1 # P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB # P45954 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 # P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 # Q5VVC8 Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 # P62913 P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 # P09543-2 Isoform CNP1 of 2'#3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP # P09543 2'#3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2 # Q9NQC3-2 Isoform 2 of Reticulon-4 OS=Homo sapiens GN=RTN4 # F8W914 F8W914 Reticulon OS=Homo sapiens GN=RTN4 PE=1 SV=1 # P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 # P62258-2 Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE # P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 # H3BPX2 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=2 # A6NGQ3 A6NGQ3 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=4 # P21980 Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 # Q9HA64 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 # A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 # Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL # B5MD87 B5MD87 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2 #
VGSFC*LSEAGAGSDSFALK	C73;C175	1.746838066	P45954 P45954	
LC*LNICVGESGDR	C21;C19;C20	1.741413583	P62913 Q5VVC8 P62913	
DKPELQFPFLQDEDTVATLLE C*K	C29;C49	1.735474124	P09543 P09543	
YSNSALGHVNC*TIK	C282;C254	1.711875281	Q9NQC3 F8W914	
LIC*CDILDVLDKHLIPAANTGE SK	C97;C75	1.707815	P62258 P62258	
GC*IVDANLSVLNLVIVK	C100	1.695237542	P62753	
ECISIHVGGAGVQIGNACWEL YC*LEHGIQPDGQMPSDK	C25	1.675292792	P68363 Q9BQE3 F5H5D3 Q71U36	
AFVNPFPDYEAAGALLASG AAEETGC*VRPPATTDEPLP FHQDGK	C49	1.674356319	Q9NS86	
APEVTILEPLQDVQLSEGQDA SFQC*R	C5228;C5228	1.671970435	H3BPX2 A6NGQ3	
SEGTYC*CGPVPVR	C370	1.653555601	P21980	
ATGHSGGGC*ISQGR	C24	1.634722168	Q9HA64	
AATMSAVEAATC*R	C278;C266;C246;C129	1.625713506	A0A0A0MQS1 Q53H96 Q53H96 B5MD87	

VFIMDNC*EELIPEYLNfir	C496;M371 C374	1.615153174	P07900 P07900	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDICFR	C201;C201;C201; C164;C183;C201	1.609039719	P68371 Q9BVA1 P04350 K7ESM5 Q5JP53 Q9BUF5	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # P60468 Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2 #
KNASC*GTR	C39	1.599159383	P60468	Q5T0N5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=1 # Q5T0N5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=3 # Q5T0N5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L #
FTSC*VAFFNILNELNDYAGQR	C69;C69;C69;C69; C69;C69	1.594200366	Q5T0N5 S4R347 Q5T0N5 Q5T0N5 Q5T0N5 Q5T0N5	Q5T0N5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=1 # Q5T0N5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=3 # Q5T0N5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L #
ISAFGYLEC*SAK	C159;C159;C159; C159	1.590293934	Q5JR08 P08134 E9PQH6	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 #
SLLINAVEASC*IR	C262;C262;C289; C262;C232	1.585855697	P32322 P32322 P32322 Q96C36 J3QKT4	P32322 Pyroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322-2 Isoform 2 of Pyroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # P32322-3 Isoform 3 of Pyroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # Q96C36 Pyroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 # J3QKT4 Pyroline-5-carboxylate reductase (Fragment) OS=Homo sapiens GN=PYCR1 PE=1 SV=1 #
TSC*GSPNYAAPEVISGR	C174;C185;C200; C174;C176	1.569701373	A0A087WXX9 Q13131 Q13131 P54646 Q96E92	A0A087WXX9 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=1 # Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 # Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 # P54646 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=2 # Q96E92 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=1 #
FQSSAVMALQEACEAYLVGL FEDTNLC*AIHAK	C111	1.554901515	P68431	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 #

AVLLASDAQEC*TLEEVVER	C332;C332	1.552508315	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
SELEC*VTNITLANVIR	C27;C27	1.546597307	Q9Y6W5 Q9Y6W5	Q9Y6W5-2 Isoform 2 of Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 # Q9Y6W5 Wiskott- Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3 #
HEFSVDMTC*GGCAEAVSR	C12 C17;M10	1.540940067	E5RIM7 O00244	E5RIM7 Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 # O00244 Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 #
GHSSDSNPAIC*R	C31;C31;C31	1.52365893	Q5JTH9 Q5JTH9 Q5JTH9	Q5JTH9-3 Isoform 3 of RRP12-like protein OS=Homo sapiens GN=RRP12 # Q5JTH9 RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 # Q5JTH9-2 Isoform 2 of RRP12-like protein OS=Homo sapiens GN=RRP12 #
C*PFTGNVSIR	C60	1.515506543	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 # P26583 High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 # Q5T7C4 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=1 #
MSSYAFFVQTC*R	C23;M13 C23	1.508906351	P26583 Q5T7C4 B2RPK0 D6R9A6 P09429	B2RPK0 Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 # D6R9A6 High mobility group protein B2 (Fragment) OS=Homo sapiens GN=HMGB2 PE=1 SV=1 # P09429 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 #
VGMGSGSIC*ITQEVLACGRP QATAVYK	C331	1.507247985	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
NC*LNPQFSK	C54	1.498441485	O75131	O75131 Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 #
C*SGVMEFSTSGHAYTDTGK	C36	1.496224598	Q9Y277	Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 #
YGSQCMQPNNIMGIENIC*EL AAR	C220 C195;M214	1.495929626	F1DAL9 P10589	F1DAL9 COUP transcription factor 1 OS=Homo sapiens GN=NR2F1 PE=1 SV=1 # P10589 COUP transcription factor 1 OS=Homo sapiens GN=NR2F1 PE=1 SV=1 #
LPSGLGC*STVLSPEGSAQFA AQIFGLSNHLVWSK	C374;C374	1.491267164	E9PBS1 P22234	E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
GLC*AIAQAESLR	C97	1.487860312	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #
VQENSAYIC*SR	C585	1.482537761	Q9Y3T9	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 # P49189 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 # P49189-2 Isoform 2 of 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 #
GALMANFLTQQQVC*CNGTR	C288;C218	1.473975	P49189 P49189	Q7Z7H8 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 # Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 #
LPSLPLVQGELVGGGLTC*LTA QTHSLLQHQLQLTLLDQYI R	C213;C223	1.463461637	Q7Z7H8 Q7Z7H8	Q7Z7H8 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 # Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 #

TIYAGNALC*TVK	C51;C155;C59;C106;C155	1.462725846	H0YK49 P13804 H0YNX6 P13804 H0YLU7	H0YK49 Electron transfer flavoprotein subunit alpha# mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 # P13804 Electron transfer flavoprotein subunit alpha# mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 # H0YNX6 Electron transfer flavoprotein subunit alpha# mitochondrial (Fragment) OS=Homo sapiens GN=ETFA PE=1 SV=1 # P13804-2 Isoform 2 of Electron transfer flavoprotein subunit alpha# mitochondrial OS=Homo sapiens GN=ETFA # H0YLU7 Electron transfer flavoprotein subunit alpha# mitochondrial (Fragment) OS=Homo sapiens GN=ETFA PE=1 SV=1 #
KAQC*PIVER	C66;C87;C66	1.461660906	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
VC*TLAIIDPGDSDIIR	C92;C92	1.459000402	P62888 E5RI99	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #
LNISFPATGC*QK	C12	1.453813114	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
QEPLGSDSEGVNC*LAYDEAI MAQQDR	C23	1.44709777	F5H6Q1 F5H3F0 J3KR44 F5GYJ8 Q96FW1	F5H6Q1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # F5H3F0 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # J3KR44 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 # F5GYJ8 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # Q96FW1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 #
NLSFFLTPPC*AR	C492;C492;C494	1.446621741	P42224 P42224 J3KPM9	P42224-2 Isoform Beta of Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 # P42224 Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 # J3KPM9 Signal transducer and activator of transcription OS=Homo sapiens GN=STAT1 PE=1 SV=1 #
YVFNLAEELVPMYVGIPE C*IK	C416 C295;M165 C357;M287 C173;M408	1.443194477	Q12982 Q12982 H7C096 J3KN59	Q12982-2 Isoform 2 of BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 # Q12982 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # H7C096 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 (Fragment) OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # J3KN59 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 #
IGAAIQEELGYNC*QTGGVIAE ILR	C112	1.440936823	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
AYEYVEC*PIR	C66	1.438404391	P53701	P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 #
NC*IVLIDSTPYR	C100	1.436219371	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #
FQSAAGALQEASEAYLVGLF EDTNLC*AIHAK	C111;C111	1.436161479	K7EK07 P84243	K7EK07 Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1 # P84243 Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 #

LC*SGPGIVGNVLVDPSAR	C245;C245	1.425726919	Q9Y5P6 Q9Y5P6	Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 #
MVYSTC*SLNPIEDEAVIASLL EK	C85;M316 C321;M281 C286	1.419235	Q08J23 Q08J23 Q08J23	Q08J23-3 Isoform 3 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 # Q08J23 tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 # Q08J23-2 Isoform 2 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 #
FMADC*PHTIGVEFGTR	C40;M37 C40	1.416822036	X6RFL8 P61106	X6RFL8 Ras-related protein Rab-14 (Fragment) OS=Homo sapiens GN=RAB14 PE=1 SV=1 # P61106 Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 #
FGVIC*LEDLIEIAFP GK	C184	1.401979012	Q6DKI1	Q6DKI1 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 #
LLACIASRPGQC*GR	C182;C162	1.400524121	P62241 Q5JR95	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 # Q5JR95 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=1 #
NAIDDGC*VVPGAGAVEVAM AEALIK	C406;C361	1.399596553	P40227 P40227	P40227 T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 # P40227-2 Isoform 2 of T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A #
SC*SGVEFSTSGSSNTDTGK VTGTLETK	C47;C47	1.396652407	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
FLSQIESDC*LALLQVR	C766;C794	1.393950708	E9PB90 P52789	E9PB90 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=1 # P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
AVAC*SGAAQVR	C578	1.39265	Q92797	Q92797 Symplekin OS=Homo sapiens GN=SYMPK PE=1 SV=2 #
TGC*TFPEKPDFH	C318;C353;C33 6	1.392237106	P55263 P55263 P55263	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK # P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 # P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK #
YLEC*SALQQDGVK	C157	1.39196269	P84095	P84095 Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHO G PE=1 SV=1 #
YIYDQC*PAVAGYGPIQLPD YNR	C453	1.390050513	P31930	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 #
VTFSC*AAGFGQR	C1113;C1227;C 1118;C1245;C12 10;C1252;C1230	1.388191454	Q14203 Q14203 Q14203 Q14203 Q14203 E7EX90	Q14203-5 Isoform 5 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-4 Isoform 4 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-2 Isoform 2 of Dynactin subunit 1 OS=Homo sapiens p135 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-6 Isoform 6 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203-3 Isoform 3 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 # Q14203 Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3 # E7EX90 Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=1 #
IHMGC*AENTAK	C196	1.374672427	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #

SVLC*STPTINIPASPFMQK	C22	1.374662192	E5RIE1 Q96KB5 Q96KB5	E5RIE1 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=1 # Q96KB5 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 # Q96KB5-2 Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
VIGIEC*SSISDYAVK	C101	1.37188185	Q99873	Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
SGETEDTFIADLVVGLC*TGQIK	C389	1.369172348	P06733	P06733 Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 # Q9Y508 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNV3 E3 ubiquitin-protein ligase RNF114 (Fragment) OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNT1 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 # A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 #
DC*GGAAQLAGPAAEADPLGR	C8;C8;C8;C8;C8;C8;C8	1.356827161	A0A096LP02 Q9Y508 A0A096LNN8 A0A096LPF9	A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 # A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 #
MPC*QLHQVIVAR	C640;C562	1.356419285	P17655 P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P17655-2 Isoform 2 of Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 # H0YLV5 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # Q9P2T1 GMP reductase 2 OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNJ6 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # Q9P2T1-2 Isoform 2 of GMP reductase 2 OS=Homo sapiens GN=GMPR2 # H0YMB3 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # F8WAN9 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # A0A087WWM4 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 #
VGIGPGSVC*TTR	C171;C186;C204;C153;C187;C186	1.346321182	H0YLV5 Q9P2T1 H0YNJ6 Q9P2T1 H0YMB3 F8WAN9 A0A087WWM4	H0YLV5 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # Q9P2T1 GMP reductase 2 OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNJ6 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # Q9P2T1-2 Isoform 2 of GMP reductase 2 OS=Homo sapiens GN=GMPR2 # H0YMB3 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # F8WAN9 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # A0A087WWM4 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 #
SGQGAFGNMC*R	C96	1.332007045	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
AAVEEGIVLGGGC*ALLR	C442	1.330258679	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
GTPEQPQC*GFSNAVQILR	C67	1.325783845	Q86SX6	Q86SX6 Glutaredoxin-related protein 5# mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 #
QGEYGLASIC*NGGGGASAMLIQK	C413	1.32568152	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #

					Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=7 # C9JX21 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # C9JNR4 Transforming protein RhoA (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOA PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q02338 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 # G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 # Q9Y6C9 Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 # P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 # O75477 Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 # Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # Q9Y3D2 Methionine-R-sulfoxide reductase B2# mitochondrial OS=Homo sapiens GN=MSRB2 PE=1 SV=2 # P21281 V-type proton ATPase subunit B# brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 # P49411 Elongation factor Tu# mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 # P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 # P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB # Q9UJW0 Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1 # Q9UJW0-2 Isoform 2 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # Q9UJW0-3 Isoform 3 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
LVIVGDGAC*GK	C16;C16;C16;C16;C16;C16	1.323941484	Q5JR08 C9JX21 C9JNR4 P61586 P08134 E9PQH6		
ECISIHVQGAGVQIGNAC*WE LYCLEHGIQPDGQMPSDK	C20	1.318483719	P68363 Q9BQE3 F5H5D3 Q71U36		
METYC*SSGSTDTSPVIDAVT HALTATTPYTR	C288	1.318235137	Q02338		
C*LHNFLTDGVP AEGAFTEDF QGLR	C316;C268	1.316345474	G3V1A6 P57764		
QVC*QLPGLFSYAQHIASIDG R	C49	1.314866672	Q9Y6C9		
IIPGFMC*QGGDFTR	C62	1.313497984	P62937		
IYFGSNIPNMFVDSSC*ALK	C310	1.305877777	O75477		
HDDSSDNFC*EADDIQSPEAE YVDLLNPER	C166	1.304351509	Q96HE7		
GQAGGGGPGTGPGLGEAGS LATC*ELPLAK	C45	1.30317	Q9Y3D2		
GPVLAEDFLDIMGQPINPQC *R	C162	1.297193596	P21281		
GEETPVIVGSALC*ALEGRDP ELGLK	C222	1.290499622	P49411		
VADSSPFALELLISDDCFVLD NGLC*GK	C275;C290	1.282245546	P40121 P40121		
AGAIAPC*EVTVPAQNTGLGP EK	C119	1.281674068	P05388		
HSMNPF*EIAVEEAVR	C42;M129 C133	1.280361778	P38117 P38117		
LLQPDFQPVC*ASQLYPR	C258;C201;C265	1.279906738	Q9UJW0 Q9UJW0 Q9UJW0		
SIQFVDWC*PTGFK	C332;C347;C347	1.278564814	P68366 P68363 P68366		



LC*PQFLQLASANTAR	C264;C264;C264	1.276311812	O95630 O95630 C9JK83	O95630 STAM-binding protein OS=Homo sapiens GN=STAMBP PE=1 SV=1 # O95630-2 Isoform 2 of STAM-binding protein OS=Homo sapiens GN=STAMBP # C9JK83 STAM-binding protein (Fragment) OS=Homo sapiens GN=STAMBP PE=1 SV=1 # P68036 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 # P68036-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 # P68036-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 # P36542 ATP synthase subunit gamma# mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 # P36542-2 Isoform Heart of ATP synthase subunit gamma# mitochondrial OS=Homo sapiens GN=ATP5C1 #
GQVC*LPVISAENWKPATK	C86;C54;C144	1.26735991	P68036 P68036 P68036	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
GLC*GAIHSSIAK	C103;C103	1.266508306	P36542 P36542	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # Q96EY8 Cob(I)yrinic acid a#c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 #
IQFNDLQSLLC*ATLQNVLR	C585;C440	1.26468	Q14974 Q14974	S4R3P5 Cob(I)yrinic acid a#c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # F5H4Z7 Cob(I)yrinic acid a#c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 #
PMC*IPPSYADLGK	C13;C13	1.264423604	A0A0A0MR02 R02 P45880	
GDLENAFLNLVQC*IQNKPLY FADR	C280;C262	1.25905173	P07355 P07355	
IQCTLQDVGSALATPC*SSAR	C132;C80;C132	1.256787404	Q96EY8 S4R3P5 F5H4Z7	

					A0A140T9H3 HLA class I histocompatibility antigen# B-46 alpha chain (Fragment) OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
					A0A140T951 HLA class I histocompatibility antigen# B-46 alpha chain (Fragment) OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
					P30481 HLA class I histocompatibility antigen# B-44 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P18465 HLA class I histocompatibility antigen# B-57 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
				A0A140T9H3	P30460 HLA class I histocompatibility antigen# B-8 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # A0A140T9A9 HLA class I histocompatibility antigen# B-46 alpha chain (Fragment) OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30461 HLA class I histocompatibility antigen# B-13 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
				A0A140T951	P30480 HLA class I histocompatibility antigen# B-42 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # P30485 HLA class I histocompatibility antigen# B-47 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
				P30481	P01889 HLA class I histocompatibility antigen# B-7 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=3 # Q04826 HLA class I histocompatibility antigen# B-40 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
				P18465	P30486 HLA class I histocompatibility antigen# B-48 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 # Q31610 HLA class I histocompatibility antigen# B-81 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
				P30460	P03989 HLA class I histocompatibility antigen# B-27 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=2 # P30479 HLA class I histocompatibility antigen# B-41 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1 #
				A0A140T9A9	Q9P0L0 Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 # Q9P0L0-2 Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA #
				A9	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
				P30461	Q2TAA2 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 # C9JE02 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 # C9JDY4 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 # Q2TAA2-2 Isoform 2 of Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 #
				P30480	H7C5G1 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 # C9J5J2 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 #
				P30485	
				P01889	
				Q04826	
				P30486	
				Q31610	
				P03989	
				P30479	
GGSYSQAAC*SDSAQGS DVS LTA	C228;C228;C349;C349;C28;C349;C349;C349;C349;C349;C349;C349	1.254890394			
YC*VRPNSGIIDPGSTVTVSV MLQPFDYDPNEK	C60	1.250707617		Q9P0L0 Q9P0L0	
FSFC*CSPEPEAEAEAAAGPG PCER	C26;C26	1.247944219		E7EMC7 Q13501	
VILITPTPLC*ETAWEEQCIQG CK	C137;C112;C24;C24;C117;C24	1.242911185		Q2TAA2 C9JE02 C9JDY4 Q2TAA2 H7C5G1 C9J5J2	

VGSFGSSPPGLSSTYTGGPL GNEIASGNNGAAAGDDEDG QNLWSC*ILSEVSTR	C51;C51;C51	1.240798006	Q9Y6G9 C9JLW1 E9PHI6	Q9Y6G9 Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1L1 PE=1 SV=3 # C9JLW1 Cytoplasmic dynein 1 light intermediate chain 1 (Fragment) OS=Homo sapiens GN=DYNC1L1 PE=1 SV=1 # E9PHI6 Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1L1 PE=1 SV=1 #
AQLSGLQLQPC*LYK	C451;C135	1.237570025	O43159 E9PPP6	O43159 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 # E9PPP6 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=1 # P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 # Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 # P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 #
LCLNIC*VGESGDR	C25;C23;C24	1.237033352	P62913 Q5VVC8 P62913	P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 #
NLVFSSSATVYGNPQYLPLDE AHPTGGC*TNPYGK	C153	1.236468648	Q14376	Q14376 UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 # Q9BRJ7 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # W4VSQ8 Nudix (Nucleoside diphosphate linked moiety X)-type motif 16-like 1# isoform CRA_b OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # K7EIN2 Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # Q9BRJ7-2 Isoform 2 of Protein syndesmos OS=Homo sapiens GN=NUDT16L1 # K7ENA3 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 #
VLGLGLGC*LR	C88;C88;C75;C8 8;C88	1.235877922	Q9BRJ7 W4VSQ8 K7EIN2 Q9BRJ7 K7ENA3	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 # P17676 CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB PE=1 SV=2 # P17676-3 Isoform 3 of CCAAT/enhancer- binding protein beta OS=Homo sapiens GN=CEBPB # P17676-2 Isoform 2 of CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB # Q99961-3 Isoform 3 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 # Q99961 Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 # Q99961-2 Isoform 2 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65- 2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q8TCJ2 Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1 # P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 # P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 #
C*ELSSSVQTDINLPYLTMDS SGPK	C317	1.230512969	P38646	
APPTAC*YAGAAPAPSQVK	C248;C50;C225	1.230291332	P17676 P17676 P17676	
EPFDLGEPEQSNNGFPC*TT APK	C213;C277;C22 9	1.229677535	Q99961 Q99961 Q99961	
TIQFVDWC*PTGFK	C347;C281;C41 7;C371;C347;C3 47	1.227890956	Q9BQE3 Q9NY65 F5H5D3 C9J2C0 Q71U36 Q9NY65	
AGSPTLLNC*LMYK	C715	1.227524332	Q8TCJ2	
VTDDLVC*LVIKTDQAQDVK	C48	1.227309849	P49458	
QNSDFLC*QMDLLQEFYETTL EALKDAK	C130	1.226105283	P61201	

YNLSPSIFFC*ATPPDDGNLC R	C120;C99	1.217695	Q00796 H0YLA4	Q00796 Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 # H0YLA4 Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=1 #
VC*FGIQLLNAVSR	C182;C218;C114;C208	1.215154033	E7EWX8 A0A0C4D FN3 H7C4E0 Q99685	E7EWX8 Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=1 # A0A0C4DFN3 Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=1 # H7C4E0 Monoglyceride lipase (Fragment) OS=Homo sapiens GN=MGLL PE=1 SV=1 # Q99685 Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=2 #
ALVDGPC*TQVR	C42;C42	1.212737738	E7EPB3 P50914	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 #
AEGSDVANAVLDGADC*IMLS GETAKGDYPLEAVR	C358;C284	1.211485	P14618 B4DNK4	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # B4DNK4 Pyruvate kinase OS=Homo sapiens GN=PKM PE=1 SV=1 #
LDINLLDNVNC*LYHGEGAQ QR	C34	1.210473357	O14980	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 #
LTNTYCLVAIGGSENFYSVFE GELSDTIPVVHASIAGC*R	C56	1.20938456	P56537	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 #
TLIQCNC*GASTIR	C417;C410;C455	1.206519068	P49368 B4DUR8 P49368	P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 # B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 # P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 #
SQSVSVSGPGPGPGGLC*P GPNVLLNQNPAPQPQH LA R	C222	1.204198081	Q9H0L4	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 #
AYHEQLSVAEITNAC*FEPAN QMVK	C280	1.204045844	P68366 P68363 Q71U36 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
VTEDENDEPIEPSDDGTVLL STVTAQFPGAC*GLR	C39;C39;C39;C39;C39	1.202413666	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
VAC*ITEQVLTLVNKR	C477	1.201919134	P04843	P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 #
GMLLGVFDGHAGCAC*SQAV SER	C151;M163 C176	1.198047885	Q9P0J1 Q9P0J1	Q9P0J1 [Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1# mitochondrial OS=Homo sapiens GN=PDP1 PE=1 SV=3 # Q9P0J1-2 Isoform 2 of [Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1# mitochondrial OS=Homo sapiens GN=PDP1 #
FLENTPSSLNIEDLFLSLAQ YYC*SK	C283;C146;C283	1.192861961	Q9NUY8 E9PGE5 Q9NUY8	Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 # E9PGE5 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=1 # Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 #

VEPC*SLTPGYTK	C219;C218;C218; 8;C218	1.191624679	Q96EB1 Q96EB1 Q96EB1 G5E9D4	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1-2 Isoform 2 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 # G5E9D4 Elongation protein 4 homolog (S. cerevisiae)# isoform CRA_b OS=Homo sapiens GN=ELP4 PE=1 SV=1 #
LEGLTGPSVDVEVPDVELE C*PDAK	C2162	1.186269227	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
LTWHSC*PEDEAQ	C177	1.185929158	Q13185	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 #
FHADSVK*K	C25	1.184463974	Q9BW61	Q9BW61 DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1 #
LC*DFGVSGQLIDSMANSFVG TR	C207	1.181620024	Q02750	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 #
LEVDAIVNAANSLLGGGGVD GC*IHR	C186	1.180289947	Q9BQ69	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #
AIC*TEAGLMALR	C399;C326	1.179645	P62191 P62191	P62191 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 # P62191-2 Isoform 2 of 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 #
EVIAVSCGPAQC*QETIR	C71;C162	1.179031866	P38117 P38117	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB #
PGHLQEGFGC*VVTNRFDQL FDDESDPFVLEK	C11;C11;C11;C1 1	1.176890609	Q8NC51 Q8NC51 Q8NC51 Q8NC51	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 # Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 #
AIVDC*GFEHPSEVQHECIPQ AILGMDVLCQAK	C63	1.175875369	Q13838 Q5STU3 O00148 Q13838	Q13838-2 Isoform 2 of Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B # Q5STU3 Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=2 # O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 # Q13838 Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1 #
LNCQVIGASVDSHFC*HLAWV NTPK	C83;C83	1.170108664	Q06830 A0A0A0MSI0 SI0	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 # A0A0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 #
LLAPDC*EIIQEVGKLYPLEIVF GMNGR	C215	1.169015594	Q9NQT5	Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 #
EITSLDTENIDEILNNADVALV NFYADWC*R	C58	1.168410828	Q9BS26	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 #
TWYVQATC*ATQGTGLYEGL DWLSNELSKR	C159;C132	1.167228447	P18085 C9JAK5	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 # C9JAK5 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=1 #

PPMEAAGFTAQVILNHPGQI SAGYAPVLDCHTAHIAC*K	C370;M314 C349	1.165797097	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
VC*NFLASQVPPFSR	C214	1.163581303	Q99714	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 #
HC*SQVDSVR	C112;C112;C11 2	1.162641021	Q14247 Q14247 Q14247	Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN # Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 # Q14247-2 Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN #
GGC*PGGEATLSQPPPR	C22	1.161209474	P20290	P20290 Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1 # B3KQV6 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=1 # P30153
LNIISNLDC*VNEVIGIR	C211;C390	1.160981476	B3KQV6 P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
EVFSSC*SSEVVLSGDDEEYQ R	C108	1.160950522	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
DLC*FSPGLMEASHVVNDVN EAVQLVFRK	C392	1.159835226	Q9BXW7 Q9BXW7 A8MYZ9	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 # Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 # A8MYZ9 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 #
ALLVTASQC*QQPAENK	C93;C92	1.158092238	Q01518 Q01518	Q01518 Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 # Q01518-2 Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 #
IGTSGGIGLEPGTVVITEQAVD TC*FK	C162	1.157968169	Q16831	Q16831 Uridine phosphorylase 1 OS=Homo sapiens GN=UPP1 PE=1 SV=1 #
LVPATQC*GSLIGK	C109	1.151007901	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
TATAVAHC*R	C25	1.150930152	A0A087W Z27	A0A087WZ27 Zinc finger protein 90 OS=Homo sapiens GN=ZNF90 PE=4 SV=2 #
LMSSLPNFC*GIFNHLER	C35 C35;M28	1.148038904	Q96PU8 Q96PU8 Q96PU8 Q96PU8	Q96PU8-8 Isoform 5 of Protein quaking OS=Homo sapiens GN=QKI # Q96PU8-9 Isoform 6 of Protein quaking OS=Homo sapiens GN=QKI # Q96PU8 Protein quaking OS=Homo sapiens GN=QKI PE=1 SV=1 # Q96PU8-6 Isoform 4 of Protein quaking OS=Homo sapiens GN=QKI #
NQSFC*PTVNLDKLWTLVSEQ TR	C70;C70;C13	1.147333229	P46776 E9PLL6 E9PJD9	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 # E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 # E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 #
LAPILC*DGTATFVDLVPGR	C568;C568	1.146333471	O43264 O43264	O43264 Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 # O43264-2 Isoform 2 of Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 #
FIC*TTSAIQNR	C20;C20	1.145478645	P53396 P53396	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 # P53396-2 Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY #
DVQIGDIVTVGEC*RPLSK	C131	1.145234038	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #

AGAVVAVPTDTLYGLACAAS C*SAALR	C99	1.145227446	Q86U90	Q86U90 YrdC domain-containing protein# mitochondrial OS=Homo sapiens GN=YRDC PE=1 SV=1 #
SC*SGVEFSTSGHAYTDTGK	C36	1.144260678	Q9Y277	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #
QMEKDETVSDC*SPHIANIGR	C206;C206;C23 5;C194;C232	1.141412421	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
EEFASTC*PDDEEIELAYEQV AK	C223	1.138880295	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
AAQLEPITYMQLSAC*EQIR	C162	1.134046667	Q9HBH0	Q9HBH0 Rho-related GTP-binding protein RhoF OS=Homo sapiens GN=RHOPE=1 SV=1 #
TDVLVLSCLITDVALHEVVD LFR	C106;C106;C10 6	1.133440355	Q9NR50 Q9NR50 Q9NR50	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 #
GC*WDSIHVVEVQEK	C147;C147;C17 6;C135;C173	1.133211641	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # Q9Y6B6 GTP-binding protein SAR1b OS=Homo sapiens GN=SAR1B PE=1 SV=1 # D6RDB2 GTP-binding protein SAR1b OS=Homo sapiens GN=SAR1B PE=1 SV=1 # D6RD69 GTP-binding protein SAR1b (Fragment) OS=Homo sapiens GN=SAR1B PE=1 SV=1 #
NYLPAINGIVFLVDC*ADHER	C102;C102;C10 2	1.132701448	Q9Y6B6 D6RDB2 D6RD69	Q9Y6B6 GTP-binding protein SAR1b OS=Homo sapiens GN=SAR1B PE=1 SV=1 # D6RDB2 GTP-binding protein SAR1b OS=Homo sapiens GN=SAR1B PE=1 SV=1 # D6RD69 GTP-binding protein SAR1b (Fragment) OS=Homo sapiens GN=SAR1B PE=1 SV=1 #
VAHALAEGLVIAIC*IGEK	C127;C164	1.13041783	P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 # Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=2 SV=1 # F8WDZ3 CKLF-like MARVEL transmembrane domain- containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 # Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 #
TTC*SSGSALGPGAGAAQPS ASPLEGLLDLSYPR	C12;C12;C12	1.130124803	Q96FZ5 F8WDZ3 Q96FZ5	Q96FZ5 CKLF-like MARVEL transmembrane domain- containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 # Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 #

				F8VYE8 Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=1 SV=1 # P62136-2 Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA # P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 # E7ETD8 Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CB PE=1 SV=1 # P36873 Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1 # F8VR82 Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=1 SV=1 # P36873-2 Isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC # F8W0W8 Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=1 SV=1 #
GNHEC*ASINR	C127;C138;C126;C127;C98;C127;C127;C136	1.128048194	F8VYE8 P62136 P62140 P62136 E7ETD8 P36873 F8VR82 P36873 F8W0W8	
TYAIC*GAIR	C56;C56	1.126896346	Q8WVC2 P63220	Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # P63220 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 # M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
WLSDEC*TNAAVNFSLR	C345;C350;C380	1.125286949	O75521 A0A0C4DGA2 O75521	
QPAIMPQSYGLEDSK	C413;C472	1.125034593	M0QXS5 P14866	
KC*EPIVMTVPR	C345	1.121557616	Q9BR76	Q9BR76 Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 # K7EIR2 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 # A0A140TA84 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 # Q5XKP0 MICOS complex subunit MIC13 OS=Homo sapiens GN=MIC13 PE=1 SV=1 # A0A140TA86 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 #
AGEVPPAMYQFSQYVC*QQ TGLQIPQLPAPPK	C82 C60;M74 C82;M52	1.121022811	K7EIR2 A0A140TA84 84 Q5XKP0 A0A140TA86	
AINC*ATSGVGLVNCLR	C1448	1.119569024	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P09110 3-ketoacyl-CoA thiolase# peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 # H7C131 3-ketoacyl-CoA thiolase# peroxisomal (Fragment) OS=Homo sapiens GN=ACAA1 PE=1 SV=1 # C9JDE9 3-ketoacyl-CoA thiolase# peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=1 # Q14258 E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 # P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
VNPLGGAVALGHPLGC*TGAR	C381;C271;C340	1.119491473	P09110 H7C131 C9JDE9	
NTVLC*NVVEQFLQADLAR	C70	1.118551165	Q14258	
C*EFQDAYVLLSEKK	C237	1.118425153	P10809	



SLHDALC*VLAQTVK	C395;C395;C395	1.118070111	P78371 F8VQ14 F5GWF6	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 # F8VQ14 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=1 # F5GWF6 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=2 #
NMSVHLSPC*FR	C116	1.116856093	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
LSTAC*PGR	C939	1.114001315	P55060	P55060 Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 #
C*ASQSGMTAYGTR	C175	1.112023333	Q99439 B4DDF4 B4DUT8 A0A087X1 X5	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X1X5 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #
IYHPNINSNGSIC*LDILR	C87;C85;C85;C79;C56;C56;C85;C56;C86;C85	1.110594924	P61077 P61077 P61077 H9KV45 P62837 D6RAH7 A0A0A0M QU3 D6RFM0 A0A087W Y85 P62837	P61077-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # H9KV45 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 # D6RAH7 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # A0A0A0MQU3 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # D6RFM0 Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=3 SV=1 # A0A087WY85 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 #
TPC*NAGTFSQPEK	C129;C129;C129;C129	1.109246667	O43684 J3QT28 O43684 J3QSX4	O43684 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 # J3QT28 Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=1 SV=1 # O43684-2 Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 # J3QSX4 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 #
VC*EDLDTSVNLAWTSGTNC TR	C210;C210	1.108683853	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
ALANVNIGSLIC*NVGAGGPA PAAGAAPAGGPAPSTAAAPA EEK	C36;C61	1.107551767	P05386 P05386	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 # P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 #
EGDVAAC*YANPSLAQEELG WTAALGLDR	C307	1.106824128	Q14376	Q14376 UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 #
TATAVAHC*K	C25;C25	1.104978695	M0R3H0 P62249	M0R3H0 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 # P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 #

TVPFLPLLGGC*IDDTILSR	C180;C190	1.104137567	Q7Z7H8 Q7Z7H8	Q7Z7H8 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 # Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 #
HELQANC*YEEVKDR	C177;C122;C139; C139	1.103059148	E9PK25 G3V1A4 P23528 E9PP50	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 # E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
FSFCC*SPEPEAEAEAAAGPG PCER	C27;C27	1.098991866	E7EMC7 Q13501	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
C*ASQAGMTAYGTR	C132;C173;C132 2	1.098776805	E9PDU6 Q15417 Q15417	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 # P00492 Hypoxanthine-guanine
SYC*NDQSTGDIK	C106	1.097582521	P00492	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
VGVGTC*GIADKPMYQYQDT SK	C214	1.096041977	O75940	O75940 Survival of motor neuron-related- splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 #
TDC*SPIQFESAWALTNIASGT SEQTK SSSSSSASAAAAAAAASSSA SC*SR	C133  C100	1.094485302  1.09439123	P52292  Q07065	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 # Q07065 Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 # K7ENV7 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=7 # K7EKW4
SVLLCGIEAQAC*ILNTTLDLL DR	C114;C114;C114 4	1.092383388	K7ENV7 K7EKW4 Q96AB3	K7ENV7 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=1 # Q96AB3 Isochorismatase domain-containing protein 2 OS=Homo sapiens GN=ISOC2 PE=1 SV=1 # Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2
VAAASGHC*GAFSGDSSR	C947;C919	1.091814334	Q9NZB2 Q9NZB2	Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 #
FLEGTSC*IAGVFVDATEK	C3902;C3920;C3912; C3957;C4071; C3934;C3961; ;C3938;C3934	1.09117	Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
VVSGMVNC*NDDQGVLLGR	C230	1.090416839	P21980	P21980 Protein-glutamine gamma- glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 #

MAAAAAAAAAAAAAAQC*RS PR	C24 C24;M8	1.089553801	Q8N3X6 Q8N3X6 D6RA10	Q8N3X6 Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens GN=LCORL PE=1 SV=4 # Q8N3X6-3 Isoform 3 of Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens GN=LCORL # D6RA10 Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens GN=LCORL PE=1 SV=1 #
ALC*HLNVPVTVVLDAAVGYI MEK	C169	1.088587618	Q14232	Q14232 Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=1 SV=1 #
IHEGC*EEPATHNALAK	C874;C870;C870	1.088495	A0A087W VQ6 Q00610 Q00610	A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #
INISEGNC*PER	C54;C54;C54;C54;C54	1.086338616	Q15366 Q15366 Q15366 Q15366 Q15366	Q15366-7 Isoform 7 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-4 Isoform 4 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
ISLGLPVGAVINC*ADNTGAK	C28	1.085045826	P62829	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 #
ITAFVPNDGC*LNFIENDEVL VAGFGR	C90	1.084633962	P62266	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 #
DHQPC*IIFMDEIDAIGGR	C242	1.084055094	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
C*LLIHPNPESALNEEAGR	C118;C147	1.083882669	Q16763 K7EPJ1	Q16763 Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=2 # K7EPJ1 Ubiquitin-conjugating enzyme E2 S (Fragment) OS=Homo sapiens GN=UBE2S PE=1 SV=1 #
YLAEVAC*GDDR	C134	1.083314594	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 # D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 # P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 #
NC*LTNFHGMDLTR	C59;C59;C96;C76	1.082799924	D6RB09 D6RAT0 P61247 D6RG13	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 # Q5HY54 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 # Q5T2R2-3 Isoform 3 of Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 # Q5T2R2 Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 PE=1 SV=1 # H0YEE6 Decaprenyl-diphosphate synthase subunit 1 (Fragment) OS=Homo sapiens GN=PDSS1 PE=1 SV=1 #
ATC*APQHGAPGPGPADASK	C2535;C2516;C2543;C2503	1.081240226	P21333 Q60FE5 P21333 Q5HY54	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 # Q5HY54 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 # Q5T2R2-3 Isoform 3 of Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 # Q5T2R2 Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 PE=1 SV=1 # H0YEE6 Decaprenyl-diphosphate synthase subunit 1 (Fragment) OS=Homo sapiens GN=PDSS1 PE=1 SV=1 #
NVGIAFQLIDDLVDFDFTSC*SDQ MGKPTSADLK	C276	1.080391875	Q5T2R2 Q5T2R2 HOYEE6	Q5T2R2-3 Isoform 3 of Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 # Q5T2R2 Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 PE=1 SV=1 # H0YEE6 Decaprenyl-diphosphate synthase subunit 1 (Fragment) OS=Homo sapiens GN=PDSS1 PE=1 SV=1 #
VLC*ELADLQDKEVGDGTTSV VIIAAELLK	C76	1.079125314	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #

DQVAQLDDIVDISDEISPSVD DLALSIYPPMC*HLTVR	C172 C172;M299 C300;M171	1.0782	O95273 O95273 O95273 O95273	O95273 Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 PE=1 SV=2 # O95273-3 Isoform 3 of Cyclin-D1- binding protein 1 OS=Homo sapiens GN=CCNDBP1 # O95273-2 Isoform 2 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 # O95273-4 Isoform 4 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 # Q96EY7-2 Isoform 2 of Pentatricopeptide repeat domain-containing protein 3# mitochondrial OS=Homo sapiens GN=PTCD3 # Q96EY7 Pentatricopeptide repeat domain- containing protein 3# mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3 # A6NHK2 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P62304 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 # P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 # P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P03956 Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU # P62424 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 # Q5T8U2 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=1 # O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 # C9JFK9 BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=1 SV=1 # P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 # Q15233-2 Isoform 2 of Non-POU domain- containing octamer-binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 # P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 # P83881 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 # Q969Q0 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 # J3KQN4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=1 # H7BZ11 Protein RPL36A-HNRNPH2 OS=Homo sapiens GN=RPL36A-HNRNPH2 PE=3 SV=2 # H0Y5B4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=2 #
VSNSPSQAIEVVELASAFSLPI C*EGLTQR	C233;C642	1.07545672	Q96EY7 Q96EY7	
IEGC*IIGFDEYMNVLDDAEEI HSK	C6;C46	1.073573333	A6NHK2 P62304	
MYGISLC*QAILDETKGDYEK	C324	1.073350539	P04083	
LQDAFSSIGQSC*HLDLPQIAV VGGQSAGK	C27;C27;C27;C2 7;C27	1.072519002	P50570 P50570 P50570 P50570 P50570	
ANSWFNC*R	C466	1.070945715	P03956	
AVC*MLSNTTAVAEAWAR	C376;C446	1.06832891	Q9BQE3 F5H5D3	
GNFTLPEVAEC*FDEITYVELQ K	C648;C629	1.068118732	Q00839 Q00839	
AQLVIAHDVDPIELVFLPAL C*R	C174;C59	1.067117102	P62424 Q5T8U2	
SQSPAASDC*SSSSSASLPS SGR	C179;C121	1.065761127	O95817 C9JFK9	
QVQSLTC*EVDALKGTNESLE R	C328	1.065065178	P08670	
FAC*HSASLTVR	C56;C145	1.064981335	Q15233 Q15233	
VDLNSNGFIC*DYELHELK	C33	1.064803501	P13797	
LECVEPNC*R	C77;C77;C113;C 77;C77	1.064607289	P83881 Q969Q0 J3KQN4 H7BZ11 H0Y5B4	

SYIEGYVPSQADVAVFEAVSS PPPADLC*HALR	C50;C50;C50	1.064553572	P24534 F2Z2G2 C9JZW3	P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 # F2Z2G2 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 # C9JZW3 Elongation factor 1-beta (Fragment) OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 #
PPMEAAGFTAQVILNHPGQI SAGYAPVLDLC*HTAHIACK	C363;M314 C342	1.063089057	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
SGDAAIVEMVPGKPMC*VESF SQYPLGR	C411	1.061366667	Q05639	Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
GSDC*GIVNVNIPTSGAEIGGA FGGEK	C450;C478;C414; C414;C441	1.061261271	P49419 P49419 P49419 F8VS02 A0A140T9 V3	P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 # P49419-4 Isoform 4 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # F8VS02 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=1 # A0A140T9V3 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=1 # H0YBD7 Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=7 # P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6
DLNYC*FSGMSDHR	C81	1.060926253	H0YBD7 P31943 G8JLB6 H0YB39 P55795 E9PCY7 H0YBG7	H0YBD7 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=7 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # H0YB39 Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 # E9PCY7 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # H0YBG7 Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 #
VGVGPGSVC*TTR	C186	1.06063803	P36959	P36959 GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1 #
INALTAASEAAC*LIVSVDETIK NPR	C511	1.060623559	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 # Q14353-2 Isoform 2 of Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT # Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 #
VQEAPIDEHWIIEC*NDGVFQ R	C91;C91	1.059690293	Q14353 Q14353	Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 #

VLLSICSLLC*DPNPDDPLVPE IAR	C113;C111;C111; C105;C82;C82; C111;C82;C112 ;C111	1.058713912	P61077 P61077 P61077 H9KV45 P62837 D6RAH7 A0A0A0M QU3 D6RFM0 A0A087W Y85 P62837	P61077-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # H9KV45 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 # D6RAH7 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # A0A0A0MQU3 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # D6RFM0 Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=3 SV=1 # A0A087WY85 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # P56545-2 Isoform 2 of C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 # P56545 C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 # Q5SQP8 C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 # Q9Y679-2 Isoform Short of Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 # Q9Y679 Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 PE=1 SV=1 # Q7KZF4 Staphylococcal nuclease domain- containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 # Q86W42 THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1 # Q86W42-2 Isoform 2 of THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 # P12236 ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 # P05141 ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 #
AAGELGIAVCNIPSAAVEETA DSTIC*HILNLYR	C680;C140;C20 8	1.058125735	P56545 P56545 Q5SQP8	
ITSC*IFQLLQEAGIK	C63	1.05559339	P22234	
TGC*VDLTITNLLEGAVAFMP EDITK	C325	1.054643831	Q9Y679 Q9Y679	
ETCLITFLLAGIEC*PR	C560	1.053221075	Q7KZF4	
AQVPGSSPGLLSLSLNQPPA APEC*K	C314;C290	1.049978446	Q86W42 Q86W42	
YFAGNLSGGAAGATSLC*FV YPLDFAR	C129;C129	1.048146405	P12236 P05141	

					Q8WVV9-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # Q8WVV9-5 Isoform 5 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # Q8WVV9-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # Q8WVV9-3 Isoform 3 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # C9IYN3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=2 # D6W592 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # Q8WVV9 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # H7BXH8 Heterogeneous nuclear ribonucleoprotein L-like (Fragment) OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # C9JJZ7 Heterogeneous nuclear ribonucleoprotein L-like (Fragment) OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # B7WPG3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 #
GLC*ESVVEADLVEALEK	C84;C84;C79;C79;C84;C84;C19;C23;C84	1.047741068	Q8WVV9 Q8WVV9 Q8WVV9 Q8WVV9 C9IYN3 D6W592 Q8WVV9 H7BXH8 C9JJZ7 B7WPG3		
ALNALC*DGLIDELNQALK	C62	1.047321657	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #	
LLQC*DPSSASQF	C185	1.046626234	P37235	P37235 Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3 #	
LGTDESC*FNMILATR	C363	1.046588167	P20073 P20073	P20073 Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 # P20073-2 Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7 #	
IC*PVEFNPNFVAR	C33;C33;C33	1.045759188	Q9UI30 Q9UI30 F5GX77	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q9UI30-2 Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 #	
LSAPGC*WAACTNFSR	C12;C12	1.044593982	Q04941 Q04941	Q04941 Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1 # Q04941-2 Isoform 2 of Proteolipid protein 2 OS=Homo sapiens GN=PLP2 #	
WC*EYGLTFTEK	C76;C76	1.044573536	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #	
SLC*NLEESITSAGRDDLESF QLEISGFLK	C63;C63	1.04443713	Q52LJ0 Q52LJ0	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #	
VELC*SFSGYK	C6;C6;C6	1.044294776	C9JNW5 C9JXB8 P83731	C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 #	
VGC*SCVVVK	C106	1.043668591	P25398	P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 #	
LQILNSIFPGIGC*PVPR	C188	1.043517351	Q9NX47	Q9NX47 E3 ubiquitin-protein ligase MARCH5 OS=Homo sapiens GN=MARCH5 PE=1 SV=1 #	

C*ALSSPSLAFTPIIK	C120;C238;C255	1.042924659	Q8NFH5 Q8NFH5 Q8NFH5	Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 #
VPAFEGDDGFC*VFESNAIAY YVSNEELR	C68;C118	1.042098585	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
YGAVDPLLALLAVPDMSSLAC *GYLR	C223	1.041769814	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 # P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 # G3V2W0 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # G3V4W5 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # G3V5L0 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # G3V241 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # P34897-3 Isoform 3 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # G3V4T0 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # G3V3Y8 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 # G3V2E4 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # G3V540 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # G3V4X0 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 #
AALEALGSC*LNNK	C91;C70;C91;C70;C70;C70;C91;C70;C70	1.041293887	P34897 G3V2W0 G3V4W5 G3V5L0 G3V241 P34897 G3V4T0 G3V3Y8 P34897 G3V2E4 G3V540 G3V4X0	P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # G3V4T0 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # G3V3Y8 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 # G3V2E4 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # G3V540 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # G3V4X0 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 #
RPYGVGLLIAGYDDMGPHIFQ TC*PSANYFDCR	C123 C148;M115 C154;M140	1.03957974	P25786 P25786 F5GX11	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 # P25786 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 # F5GX11 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 #
LVAFC*PFASSQVALENANAV SEGVVHEDLR	C52	1.037265673	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
YINENLIVNTDELGRDC*LINA AK	C147	1.036005058	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
AAAPAPEEEMDEC*EQALAA EPK	C316 C266;M313	1.034622573	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
QMFEPVSC*TFTYLLGDR	C34;C34	1.034101392	O95571 MOQXB5	O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # MOQXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 #
NTPSFLIAC*NK	C179	1.033904276	Q9Y5M8	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 #



STFFNVLTNQASAENFPFC* TIDPNESR	C75;C55	1.033759874	J3KQ32 Q9NTK5	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 #
NESC*SENYTTDFIYQLYSEE GK	C641	1.033268734	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
LTTPTYGDLNHLVSATMSGVT TC*LR	C239;C239;C239; 9;C239;C221	1.032351846	P07437 P68371 Q9BVA1 P04350 Q5JP53	P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
ALADAQIPYSAVDQACVGYVF GDSTC*GQR	C71	1.029858794	P22307	P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 #
EMFPYEASTPTGISASC*R	C323;M348 C254 C363;M239	1.027467822	G5E972 P42167 P42167	G5E972 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 # P42167 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 # P42167-2 Isoform Gamma of Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO #
YTIVVSATASDAAPLQYLAPY SGC*SMGEYFR	C294	1.025951232	P25705 P25705	P25705 ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 # P25705-2 Isoform 2 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 #
IAVYSC*PFDGMITETK	C225	1.025590441	P50990 P50990	P50990-2 Isoform 2 of T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 # P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 # E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 # H0YA99 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 # Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 #
C*FLAQPVTLDDIYTHWQQTS ELGR	C38;C26;C38;C38; 8;C38;C38;C38; C38;C38;C38;C38; 8	1.023944435	E7ETY2 H0YA99 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 J3KQ96	Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 # Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-5 Isoform 5 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 # J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 #
VIGSGC*NLDSAR	C192;C164;C163	1.022029139	P00338 P07195 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #

SGTIC*SSELPGAFAFEAAGFHL NEHLYNMIIR	C122;C190;C14 1;C190	1.021412847	U3KQE2 A0A0C4D GQ5 A0A075B7 C0 P04632	U3KQE2 Calpain small subunit 1 (Fragment) OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # A0A0C4DQG5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # A0A075B7C0 Calpain small subunit 1 (Fragment) OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #
AVLC*PQPTR	C178;C134;C17 1	1.020498489	P15153 B1AH77 B1AH80	P15153 Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 # B1AH77 Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 # B1AH80 Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 #
VAASC*GAIQYIPTELDQVRK	C134	1.019935462	Q7L2H7	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #
YYALCGFGGVLSC*GLTHTAV VPLDLVK	C75	1.019823225	Q00325	Q00325-2 Isoform B of Phosphate carrier protein# mitochondrial OS=Homo sapiens GN=SLC25A3 #
LDTNSDGQLDFSEFLNLIGGL AMAC*HDSFLK	C91	1.019529911	P31949	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 #
NVQLLSQFVSPFTGC*YGR	C90	1.017757396	Q9Y3D5	Q9Y3D5 28S ribosomal protein S18c# mitochondrial OS=Homo sapiens GN=MRPS18C PE=1 SV=1 #
ELEAVC*QDVLSLLDNYLIK	C97	1.015783495	P61981	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 #
TFVDFFSQC*LHEEYR	C215	1.015121095	Q53GQ0	Q53GQ0 Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 #
C*AGPTPEAELQALAR	C52	1.014293332	Q15050	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 #
FVLSGANIMC*PGLTSPGAK	C113;M113 C114 C101;M112	1.01383563	Q9ULC4 Q9ULC4 Q9ULC4	Q9ULC4-2 Isoform 2 of Malignant T-cell- amplified sequence 1 OS=Homo sapiens GN=MCTS1 # Q9ULC4 Malignant T-cell- amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1 # Q9ULC4-3 Isoform 3 of Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 #
ENSTLNC*ASFTAGIVEAVLTH SGFPAK	C139	1.013718195	Q8IUR0	Q8IUR0 Trafficking protein particle complex subunit 5 OS=Homo sapiens GN=TRAPPC5 PE=1 SV=1 #
SC*LLLQFTDKR	C21;C21;C21;C2 1	1.011129955	E9PKL7 P61019 Q8WUD1 Q5HYI5	E9PKL7 Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 # P61019 Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 # Q8WUD1 Ras-related protein Rab-2B OS=Homo sapiens GN=RAB2B PE=1 SV=1 # Q5HYI5 Putative uncharacterized protein DKFZp313C1541 OS=Homo sapiens GN=DKFZp313C1541 PE=1 SV=1 # C9J4K0 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 # Q9BVC5 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 # Q9BVC5-2 Isoform 2 of Ashwin OS=Homo sapiens GN=C2orf49 #
SC*TDESELLHPPELLSQEFLLL TLEQK	C10;C10;C48	1.00898468	C9J4K0 Q9BVC5 Q9BVC5	Q14376 UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 #
YFNPTGAHASGC*IGEDPQGI PNNLMPYVSQVAIGR	C196	1.007796222	Q14376	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
QAVLGAGLPSTPC*TTINK	C119	1.006081422	P24752	

FNNWGGSLSLGHPFGATGC* R	C435;C312;C41 3	1.005684643	P55084 B5MD38 P55084	P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 # B5MD38 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=1 # P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB #
IKSGEEDFESLASQFSDC*SS AK	C40;C113;C113	1.005480178	K7EN45 K7EMU7 Q13526	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 # K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 # Q13526 Peptidyl-prolyl cis-trans isomerase NIMA- interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 #
KAVVVC*PK	C607;C588	1.005352532	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
AYHEQLTVAEITNAC*FEPAN QMVK	C295	1.004561931	Q9BQE3 F5H5D3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
TSSVSNPQDSVSGSPC*SR	C108;C106;C10 9;C108;C108	1.004434367	P49023 F5GZ78 F5H836 P49023 P49023	P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 # F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 # F5H836 Paxillin (Fragment) OS=Homo sapiens GN=PXN PE=1 SV=7 # P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN # P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN #
YSTGSDSASFHTTPSMC*LN PDLEGPPELAYTIQQQYAIPIQ PDLTK	C217 C217;M212 C213;M216	1.004343599	Q15366 Q15366 Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
VFIMDSC*DELIPEYLNfir	C366	1.004244757	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
GVSASAVPFTPSSPLLSC*SQ EGSR	C576;C39;C576; C585	1.00377	Q9Y2X7 J3QL89 J3QRU8 Q9Y2X7	Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 # J3QL89 ARF GTPase-activating protein GIT1 (Fragment) OS=Homo sapiens GN=GIT1 PE=1 SV=1 # J3QRU8 ARF GTPase- activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 # Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 #
SAC*SLESNLEGLAGVLEADL PNYK	C44	1.00371232	Q09161	Q09161 Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 # P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 #
YDC*GEEILITVLSAMTEEAHV AIK	C159	1.00247727	P63241 P63241	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 # P48047 ATP synthase subunit O# mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 #
QVLMGPYPNDTC*PEVGFFD VLGNDR	C129	0.999403932	Q9H3P7	
GEVPC*TVTSASPLEEATLSE LK	C141	0.998238964	P48047	

VNQAIWLLC*TGAR	C155;C176;C155	0.99657487	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
YMACC*LLYR	C301;C316;C316;C283;C386;C316;C323;C316	0.996127072	P68366 P68363 Q9BQE3 A6NHL2 F5H5D3 Q71U36 A6NHL2 P68366	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 # Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 #
FQSSAVMALQEASEAYLVGL FEDTNLC*AIHAK	C111	0.995768939	Q71DI3	Q96I24 Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2 #
LTALDYHNPAGFNC*KDETEFR	C19	0.995648604	Q9Y224	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
SSGC*FPNMAAK	C460	0.99483088	Q96I24	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP # Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 #
IISNASC*TTNCLAPLAK	C152	0.994226208	P04406	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 #
AITIAGVPQSVTEC*VK	C158	0.99358087	Q15365	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
IGFPETTEEELEEIASENSDC*IFPSAPDVKA	C353;C340	0.993441657	Q9Y3F4 Q9Y3F4	J3KTF8 Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDI PE=1 SV=7 # P52565 Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI PE=1 SV=3 # P52565-2 Isoform 2 of Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI # J3QQX2 Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI PE=1 SV=1 # J3KRY1 Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDI PE=1 SV=1 #
AYGGSMC*AK	C83	0.992911512	P49207	
YMAC*CLLYR	C300;C315;C315;C282;C385;C315;C322;C315	0.990153897	P68366 P68363 Q9BQE3 A6NHL2 F5H5D3 Q71U36 A6NHL2 P68366	
VAVSADPNVNVVVVGLTLV C*SSAPGPLELDLTGDLSEFK K	C79;C79;C79;C79;C79	0.988997089	J3KTF8 P52565 P52565 J3QQX2 J3KRY1	

DCIGGC*SDLVSLQQSGELLT R	C83	0.988114648	P35754	P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 # O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # O60701-2 Isoform 2 of UDP-glucose 6- dehydrogenase OS=Homo sapiens GN=UGDH # O60701-3 Isoform 3 of UDP- glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH # Q7L1Q6 Basic leucine zipper and W2 domain- containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain- containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-2 Isoform 2 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # P82932 28S ribosomal protein S6# mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 # A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q8NBF2 NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 # Q8NBF2-2 Isoform 2 of NHL repeat- containing protein 2 OS=Homo sapiens GN=NHLRC2 # Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 # E9PLZ8 Multivesicular body subunit 12A (Fragment) OS=Homo sapiens GN=MVB12A PE=1 SV=7 # Q96EY5-2 Isoform 2 of Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A # Q96EY5 Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A PE=1 SV=1 # Q96SW2 Protein cereblon OS=Homo sapiens GN=CRBN PE=1 SV=1 # J3QT87 Protein cereblon (Fragment) OS=Homo sapiens GN=CRBN PE=1 SV=1 # J3QT51 Protein cereblon (Fragment) OS=Homo sapiens GN=CRBN PE=1 SV=1 # Q96SW2-2 Isoform 2 of Protein cereblon OS=Homo sapiens GN=CRBN #
ISSINSISALC*EATGADVVEEV ATAIGMDQR	C241	0.986692888	O60701 O60701 O60701	
TDVC*VFAAQEDLETMQAFA QVFNK	C96	0.986417774	Q7L1Q6 Q7L1Q6 Q7L1Q6 Q7L1Q6	
EC*EGIVPVPLAEK	C105	0.985045085	P82932	
AFAFVTFADDQIAQSLC*GED LIIK	C244;C244;C24 4;C244;C244	0.984703065	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	
AILFSQPLQITDTQQGC*IAPV ELR	C716;C357	0.984642366	Q8NBF2 Q8NBF2	
GPFVEAEVDPVDLEC*PDAK	C1833	0.984247372	Q09666	
ATVAPEDVSEVIFGHVLAAGC *GQNPVR	C65	0.983762536	Q9BWD1	
TIAEC*LADELINAAK	C172;C193;C17 2	0.983163581	P46782 M0R0R2 M0R0F0	
LGGSLIVAFEGC*PV	C146;C163	0.982202959	P60981 P60981	
SC*SPLAFSAFGDLTIK	C92;C191;C231	0.981914381	E9PLZ8 Q96EY5 Q96EY5	
VQILPEC*VLPSTMSAVQLES LNK	C188	0.981315629	Q96SW2 J3QT87 J3QT51 Q96SW2	

LGC*NITISEDITPR	C38;C38	0.980906852	Q96FJ0 Q96FJ0	Q96FJ0 AMSh-like protease OS=Homo sapiens GN=STAMBPL1 PE=1 SV=2 # Q96FJ0-2 Isoform 2 of AMSh-like protease OS=Homo sapiens GN=STAMBPL1 # O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # MQXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 #
TDFQQGC*AK	C170;C170	0.980819251	O95571 MQXB5	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 # Q9NS25 Sperm protein associated with the nucleus on the X chromosome B1 OS=Homo sapiens GN=SPANXB1 PE=2 SV=2 #
ILVALC*GGN	C343	0.977052054	P04083	J3KPE3 Receptor of-activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=1 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
SVPC*ESNEANEANEANK	C16	0.976081401	Q9NS25	Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EJU4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 #
VWNLANC*K	C138;C182	0.974454753	J3KPE3 P63244	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
EAVQC*VQELASPSLLFIFVR	C1265;C1225;C1179;C1266;C1178;C1069;C1226;C1101;C1272;C1102;C1070	0.973883675	Q04637 Q04637 E9PGM1 Q04637 Q04637 E7EJU4 Q04637 Q04637 E7EX73 Q04637	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 # Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 # Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 # P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 # HOYEN5 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=1 SV=1 # P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
ELEVLLMC*NK	C91;C109;C91	0.971139704	P62910 F8W727 D3YTB1	
C*MPTFQFFKK	C73	0.971069062	P10599	
VSLDPELEEALTSASDTELC* DLAAILGMHNLITNTK EGTDSSQGIPQLVSNISAC*Q VIAEAVR	C132 C29	0.970465817 0.967546462	Q9NYL9 Q99832	
GC*TATLGNFAK	C229;C131	0.967322151	P15880 HOYEN5	
SGDAAIVDMVPGKPMC*VES FSDYPLGR	C411;C390	0.965901165	P68104 P68104	

LLSNMMC*QYR	C156;C160;C160	0.962331714	P28062 X5D2R7 P28062	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 # Q9BV86 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #
IIC*SAGLSLLAEER	C195;C107	0.960399096	Q9BV86 S4R338	Q15366-7 Isoform 7 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-4 Isoform 4 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #
LVPASQC*GSLIGK	C109;C109;C109;C109	0.960125646	Q15366 Q15366 Q15366 Q15366	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
VC*NYGLTFTQK	C65	0.959592901	Q9Y277	O95573 Long-chain-fatty-acid-CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #
SYC*AEIAHNVSSK	C96;C114;C96	0.956024283	P62910 F8W727 D3YTB1	F5H248 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # Q9UBW8 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5H4U8 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 #
LLLC*GGAPLSATTQR	C450	0.954730035	O95573	# F5GYF7 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=7 # F5H7C6 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 #
KLLDLVQQSC*NYK	C34;C30	0.954426663	B1AHD1 P55769	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 #
C*IPYAVLLEALALR	C110;C110;C110;C110;C110	0.954229207	F5H248 Q9UBW8 F5H4U8 F5GYF7 F5H7C6	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 #
VDEFPLC*GHMVSDEYEQLS SEALEAAR	C49;C49	0.953321445	X1WI28 P27635	
LPACVVDC*GTGYTK	C12	0.948860943	P61158	
FRCPEALFQPSFLGMESC*GI HETTFNSIMK	C272	0.94835379	P60709	
TAFQEALDAAGDKLVVVD ATWC*GPKK	C32	0.94684869	P10599	

				Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A0A075B736 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
NMMAAC*DPR	C303;M263 C266;M282 C303 C266;M647 C285;M300 C303;M300 C650;M300	0.943316133	Q13509 P07437 P68371 A0A075B736 A0A0B4J269 Q9BVA1 P04350 K7ESM5 Q5JP53 Q9BUF5	
AQDIEAGDGTTSVVIAGSLLD SC*TK	C90;C120	0.943013759	P50991 P50991	P50991-2 Isoform 2 of T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 # P50991 T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 # Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 # F8VPD4 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 # P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
VLTC*TDLEQGNFFLDFENA QPTESEKEIYNQVNVVLK	C10	0.942898633	Q9NUQ9	
AQILVLTYPILIGNYGIPPEMD EFGLC*K	C73 C73;M67	0.940862175	F8VPD4 P27708	
LVSSPC*CIVTSTYGWTANMER	C589	0.93761722	P08238	
ATFHTPFSHLQGSPEGC*SSY TFPK	C247;C252;C282	0.937597909	O75521 A0A0C4DGA2 O75521	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 # Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X1X5 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #
AGQC*VIGLQMGTKN	C164;C153;C185;C101	0.936985	Q99439 B4DDF4 B4DUT8 A0A087X1X5	
LNLPIINIIGLAPLC*ENMPSGK	C335	0.936644864	P28838 P28838	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 # P08559 Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 # P08559-4 Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 # P08559-2 Isoform 2 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 #
NFYGGNGIVGAQVPLGAGIAL AC*K	C181;C219;C188	0.936148049	P08559 P08559 P08559	
C*TGGEVGATSALAPK	C17	0.934696793	P30050	P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 # P30044-4 Isoform 4 of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 # P30044 Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 # P30044-2 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 # P30044-3 Isoform 3 of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 #
ALNVEPDGTGLTC*SLAPNIIS QL	C115;C204;C152;C160	0.930333377	P30044 P30044 P30044 P30044	



QLFALSC*TAEQGVLPDDL GVIR	C96;C60;C112;C 75;C96	0.929330694	P04899 P04899 P04899 P04899 P04899	P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
AC*LIFFDEIDAIGGAR	C133;C270	0.929172086	P35998 P35998	P35998-2 Isoform 2 of 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 # P35998 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 #
EC*LPLIIFLR	C41	0.928173002	P62701	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 #
C*GVPDVAQFVLTEGNPR	C92	0.924849067	P03956	P03956 Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3 #
NYLPAINGIVFLVDC*ADHSR	C102;C102	0.924124352	Q5SQT8 Q9NR31	Q5SQT8 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 # Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 #
VLVTTNVC*AR	C361;C302;C39 2;C393;C310	0.920169532	I3L0H8 Q9NUU7 Q9NUU7 F6QDS0 I3L352	I3L0H8 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 # Q9NUU7-2 Isoform 2 of ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A # Q9NUU7 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 # F6QDS0 HCG2043426# isoform CRA_b OS=Homo sapiens GN=hCG_2043426 PE=1 SV=1 # I3L352 ATP-dependent RNA helicase DDX19A (Fragment) OS=Homo sapiens GN=DDX19A PE=1 SV=1 #
ELDLSNNC*LG DAGILQLVES VR	C409	0.920150401	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
GEELSC*EER	C38;C38	0.919823023	P31947 P31947	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 # P31947-2 Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN #
VAC*AEEWQESR	C87;C87	0.914925751	O75663 O75663	O75663 TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 # O75663-2 Isoform 2 of TIP41-like protein OS=Homo sapiens GN=TIPRL #
GQGVYLGMPGC*LPVYDALA GEFIR	C157 C56;M154	0.913139615	F8VY02 P30040	F8VY02 Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=1 # P30040 Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 #
SVAFFPCISTGVFGYPC*EAAA EIVLATLR	C276	0.912222415	Q9BQ69	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #
GMYGIEVFLSLPC*ILNAR	C294	0.91091953	P07195	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 #
GISEFIVMAADAEPLEIILHLPL LC*EDKNVPYVFVR	C73 C77;M56	0.909653241	B1AHD1 P55769	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #

					H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
LC*EPEVLNSLEETYSPPFR	C177;C261;C261;C106;C224;C261;C261;C227;C261;C261;C242	0.909644883		H0YJA2 Q6PJT7 Q6PJT7 G3V5I6 Q6PJT7 G3V256 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7	
NWYIQATC*ATSGDGLYEGLD WLSNQLR	C159	0.908162399	P84077	P84077 ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2 #	
ALAPLLLAFVTKPNSALESC*S FAR	C573	0.90262354	P46060	P46060 Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 #	
LC*YVALDFEQEMATAASSSS LEK	C217	0.900143088	P63261 P60709 Q6S8J3	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 #	
LC*YVALDFEQEMAMVASSS SLEK	C880	0.896510827	P0CG39	P0CG39 POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 #	
VIEINPYLLGTMSGC*AADCQ YWER	C116;C120;C120	0.896362085	P28062 X5D2R7 P28062	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 # K7ER88 3-ketoacyl-CoA thiolase# mitochondrial (Fragment) OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # A0A0B4J2A4 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # P42765 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 # K7EME0 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # K7EJB1 3-ketoacyl-CoA thiolase# mitochondrial (Fragment) OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # K7EJ68 3-ketoacyl-CoA thiolase# mitochondrial (Fragment) OS=Homo sapiens GN=ACAA2 PE=1 SV=1 #	
LC*GSGFQSIVNGCQEICVK	C37;C89;C92;C37;C37;C37	0.895485607	K7ER88 A0A0B4J2 A4 P42765 K7EME0 K7EJB1 K7EJ68		

AFC*GFEDPR	C4325;C4343;C4335;C4494;C4357;C4380;C4384;C4361;C4357	0.892005615	Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
DTAQQGVVNFYDDFIQC*V MSV	C179	0.889110436	P30626 P30626	P30626-2 Isoform 2 of Sorcin OS=Homo sapiens GN=SRI # P30626 Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 #
YEAAPFLSPC*GR	C90;C143;C98	0.884903807	Q6P1X6 H0YF29 Q6P1X6	Q6P1X6-2 Isoform 2 of UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 # H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 # Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 #
AAVLVQQWVSYADTELIPAAAC *GATLPALGLR	C112	0.880919525	P26640	P26640 Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4 #
NFNYHILSPC*DLSNYTDLAM STVK	C461	0.878705753	G5E9W3 Q9UKF6	G5E9W3 Cleavage and polyadenylation specific factor 3# 73kDa# isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 #
EEQVISLGPQVAEGENVFGV C*HIFASFNDTFVHVTDLSGK	C31;C31	0.878111667	P62263 E5RH77	P62263 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 # E5RH77 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=1 #
NAFAC*FDEEATGTIQEDYLR	C108;C114;C109	0.877652653	P19105 J3QRS3 O14950	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 # J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 # O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 #
SC*PSFSASSEGTR	C9;C9;C9;C9	0.876976052	D6RCP9 P27707 D6RFG8 D6RG38	D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RG38 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
LPLALPPASQGC*SSGGGGG GGGGSSAGGSGNSRPPR	C22	0.875879158	Q9NZL4	Q9NZL4 Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 PE=1 SV=1 #
AIVLFTSDAC*GLSDVAHVESL QEK	C193;C326;C173	0.871109517	P24468 P24468 P24468	P24468-2 Isoform 2 of COUP transcription factor 2 OS=Homo sapiens GN=NR2F2 # P24468 COUP transcription factor 2 OS=Homo sapiens GN=NR2F2 PE=1 SV=1 # P24468-3 Isoform 3 of COUP transcription factor 2 OS=Homo sapiens GN=NR2F2 #
LDNWLNELETYC*TR	C139;C110;C223;C86;C65	0.870887279	Q9NP72 Q9NP72 H0Y6T8 A0A087X163 Q5W0J0	Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # H0Y6T8 Ras-related protein Rab-18 (Fragment) OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # Q5W0J0 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 #

ADHQPLTEASYVNLPTIALC*N TDSPLR	C153;C148;C14 8	0.86382153	A0A0C4D G17 C9J9K3 P08865	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 # Q7L1Q6 Basic leucine zipper and W2 domain- containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain- containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-2 Isoform 2 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 # P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 # Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 # C9JAK5 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=1 # P07741-2 Isoform 2 of Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT # H3BQF1 Adenine phosphoribosyltransferase (Fragment) OS=Homo sapiens GN=APRT PE=1 SV=7 # H3BQB1 Adenine phosphoribosyltransferase (Fragment) OS=Homo sapiens GN=APRT PE=1 SV=1 # P07741 Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 # Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 # P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
FDPTQFQDC*IIQGLTETGTDL EAVAK	C35;C67;C39;C3 5	0.859385399	Q7L1Q6 Q7L1Q6 Q7L1Q6 Q7L1Q6	
LVSSPCC*IVTSTYGWTANME R	C590	0.856455	P08238	
VDDEILGFISEATPLGGIQAAS TESC*NQQLDLALCR	C561	0.848153688	P42166	
LEGDLTGPVSGVEVPDVELE C*PDAK	C1900	0.847555272	Q09666	
QC*TGLQGFLVFHSGGGTG SGFTSLLMER	C114	0.845534446	P68366 P68363 Q9BQE3 F5H5D3 Q71U36 P68366	
NIC*FTVWDVGGQDR	C62;C35	0.84341157	P18085 C9JAK5	
GFLFGPSLAQELGLGC*VLIR	C83;C83;C83;C8 3	0.840759568	P07741 H3BQF1 H3BQB1 P07741	
AVLLVGLC*DSGK	C73	0.84028	Q9Y5M8	
NLSDLIDLVPSLC*EDLLSSVD QPLK	C36;C36;C65;C2 4;C62	0.838390864	P47756 P47756 B1AK88 B1AK87 B1AK85	

FQLTDC*QIYEVLSVIR	C143;C179	0.837674507	Q16555 Q16555	Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
NWYVQPSC*ATSGDGLYEGL TWLTSNYK	C155	0.836819515	P62330	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 #
TDVNKIEEFLEEVLC*PPK	C100	0.836238997	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
NCGC*LGASPNLEQLQEENL K	C34	0.836132552	P54136	P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 # E9PML7 Deoxyribose-phosphate aldolase (Fragment) OS=Homo sapiens GN=DERA PE=1 SV=1 # Q9Y315 Deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2 # G3V158 2-deoxyribose-5-phosphate aldolase homolog (C. elegans)# isoform CRA_a OS=Homo sapiens GN=DERA PE=1 SV=1 # E9PPM8 Deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=1 # E9PMH9 Deoxyribose-phosphate aldolase (Fragment) OS=Homo sapiens GN=DERA PE=1 SV=1 # E9PPK3 Deoxyribose-phosphate aldolase (Fragment) OS=Homo sapiens GN=DERA PE=1 SV=1 #
AAGC*NIPVASVAAGFPAGQT HLK	C139;C118;C30; C118;C30;C30	0.82828165	E9PML7 Q9Y315 G3V158 E9PPM8 E9PMH9 E9PPK3	
ATLQAALC*LENFSSQVVER	C21;C21;C21;C2 1;C40;C21	0.826355052	P59998 A0A0A6Y YG9 P59998 F8WCF6 P59998 F8WDD7	P59998 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 # A0A0A6Y YG9 Protein ARPC4-TLL3 OS=Homo sapiens GN=ARPC4-TLL3 PE=4 SV=1 # P59998-2 Isoform 2 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 # F8WCF6 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4-TLL3 PE=3 SV=1 # P59998-3 Isoform 3 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 # F8WDD7 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=4 SV=1 #
AEPPQC*TSLAWSADGQTLF AGYTDNLVR	C286	0.825954491	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
YAIC*SALAASALPALVMSK	C125	0.822923534	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
EAVFPFQPGSVAEVC*ITFDQ ANLTVK	C89	0.818960089	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 #
LISP NLGVVFFNAC*EAASR	C316;C342	0.817284438	Q66K74 Q66K74	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 # P21964-2 Isoform Soluble of Catechol O-methyltransferase OS=Homo sapiens GN=COMT # P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 #
GSSC*FECTHYQSFLYR	C188;C238	0.816840104	P21964 P21964	
ASFENNCEIGC*FAK	C15	0.813221546	P56537	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 # P52657 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 # A0A0B4J1Z5 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 # P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 # P30048-2 Isoform 2 of Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 #
AFQYVETHGEVC*PANWTPD SPTIKPSPAASK	C229;C211	0.806812838	P30048 P30048	

GLGTDEDSLIEIC*SR	C151;C133	0.805858042	P07355 P07355	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
GC*LLYGPPGTGK	C184;C170	0.805743913	A0A087X2I1 P62333	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
AVLFC*LSEDKK	C77;C22;C39;C39	0.805262212	E9PK25 G3V1A4 P23528 E9PP50	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 # C9JQJ4 Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=1 SV=1 #
HTGPGILSMANAGPNTNGSQ FFIC*TAK	C115	0.804106387	P62937	P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 # P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
LTVVDTPGYGDAINC*R	C122	0.803876774	C9JQJ4	P52788 Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 # P52788-2 Isoform 2 of Spermine synthase OS=Homo sapiens GN=SMS #
LC*VQNSPQEAR	C150;C150;C150;C150;C141	0.803737312	P33240 E7EWR4 E9PID8 A0A0A0MT56	P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 # P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
YFTQGNC*VNLTEALSLYEEQ LGR	C318;C265	0.799624368	P52788 P52788	Q9H078 Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1 # Q9H078-4 Isoform 4 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-2 Isoform 2 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-5 Isoform 5 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-3 Isoform 3 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # H0YGM0 Caseinolytic peptidase B protein homolog (Fragment) OS=Homo sapiens GN=CLPB PE=1 SV=1 #
LPITVLNGAPGFINLC*DALNA WQLVK	C241;C240	0.799494858	P31939 P31939	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 #
TIGGGDDSFSTFFC*ETGAGK	C39;C54	0.79432222	P68366 P68366	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # Q5JPI3-2 Isoform 2 of Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 # Q5JPI3 Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 PE=1 SV=1 #
INEIVYFLPFC*HSELIQLVVK	C572;C527;C542;C371;C513;C577	0.792790704	Q9H078 Q9H078 Q9H078 Q9H078 H0YGM0	
LEKPNEGYLEFFVDC*SASAT PEFEGR	C85	0.792220161	Q15024	
C*FIVGADNVGSK	C27	0.785415374	P05388	
FEQSDLEAFYNVITVC*GTNE VR	C306;C308	0.783239915	Q5JPI3 Q5JPI3	

AAQGPPAPAVPPNTDVMAC* TQTALLQK	C146;M150 C115 C152;M113	0.782265783	H0YEB6 O60232 G3V1B8	H0YEB6 Sjogren syndrome/scleroderma autoantigen 1 (Fragment) OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # O60232 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # G3V1B8 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # Q12888-3 Isoform 3 of Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 # Q12888 Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2 # Q12888-2 Isoform 2 of Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 # A6NNK5 Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2 #
C*AEALQLPVVSQEWVIQCLI VGER	C1936;C1933;C1938;C1888	0.780471186	Q12888 Q12888 Q12888 A6NNK5	Q12888-3 Isoform 3 of Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2 # Q12888-2 Isoform 2 of Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 # A6NNK5 Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2 #
NIC*FTVWDVGGQDK	C62	0.77578	P84085	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 # F5H157 Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=1 SV=1 # Q15286 Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 #
ENVNVEEMFNC*ITELVLR	C147;M160 C163	0.774239338	F5H157 Q15286	F5H157 Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=1 SV=1 # Q15286 Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 #
VGLGIC*YDMR	C153	0.773151082	Q9NQR4	Q9NQR4 Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 #
LC*VQNSHQEAR	C150	0.769246546	Q9H0L4	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 #
VILALGDYMGATCHAC*IGGT NVR	C135 C135;M128 C136;M128	0.769074462	Q14240 Q14240 E7EQG2	Q14240-2 Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 # Q14240 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2 # E7EQG2 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=1 # P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
GLYGIKDDVFLSVPC*ILGQN GISDLVK	C322;C293	0.76628	P00338 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
STPYEC*GFDPMSPAR	C39	0.761167743	P03897	P03897 NADH-ubiquinone oxidoreductase chain 3 OS=Homo sapiens GN=MT-ND3 PE=1 SV=1 #
LTPGC*EAEAEATEAICFFVQQ FTDMEHNR	C2359	0.760684215	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
NC*GCLGASPNIQLQEENL K	C32	0.752217533	P54136	P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 #
LDSLGLCSVSC*ALEFIPNSK	C256	0.750992854	Q9BSH4	Q9BSH4 Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1 #
C*PEALFQPSFLGMESCGIHE TTFNSIMK	C257	0.750531147	P60709	P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # H0Y852 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial (Fragment) OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
SC*NGPVLVGSPQGGVDIEEV AASNPELIFK	C162;C162;C54; C162	0.743521635	Q96I99 E9PDQ8 H0Y852 Q96I99	Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # H0Y852 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial (Fragment) OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
APPWVPAMGFTLAPSLGC*F VGSR	C19;M9 C19	0.739882512	B1AH87 P30536	B1AH87 Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=1 SV=1 # P30536 Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 #

VC*ENIPIVLCGNK	C108	0.738456345	F5H018	F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=РАН PE=1 SV=7 #
EMQNLSFQDC*YSSK	C111	0.720631509	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
EERWC*ETR	C21	0.714153937	C9JWF7	C9JWF7 SRSF protein kinase 2 (Fragment) OS=Homo sapiens GN=SRPK2 PE=1 SV=1 #
SEGGSGGGAAGGGAGGAGA GAGC*GSGGSSVGV	C32;C32;C32;C3 2	0.713336667	Q9NSY1 Q9NSY1 K4DI97 Q9NSY1	Q9NSY1-3 Isoform 3 of BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K # Q9NSY1-2 Isoform 2 of BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K # K4DI97 BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=1 # Q9NSY1 BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=2 # F5H763 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980-3 Isoform Numa-m of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980 F5H6Y5 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # F5H0Z7 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # F5H4J1 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # F5H4J1 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=7 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980-4 Isoform Numa-s of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 #
APVPSTC*SSTFPEELSPPSH QAK	C160;C160;C16 0;C160;C160;C1 60;C160;C160;C 160;C160	0.706798081	F5H763 A0A087W Y61 Q14980 Q14980 Q14980 F5H6Y5 F5H0Z7 F5H4J1 Q14980 Q14980	Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # F5H6Y5 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # F5H0Z7 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # F5H4J1 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # F5H4J1 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=7 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980-4 Isoform Numa-s of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 #
VPADTEVVC*APPTAYIDFAR	C42;C79	0.704589666	P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 # Q6UUUV9 CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 PE=1 SV=2 # M0QXN6 CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 PE=1 SV=1 # M0QX46 CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 PE=1 SV=1 # Q6UUUV9-3 Isoform 3 of CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 # Q6UUUV9-2 Isoform 2 of CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 #
QADSC*PYGTMYSPPADTS WR	C131;C56;C90;C 131;C147	0.701301766	Q6UUUV9 M0QXN6 M0QX46 Q6UUUV9 Q6UUUV9	Q6UUUV9-3 Isoform 3 of CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 # Q6UUUV9-2 Isoform 2 of CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 #
LLQDYPITDVC*QILQK	C262;C387	0.699786036	Q9NVG8 Q9NVG8	Q9NVG8-2 Isoform 2 of TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 # Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
DAFEHIVTQFSSVPVSVVSDS YDIYNAC*EK	C287;C287	0.699525328	P43490 A0A0C4D FS8	P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 # A0A0C4DFS8 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 #
YGIIC*MEDLIHEIYTVGK	C186	0.69525	P18124 A8MUD9	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 # A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 #



FMTQVIQDNPSGWGPC*AVP EQFR	C19 C19;M5	0.691412415	B0QYA8 O15371 B0QYA5 B0QYA6 O15371 O15371	B0QYA8 Eukaryotic translation initiation factor 3 subunit D (Fragment) OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # B0QYA5 Eukaryotic translation initiation factor 3 subunit D (Fragment) OS=Homo sapiens GN=EIF3D PE=1 SV=1 # B0QYA6 Eukaryotic translation initiation factor 3 subunit D (Fragment) OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # P14868 Aspartate--tRNA ligase# cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 # P14868-2 Isoform 2 of Aspartate--tRNA ligase# cytoplasmic OS=Homo sapiens GN=DARS # J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 # Q07020 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 # Q07020-2 Isoform 2 of 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 # H0YHA7 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA # P49915 GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 # P49915-2 Isoform 2 of GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS # Q99986 Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 # J3KNE3 Platelet-activating factor acetylhydrolase IB subunit beta (Fragment) OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1 # P68402 Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1 # H7C0N4 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 # Q15637-6 Isoform 6 of Splicing factor 1 OS=Homo sapiens GN=SF1 # H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 #
VPTANVSVVDLTC*R	C247	0.689363766	P04406	
LEFSIYPAPQVSTAVVEPYNSI LTHTTLEHSDC*AFMVDNEA IYD	C185	0.68848	P68366 P68363 Q9BQE3 Q71U36 P68366	
LQSGIC*HLFR	C203;C103	0.68772943	P14868 P14868	
GC*GTVLLSGPR	C136;C134;C134; C105;C113	0.675763333	J3QQ67 G3V203 Q07020 Q07020 H0YHA7	
RPLNPLASGGTSEENTFYSS WLEGLC*VEK	C241	0.674841123	Q96HE7	
ALANSLAC*QGK	C339;C393	0.669331032	P04075 P04075	
TVGVQGDC*R	C523;C424	0.666617601	P49915 P49915	
VGLPIGQGGFGC*IYLADMNS SEVGS DAPCVVK	C50	0.652716795	Q99986	
LANVQLLDTDGGFVHSDGAIS C*HDMFDLHLTG GGYAK	C134	0.652655	J3KNE3 P68402	
YAC*GLWGLSPASR	C26;C457;C175	0.639075979	H7C0N4 Q15637 H7C561	

LVC*GMVSYLNDLPSQR	C449	0.631065245	Q15067 Q15067 Q15067	Q15067 Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 # Q15067-3 Isoform 3 of Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 # Q15067-2 Isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 # D6RF24 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=1 # H0Y9L0 Methionine aminopeptidase 1 (Fragment) OS=Homo sapiens GN=METAP1 PE=1 SV=1 # P53582 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=2 #
VCETDGC*SSEAK	C14;C10;C14	0.622223809	D6RF24 H0Y9L0 P53582	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
NTGIIC*TIGPASR	C49	0.622222084	P14618	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 #
ASFENNC*EIGCFAK	C11	0.587742262	P56537	Q13200-2 Isoform 2 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 # Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 #
GTLTLC*PYHSDR	C620;C779;C649	0.573464532	Q13200 Q13200 Q13200	Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 #
NVGTGLVGAPAC*GDVMK	C69	0.572631442	Q9H1K1 Q9H1K1 F5H5N2 B4DNC9 B3KQ30	Q9H1K1 Iron-sulfur cluster assembly enzyme ISCU# mitochondrial OS=Homo sapiens GN=ISCU PE=1 SV=2 # Q9H1K1-2 Isoform 2 of Iron-sulfur cluster assembly enzyme ISCU# mitochondrial OS=Homo sapiens GN=ISCU # F5H5N2 Iron-sulfur cluster assembly enzyme ISCU# mitochondrial OS=Homo sapiens GN=ISCU PE=1 SV=1 # B4DNC9 Iron-sulfur cluster assembly enzyme ISCU# mitochondrial OS=Homo sapiens GN=ISCU PE=1 SV=1 # B3KQ30 Iron-sulfur cluster assembly enzyme ISCU# mitochondrial OS=Homo sapiens GN=ISCU PE=1 SV=1 #
ASVGFGGSC*FQK	C276;C209;C179	0.56981715	O60701 O60701 O60701	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # O60701-2 Isoform 2 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH # O60701-3 Isoform 3 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH #
LC*PGGQLPFLLYGTEVHTDTNK	C59	0.510786425	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
GVLMYGPPGC*GK	C179;C210	0.504210911	P43686 P43686	P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 #
EDPTVSALLTSEKDWQGFLELYLQNSPEAC*DYGL	C209;C237	0.472099433	P78417 P78417	P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
LTESPC*ALVASQYGWSGNMER	C645	0.462111623	P14625	P14625 Endoplasmic reticulum chaperone protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 #
ADIIHAC*DIVEDAAIAYGYNNIQMTLPK	C362	0.456901414	Q9NSD9	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 #

SPWLAGNELTVADVVLWSVL QQIGGC*SVTPANVQR	C213;C291;C22 2	0.454736795	A8MU58 Q13155 F8W950	A8MU58 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 # Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 # F8W950 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=1 #
EALAEASAWC*YLYGTGSVA GVYLPGSR	C3652;C3670;C3662;C3821;C3684;C3707;C3711;C3688;C3684	0.443418017	Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
AFDTAGNGYC*R	C223	0.440787534	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P10155-5 Isoform 5 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 # G5E9R9 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=1 # P10155-4 Isoform 4 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 # P10155 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2 # P10155-3 Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 #
VLGSILNASTVAAAMC*MVVT R	C400;M124 C400;M399 C125;M399 C400	0.440390328	P10155 G5E9R9 P10155 P10155 P10155	P10155-5 Isoform 5 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 # P10155 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2 # P10155-3 Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 #
GEFYVIEYAAC*DATYNEIVTF ER	C99;C86;C50;C1 4;C14;C99	0.437499298	P51114 B4DXZ6 E9PFF5 E7EU85 P51114 P51114	P51114-2 Isoform 2 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # B4DXZ6 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # E9PFF5 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # E7EU85 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # P51114-3 Isoform 3 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # P51114 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3 #
TC*DGVQCAFEELVEK	C184;C155;C13 1;C110	0.41882191	Q9NP72 Q9NP72 A0A087X1 63 Q5W0J0	Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # Q5W0J0 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 #

					Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 # D6R927 Recombining-binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=1 # Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-3 Isoform APCR-3 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-2 Isoform APCR-1 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # J3KQ69 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=2 # P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 # P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 # Q7Z434-3 Isoform 3 of Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS # Q7Z434-6 Isoform 6 of Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS # Q7Z434-2 Isoform 2 of Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS # Q7Z434 Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2 # Q7Z434-5 Isoform 5 of Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS # A0A087WUJ4 Zinc finger protein 516 (Fragment) OS=Homo sapiens GN=ZNF516 PE=1 SV=1 # Q92618 Zinc finger protein 516 OS=Homo sapiens GN=ZNF516 PE=1 SV=1 # G3V1V0 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660-2 Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 # P60660 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 # F8W1R7 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P55036-2 Isoform Rpn10E of 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 # Q5VWC4 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 # A6PVX3 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=1 SV=1 # P55036 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 # A0A087WTS8 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=1 # A0A087WYC1 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=1 # P34932 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 #
IIQFQATPC*PK	C300;C313;C299;C298;C224;C299;C278;C238	0.410302953	Q06330 Q06330 D6R927 Q06330 Q06330 Q06330 Q06330		
TLTSC*FLSCVVCVEGIVTK	C129;C119;C164	0.392640315	J3KQ69 P25205 P25205		
NFSNFCNVDVVEILPYLPC*LTAR	C33;C33;C33;C33;C33	0.299099124	Q7Z434 Q7Z434 Q7Z434 Q7Z434 Q7Z434		
QTKPC*HGQEPHGAATQGPLAK	C282;C891	0.28294357	A0A087WUJ4 Q92618		
MC*DFTEDQTAEFK	C2 C2;M1	0.268963115	G3V1V0 P60660 P60660 F8W1R7		
SNPENNVGLITLANDC*EVLTTLTPDTGR	C58;C58;C43;C58	0.265272637	P55036 Q5VWC4 A6PVX3 P55036		
C*TPACISFGPK	C34;C34;C34	0.169114831	A0A087WTS8 A0A087WYC1 P34932		

STLTDSLVC*K	C41	0.167578872	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
QSRTC*STQVC*R	C3687 C3692;C3688 C3693	0.144917011	A2VEC9 A0A096LN W2	A2VEC9 SCO-spondin OS=Homo sapiens GN=SSPO PE=2 SV=1 # A0A096LNW2 SCO-spondin OS=Homo sapiens GN=SSPO PE=4 SV=1 #
KQC*QQLQTAIAEAEQR	C383	0.142150497	Q5XKE5	Q5XKE5 Keratin# type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 #
MAC*GLVASNLNLKPGECLR	C3	0.050275553	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 #
DQVLKLC*ANHR	C1400;C1405;C1405;C1406;C1398;C2381;C1398 ;C1390;C1265	0.043120462	J3KNE0 Q99666 O14715 A6NKT7 F8VYC4 P49792 P0DJJ1 P0DJJ0 J3KQ37	J3KNE0 RanBP2-like and GRIP domain-containing protein 3 OS=Homo sapiens GN=RGPD3 PE=4 SV=2 # Q99666 RANBP2-like and GRIP domain-containing protein 5/6 OS=Homo sapiens GN=RGPD5 PE=1 SV=3 # O14715 RANBP2-like and GRIP domain-containing protein 8 OS=Homo sapiens GN=RGPD8 PE=1 SV=2 # A6NKT7 RanBP2-like and GRIP domain-containing protein 3 OS=Homo sapiens GN=RGPD3 PE=3 SV=2 # F8VYC4 RANBP2-like and GRIP domain-containing protein 1 OS=Homo sapiens GN=RGPD1 PE=4 SV=1 # P49792 E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 # P0DJJ1 RANBP2-like and GRIP domain-containing protein 2 OS=Homo sapiens GN=RGPD2 PE=2 SV=1 # P0DJJ0 RANBP2-like and GRIP domain-containing protein 1 OS=Homo sapiens GN=RGPD1 PE=2 SV=1 # J3KQ37 RANBP2-like and GRIP domain-containing protein 8 OS=Homo sapiens GN=RGPD8 PE=1 SV=1 #
ALSGYC*GFMAANLYAR	C888	0.013825823	P53618	P53618 Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 #
FFAFWGQDINNLTTPLEC*GR ESR	C93;C118;C93;C80;C93;C635;C735	0.002249817	H3BU60 H3BUH3 B7ZAR9 Q8NCN5 H3BV59 A8MT40 Q8NCN5	H3BU60 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # H3BUH3 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # B7ZAR9 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=1 # Q8NCN5-2 Isoform 2 of Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR # H3BV59 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # A8MT40 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # Q8NCN5 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # B3KQV6 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=1 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
DNTIEHLLPLFLAQLKDEC*PE VR	C198;C377	34.48272141	B3KQV6 P30153	B3KQV6 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=1 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #

**Table A3.4**

IsoTOP-ABPP analysis of DKM 2-90 (100 µM) in situ in 231MFP proteomes.

Peptide	Modified residue	Average area ratio	Uniprot ID	Protein
SWC*PDCVQAEPVVR	C43	73.55701891	Q9BRA2	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 #
AGSDGESIGNC*PFSQR	C35	38.32201299	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
IHMGC*AENTAK	C196	16.60018199	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
SGLTPNDIDVIELHDC*FSTNE LLTYEALGLCPEGQGATLVD R	C307;C307	7.868026003	E9PLD1 P22307	E9PLD1 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=1 # P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 #
DNTIEHLLPLFLAQLKDEC*PE VR	C377	5.863928818	P30153	P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
LPPQSSGVDTSPC*PNSPV R	C360;C269	4.979991729	O75815 O75815	O75815 Breast cancer anti-estrogen resistance protein 3 OS=Homo sapiens GN=BCAR3 PE=1 SV=1 # O75815-3 Isoform 3 of Breast cancer anti-estrogen resistance protein 3 OS=Homo sapiens GN=BCAR3 # Q14669-2 Isoform 2 of E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 # Q14669-3 Isoform 3 of E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 # Q14669 E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1 # Q14669-4 Isoform 4 of E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 #
LQVIQC*IDVAEQALTALEMLS R	C541	4.88980148	Q14669 Q14669 Q14669 Q14669	Q14669 E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 # Q14669 E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1 # Q14669-4 Isoform 4 of E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 #
NSPLPNC*TYATR	C340;C350;C27 5	4.878756907	Q5JTD0 Q5JTD0 Q5JTD0	Q5JTD0-2 Isoform 2 of Tight junction-associated protein 1 OS=Homo sapiens GN=TJAP1 # Q5JTD0 Tight junction-associated protein 1 OS=Homo sapiens GN=TJAP1 PE=1 SV=1 # Q5JTD0-4 Isoform 4 of Tight junction-associated protein 1 OS=Homo sapiens GN=TJAP1 #
NFNYHILSPC*DLSNYTDLAM STVK	C461	4.854704699	G5E9W3 Q9UKF6	G5E9W3 Cleavage and polyadenylation specific factor 3# 73kDa# isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 #
FICVTPTTC*SNTIDLPMSPR	C718	4.850660333	P40763	P40763 Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 #
TMPIGPDVSLLENLAAETC*FF SGADLR	C685	4.817929611	Q9BVQ7	Q9BVQ7 Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2 #
C*ALSSPSLAFTPIIK	C238;C255	4.73835307	Q8NFH5 Q8NFH5	Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 #
GPADMASQC*WGAAAAAAA AAAASGGAQQR	C336 C336;M332	4.737855087	O14497 O14497	O14497 AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3 # O14497-2 Isoform 2 of AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A #

NNQESDC*VSK	C297;C33	4.733083464	A6NDG6 H3BV17	A6NDG6 Glycerol-3-phosphate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 # H3BV17 Glycerol-3-phosphate phosphatase (Fragment) OS=Homo sapiens GN=PGP PE=1 SV=1 #
FTSC*VAFFNILNELNDYAGQ R	C69;C69;C69;C6 9;C69;C69	4.699959888	Q5T0N5 S4R347 Q5T0N5 Q5T0N5 Q5T0N5	Q5T0N5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=1 # Q5T0N5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=3 # Q5T0N5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L #
C*WDPSQAYFTLPR	C354;C348	4.568998279	O14641 I3L2N2	O14641 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 # I3L2N2 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 #
TGLC*YLPEELALQK	C46;C35	4.553772952	Q13045 Q13045	Q13045 Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2 # Q13045-3 Isoform 3 of Protein flightless-1 homolog OS=Homo sapiens GN=FLII # P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK #
KIIPTLEEGQLPSPTATSQLP LESDAVEC*LNYQHYYK	C132;C132	4.552250151	P61978 P61978	O00170 AH receptor-interacting protein OS=Homo sapiens GN=AIP PE=1 SV=2 #
YYDAIAC*LK	C208	4.511389434	O00170	Q9UPM9-2 Isoform 2 of B9 domain-containing protein 1 OS=Homo sapiens GN=B9D1 #
FTSLC*LVASSDLQAAPPTED K	C137	4.506947313	Q9UPM9	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 #
VQENSAYIC*SR	C585	4.496078451	Q9Y3T9	O75569-2 Isoform 2 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA # O75569 Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=1 SV=1 # O75569-3 Isoform 3 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA #
ANASIC*FAVPDPLMPDPSK	C95	4.431799903	O75569 O75569 O75569	Q99704 Docking protein 1 OS=Homo sapiens GN=DOK1 PE=1 SV=1 # Q99704-3 Isoform 3 of Docking protein 1 OS=Homo sapiens GN=DOK1 #
IAPC*PSQDSLYSDDLSTSA QAGEGVQR	C308;C169	4.410125448	Q99704 Q99704	Q9BST9-2 Isoform 2 of Rhotekin OS=Homo sapiens GN=RTKN #
LELYGAC*VEEEGALTGGPK	C186	4.383205565	Q9BST9	Q3V6T2-3 Isoform 3 of Girdin OS=Homo sapiens GN=CCDC88A # Q3V6T2-4 Isoform 4 of Girdin OS=Homo sapiens GN=CCDC88A # H7C2C6 Girdin (Fragment) OS=Homo sapiens GN=CCDC88A PE=1 SV=1 # H0Y7K3 Girdin (Fragment) OS=Homo sapiens GN=CCDC88A PE=1 SV=1 # Q3V6T2-2 Isoform 2 of Girdin OS=Homo sapiens GN=CCDC88A # H0Y470 Girdin (Fragment) OS=Homo sapiens GN=CCDC88A PE=1 SV=1 # H0Y7U8 Girdin (Fragment) OS=Homo sapiens GN=CCDC88A PE=1 SV=7 # Q3V6T2 Girdin OS=Homo sapiens GN=CCDC88A PE=1 SV=2 #
DKPVSC*GLAR	C1728;C1700;C 904;C232;C1701 ;C746;C682;C17 29	4.382245123	Q3V6T2 Q3V6T2 H7C2C6 H0Y7K3 Q3V6T2 H0Y470 H0Y7U8 Q3V6T2	

TC*YPLESRPSSLGTTITDEE MK	C1921	4.350820549	A0A087W Y61 Q14980 Q14980 Q14980	A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 # P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 # F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 # P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN # P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN # Q9UL15-2 Isoform 2 of BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 # Q9UL15 BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 PE=1 SV=1 # Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 # P54274-2 Isoform 2 of Telomeric repeat-binding factor 1 OS=Homo sapiens GN=TERF1 # P54274 Telomeric repeat-binding factor 1 OS=Homo sapiens GN=TERF1 PE=1 SV=3 # Q06203 Amidophosphoribosyltransferase OS=Homo sapiens GN=PPAT PE=1 SV=1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 # H3BVG0 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=1 # Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 # Q15084-2 Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-4 Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-5 Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 # Q15084-3 Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # P21980 Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 #
VC*EEIAIIPSKK	C35;C35;C35	4.304673333	H0YN88 A0A075B7 16 P08708	
ECENCDC*LQGFQLTHSLGG GTGSGMGTLLISK	C129	4.290445735	Q13509 Q13509	
TSSVSNPQDSVSGSPC*SR	C108;C106;C10 8;C108	4.267393988	P49023 F5GZ78 P49023 P49023	
TELQGLIGQLDEVSLEKNPC* R	C368;C327	4.262636039	Q9UL15 Q9UL15	
VWLQYQC*LWDMQAENIYNR	C1059	4.257811662	Q14204	
NSAEAIHGLSSLTAC*QLR	C118;C118	4.228690315	P54274 P54274	
C*ELENCQPFVETLHGK	C100	4.125995019	Q06203	
QLC*EDWEVPEPVAR	C45;C45	4.117181945	P27707 D6RFG8	
ELETVC*NDVLSLLDK	C97	4.114387439	Q04917	
LNQVC*FDDDGTSPPQDR	C422;C422	4.089522217	H3BVG0 Q8N1F7	
DVIELTDDSFDKNVLDSEDEV WMVEFYAPWC*GHCK	C238;M182 C187 C242;M187 C195;M230 C190;M179	4.064609963	Q15084 Q15084 Q15084 Q15084 Q15084	
VVSGMVNC*NDDQGVLLGR	C230	4.055556037	P21980	



AADETLK*QTK	C929;C842;C929;C842	4.011935	P49916 P49916 P49916 P49916	P49916-2 Isoform 2 of DNA ligase 3 OS=Homo sapiens GN=LIG3 # P49916-4 Isoform 4 of DNA ligase 3 OS=Homo sapiens GN=LIG3 # P49916 DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2 # P49916-3 Isoform 3 of DNA ligase 3 OS=Homo sapiens GN=LIG3 #
AQILVLTYPILIGNYGIPPEMD EFGLC*K	C73	3.995267812	P27708	P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
ENFDEVVNDADIILVEFYAPW C*GHCK	C206	3.93833	P13667	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 #
C*SFDVVKR	C169	3.935097148	Q9Y678	Q9Y678 Coatmer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 #
TGC*VDLTITNLLGAVAFMP EDITK	C325	3.922858949	Q9Y679 Q9Y679	Q9Y679-2 Isoform Short of Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 # Q9Y679 Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 PE=1 SV=1 #
MEC*PEIDCEEGWALLK	C138;M105 C107	3.896230813	P09914 P09914	P09914 Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 # P09914-2 Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 #
TWALTAVSIPEQDNIAC*TSP HVLKGTPLSR	C210	3.869202606	O14498	O14498 Immunoglobulin superfamily containing leucine-rich repeat protein OS=Homo sapiens GN=ISLR PE=2 SV=1 #
C*SVLAAANSVFR	C482	3.845227938	P33992	P33992 DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 #
VLILDEATSALDVQC*EQALQ DWNSR	C641;C641;C641 1;C641	3.841442654	X5CMH5 Q03519 A0A0G2JL V0 A0A087W YD6	X5CMH5 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # Q03519 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # A0A0G2JLV0 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # A0A087WYD6 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # Q9BTW9-4 Isoform 4 of Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD #
AGAPDEAVCGENVSIQY*AL LGCMDYYTDSR	C850;C850;C850 0	3.836065483	Q9BTW9 Q9BTW9 J3KR97	Q9BTW9 Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2 # J3KR97 Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=1 #
YAC*GLWGLSPASR	C457;C175	3.811204909	Q15637 H7C561	Q15637-6 Isoform 6 of Splicing factor 1 OS=Homo sapiens GN=SF1 # H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 #
VTAVDWHFEEAVDGEK*PPQ R	C1374	3.809582637	P27708	P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
ADASSTPSFQQAFASSC*TIS SNGPGQR	C688;C928	3.795790607	Q68CZ2 Q68CZ2	Q68CZ2-2 Isoform 2 of Tensin-3 OS=Homo sapiens GN=TNS3 # Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 # B1AKL4 Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 PE=1 SV=1 # Q9NRA8 Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 PE=1 SV=2 # Q9NRA8-3 Isoform 3 of Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 # Q9NRA8-2 Isoform 2 of Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 #
DAVLPEQSPGDFDFNEFFNL DKVPC*LASMIEDVLGEGSVS ASR	C318	3.793796843	B1AKL4 Q9NRA8 Q9NRA8 Q9NRA8	B1AKL4 Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 PE=1 SV=2 # Q9NRA8-3 Isoform 3 of Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 # Q9NRA8-2 Isoform 2 of Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 #

FTSGAFLSPSVSVQEC*R	C1051;C1068;C1068;C107	3.768813333	P52948 P52948 P52948 H7C3P6	P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
NQLC*DLETK	C62;C62	3.767302261	P26358 P26358	P26358 DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2 # P26358-2 Isoform 2 of DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 #
RVDDFEAGAAAGAAPGEEDL C*AAFNVIC*DNVVK	C105 C98	3.735232045	Q13158	Q13158 FAS-associated death domain protein OS=Homo sapiens GN=FADD PE=1 SV=1 #
VLESTPNNGYLYHQIGCC*YK	C284	3.722777264	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
KIPC*DVTEAEIISLGLPFGK	C74;C40;C37;C68;C71;C40	3.703433333	O95758 O95758 O95758 O95758 O95758	O95758-4 Isoform 4 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758-2 Isoform 2 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758-1 Isoform 1 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758 Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 PE=1 SV=2 # O95758-5 Isoform 5 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758-6 Isoform 6 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 #
EGIC*ALGGTSELSSEGTQHS YSEEEKYAFVNWINK	C104	3.682483423	P13797	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
AC*DLPAAVWHFPDTER	C181;C181;C153;C123;C181	3.675788706	A0A087W XU3 A0FGR8 A0FGR8 H7BX11 A0FGR8	A0A087WXU3 Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8 Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8-2 Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 # H7BX11 Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8-6 Isoform 6 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 #
MTEEEVEMLVAGHEDSNGC* INYEELVR	C139;M120 C138	3.6745125	G8JLA2 P60660	G8JLA2 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660-2 Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 #
DIVENIC*GR	C330	3.67450157	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
LC*VQNSHQEAR	C150	3.670864995	Q9H0L4	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 #
IATPFQVYSWTAPQAEHAMD C*VR	C333;M272 C274	3.665859677	O75153 K7EIG1	O75153 Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2 # K7EIG1 Clustered mitochondria protein homolog (Fragment) OS=Homo sapiens GN=CLUH PE=1 SV=2 #
EQPQLTSTC*HIAISNSENLLG K	C772;C773	3.645333876	A0A087W V66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
VMALQEAC*EAYLVGLFEDTN LCAIHAK	C97	3.633799495	P68431	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 #

GC*LEGSQGTQALHK	C76;C76	3.633402004	Q86WQ0 Q86WQ0	Q86WQ0-2 Isoform 2 of Nuclear receptor 2C2-associated protein OS=Homo sapiens GN=NR2C2AP # Q86WQ0 Nuclear receptor 2C2-associated protein OS=Homo sapiens GN=NR2C2AP PE=1 SV=1 #
STC*SLTPALAAHFSENLIK	C553;C450;C508;C401	3.615939947	Q9BTA9 Q9BTA9 Q9BTA9 A0A0A0MRT2	Q9BTA9 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=3 # Q9BTA9-5 Isoform 4 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC # Q9BTA9-2 Isoform 2 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC # A0A0A0MRT2 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=1 #
VANVIVDHSLQDC*VFSK	C90;C90;C49;C49;C49;C83;C83;C49	3.542495785	A9UHW6 J3KSU6 J3QLJ5 J3QLD1 J3KSB8 J3QRZ6 A9UHW6 J3QKW3 A9UHW6	A9UHW6-3 Isoform 3 of MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD # J3KSU6 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=1 # J3QLJ5 MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD PE=1 SV=1 # J3QLD1 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=1 # J3KSB8 MIF4G domain containing isoform 4 OS=Homo sapiens GN=MIF4GD PE=1 SV=1 # J3QRZ6 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=7 # A9UHW6-2 Isoform 2 of MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD # J3QKW3 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=7 # A9UHW6 MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD PE=1 SV=1 #
LFTEYPC*GSGNVYAGVLAVAR	C280	3.517786818	Q8IU81	Q8IU81 Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens GN=IRF2BP1 PE=1 SV=1 #
VGMGSGSIC*ITQEV LACGRP QATAVYK	C331	3.456038975	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
SFC*PGGTDSVSPPPSVITQENLGR	C314	3.44744	Q9C0C9	Q9C0C9 (E3-independent) E2 ubiquitin-conjugating enzyme OS=Homo sapiens GN=UBE2O PE=1 SV=3 #
AAEEEEEEEEVDLAC*TPTDVR	C285	3.417124162	P24385	P24385 G1/S-specific cyclin-D1 OS=Homo sapiens GN=CCND1 PE=1 SV=1 #
QEEVC*VIDALLADIR	C971;C971	3.402581115	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
LLEEEGVSLPDLEPAPLDSLC*SGASAEPTSHR	C198;C300	3.369495	Q9H6Q4 Q9H6Q4	Q9H6Q4-3 Isoform 3 of Cytosolic Fe-S cluster assembly factor NARFL OS=Homo sapiens GN=NARFL # Q9H6Q4 Cytosolic Fe-S cluster assembly factor NARFL OS=Homo sapiens GN=NARFL PE=1 SV=1 #
ADELLC*WEDSAGHWLYE	C158	3.364136497	Q13232	Q13232 Nucleoside diphosphate kinase 3 OS=Homo sapiens GN=NME3 PE=1 SV=2 #
DPDMAMEIC*ATDAVDDMEEGLK	C329	3.35393	Q2NL82	Q2NL82 Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 #
AVASQLDC*NFLK	C207;C193	3.35026	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
LPLMEC*VQMTQDVQK	C360	3.345659924	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #

NC*LQVLNPETR	C115	3.336793781	Q7Z6M1	Q7Z6M1 Rab9 effector protein with kelch motifs OS=Homo sapiens GN=RABEPK PE=1 SV=1 #
				Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 # Q92841-2
TTSSANNPNLMYQDEC*DRR	C586;M502 C507;M579 C507;M581 C584;M500 C505	3.324725671	Q92841 H3BLZ8 Q92841 Q92841 Q92841	Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 # Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 #
VVNSETPVVDFHAQWC*GPCK	C90;C90	3.322092501	Q99757 F8WDN2	Q99757 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 # F8WDN2 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 #
HSSSC*LPLPEFVDNTQVPSYCLNAR	C89;C89	3.319521146	Q9ULP9 Q9ULP9	Q9ULP9-2 Isoform 2 of TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 # Q9ULP9 TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 PE=1 SV=2 #
GTPEQPQC*GFSNAVQILR	C67	3.312144314	Q86SX6	Q86SX6 Glutaredoxin-related protein 5# mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 #
ESTGNMVTGQTVCK	C596	3.30798459	Q15021	Q15021 Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 #
NGSFGGQYSEC*RDPAR	C173	3.281095	O43823	O43823 A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1 #
SLDDSQC*GITYK	C282	3.260545177	Q9NVG8	Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
QIPAITC*IQSQWR	C781	3.233829932	P46940	P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 #
TFC*GTPEYLAPEVLEDNDYGR	C310;C311;C248; C307;C307	3.233338174	P31749 P31751 P31749 Q9Y243 Q9Y243	P31749 RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2 # P31751 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 # P31749-2 Isoform 2 of RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 # Q9Y243-2 Isoform 2 of RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 # Q9Y243 RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 PE=1 SV=1 #
SFFDNISC*DDNRER	C311;C375;C50; C375;C334;C54	3.232874073	A0A140TA76 Q8ND56 A0A0G2JQ95 Q8ND56 Q8ND56 A0A096LP11	A0A140TA76 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 # Q8ND56-2 Isoform 2 of Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A # A0A0G2JQ95 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 # Q8ND56 Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A PE=1 SV=3 # Q8ND56-3 Isoform 3 of Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A # A0A096LP11 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 #
VMTIPYQPMPASSPVIC*AGGQDR	C194	3.184385769	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #

GMLLGVDGHAGC*ACSQAV SER	C149;M163 C174	3.145185	Q9P0J1 Q9P0J1	Q9P0J1 [Pyruvate dehydrogenase [acetyl- transferring]]-phosphatase 1# mitochondrial OS=Homo sapiens GN=PDP1 PE=1 SV=3 # Q9P0J1-2 Isoform 2 of [Pyruvate dehydrogenase [acetyl-transferring]]- phosphatase 1# mitochondrial OS=Homo sapiens GN=PDP1 #
FC*NIMGSSNGVDQEHSNV VK	C150	3.141591086	Q9NYL9	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 #
SMVSPVPSPTGTISV PNSC*P ASPR	C254	3.125362541	P85037	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 #
VLVTQQFPC*QNPLPVNSGQ AQR	C33;C33	3.095516245	O14965 A3KFJ0	O14965 Aurora kinase A OS=Homo sapiens GN=AURKA PE=1 SV=2 # A3KFJ0 Aurora kinase A OS=Homo sapiens GN=AURKA PE=1 SV=1 #
NYVTVMQNNPLTSGLEPSP QC*DYIRPSLTGK	C202 C266;M186	3.07418	P16333 P16333	P16333 Cytoplasmic protein NCK1 OS=Homo sapiens GN=NCK1 PE=1 SV=1 # P16333-2 Isoform 2 of Cytoplasmic protein NCK1 OS=Homo sapiens GN=NCK1 #
GYWASLDASTQTTHELTIPNN LIGC*IIGR	C293	3.074130654	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # Q9Y4P8-2 Isoform 2 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 # Q9Y4P8 WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 PE=1 SV=1 # Q9Y4P8-4 Isoform 4 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 # Q9Y4P8-6 Isoform 6 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 #
FFSLSSVDKLEQIYEC*TDTED VCIVER	C52;C70;C52;C7 0	3.047755731	Q9Y4P8 Q9Y4P8 Q9Y4P8 Q9Y4P8	P23497-6 Isoform 6 of Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 # P23497 Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 PE=1 SV=3 # P23497-2 Isoform Sp100-A of Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 # P23497-7 Isoform 7 of Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 # P23497-4 Isoform Sp100-C of Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 # P23497-3 Isoform Sp100-B of Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 # E9PHV6 Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 PE=1 SV=1 # F1T0I1 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 # J3KNL6 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 #
AEPTEC*EQIAVQVNNGDA GR	C223;C248;C24 8;C213;C248;C2 48;C223	3.04484836	P23497 P23497 P23497 P23497 P23497 E9PHV6	
ANNNAVAPTTC*PLQPVTDP FAFSR	C46;C46	3.040028424	F1T0I1 J3KNL6	
LPSSSTWQQSNTTAC*QSQ ATLSLAEIQK	C960;C959;C93 2;C938;C932	3.035621149	I1E4Y6 Q6Y7W6 Q6Y7W6 Q6Y7W6 Q6Y7W6	I1E4Y6 PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1 # Q6Y7W6- 3 Isoform 2 of PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 # Q6Y7W6-4 Isoform 3 of PERQ amino acid-rich with GYF domain- containing protein 2 OS=Homo sapiens GN=GIGYF2 # Q6Y7W6 PERQ amino acid- rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1 # Q6Y7W6-5 Isoform 4 of PERQ amino acid- rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 # Q8WWH5 Probable tRNA pseudouridine synthase 1 OS=Homo sapiens GN=TRUB1 PE=1 SV=1 #
SKPESNEQVLSC*EYITLNEP K	C331	3.016928352	Q8WWH5	

SGIQPLC*PER	C341	3.016053533	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
VDDEILGFISEATPLGGIQAAS TESC*NQQLDLALCR	C561	3.01392263	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
GAVEC*CPNCR	C149	3.006059091	P31689	P31689 DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 #
ATGNLSASC*GSALR	C81;C81	3.003595396	Q96T51 Q96T51	Q96T51 RUN and FYVE domain-containing protein 1 OS=Homo sapiens GN=RUFY1 PE=1 SV=2 # Q96T51-3 Isoform 3 of RUN and FYVE domain-containing protein 1 OS=Homo sapiens GN=RUFY1 # Q9H4L5-2 Isoform 1b of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5-3 Isoform 1c of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5-4 Isoform 1d of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 #
QNLFQTGSNVSFSC*GGETR	C203;C203;C203;C203	2.995370209	Q9H4L5 Q9H4L5 Q9H4L5 Q9H4L5	Q9H4L5 Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5 Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1 # Q9H4L5-4 Isoform 1d of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 #
SC*PSFSASSEGTR	C9;C9	2.994804022	P27707 D6RFG8	P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # Q13126-5 Isoform 5 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP # Q13126-6 Isoform 6 of S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP # J3KRN1 S-methyl-5'-thioadenosine phosphorylase (Fragment) OS=Homo sapiens GN=MTAP PE=1 SV=1 #
EAGICYASIAMATDYDC*WKE HEEAMIK	C223;M36 C42 C223;M217	2.97704	Q13126 Q13126 J3KRN1	P50995 Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 # P50995-2 Isoform 2 of Annexin A11 OS=Homo sapiens GN=ANXA11 #
GVTGDEAC*LIEILASR	C294;C261	2.969163389	P50995 P50995	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 #
FQSSAVMALQEACEAYLVGL FEDTNLC*AIHAK	C111	2.96589355	P68431	Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
LLQDYPITDVC*QILQK	C387	2.952818112	Q9NVG8	P04183 Thymidine kinase# cytosolic OS=Homo sapiens GN=TK1 PE=1 SV=2 #
KLFAPQQILQC*SPAN	C230	2.948415786	P04183	P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
KVAEPELMGTPDGTC*YPPP PVPR	C1889	2.932376339	P27708	Q5VUC6 Glycylpeptide N-tetradecanoyltransferase OS=Homo sapiens GN=NMT2 PE=1 SV=1 # O60551 Glycylpeptide N-tetradecanoyltransferase 2 OS=Homo sapiens GN=NMT2 PE=1 SV=1 #
AMELLSAC*QGPAR	C104 C91;M98	2.916896667	Q5VUC6 O60551	Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
YSLADQTSQDQSPLPPCTPT PPC*AEMR	C569	2.901269356	Q06124 Q06124	Q8TF05 Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens GN=PPP4R1 PE=1 SV=1 # Q8TF05-2 Isoform 2 of Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens GN=PPP4R1 #
SDLQDELINELPNC*K	C566;C549	2.88685	Q8TF05 Q8TF05	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 # O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 #
AGEGTYALDSESC*MEK	C272	2.880469891	O00541 O00541	

LDC*NIEIQNIAIELTKPQYLSM IDLLESVDYIMVR	C279	2.879738394	Q709C8 Q709C8 Q709C8 Q709C8	Q709C8-3 Isoform 3 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C # Q709C8-4 Isoform 4 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C # Q709C8 Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1 # Q709C8-2 Isoform 2 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C # P54886 Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 #	
CEYPAAC*NALETLIHR	C612	2.851280576	P54886	Q96T76-8 Isoform 5 of MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 # Q96T76 MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 # O60934 Nibrin OS=Homo sapiens GN=NBPN PE=1 SV=1 #	
VGESNLNNGDEPTQC*SR	C570;C549	2.84913007	Q96T76 Q96T76	P23381 P23381	P23381 Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 # P23381-2 Isoform 2 of Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS # P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-5 Isoform 5 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 # E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 # E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 #
IETSC*SLLEQTQPATPSLWK	C487	2.848381176	O60934	P49327	M0R073 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 # Q8IV63-2 Isoform 2 of Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 # M0QX88 Inactive serine/threonine-protein kinase VRK3 (Fragment) OS=Homo sapiens GN=VRK3 PE=1 SV=7 # Q8IV63-3 Isoform 3 of Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 # M0QYG0 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 # M0R200 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 # Q8IV63 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=2 # M0QYA8 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 #
GIFGFTDSDC*IGK	C274;C233	2.847435839	P23381 P23381	P35611 P35611 E7ENY0 P35611 E7EV99 P35611 P35611	
LTPGC*EAEAEIEAICFFVQQ FTDMEHNR	C2359	2.846895163	P49327		
YSDVEVPASVTGYFASDGD SGTC*SPLR	C430;C430;C430; 0;C430;C430;C430; 30;C430;C430	2.837496587	E7ENY0 P35611 E7EV99 P35611 P35611		
DNQGILYEAAPTSTLTC*DSG PQK	C141;C191;C141; 1;C141;C191;C141; 41;C191;C191	2.808292541	M0R073 Q8IV63 M0QX88 Q8IV63 M0QYG0 M0R200 Q8IV63 M0QYA8		
C*PGESLINPGFK	C180	2.801553095	Q9BUH6		Q9BUH6 Protein PAXX OS=Homo sapiens GN=C9orf142 PE=1 SV=2 #
ILYLDSEICFPTVPGC*PGA WDVDSNPQR	C611	2.79232861	Q9BSJ8		Q9BSJ8 Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 #
SLITSDKGFVTMTLESLEEIQD VSC*AWK	C603	2.791251306	Q9BQ39		Q9BQ39 ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1 #

KTYITDPVSAPC*APPLQPK	C342;C364;C364	2.78994	A0A087WZF1 C9JUT4 Q93052	A0A087WZF1 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 # C9JUT4 LIM domain containing preferred translocation partner in lipoma# isoform CRA_e OS=Homo sapiens GN=LPP PE=1 SV=1 # Q93052 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 #
RPYEDQQLGETTPLTIIC*QP MQPLR	C367	2.785097322	Q8TF42	Q8TF42 Ubiquitin-associated and SH3 domain-containing protein B OS=Homo sapiens GN=UBASH3B PE=1 SV=2 #
SGQAGYVPC*NILGEARPEDA GAPFEQAGQK	C543	2.784576408	Q9H6S3	Q9H6S3 Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2 #
C*AIQNAPNPGGGDLQK	C137;C137	2.782621708	P48200 A0A0A6Y96	P48200 Iron-responsive element-binding protein 2 OS=Homo sapiens GN=IREB2 PE=1 SV=3 # A0A0A6Y96 Iron-responsive element-binding protein 2 OS=Homo sapiens GN=IREB2 PE=1 SV=1 #
YSNSALGHVNC*TIK	C282	2.776027057	Q9NQC3	Q9NQC3-2 Isoform 2 of Reticulon-4 OS=Homo sapiens GN=RTN4 #
VTINDLNENSVTLIQENC*HLN K	C320	2.772951856	Q7Z2T5	Q7Z2T5 TRMT1-like protein OS=Homo sapiens GN=TRMT1L PE=1 SV=2 #
LC*GSGFQSIVNGCQEICVK	C89;C92	2.764083059	A0A0B4J2 A4 P42765	A0A0B4J2A4 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # P42765 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 #
SC*TPSPDQISHR	C272;C272	2.758545	C9J6P4 Q7Z2W4	C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
EGALC*EENMR	C693	2.74646	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
NAEFLTC*NIPTSNASNMV TEK	C97	2.74599757	P55265 P55265 P55265	P55265-5 Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265-4 Isoform 4 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265 Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 #
C*NYLALVGGGK	C56;C63	2.726798748	I3L4S6 Q5MNZ6	I3L4S6 WD repeat domain phosphoinositide-interacting protein 3 (Fragment) OS=Homo sapiens GN=WDR45B PE=1 SV=1 # Q5MNZ6 WD repeat domain phosphoinositide-interacting protein 3 OS=Homo sapiens GN=WDR45B PE=2 SV=2 #
SRGWGQQDGPSPSPGQS PSPC*R	C1287;C1323	2.723819686	Q6F5E8 Q6F5E8	Q6F5E8-2 Isoform 2 of F-actin-uncapping protein RLTPR OS=Homo sapiens GN=RLTPR # Q6F5E8 F-actin-uncapping protein RLTPR OS=Homo sapiens GN=RLTPR PE=1 SV=2 #
SSVQEEC*VSTISSKDEDPL AATR	C78;C78	2.719493124	Q7L0Y3 C9JVB6	Q7L0Y3 Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2 # C9JVB6 Mitochondrial ribonuclease P protein 1 (Fragment) OS=Homo sapiens GN=TRMT10C PE=1 SV=1 #
NLLC*GFYGR	C247;C247	2.711948744	B0QYD3 Q9UH17	B0QYD3 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 # Q9UH17 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 #
EYTAC*ELMNIYK	C195	2.709661562	Q9NSD9	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 #
AWSTGDC*DNGGDEWEQE R	C54	2.707956618	Q9BRF8	Q9BRF8 Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3 #



SSGC*FPNMAAK	C460	2.683440265	Q96I24	Q96I24 Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2 #
STDWEDDGGWAWEENEPQ EPEEEGNTC*K	C67	2.659131521	Q9H2M9	Q9H2M9 Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1 #
VEPC*SLTPGYTK	C219;C218	2.647635352	Q96EB1 Q96EB1	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 # C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ELP4 PE=1 SV=2 #
NSNVDSYLESLEYQSC*PR	C767;C645	2.635688525	C9J6P4 Q7Z2W4	Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 # Q07000 HLA class I histocompatibility antigen# Cw-15 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 #
GGSC*SQAASSNSAQGSDES LIACKA	C345	2.635212473	Q07000	Q07000 HLA class I histocompatibility antigen# Cw-15 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q9BQG2 Peroxisomal NADH pyrophosphatase NUDT12 OS=Homo sapiens GN=NUDT12 PE=1 SV=1 #
KPWFLTNEVEEC*ENYFSK	C117	2.633169607	Q9BQG2	Q9BQG2 Peroxisomal NADH pyrophosphatase NUDT12 OS=Homo sapiens GN=NUDT12 PE=1 SV=1 # P50991-2 Isoform 2 of T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 #
IGLIQFC*LSAPK	C222;C252	2.629216445	P50991 P50991	P50991 T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 # Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 #
TSC*GSPNYAAPEVISGR	C185;C200	2.620593779	Q13131 Q13131	Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 #
TTPVDLC*LLEESVGSLEGR	C1499	2.601002436	Q9UKK3	Q9UKK3 Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3 # E9PBZ2 15-hydroxyprostaglandin dehydrogenase [NAD(+)] OS=Homo sapiens GN=HPGD PE=1 SV=1 #
QNGGEGGIINMSSLAGISSV C*RHLK	C146	2.594071474	E9PBZ2	E9PBZ2 15-hydroxyprostaglandin dehydrogenase [NAD(+)] OS=Homo sapiens GN=HPGD PE=1 SV=1 # O96011 Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B PE=1 SV=1 #
LLMEQESSAC*SR	C153;M132 C139	2.590288178	O96011 O96011	O96011-2 Isoform 2 of Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B #
LPLC*SLPGEPNGPDQQLQ R	C75	2.588571504	Q96GX2	Q96GX2 Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 #
VQILPEC*VLPSTMSAVQLES LNK	C188	2.582360321	Q96SW2 Q96SW2	Q96SW2 Protein cereblon OS=Homo sapiens GN=CRBN PE=1 SV=1 # Q96SW2-2 Isoform 2 of Protein cereblon OS=Homo sapiens GN=CRBN #
DLNYC*FSGMSDHR	C267	2.567892662	P31943 G8JLB6	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 #
KSQTGILLGVC*SK	C798;C798;C798; 8;C798	2.563733758	Q12923 Q12923 Q12923 Q12923	Q12923-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-4 Isoform 4 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-3 Isoform 3 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923 Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2 #
C*AGPTPEAELQALAR	C52	2.531388818	Q15050	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 #

AGQC*VIGLQMGTNK	C164	2.5258581	Q99439 B4DDF4 B4DUT8 A0A087X1 X5	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X1X5 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #
VLGLGLGC*LR	C88;C75	2.515892001	Q9BRJ7 K7EIN2	Q9BRJ7 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # K7EIN2 Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 #
IHEGC*EEPATHNALAK	C874;C870;C87 0	2.485969704	A0A087W VQ6 Q00610 Q00610	A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #
SSSQPSSC*CSDPSKPGGNV EGATQSLAEQMR	C289	2.481038083	Q13501	Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
ADEASELAC*PTPK	C2202	2.466873732	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
HPSAVTAC*NLDLENLVTDSN R	C325	2.46343	Q9Y678	Q9Y678 Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 #
VVETSALLC*TAQHLLAAVQSS GAPATASGPQVDNTGGPEA WDSPLRR	C150	2.44536255	Q9H6W3	Q9H6W3 Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 OS=Homo sapiens GN=NO66 PE=1 SV=2 #
IYFGSNIPNMFVDSSC*ALK	C310	2.440649547	O75477	O75477 Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 #
C*ASQSGMTAYGTR	C175;C164;C19 6;C112	2.438541164	Q99439 B4DDF4 B4DUT8 A0A087X1 X5	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X1X5 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #
AHSNPDFLPVDNC*LQSVLG QR	C703;C798	2.433908652	Q5VSL9 Q5VSL9	Q5VSL9-2 Isoform 2 of Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 # Q5VSL9 Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 PE=1 SV=1 #
YDESGNMDFDNFISC*LVR	C232 C232;M224	2.433836667	A0A0C4D GQ5 P04632	A0A0C4DGGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #
ESGC*VLGLRPGAQESPVS W PEGSK	C369;C437;C22 7	2.433820869	Q6ZUT6 Q6ZUT6 Q6ZUT6	Q6ZUT6-4 Isoform 4 of Uncharacterized protein C15orf52 OS=Homo sapiens GN=C15orf52 # Q6ZUT6 Uncharacterized protein C15orf52 OS=Homo sapiens GN=C15orf52 PE=1 SV=1 # Q6ZUT6-2 Isoform 2 of Uncharacterized protein C15orf52 OS=Homo sapiens GN=C15orf52 #
GLNPLNAYSDLAEFLETEC*Y QTPFNK	C343	2.432727451	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
C*SSYSESSEAAQLEEVTSVL EANSK	C94;C179;C137	2.428286995	Q7Z5K2 Q7Z5K2 Q7Z5K2	Q7Z5K2 Wings apart-like protein homolog OS=Homo sapiens GN=WAPL PE=1 SV=1 # Q7Z5K2-3 Isoform 3 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL # Q7Z5K2-2 Isoform 2 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL #
NC*GC*LGASPNLEQLQEENL K	C34 C32	2.425591052	P54136	P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 #
VC*NQIEFLNTEFK	C39	2.420865614	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
LEC*PETDCEKGWALLK	C137	2.41908181	Q13325	Q13325 Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 PE=1 SV=1 #

NKDTPAC*SR	C1484	2.415908796	P42695	P42695 Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=1 SV=2 #
DDFAYCLNCFC*DLYAK	C330;C324;C214	2.413115045	A0A0A0MSG2 SG2 J3KNW4 Q14192	A0A0A0MSG2 Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=1 # J3KNW4 Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=1 # Q14192 Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3 #
C*LHNFLTDGVPAEGAFTEDF QGLR	C316;C268	2.408846393	G3V1A6 P57764	G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 #
C*LLIHPNPESALNEEAGR	C118;C147	2.400537996	Q16763 K7EPJ1	Q16763 Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=2 # K7EPJ1 Ubiquitin-conjugating enzyme E2 S (Fragment) OS=Homo sapiens GN=UBE2S PE=1 SV=1 #
NVLVIGTTGSQTTFLPEGELP EC*AR	C361;C361	2.394564685	Q5TDH0 Q5TDH0	Q5TDH0-3 Isoform 3 of Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 # Q5TDH0 Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1 #
INPIC*NDHYR	C70;C70	2.393832366	Q96KB5 Q96KB5	Q96KB5 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 # Q96KB5-2 Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK #
VLQNMEQC*QK	C365;C368;C366	2.390808917	J3KND1 E9PRZ1 Q96ER3	J3KND1 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=1 # E9PRZ1 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=1 # Q96ER3 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=2 #
LDNWLNELETYC*TR	C139;C110;C223;C86	2.384988412	Q9NP72 Q9NP72 H0Y6T8 A0A087X163	Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # H0Y6T8 Ras-related protein Rab-18 (Fragment) OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 #
HGEVC*PAGWKPGSETIIPDP AGK	C245	2.375642821	Q13162	Q13162 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 #
TTEEQVQASTPC*PR	C108	2.369409923	Q14137	Q14137 Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 #
TVEIC*PFSFDSR	C572;C536	2.35939612	Q9ULW0 Q9ULW0	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 # Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 #
VHVDC*MTSQK	C1455	2.35623	P27708	P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
EVFSSC*SSEVVLSGDDEEY QR	C108	2.351583014	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
DAATTVC*SK	C1066	2.348923832	Q52LW3	Q52LW3 Rho GTPase-activating protein 29 OS=Homo sapiens GN=ARHGAP29 PE=1 SV=2 #
VC*ENIPIVLCGNK	C112;C130;C129;C108	2.348726925	P62826 J3KQE5 B5MDF5 F5H018	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 # J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 # B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 # F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 #

TASLELGEDDDDEQEDDDIEYF C*QAVGEAPSEDLFPEAK	C391;C391;C33 8;C391;C391;C3 91	2.348063676	Q9NQ55 Q9NQ55 A8MV53 A0A0B4J1 V8 Q9NQ55 A0A0A6Y YI3	Q9NQ55 Suppressor of SWI4 1 homolog OS=Homo sapiens GN=PPAN PE=2 SV=1 # Q9NQ55-3 Isoform 3 of Suppressor of SWI4 1 homolog OS=Homo sapiens GN=PPAN # A8MV53 HCG2033702# isoform CRA_a OS=Homo sapiens GN=PPAN PE=4 SV=1 # A0A0B4J1V8 HCG2039996 OS=Homo sapiens GN=PPAN-P2RY11 PE=3 SV=1 # Q9NQ55-2 Isoform 2 of Suppressor of SWI4 1 homolog OS=Homo sapiens GN=PPAN # A0A0A6YYI3 Protein PPAN-P2RY11 OS=Homo sapiens GN=PPAN-P2RY11 PE=4 SV=1 #
EADQKEQFSQGSNSC*LET SLAEIFPLGK	C161;C102	2.345546432	Q9NQ88 A0A0U1R QD1	Q9NQ88 Fructose-2#6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 # A0A0U1RQD1 Chromosome 12 open reading frame 5# isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 # Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 #
EAEVMDAGC*QESAGPER	C777	2.316855	Q99575	P49189 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 # Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 # J3QL89 ARF GTPase-activating protein GIT1 (Fragment) OS=Homo sapiens GN=GIT1 PE=1 SV=1 # J3QRU8 ARF GTPase- activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 # Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 # Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 # Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 #
GALMANFLTQGGVC*CNGTR	C288	2.31224	P49189	
GVSASAVPFTPSSPLLSC*SQ EGSR	C576;C39;C576; C585	2.311005	Q9Y2X7 J3QL89 J3QRU8 Q9Y2X7	
FLENTPSSLNIEDIEDLFLAQ YYC*SK	C283;C283	2.310676837	Q9NUY8 Q9NUY8	
LLC*SQLQVADFLQNILAQED TAK	C54;C54	2.295588007	Q95229 Q95229	O95229-2 Isoform 2 of ZW10 interactor OS=Homo sapiens GN=ZWINT # O95229 ZW10 interactor OS=Homo sapiens GN=ZWINT PE=1 SV=2 # P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 # Q9Y508 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNV3 E3 ubiquitin-protein ligase RNF114 (Fragment) OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNT1 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 # A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 #
AYEYVEC*PIR	C66	2.292093797	P53701	
DC*GGAAQLAGPAEADPLG R	C8;C8;C8;C8;C8 ;C8;C8	2.291055684	Q9Y508 A0A096LN V3 A0A096LN T1 A0A096LP 02 Q9Y508 A0A096LN N8 A0A096LP F9	
VAAASGHC*GAFSGSDSSR	C947;C919	2.283801834	Q9NZB2 Q9NZB2	

ELEVLLMC*NK	C109;M90 C91 C91;M108	2.280069883	P62910 F8W727 D3YTB1	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
EMASC*ITQR	C114	2.276330546	Q969E8	Q969E8 Pre-rRNA-processing protein TSR2 homolog OS=Homo sapiens GN=TSR2 PE=1 SV=1 #
SCYDLSC*HAR	C471	2.261119961	P41250	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 #
SHSSDFPC*SDTFSNFTFWR	C905;C863;C89 9;C948;C869;C8 89	2.259007081	Q14693 Q14693 Q14693 Q14693 Q14693	Q14693-5 Isoform 5 of Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 # Q14693 Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 PE=1 SV=2 # Q14693-3 Isoform 3 of Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 # Q14693-7 Isoform 7 of Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 # Q14693-2 Isoform 2 of Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 # Q14693-4 Isoform 4 of Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 #
EANTLNLAPYDACWNAC*R	C285;C285;C28 5	2.257477277	Q9NR50 Q9NR50 Q9NR50	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 #
YSSSFC*THDR	C66;C66	2.256994804	P04183 K7ERV3	P04183 Thymidine kinase# cytosolic OS=Homo sapiens GN=TK1 PE=1 SV=2 # K7ERV3 Thymidine kinase OS=Homo sapiens GN=TK1 PE=1 SV=1 #
VIEINPYLLGTMSGC*AADCQ YWER	C120 C116;M117 C120;M117	2.241494629	P28062 X5D2R7 P28062	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSMB8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 #
LGTTAGQMC*SGLPGLSSVDI NNFGDSINESEGIPLKR	C475 C475;M474	2.24124	A0A087W V66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
TTC*SSGSALGPGAGAAQPS ASPLEGLLDLSYPR	C12;C12;C12	2.239974259	Q96FZ5 F8WDZ3 Q96FZ5	Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=2 SV=1 # F8WDZ3 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 # Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 #
RVDDFEAGAAAGAAPGEEDL C*AANVICDNVVK	C98	2.236582708	Q13158	Q13158 FAS-associated death domain protein OS=Homo sapiens GN=FADD PE=1 SV=1 #
YDSYESC*DSR	C128;C117;C14 7;C94;C66	2.235489439	Q9ULX6 MQYT7 M0R010 V9GZ50 M0R1Y5	Q9ULX6 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 # M0R010 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 # V9GZ50 A kinase (PRKA) anchor protein 8-like# isoform CRA_c OS=Homo sapiens GN=AKAP8L PE=1 SV=1 # M0R1Y5 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=2 #

VTPTEEHVEGPLPSPVTNGT SPAQLNGGSAC*SSR	C160;C165;C27 1;C158;C271;C1 43	2.226542927	Q15599 H3BQS0 Q15599 H3BN50 Q15599 H3BUQ9	Q15599-3 Isoform 3 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 # H3BQS0 Na(+)/H(+) exchange regulatory cofactor NHE- RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=1 # Q15599-2 Isoform 2 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 # H3BN50 Na(+)/H(+) exchange regulatory cofactor NHE- RF2 (Fragment) OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=1 # Q15599 Na(+)/H(+) exchange regulatory cofactor NHE- RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=2 # H3BUQ9 Na(+)/H(+) exchange regulatory cofactor NHE-RF2 (Fragment) OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=1 #
QSLLC*PK	C27	2.22144144	Q56VL3	Q56VL3 OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 #
GALEGGSSC*PFR	C336;C282;C25 3	2.21953722	A0A087W T44 P30519 P30519	A0A087WT44 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=1 # P30519 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2 # P30519-2 Isoform 2 of Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 #
FAEMYPAFAEEYLYPDQTHF ESCAETSPAPIPNGFC*ADFS PENS DAGR	C514	2.219394396	Q8NF37	Q8NF37 Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 #
AVQDLC*GWR	C428	2.215861215	Q9P258	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 #
APELLGC*K	C177;C177	2.215512031	P24941 G3V5T9	P24941 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2 # G3V5T9 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=1 #
NGDIC*ETSGKPK	C60;C60;C60;C6 0	2.210871572	Q16637 E7EQZ4 Q16637 B4DP61	Q16637 Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1 # E7EQZ4 Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1 # Q16637-3 Isoform SMN-delta7 of Survival motor neuron protein OS=Homo sapiens GN=SMN1 # B4DP61 Survival motor neuron protein OS=Homo sapiens GN=SMN2 PE=1 SV=1 #
SEFYANEAC*KR	C339;C339;C21 9;C401;C381	2.21073036	Q86TX2 A0A087X0 W7 P49753 P49753 A0A087W T95	Q86TX2 Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 # A0A087X0W7 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # P49753-2 Isoform 2 of Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 # P49753 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 # A0A087WT95 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 #
GMETC*AMETR	C441	2.2058	Q9H0L4	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 #

NDKIELLVGC*IAELSEIENMLLR	C230	2.20323684	B5MCB3 A0A0A0M T19 Q4FZB7 B7WNX0 Q4FZB7 Q4FZB7	B5MCB3 Histone-lysine N-methyltransferase KMT5B OS=Homo sapiens GN=KMT5B PE=1 SV=2 # A0A0A0MT19 Histone-lysine N-methyltransferase KMT5B OS=Homo sapiens GN=KMT5B PE=1 SV=1 # Q4FZB7-2 Isoform 2 of Histone-lysine N-methyltransferase KMT5B OS=Homo sapiens GN=KMT5B # B7WNX0 Histone-lysine N-methyltransferase KMT5B OS=Homo sapiens GN=KMT5B PE=1 SV=3 # Q4FZB7-4 Isoform 3 of Histone-lysine N-methyltransferase KMT5B OS=Homo sapiens GN=KMT5B # Q4FZB7 Histone-lysine N-methyltransferase KMT5B OS=Homo sapiens GN=KMT5B PE=1 SV=4 # E9PBC6 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E7EMZ9 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3 # O95359-3 Isoform 3 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 #
MSESPTPC*SGSSFEETALVNTAAK	C2528;M2566 C2573;M2566 C2577;M2521 C2573	2.202056355	E9PBC6 E7EMZ9 O95359 O95359	O14929 Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1 # F8WBU3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # F8WCL3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # C9JNL5 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=8 # Q96115-2 Isoform 2 of Selenocysteine lyase OS=Homo sapiens GN=SCLY # H7C2M1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=1 # H7C4A1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=7 # A0A0A0MQU4 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # Q96115 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=4 # Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 # Q06587 E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 PE=1 SV=2 # Q06587-2 Isoform 2 of E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 #
VDENFDC*VEADDVEGK	C101	2.200630317	O14929	O14929 Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1 # F8WBU3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # F8WCL3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # C9JNL5 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=8 # Q96115-2 Isoform 2 of Selenocysteine lyase OS=Homo sapiens GN=SCLY # H7C2M1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=1 # H7C4A1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=7 # A0A0A0MQU4 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # Q96115 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=4 # Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 # Q06587 E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 PE=1 SV=2 # Q06587-2 Isoform 2 of E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 #
DAPAPAASQPSGC*GK	C22;C22;C30;C2 2;C13;C23;C30; C22	2.198280673	F8WBU3 F8WCL3 C9JNL5 Q96115 H7C2M1 H7C4A1 A0A0A0M QU4 Q96115	O14929 Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1 # F8WBU3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # F8WCL3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # C9JNL5 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=8 # Q96115-2 Isoform 2 of Selenocysteine lyase OS=Homo sapiens GN=SCLY # H7C2M1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=1 # H7C4A1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=7 # A0A0A0MQU4 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # Q96115 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=4 # Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 # Q06587 E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 PE=1 SV=2 # Q06587-2 Isoform 2 of E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 #
LLAPDC*EIIQEVGK	C215	2.197803337	Q9NQT5	Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 # Q06587 E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 PE=1 SV=2 # Q06587-2 Isoform 2 of E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 #
FC*SDCIVTALR	C69;C40	2.186807911	Q06587 Q06587	Q06587 E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 PE=1 SV=2 # Q06587-2 Isoform 2 of E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 #
NVTC*QDTR	C124	2.181085	Q8N511	Q8N511 Transmembrane protein 199 OS=Homo sapiens GN=TMEM199 PE=1 SV=1 #
HFLIEC*TPK	C1001;C1241	2.173293018	Q68CZ2 Q68CZ2	Q68CZ2-2 Isoform 2 of Tensin-3 OS=Homo sapiens GN=TNS3 # Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 # Q14694-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 # Q14694 Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 # Q14694-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 #
TAGQPEGGPGADFGQSC*FP AEAGR	C302;C254;C25 8	2.163623253	Q14694 Q14694 Q14694	Q14694 Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 # Q14694-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 #
GEASEDLC*EMALDPELLLLR DDGEEEFAGAK	C644	2.16259277	Q8N163 Q8N163	Q8N163 Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2 # Q8N163-2 Isoform 2 of Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 #

LEQC*PLQLNPFNEYSK	C149;C149;C149; 9;C149;C149	2.162022904	Q9BPZ7 Q9BPZ7 Q9BPZ7 Q9BPZ7 Q9BPZ7	Q9BPZ7 Target of rapamycin complex 2 subunit MAPKAP1 OS=Homo sapiens GN=MAPKAP1 PE=1 SV=2 # Q9BPZ7-6 Isoform 6 of Target of rapamycin complex 2 subunit MAPKAP1 OS=Homo sapiens GN=MAPKAP1 # Q9BPZ7-5 Isoform 5 of Target of rapamycin complex 2 subunit MAPKAP1 OS=Homo sapiens GN=MAPKAP1 # Q9BPZ7-2 Isoform 2 of Target of rapamycin complex 2 subunit MAPKAP1 OS=Homo sapiens GN=MAPKAP1 # Q9BPZ7-3 Isoform 3 of Target of rapamycin complex 2 subunit MAPKAP1 OS=Homo sapiens GN=MAPKAP1 #
YNPGSMNIVSNASC*TTNCLA PLAK	C156 C224;M148	2.160241581	O14556 K7EP73	O14556 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 # K7EP73 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific (Fragment) OS=Homo sapiens GN=GAPDHS PE=1 SV=1 #
C*DQDAQNPLSAGLQGACLM ETVELLQAK	C240	2.15968926	Q13561 Q13561 H0Y198 Q13561	Q13561 Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4 # Q13561-3 Isoform 3 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 # H0Y198 Dynactin subunit 2 (Fragment) OS=Homo sapiens GN=DCTN2 PE=1 SV=1 # Q13561-2 Isoform 2 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 #
VMAEANHFIDLSQIPC*NGK	C620	2.153711978	O15294	O15294 UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3 #
VNSDC*DSVLPSNFLGGNIF DPLNLNSLLDEEVSR	C177	2.153688249	Q7L2J0	Q7L2J0 7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1 #
RPLNPLASGQGTSEENTFY S WLEGLC*VEK	C241	2.15231158	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 #
LGAEAAAGAVDDGGC*SRGG GAGEK	C55	2.148886488	O95935	O95935 T-box transcription factor TBX18 OS=Homo sapiens GN=TBX18 PE=1 SV=3 #
PC*GEDWLSHPLGIVQGFFA QNGVNPDWEK	C3;C3	2.147278431	Q9BTE3 Q9BTE3	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 # Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP #
ENPDLAC*LQSIIFDEERSPEE QAK	C63	2.143242314	O95801	O95801 Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 #
LTNTYCLVAIGGSENFYSVFE GELSDTIPVVHASIAGC*R	C56	2.141374321	P56537	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 #
DQVAQLDDIVDISDEISPSVD DLALSIYPPMC*HLTVR	C300	2.138599006	O95273	O95273 Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 PE=1 SV=2 #
DADANAGLTSC*PR	C676	2.134253856	H0Y507	H0Y507 SH3 and PX domain-containing protein 2A (Fragment) OS=Homo sapiens GN=SH3PXD2A PE=1 SV=1 #
LQEVEC*EEQR	C318;C318;C10 0;C253	2.131866777	Q13596 Q13596 H0YK42 Q13596	Q13596 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3 # Q13596-3 Isoform 3 of Sorting nexin-1 OS=Homo sapiens GN=SNX1 # H0YK42 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=1 # Q13596-2 Isoform 1A of Sorting nexin-1 OS=Homo sapiens GN=SNX1 #
C*ASQVGMTAPGTR	C215	2.126112079	Q99439 B4DDF4 B4DUT8	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 #



GC*WDSIHVVEVQEK	C147;C147	2.117819523	P47756 P47756	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST # A0A087WZU8 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-8 Isoform 8 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # E7ESS1 Cellular tumor antigen p53 (Fragment) OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-7 Isoform 7 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-9 Isoform 9 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # Q96N67-3 Isoform 3 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67-2 Isoform 2 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67-4 Isoform 4 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # H0Y7L2 Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=2 # Q96N67-6 Isoform 6 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67 Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4 # Q96N67-5 Isoform 5 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q9NPF4 Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens GN=OSGEP PE=1 SV=1 #
SESELIDELSEDFDRSEC*K	C442;C464;C340;C367;C423;C381;C367;C427;C445;C359	2.11105	P20810 P20810 E7EVY3 P20810 P20810 B7Z574 A0A0C4DGB5 GB5 P20810 P20810	
C*SDSDGLAPPQHLIR	C171;C182;C182;C50;C143;C182;C182;C50;C143;C50;C143;C143;C50	2.105148905	A0A087WZU8 J3KP33 P04637 P04637 P04637 P04637 E7ESS1 P04637 A0A0U1RQC9 QC9 P04637 P04637	
FMYC*TPFTLDGR	C1933;M1933 C1904;M1931 C1902;M1931 C1944;M1911 C1913 C1935;M1942 C1933;M1900	2.10466626	Q96N67 Q96N67 Q96N67 H0Y7L2 Q96N67 Q96N67 Q96N67	
AMAHCGSQEALIVGGVGC*NVR	C265	2.103335	Q9NPF4	

AAIGC*GIVESILNWVK	C441;C431;C405;REVERSE;C486	2.09164556	P11388 P11388 P11388 P11388	P11388-3 Isoform 3 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A # P11388-2 Isoform 2 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A # P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 # Reverse_sp P01775 HV314_HUMAN Ig heavy chain V-III region LAY OS=Homo sapiens PE=1 SV=1 # P11388-4 Isoform 4 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A #
SISSSSFGAEPSAPGGGGSP GAC*PALGTK	C34;C34;C34;C34;C34	2.085865452	O95197 O95197 O95197 O95197 O95197	O95197-7 Isoform 7 of Reticulon-3 OS=Homo sapiens GN=RTN3 # O95197-2 Isoform 2 of Reticulon-3 OS=Homo sapiens GN=RTN3 # O95197 Reticulon-3 OS=Homo sapiens GN=RTN3 PE=1 SV=2 # O95197-3 Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3 # O95197-4 Isoform 4 of Reticulon-3 OS=Homo sapiens GN=RTN3 #
SSSQPSSCC*SDPSKPGGNV EGATQSLAEQMR	C290	2.070478	Q13501	Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # A0A087X0W8 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206-2 Isoform 2 of Transcription factor p65 OS=Homo sapiens GN=RELA # E9PKH5 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # Q2TAM5 RELA protein OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=2 # Q8NF37 Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 #
DGFYEAELC*PDR	C105;C92;C116;C105;C105	2.064128596	A0A087X0W8 Q04206 E9PKH5 Q2TAM5 Q04206	Q7KZF4 Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 # Q68CZ2-2 Isoform 2 of Tensin-3 OS=Homo sapiens GN=TNS3 # Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 # P55209-2 Isoform 2 of Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 # F8W543 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # H0YIV4 Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # P55209 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F8VV59 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F5H4R6 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 #
LPADTC*LLEFAR	C330	2.063831642	Q8NF37	
ETCLITFLLAGIEC*PR	C560	2.062251837	Q7KZF4	
SC*PETLTHAVGMSESPIGPK	C648	2.044575	Q68CZ2 Q68CZ2	
FEIINAIYEPTEEEEC*EWKPDE EDEISEELK	C132;C69;C126;C132;C91;C132	2.040635	P55209 F8W543 H0YIV4 P55209 F8VV59 F5H4R6	
HEEFEEGC*K	C41;C41;C41;C245;C41	2.040215663	I3L3Q4 Q9HC38 Q9HC38 F6TLX2 I3L1F4	I3L3Q4 Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=1 SV=1 # Q9HC38-2 Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 # Q9HC38-3 Isoform 3 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 # F6TLX2 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 # I3L1F4 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 #

ETTQNALQTPC*YTPYYVAPE VLGPEK	C203;C203	2.039703883	C9J8E1 Q16644	C9J8E1 MAP kinase-activated protein kinase 3 (Fragment) OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 # Q16644 MAP kinase-activated protein kinase 3 OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 # O15270 Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1 #
ANGC*VANGEVR	C19	2.029002584	O15270	Q9NVM9-2 Isoform 2 of Protein asunder homolog OS=Homo sapiens GN=ASUN # Q9NVM9 Protein asunder homolog OS=Homo sapiens GN=ASUN PE=1 SV=2 # H0YH12 Protein asunder homolog (Fragment) OS=Homo sapiens GN=ASUN PE=1 SV=1 # O75663 TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 # Q9BVS4 Serine/threonine-protein kinase RIO2 OS=Homo sapiens GN=RIOK2 PE=1 SV=2 # Q9BVS4-2 Isoform 2 of Serine/threonine-protein kinase RIO2 OS=Homo sapiens GN=RIOK2 #
ISPV DVNSRPSSC*LTN FLLN GR	C248;C349;C53	2.023506046	Q9NVM9 Q9NVM9 H0YH12	O95985-3 Isoform 3 of DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B # O95985 DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B PE=1 SV=1 # O95985-2 Isoform 2 of DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B # Q9Y6Y8 SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1 # Q9Y6Y8-2 Isoform 2 of SEC23-interacting protein OS=Homo sapiens GN=SEC23IP # Q8N490-3 Isoform 3 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490-4 Isoform 4 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490 Probable hydrolase PNKD OS=Homo sapiens GN=PNKD PE=1 SV=2 # P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 # P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 # P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 # Q9UEW8 STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens GN=STK39 PE=1 SV=3 # O95747 Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 # C9JIG9 Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 # Q9UEW8-2 Isoform 2 of STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens GN=STK39 # P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 # D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 # J3QSY4 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 #
VAC*AEEWQESR	C87	2.020650104	O75663	
VQGGVPAGSDEYEDEC*PHLI ALSSLNR	C449;C449	2.00506	Q9BVS4 Q9BVS4	
YGDLDSSLISFGPC*QTPTLG FCVER	C217;C217;C217	2.004449816	O95985 O95985 O95985	
C*PGPLAVANGVVK	C604;C604	2.00218759	Q9Y6Y8 Q9Y6Y8	
THC*LALQEALGPGPGPTGD DDYSR	C323;C287;C347	1.991574549	Q8N490 Q8N490 Q8N490	
DLSYC*LSGMYDHR	C267	1.98639636	P52597	
SVHYC*PATK	C148;C193	1.981779037	P25205 P25205	
TFVGTPC*WMAPEVMEQVR	C237	1.981635	Q9UEW8 O95747 C9JIG9 Q9UEW8	
LKNCGC*LGASPNLEQLQEE NLK	C34	1.979817495	P54136	
ADPDGPEAQAEAC*SGER	C18;C18;C18;C18	1.973110333	D6RCB9 D6RC52 Q9NX24 J3QSY4	

EITAISSVPC*QLLESVLQEL K	C645;C704	1.970996209	O75694 O75694	O75694-2 Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 # O75694 Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 #
VC*EDLDTSVNLAWTSGTNC TR	C210;C210	1.969563711	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
EHGVGGVQC*PEPGLR	C1373	1.968321722	Q9C0C2	Q9C0C2 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4 #
AAC*SAAAMEEDSEASSSR	C198	1.959098075	Q05086 Q05086 Q05086	Q05086 Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A PE=1 SV=4 # Q05086-2 Isoform I of Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A # Q05086-3 Isoform III of Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A #
VETNQDWSLMC*PNECPGLD EVWGEEFEK	C352	1.958721964	P23921	P23921 Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 #
C*ASQAGMTAYGTR	C173	1.9583017	Q15417	Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 #
LC*VQNSPQEAR	C150;C150;C150; C150;C141	1.957575233	P33240 P33240 E7EWR4 E9PID8 A0A0A0M T56	P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 # P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
SLEPSPSPGPQEEDGEVALV LLGRPSPGAVGPEDVALC*SS R	C1612;C1612;C1531; C1637;C1637;C1531	1.952729726	A0A0G2J NZ2 Q14160 A0A0G2J MS7 A0A0G2J PP5 Q14160 Q14160	A0A0G2JNZ2 Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=1 # Q14160 Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4 # A0A0G2JMS7 Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=1 # A0A0G2JPP5 Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=1 # Q14160-3 Isoform 3 of Protein scribble homolog OS=Homo sapiens GN=SCRIB # Q14160-2 Isoform 2 of Protein scribble homolog OS=Homo sapiens GN=SCRIB # P19447 TFIIH basal transcription factor complex helicase XPB subunit OS=Homo sapiens GN=ERCC3 PE=1 SV=1 #
SGVIVLPC*GAGK	C342	1.948370142	P19447	E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
GC*STVLSPEGSAQFAAQIFG LSNHLVWSK	C374;C374	1.945808515	E9PBS1 P22234	Q8WTW3 Conserved oligomeric Golgi complex subunit 1 OS=Homo sapiens GN=COG1 PE=1 SV=1 # A0A087WV10 Conserved oligomeric Golgi complex subunit 1 OS=Homo sapiens GN=COG1 PE=1 SV=1 # E9PBL8 Conserved oligomeric Golgi complex subunit 1 (Fragment) OS=Homo sapiens GN=COG1 PE=1 SV=2 #
AQAISPC*VQNFCALDSK	C513;C513;C513 3	1.943344204	Q8WTW3 A0A087W V10 E9PBL8	Q8N556 Actin filament-associated protein 1 OS=Homo sapiens GN=AFAP1 PE=1 SV=2 # Q8N556-2 Isoform 2 of Actin filament-associated protein 1 OS=Homo sapiens GN=AFAP1 #
SQAAPGSSPC*R	C713;C797	1.941371319	Q8N556 Q8N556	

LNIIINLDC*VNEVIGIR	C402;C402;C390	1.938265652	P30154 P30154 P30153	P30154-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B # P30154 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
QEPLGSDSEGVNC*LAYDEAI MAQQDR	C23	1.927672076	F5H6Q1 J3KR44 Q96FW1	F5H6Q1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # J3KR44 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 # Q96FW1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 #
QGFWEETFELQQQEC*K	C259;C259	1.923161903	Q06124 Q06124	Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
INQMVC*NSDR	C853	1.918880372	P06400	P06400 Retinoblastoma-associated protein OS=Homo sapiens GN=RB1 PE=1 SV=2 #
MNLYSLC*K	C247	1.91866	Q8TDX7	Q8TDX7 Serine/threonine-protein kinase Nek7 OS=Homo sapiens GN=NEK7 PE=1 SV=1 #
TIC*AILENYQTEK	C460;C438	1.916803333	Q5T5C7 P49591	Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 #
YSLADQTSQDQSPLPPC*TPT PPCAEMR	C563	1.916669334	Q06124 Q06124	Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
C*IPYAVLLEALALR	C110;C110;C1100;C110;C110	1.910377376	F5H248 Q9UBW8 F5H4U8 F5GYF7 F5H7C6	F5H248 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # Q9UBW8 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5H4U8 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5GYF7 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=7 # F5H7C6 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 #
C*FVCPVEYNNDTNSFTVDC EPSDLFR	C286	1.906296801	O95674	O95674 Phosphatidate cytidyltransferase 2 OS=Homo sapiens GN=CDS2 PE=1 SV=1 #
MSYLTAMGADYLSC*DSR	C891;M878 C914;M932 C914;M905 C914;M878 C945;M901 C891;M901 C918	1.903125	Q9UDY2 Q9UDY2 Q9UDY2 Q9UDY2 Q9UDY2 Q9UDY2 Q9UDY2	Q9UDY2-2 Isoform A2 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 # Q9UDY2-3 Isoform C1 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 # Q9UDY2-4 Isoform C2 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 # Q9UDY2-5 Isoform A3 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 # Q9UDY2-7 Isoform 7 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 # Q9UDY2 Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2 #
QPPWC*DPLGPFVVGEDLD PFGPR	C185;C185	1.90046102	Q5QPM7 Q92530	Q5QPM7 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 # Q92530 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 #

GSDelfSTC*VTNGPFIMSSN SASAANGNSKK	C23	1.897851522	A0A0U1R RM4 P26599 P26599 P26599	A0A0U1RRM4 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 # P26599-3 Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 # P26599-2 Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 # P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 # Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 # Q96FJ0 AMSH-like protease OS=Homo sapiens GN=STAMBPL1 PE=1 SV=2 # Q96FJ0-2 Isoform 2 of AMSH-like protease OS=Homo sapiens GN=STAMBPL1 # P16615 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 # H7C360 Mitogen-activated protein kinase kinase kinase kinase 4 (Fragment) OS=Homo sapiens GN=MAP4K4 PE=1 SV=1 # O95819 Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2 # E7ESS2 Mitogen- activated protein kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=3 # G3XAA2 Mitogen-activated protein kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2 # E7ENQ1 Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=1 # E7EN19 Mitogen- activated protein kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=1 # A0A0D9SEY1 Mitogen-activated protein kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=1 # G5E948 Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2 # O95819-2 Isoform 2 of Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 # O95819-5 Isoform 5 of Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 # O95819-3 Isoform 3 of Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 # O95819-4 Isoform 4 of Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # P36959 GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1 #
SGEEDFESLASQFSDC*SSAK	C113	1.888266174	Q13526	
LGC*NITISEDITPR	C38;C38	1.886794079	Q96FJ0 Q96FJ0	
NYLEPGKEC*VQPATK	C997	1.885060024	P16615	
NTFIGTPYWMAPEVIAC*DEN PDATYDYR	C164;M195 C202;M195 C202	1.87462485	H7C360 O95819 E7ESS2 G3XAA2 E7ENQ1 E7EN19 A0A0D9S EY1 G5E948 O95819 O95819 O95819 O95819	
YSTGSDSASFPHHTPSMC*LN PDLEGPPLEAYTIQGGYAIQ PDLTK	C217 C217;M212 C213;M216	1.871479271	Q15366 Q15366 Q15366 Q15366	
VGVGPGSVC*TTR	C186	1.870597076	P36959	

VNC*SQFLGLCALPGCK	C39;C39;C39;C39; 9;C39;C39	1.866279841	A0A087W WK3 Q16667 G3V1K6 H7C0S3 G3V2J7 F5H232	A0A087WWK3 Cyclin-dependent kinase inhibitor 3 OS=Homo sapiens GN=CDKN3 PE=1 SV=1 # Q16667 Cyclin-dependent kinase inhibitor 3 OS=Homo sapiens GN=CDKN3 PE=1 SV=1 # G3V1K6 Cyclin-dependent kinase inhibitor 3 OS=Homo sapiens GN=CDKN3 PE=1 SV=1 # H7C0S3 Cyclin-dependent kinase inhibitor 3 OS=Homo sapiens GN=CDKN3 PE=1 SV=1 # G3V2J7 Cyclin-dependent kinase inhibitor 3 OS=Homo sapiens GN=CDKN3 PE=1 SV=1 # F5H232 Cyclin-dependent kinase inhibitor 3 OS=Homo sapiens GN=CDKN3 PE=1 SV=1 # P57721 Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 PE=2 SV=2 # P57721-4 Isoform 4 of Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 # J3QT27 Poly(rC)-binding protein 3 (Fragment) OS=Homo sapiens GN=PCBP3 PE=1 SV=1 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # P57721 J3QT27 Q15366 protein 2 OS=Homo sapiens GN=PCBP2 # P57721-2 Isoform 2 of Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # P57721 E9PFP8 P57721-3 Isoform 3 of Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 # E9PFP8 Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 PE=1 SV=1 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # P57721-5 Isoform 5 of Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # Q96RS6-2 Isoform 2 of NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 # Q9UJW0 Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1 # Q9UJW0-2 Isoform 2 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # Q9UJW0-3 Isoform 3 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
INISEGNC*PER	C86;C86;C62;C54; C54;C86;C54;C86; C54;C54;C86;C54;C86; 6;C54	1.864060205	P57721 P57721 J3QT27 Q15366 Q15366 P57721 Q15366 P57721 E9PFP8 Q15366 P57721 Q15365	
DSAQC*AAIAER	C376;C347	1.85683322	Q96RS6 Q96RS6	
LLQPDFQPVC*ASQLYPR	C258;C201;C265	1.856247326	Q9UJW0 Q9UJW0 Q9UJW0	
FC*DNSSAIQ GK	C270	1.848910158	O15067	

				Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7Euu4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # P09543-2 Isoform CNP1 of 2#3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP # P09543 2#3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2 # P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 # Q8N3X6 Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens GN=LCORL PE=1 SV=4 # Q8N3X6-3 Isoform 3 of Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens GN=LCORL # D6RA10 Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens GN=LCORL PE=1 SV=1 # Q9H668 CST complex subunit STN1 OS=Homo sapiens GN=OBFC1 PE=1 SV=2 # Q9UGI8 Testin OS=Homo sapiens GN=TES PE=1 SV=1 # Q9UGI8-2 Isoform 2 of Testin OS=Homo sapiens GN=TES # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 # Q96EY7 Pentatricopeptide repeat domain-containing protein 3# mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3 #
LQGINC*GPDFTPSFANLGR	C662;C622;C575;C662;C575;C466;C622;C498;C669;C498;C466	1.845606518	Q04637 Q04637 E9PGM1 Q04637 Q04637 E7Euu4 Q04637 Q04637 E7EX73 Q04637	
DKPELQFPFLQDEDTVATLLE C*K	C29;C49	1.836499006	P09543 P09543	
YACSPLPSYLEGSGC*VIAEE QNSQTPLR	C1459;C1476;C1373;C412	1.825386217	P52948 P52948 P52948 H7C3P6	
MAAAAAAAAAAAAAAQC*RS PR	C24 C24;M8	1.824237971	Q8N3X6 Q8N3X6 D6RA10	
C*EEETPSLLWGLDPVFLAFA K	C8	1.823314704	Q9H668	
SEALGVGDVKLPC*EMDAQG PK	C196	1.820963046	Q9UGI8 Q9UGI8	
PMC*IPPSYADLGK	C13;C13	1.820426041	A0A0A0MR02 R02 P45880	
DIAEPHIPC*LMPEYFEPQIK	C139	1.819527452	Q96EY7	



TGNPMSVC*GR	C574;C493;C499;C490;C491	1.810269443	O95793 O95793 O95793 A0A087X1A5 Q5JW30	O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 # O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 # O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 # Q5JW30 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 # H0YND7 Diphthine--ammonia ligase (Fragment) OS=Homo sapiens GN=DPH6 PE=1 SV=1 # Q7L8W6-2 Isoform 2 of Diphthine--ammonia ligase OS=Homo sapiens GN=DPH6 PE=1 SV=3 #
C*EGDEVEDLYELLK	C40;C88;C88	1.806664964	H0YND7 Q7L8W6 Q7L8W6	P00533 Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 # Q96TA1 Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 # Q96TA1-2 Isoform 2 of Niban-like protein 1 OS=Homo sapiens GN=FAM129B # Q9UPN7 Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q99661 Kinesin-like protein KIF2C OS=Homo sapiens GN=KIF2C PE=1 SV=2 # A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 # J3KT29 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 # H3BTQ7 Origin recognition complex subunit 6 OS=Homo sapiens GN=ORC6 PE=1 SV=1 # H3BT22 Origin recognition complex subunit 6 OS=Homo sapiens GN=ORC6 PE=1 SV=1 # Q9Y5N6 Origin recognition complex subunit 6 OS=Homo sapiens GN=ORC6 PE=1 SV=1 # Q16576-2 Isoform 2 of Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 # Q16576 Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 # Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 # P46934-4 Isoform 4 of E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 # P46934 E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 PE=1 SV=4 # H0Y8X6 E3 ubiquitin-protein ligase NEDD4 (Fragment) OS=Homo sapiens GN=NEDD4 PE=1 SV=1 # Q96F86 Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1 #
TPLLSSLSATSNNSTVAC*IDR	C1049	1.802716086	P00533	
GPTKEELC*K	C466;C453	1.800450446	Q96TA1 Q96TA1	
VTEPSAPC*QALVSIQDLQAT FHGIR	C795	1.797591321	Q9UPN7	
ALQSNIIIFC*DEVMLLLENL GNENVHR	C689	1.79659692	Q14974	
ELSPHSGPSGEQLIQMETEE MEAC*SNGALIPGNLSK	C610	1.79512	Q99661	
NSFYMGTC*QDEPEQLDDW NR	C1907;M768 C1891;M1890 C771 C1893;M1904	1.794385716	A0A087WY61 Q14980 Q14980 Q14980	
ISLGLPVGAVINC*ADNTGAK	C28;C28	1.787053211	P62829 J3KT29	
SFEC*LLGLNSNIGIR	C88;C39;C88	1.786768968	H3BTQ7 H3BT22 Q9Y5N6	
VHIPNDDAQFDASHC*DSDK GEFGGFGSVTGK	C141;C97	1.785840748	Q16576 Q16576	
VSLDPELEEALTSASDTELC* DLAAILGMHNLITNTK	C132	1.785271906	Q9NYL9	
TSGSEDDNAEQAELEPGW VVLDQPDAAAC*HLQQQPEPS PLPPGWEEER	C182;C601;C192	1.782063202	P46934 P46934 H0Y8X6	
DLPTSPVDLVINCLDC*PENV FLR	C413	1.77741	Q96F86	



DGVADSTVISSMPC*LLMELR	C57 C57;M55	1.74471	Q5BIX2 Q96B23 A0A087W VF1 K7EQH1 Q96B23	Q5BIX2 Chromosome 18 open reading frame 25# isoform CRA_a OS=Homo sapiens GN=ARKL1 PE=1 SV=1 # Q96B23-2 Isoform 2 of Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 # A0A087WVF1 Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=1 # K7EQH1 Uncharacterized protein C18orf25 (Fragment) OS=Homo sapiens GN=C18orf25 PE=1 SV=1 # Q96B23 Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=2 #
SAC*SLESNLEGLAGVLEADL PNYK	C44	1.741098862	Q09161	Q09161 Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 #
C*PICVPCGLR	C44	1.740733678	Q9HAV4	Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 # Q9BY32-3 Isoform 3 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA # Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 # Q9BY32-2 Isoform 2 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA # P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #
GC*QDFGWDPFCQPDGYEQ TYAEMPK	C105	1.73925511	Q9BY32 Q9BY32 Q9BY32	Q9BY32-3 Isoform 3 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA # Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 # Q9BY32-2 Isoform 2 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA # P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #
INQVFHGSC*ITEGNELTK	C1904	1.738755354	P78527	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #
LAC*LSEEGNEIESGK	C213;C183;C51	1.737652747	Q9Y2L1 Q9Y2L1 G3V1J5	Q9Y2L1 Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2 # Q9Y2L1-2 Isoform 2 of Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 # G3V1J5 Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=1 # Q7Z2Z2 Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2 # Q7Z2Z2-2 Isoform 2 of Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 # Q15102 Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1 #
LAAAQGGAPLEPTQDGSAIET C*PK	C474;C423	1.736618388	Q7Z2Z2 Q7Z2Z2	Q7Z2Z2 Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2 # Q7Z2Z2-2 Isoform 2 of Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 # Q15102 Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1 #
DKEPEVVFIGDSLVLQMHQC* EIWR	C55	1.730708017	Q15102	Q15102 Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1 #
KLDTNSDGLDFSEFLNLIGG LAMAC*HDSFLK	C91	1.72917488	P31949	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 # Q9P0V9-2 Isoform 2 of Septin-10 OS=Homo sapiens GN=SEPT10 # Q9P0V9 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EW69 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 # B5ME97 Septin 10# isoform CRA_c OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EX04 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 #
TTC*MSSQGSDDDEQIKR	C22;C22;C22;C2 2;C7	1.728956725	Q9P0V9 Q9P0V9 E7EW69 B5ME97 E7EX04	Q9P0V9-2 Isoform 2 of Septin-10 OS=Homo sapiens GN=SEPT10 # Q9P0V9 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EW69 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 # B5ME97 Septin 10# isoform CRA_c OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EX04 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 #
GYDAPLC*NLLLFK	C420;C379	1.723245	O60488 O60488	O60488 Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2 # O60488-2 Isoform Short of Long-chain-fatty- acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 #

				P04150-11 Isoform Alpha-C1 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
				P04150-16 Isoform Alpha-D3 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
				P04150-3 Isoform Alpha-2 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
			P04150	P04150-12 Isoform Alpha-C2 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
			P04150	P04150-13 Isoform Alpha-C3 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
			P04150	P04150-10 Isoform 10 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
			P04150	P04150-15 Isoform Alpha-D2 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
			P04150	P04150-14 Isoform Alpha-D1 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
				P04150-8 Isoform Alpha-B of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 #
				P04150 Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 PE=1 SV=1 #
				P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 #
			P50570	P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 # P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 #
			P50570	P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 #
				Q96RU3-3 Isoform 3 of Formin-binding protein 1 OS=Homo sapiens GN=FNBP1 # Q96RU3-2 Isoform 2 of Formin-binding protein 1 OS=Homo sapiens GN=FNBP1 # Q96RU3 Formin-binding protein 1 OS=Homo sapiens GN=FNBP1 PE=1 SV=2 # Q96RU3-4 Isoform 4 of Formin-binding protein 1 OS=Homo sapiens GN=FNBP1 # Q96RU3-5 Isoform 5 of Formin-binding protein 1 OS=Homo sapiens GN=FNBP1 # H0Y7W6 Formin-binding protein 1 (Fragment) OS=Homo sapiens GN=FNBP1 PE=1 SV=2 # B7ZL14 FNBP1 protein OS=Homo sapiens GN=FNBP1 PE=1 SV=1 # Q8NCF5 NFATC2-interacting protein OS=Homo sapiens GN=NFATC2IP PE=1 SV=1 #
				O75131 Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 #
				O94804 Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1 #
				F8W881 Constitutive coactivator of PPAR-gamma-like protein 2 OS=Homo sapiens GN=FAM120C PE=1 SV=2 # Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NX05 Constitutive coactivator of PPAR-gamma-like protein 2 OS=Homo sapiens GN=FAM120C PE=2 SV=3 # Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 #
				Q96MG7 Non-structural maintenance of chromosomes element 3 homolog OS=Homo sapiens GN=NSMCE3 PE=1 SV=1 #
C*QGS GDDNLTSLGTLNFPGR	C282;C32;C367;C278;C270;C341;C37;C52;C341;C367	1.719335535		
LQDAFSSIGQSC*HLDLPQIAV VGGQSAGK	C27;C27;C27;C27;C27	1.717480518		
NEDEEGYVPTSYVEVC*LDK	C580;C604;C609;C543;C604;C556;C543	1.716744739		
SC*LSPKPPQGQEQGQGEDEVVLVEGPTLPETPR	C232	1.716285354	Q8NCF5	
NC*LNPQFSK	C54	1.71589643	O75131	
LSEEAEC*PNPSTPSK	C947	1.715236763	O94804	
AHQLVLPPC*DVIK	C354;C279;C354;C279	1.713808459	F8W881 Q9NZB2 Q9NX05 Q9NZB2	
DWPAQYC*EALADEENR	C283	1.712794238	Q96MG7	

					P60484-2 Isoform alpha of Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN # A0A087X033
VENGSLC*DQEIDSICSIER	C469;C105;C296;C469	1.709055855	P60484 A0A087X033 P60484 A0A0U1R63		Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # P60484 Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # A0A0U1RR63 Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 # Q9Y570-4 Isoform 4 of Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 # Q9Y570 Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 # P40616 ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=1 SV=1 # P40616-2 Isoform 2 of ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 # F8VYN9 ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=1 SV=1 #
C*DYMDEVTYGELEKEEAQPI VTK	C602	1.707423156	H3BQZ7 Q1KMD3		
QC*EGITSPPEGSK	C238;C238	1.706292449	Q9Y570 Q9Y570		
C*YYSNDAVIYVVDSCDRDR	C80;C63;C80	1.706064186	P40616 P40616 F8VYN9		
LTIIVSDPShc*NVLr	C87;C87	1.704861649	P78346 P78346		P78346-2 Isoform 2 of Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 # P78346 Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1 # P61289-3 Isoform 3 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 # B3KQ25 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 # P61289 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 # K7ESG5 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 # P61289-2 Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 # P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #
LDEC*EEAFQGTK	C103;C31;C92;C36;C92	1.703394797	P61289 B3KQ25 P61289 K7ESG5 P61289		
DVLKEEGVSFLINTFEGGGC* GQPSGILAQPTLLYLr	C1229	1.701859632	P78527		
LELLVGSPASC*MELELYGVD DKFYSK	C51	1.699925	Q99426		Q99426 Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2 # Q8TAF3-4 Isoform 4 of WD repeat-containing protein 48 OS=Homo sapiens GN=WDR48 # Q8TAF3 WD repeat-containing protein 48 OS=Homo sapiens GN=WDR48 PE=1 SV=1 # Q8TAF3-3 Isoform 3 of WD repeat-containing protein 48 OS=Homo sapiens GN=WDR48 # P36551 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 # P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 # P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 #
ASGDYDNDc*TNpITPLCTQP DQVIK	C260;C342;C333	1.69943	Q8TAF3 Q8TAF3 Q8TAF3		
EGGGGISCVLQDGC*VFEK	C198	1.697875992	P36551		
NC*DKGQSFFIDAPDSPA TLAYR	C266;C277	1.695301676	P53384 P53384		

ILYLDSEIC*FPTVPGCPGA WDVDSNPQR	C604	1.688280337	Q9BSJ8	Q9BSJ8 Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 #
LFNTAVC*ESK	C721	1.686720596	Q9BXJ9	Q9BXJ9 N-alpha-acetyltransferase 15# Nata auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
VICAEOPYIC*K	C456;C357	1.685884008	P49915 P49915	P49915 GMP synthase [glutamine- hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 # P49915-2 Isoform 2 of GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS #
NCAVSC*AGEK	C141;C141	1.681503004	Q15813 Q15813	Q15813 Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 # Q15813-2 Isoform 2 of Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE #
LPITVLNGAPGFINLC*DALNA WQLVK	C241;C240	1.680911014	P31939 P31939	P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 # P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC #
EREDESSMFDEYFQEC*QD E	C320 C291;M312 C281;M283	1.679811324	Q9UHW5 Q9UHW5 Q9UHW5	Q9UHW5 GPN-loop GTPase 3 OS=Homo sapiens GN=GPN3 PE=1 SV=2 # Q9UHW5-2 Isoform 2 of GPN-loop GTPase 3 OS=Homo sapiens GN=GPN3 # Q9UHW5-3 Isoform 3 of GPN-loop GTPase 3 OS=Homo sapiens GN=GPN3 #
SNLPNC*ANSDTDFMGLFK	C1384	1.679805	A0A0J9Y WLO	A0A0J9YWLO Absent in melanoma 1 protein OS=Homo sapiens GN=AIM1 PE=1 SV=1 #
GDFYVIEYAAAC*DATYNEIVTL ER	C109	1.6796071	P51116	P51116 Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 #
AFDLIEHYFGTEDEDSSIAPQ VDLNQQYIFQQC*EAPMEG FQL	C529	1.675625	P52294	P52294 Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3 #
AHFDYDPSDDPYVPC*R	C366;C332	1.67441849	Q8N3R9 Q8N3R9	Q8N3R9 MAGUK p55 subfamily member 5 OS=Homo sapiens GN=MPP5 PE=1 SV=3 # Q8N3R9-2 Isoform 2 of MAGUK p55 subfamily member 5 OS=Homo sapiens GN=MPP5 #
HELQANC*YEEVK	C177;C122;C13 9;C139	1.670158552	E9PK25 G3V1A4 P23528 E9PP50	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
FAEMYPAFAEEYLYPDQTHF ESC*AETSPAPIPNGFCADFS PENS DAGR	C501	1.667001057	Q8NF37	Q8NF37 Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 #
NWISQLQMHAYC*ENPDIVLC GNK	C123;C123;C12 3	1.665453836	P51159 P51159 H3BN55	P51159 Ras-related protein Rab-27A OS=Homo sapiens GN=RAB27A PE=1 SV=3 # P51159-2 Isoform Short of Ras-related protein Rab-27A OS=Homo sapiens GN=RAB27A # H3BN55 Ras-related protein Rab-27A (Fragment) OS=Homo sapiens GN=RAB27A PE=1 SV=1 #
SIC*TTVLELLDKYLIANATNPE SK	C94	1.660696278	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #
IPC*DSPQSDPVDTPSTK	C1250;C1251	1.65960117	A0A087W V66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
LEGDLTGPSVGVVDPDVELE C*PDAK	C1900	1.65798978	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #

ELHGQNPVWTPC*NK	C159;C159;C159; 9;C159	1.657698665	Q16630 Q16630 F8WJN3 Q16630	Q16630-2 Isoform 2 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 # Q16630-3 Isoform 3 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 # F8WJN3 Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=1 # Q16630 Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2 # O94901 SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=3 # O94901-5 Isoform 5 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-8 Isoform 8 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-6 Isoform 6 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-9 Isoform 9 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # E9PHI4 SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=1 #
TGC*ETVDAVQER	C526;C416;C499; C396;C630;C536	1.654266586	O94901 O94901 O94901 O94901 E9PHI4	Q9901 SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-8 Isoform 8 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-6 Isoform 6 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-9 Isoform 9 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # E9PHI4 SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=1 #
FHADSVC*K	C25	1.65310409	Q9BW61	Q9BW61 DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1 #
SEGGFIWAC*K	C269	1.65050995	O75874	O75874 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 #
MSDSADKPIDNDAEGVWSPD IEQSFQEALAIYPPC*GR	C53;M19 C53	1.650441749	P28347 H0YE88	P28347 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=2 # H0YE88 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=1 #
VADSSPFALELLISDDCFVLD NGLC*GK	C275;C290	1.650262377	P40121 P40121	P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
LTPTYGDLNHLVSATMSGV TTC*LR	C239;C239;C239; 9;C221	1.64795878	P68371 Q9BVA1 P04350 Q5JP53	P68371 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
LANLAATIC*SWEDDVNHSFA K	C210;C210	1.647462222	Q9NQW6 Q9NQW6	Q9NQW6-2 Isoform 2 of Actin-binding protein anillin OS=Homo sapiens GN=ANLN # Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 #
LISPNLGVVFFNAC*EAASR	C316;C342	1.64545255	Q66K74 Q66K74	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 # Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 # P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 # Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 #
AYSFC*GTVEYMAPEVVNR	C232;C207;C223; C229;C131;C223	1.641235	Q15418 Q15418 E9PGT3 P51812 Q15418 Q15418	Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 # P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 # Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 #

EITSLDTENIDEILNNADVALV NFYADWC*R	C58	1.640720013	Q9BS26	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 # Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 # P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 # Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 # Q9Y2H1-2 Isoform 2 of Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L # Q9Y2H1 Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3 # Q15208 Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1 # F5H277 Serine/threonine-protein kinase 38-like (Fragment) OS=Homo sapiens GN=STK38L PE=1 SV=7 #
AENGLLMTPC*YTANFVAPEV LKR	C579;M480 C483;M572 C584;M556 C575 C564;M576 C559;M561	1.63744	Q15418 Q15418 E9PGT3 P51812 Q15418 Q15418	
LSDFGLC*TGLK	C142;C235;C234;C194	1.633392183	Q9Y2H1 Q9Y2H1 Q15208 F5H277	
PAVC*NDLSIMSKFK	C1525	1.63018881	O95714	O95714 E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 # Q8IWB1 Inositol 1#4#5-trisphosphate receptor-interacting protein OS=Homo sapiens GN=ITPRIP PE=1 SV=1 #
QDHQEGPSPEC*LGGEDEL PGLGGAPLQGLTLPNK	C115	1.629285701	Q8IWB1	P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
FLSQIESDC*LALLQVR	C794	1.627018409	P52789	O00743 Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1 # O00743-3 Isoform 3 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C # O00743-2 Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C # D6RER6 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=1 # P36551-2 Isoform 2 of Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX # P36551 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 #
GAFC*DLVWSDPEDVDTWAI SPR	C192;C229;C170	1.62689363	O00743 O00743 O00743	
C*SSFMAPPVTDLGELR	C127	1.625387235	D6RER6 P36551 P36551	
MTGESEC*LNPSTQSR	C1212;C1181	1.621422531	Q9H2G2 Q9H2G2	Q9H2G2 STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 # Q9H2G2-2 Isoform 2 of STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK #
FDDLQFFENC*GGGSFGSVY R	C22	1.620853772	Q9NYL2	Q9NYL2 Mitogen-activated protein kinase kinase MLT OS=Homo sapiens GN=ZAK PE=1 SV=3 #
DFQDYMEPEEGC*QGSPQR	C191	1.61967	O43237	O43237 Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1 # H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #
EGC*TEVSLLR	C308;C308	1.619235	H3BQZ7 Q1KMD3	



KC*DLISIPK	C426;C420;C47 3	1.619149473	Q9ULV4 Q9ULV4 Q9ULV4	Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C #
C*SGIGDNPGSETAAPR	C2675	1.619124746	P50851	P50851 Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4 #
VSVC*AETYNPDEEEEDTDP R	C101;C101	1.615785339	P13861 P13861	P13861 cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2 # P13861-2 Isoform 2 of cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A #
EEC*PVFTPPGGETLDQVK	C114;C55	1.61073614	Q9NQ88 A0A0U1R QD1	Q9NQ88 Fructose-2#6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 # A0A0U1RQD1 Chromosome 12 open reading frame 5# isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 #
DAWASPC*HSYPLVATR	C374	1.608602875	Q13425	Q13425 Beta-2-syntrophin OS=Homo sapiens GN=SNTB2 PE=1 SV=1 #
NMITGTSQADC*AVLIVAAGV GEFEAGISK	C111;M102 C111	1.607548046	P68104 Q05639 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
TC*ETGEPMEAESGDSSEG PAQVYLPGR	C11	1.604575435	Q9BQ67	Q9BQ67 Glutamate-rich WD repeat-containing protein 1 OS=Homo sapiens GN=GRWD1 PE=1 SV=1 #
TGTQEVGQDPGEAVQPC*R	C443;C443	1.603529974	Q9NZT2 Q9NZT2	Q9NZT2 Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3 # Q9NZT2-2 Isoform 2 of Opioid growth factor receptor OS=Homo sapiens GN=OGFR # Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 #
IIQFQATPC*PK	C300;C313;C29 8;C278;C299	1.602342882	Q06330 Q06330 Q06330 Q06330 Q06330	Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q12800-3 Isoform 3 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 # Q12800-2 Isoform 2 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 # Q12800-4 Isoform 4 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 # F8VWL0 Alpha-globin transcription factor CP2 (Fragment) OS=Homo sapiens GN=TFCP2 PE=1 SV=1 # F8VX55 Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 PE=1 SV=1 # Q12800 Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 PE=1 SV=2 #
IAQLFSISPC*QISQIYK	C402;C402;C45 3;C355;C375;C4 53	1.60178	Q12800 Q12800 Q12800 F8VWL0 F8VX55 Q12800	Q12800-3 Isoform 3 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 PE=1 SV=2 # Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 # Q15019-2 Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2 # Q15019 Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 # Q15019-3 Isoform 3 of Septin-2 OS=Homo sapiens GN=SEPT2 #
LTWHSC*PEDEAQ	C177	1.599704805	Q13185	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 # Q15019-2 Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2 # Q15019 Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 # Q15019-3 Isoform 3 of Septin-2 OS=Homo sapiens GN=SEPT2 #
LTVVDPGYGDAINC*R	C146;C111;C12 1	1.597800974	Q15019 Q15019 Q15019	Q15019-2 Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2 # Q15019 Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 # Q15019-3 Isoform 3 of Septin-2 OS=Homo sapiens GN=SEPT2 #

SLPDC*TPHPNSISIDAGPR	C42;C29;C197;C736;C733	1.596098531	F8WF49 A0A0B4J2 C2 Q9Y2H0 Q9Y2H0 Q9Y2H0	F8WF49 Disks large-associated protein 4 OS=Homo sapiens GN=DLGAP4 PE=1 SV=1 # A0A0B4J2C2 Discs# large (Drosophila) homolog-associated protein 4# isoform CRA_b OS=Homo sapiens GN=DLGAP4 PE=1 SV=1 # Q9Y2H0-3 Isoform 3 of Disks large-associated protein 4 OS=Homo sapiens GN=DLGAP4 # Q9Y2H0 Disks large-associated protein 4 OS=Homo sapiens GN=DLGAP4 PE=1 SV=3 # Q9Y2H0-1 Isoform 2 of Disks large-associated protein 4 OS=Homo sapiens GN=DLGAP4 # Q9Y285-2 Isoform 2 of Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA # Q9Y285 Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 # K7ER00 Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=1 # G5EA39 Anaphase-promoting complex subunit 15 OS=Homo sapiens GN=ANAPC15 PE=1 SV=1 #
VNLQMVYDSPLC*R	C533 C493;M526 C462;M486	1.59349764	Q9Y285 Q9Y285 K7ER00	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 # P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 # P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 # B3KVZ3 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 # Q9H3R5 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 #
VTETLWFNLDRPC*VEETELQ QQEQHQAWLQSIQAEK	C24	1.586469015	G5EA39	P04183 Thymidine kinase# cytosolic OS=Homo sapiens GN=TK1 PE=1 SV=2 # K7ERV3 Thymidine kinase OS=Homo sapiens GN=TK1 PE=1 SV=1 #
HDDSSDNFC*EADDIQSPEAE YVDLLLNP	C166	1.585991123	Q96HE7	Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
GSSC*FECTHYQSFLEYR	C238	1.585101759	P21964	O60831 PRA1 family protein 2 OS=Homo sapiens GN=PRAF2 PE=1 SV=1 # A6NP52 PRA1 family protein 2 OS=Homo sapiens GN=PRAF2 PE=1 SV=1 #
TWYVQATC*ATQGTGLYEGL DWLSNELSK	C159	1.579087609	P18085	Q2TAA2 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 # H7C5G1 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 #
LMDLDVEQLGIPEQEYSC*VV K	C135	1.578951682	P12004	Q8NBF2 NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 #
AGGPPQVAGAQAAC*SEDR	C35;C35	1.577460098	B3KVZ3 Q9H3R5	O75683 Surfeit locus protein 6 OS=Homo sapiens GN=SURF6 PE=1 SV=3 # Q99661 Kinesin-like protein KIF2C OS=Homo sapiens GN=KIF2C PE=1 SV=2 #
ENC*PVPGKPGEAVAAR	C206;C239	1.574892175	P04183 K7ERV3	O95999 B-cell lymphoma/leukemia 10 OS=Homo sapiens GN=BCL10 PE=1 SV=1 #
FSFCC*SPEPEAEAEAAAGP GPCER	C27	1.574571152	Q13501	Q86U90 YrdC domain-containing protein# mitochondrial OS=Homo sapiens GN=YRDC PE=1 SV=1 #
LAAPDPC*DPQR	C28;C28	1.573542432	O60831 A6NP52	A0A024R4E5 High density lipoprotein binding protein (Vigilin)# isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1 #
VILITPTPLC*ETAWEEQCIQGC CK	C137;C117	1.567171644	Q2TAA2 H7C5G1	
AILFSQPLQITDTQQGC*IAPV ELR	C716	1.566962462	Q8NBF2	
KAEEATEAQEVVEATPEGAC* TEPR	C189	1.56300813	O75683	
ATLEC*HPLTMTDPIEEHR	C245	1.562285	Q99661	
TENTIFSSTTLPRPGDPGAPP LPPDLQLEEEGTC*ANSSEMF LPLR	C215	1.5617225	O95999	
AGAVVAVPTDTLYGLACAAS C*SAALR	C99	1.560968547	Q86U90	
AAC*LESAQEPAGAWGNK	C53	1.559677769	A0A024R4 E5	

HLNEIDL FHC*IDPNDSK	C62;C58;C58;C58	1.559586472	A0A087WYT3 Q15185 Q15185 Q15185	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q15185-3 Isoform 3 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q96S55 ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 PE=1 SV=2 # Q96S55-3 Isoform 3 of ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # Q14247 Src substrate corctactin OS=Homo sapiens GN=CTTN PE=1 SV=2 # Q9BTY7 Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1 # Q9NR30 Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 # Q9NR30-2 Isoform 2 of Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 # Q96RN5-3 Isoform 3 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 # Q96RN5-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 # Q96RN5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=2 # G3V1P5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=1 # P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 # Q9P0L0 Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 # Q9P0L0-2 Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA # Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 # P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 # E7ESC6 Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=1 # Q9UIA9 Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3 # A6NDU8 UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 # Q9H4A6 Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 # Q9H4A5 Golgi phosphoprotein 3-like OS=Homo sapiens GN=GOLPH3L PE=1 SV=1 # Q8N6S5 ADP-ribosylation factor-like protein 6-interacting protein 6 OS=Homo sapiens GN=ARL6IP6 PE=1 SV=1 # Q9BQP7 Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens GN=MGME1 PE=1 SV=1 #
SQQDTFLPHVEC*GTITLIGAT TENPSFQVNAALLSR	C347;C127	1.558891345	Q96S55 Q96S55	
WC*NVQSTQDEFEEELTMSQK	C59	1.55856838	P27707 D6RFG8	
HC*SQVDSVR	C112	1.55778	Q14247	
GMENLLEVVQVPEDVEQQLQ QLDC*R	C368	1.557617007	Q9BTY7	
DSEDNPQTLIFSATC*PHWV FNVAK	C378;C310	1.557224756	Q9NR30 Q9NR30	
QQYLC*QPLLDVLANIR	C507;C578;C618;C552	1.556489079	Q96RN5 Q96RN5 Q96RN5 G3V1P5	
WNDNC*PSWNTIDPEER	C301	1.55643083	P17655	
DAANC*WTSLLESEYAADPW VQDQMQR	C99	1.551206552	Q8WVJ2	
YC*VRPNSGIIDPGSTVTVSV MLQPFYDPNEK	C60	1.549876066	Q9P0L0 Q9P0L0	
LGPQSDPTEANLESADPEL C*IR	C38;C38	1.549694689	Q27J81 Q27J81	
YDC*GEEILITVLSAMTEEA AAIK	C159	1.548397409	P63241 P63241	
LTHNCLNDFIGTSTDESSDD LC*TVQIPTSWR	C245;C244	1.547771133	E7ESC6 Q9UIA9	
EC*SNPSNLELYTQAILDMT YFEENKLVDEDFPEDSSSQK	C57	1.538729833	A6NDU8	
EGYTSFWNDC*ISSGLR	C84;C70	1.538585	Q9H4A6 Q9H4A5	
PSYSSTQGDWSWGEGEVDE EEGC*DQVAR	C48	1.537148414	Q8N6S5	
GVAQTGPSVEEDALLC*GPV SK	C79	1.537077693	Q9BQP7	

LIC*DFPFDGLLEER	C670;C681	1.533740787	Q96JC1 Q96JC1	Q96JC1-2 Isoform 2 of Vam6/Vps39-like protein OS=Homo sapiens GN=VPS39 # Q96JC1 Vam6/Vps39-like protein OS=Homo sapiens GN=VPS39 PE=1 SV=2 #
GGNAVVDGC*GK	C501	1.53293288	P48506	P48506 Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 #
NC*MTDLLAK	C18	1.52967995	Q00765	Q00765 Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3 # P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
VSDTVVEPYNATLSVHQLVE NTDETYCIDNEALYDIC*FR	C211;C211;C211; 1;C211;C211	1.529229842	P07437 P68371 Q9BVA1 P04350 Q9BUF5	
APVPSTC*SSTFPEELSPPSH QAK	C160;C160;C160; 0;C160	1.519813199	A0A087W Y61 Q14980 Q14980 Q14980	A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 #
DLC*FSPGLMEASHVVNDVN EAVQLVFR	C392	1.519412699	Q9BXW7 Q9BXW7	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 # Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 #
LLDRDAC*DTVR	C247;C204	1.518337712	Q9NZL4 Q9NZL4	Q9NZL4-3 Isoform 3 of Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 # Q9NZL4 Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 PE=1 SV=1 #
VWNLANC*K	C182	1.518259368	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
C*STPEEIK	C6;C23	1.517306185	P60981 P60981	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
TDICQGALGDC*WLLAAIASLT LNEEILAR	C105	1.513197063	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
GEAYNLFEHNC*NTFSNEVA QFLTGR	C108	1.51139444	Q6ICB0	Q6ICB0 Desumoylating isopeptidase 1 OS=Homo sapiens GN=DESI1 PE=1 SV=1 #
AVMEQIPEIQKDSLQDFDC*K	C246 C1131;M230	1.511278996	Q9HAV4 H0Y3W3	Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 # H0Y3W3 Exportin-5 (Fragment) OS=Homo sapiens GN=XPO5 PE=1 SV=1 #
QNSDFLC*QMDLLQEFYETTL EALKDAK	C130	1.510567118	P61201	P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 #
LFDDPDLGGAIPLGDSLPA AC*ESGGPTPSLSHR	C287	1.50881695	Q53T59	Q53T59 HCLS1-binding protein 3 OS=Homo sapiens GN=HS1BP3 PE=1 SV=1 #
VDSTTC*LFPVEEK	C246;C264	1.506023017	Q06210 Q06210	Q06210-2 Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 # Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 #
INDALSC*EYECR	C216	1.502334652	Q52LJ0	Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #
LEVDAIVNAANSSLLGGGGV DGC*IHR	C186	1.500551835	Q9BQ69	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #
SFC*SQFLPEEQAEIDQLFDA LSSDKNSPNVSSK	C13	1.49883656	Q6P9B6	Q6P9B6 TLD domain-containing protein 1 OS=Homo sapiens GN=TLDC1 PE=1 SV=2 #

				O00233-2 Isoform p27-S of 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 # O00233 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 #
GIGMNEPLVDC*EGYPR	C59;M52 C59	1.498802379	O00233 O00233 J3KN29 F5H7X1 F5H5V4 F5GX23	J3KN29 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H7X1 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H5V4 26S proteasome non-ATPase regulatory subunit 9 (Fragment) OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5GX23 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 #
GPC*GSFDVR	C1183;C1211	1.498062921	Q7L2E3 Q7L2E3	Q7L2E3 Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1 # Q7L2E3-2 Isoform 2 of Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 #
VAHALAEGLGVIAC*IGEK	C127;C45;C164	1.494266982	P60174 P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174-4 Isoform 4 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 #
LTALDYHNPAGFNC*KDETEFR	C19	1.490179358	Q9Y224	Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 #
SSGGFVWAC*K	C308;C256	1.488137194	P48735 P48735	P48735 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 # P48735-2 Isoform 2 of Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 #
SVLC*STPTINIPASPFMQK	C22	1.485602247	Q96KB5	Q96KB5 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 #
AGC*AVTSLASELTK	C1218;C1203;C1218;C1227;C1183;C1227	1.48389659	O60610 O60610 A0A140T8Z0 A0A0G2JH68 H9KV28 O60610	O60610-3 Isoform 3 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # O60610-2 Isoform 2 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # A0A140T8Z0 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # A0A0G2JH68 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # H9KV28 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 # O60610 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 #
GPFVEAEVDPVDLEC*PDAK	C1833	1.481792334	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
VAGINAC*GR	C1803;C1872;C1916;C1917	1.480405	P51610 P51610 P51610 A6NEM2	P51610-2 Isoform 2 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 # P51610 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 # P51610-4 Isoform 4 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 # A6NEM2 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 #
SVPTTQC*LDNSK	C226;C226	1.47954526	A0A087WV66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
AINC*ATSGVVGLVNCLR	C1448	1.476297739	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #

FQSAAGALQEASEAYLVGLF EDTNLC*AIHAK	C111;C111	1.475916531	K7EK07 P84243	K7EK07 Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1 # P84243 Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 #
SPC*QTDVLR	C239	1.475249724	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
NDITAWQEC*VNNSMAQLEH QAVR	C106	1.47339983	O75934	O75934 Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 #
LC*DFGISGQLVDSIAK	C257;C246	1.472964223	P45985 P45985	P45985-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens GN=MAP2K4 # P45985 Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens GN=MAP2K4 PE=1 SV=1 #
NLQTCMEVLEALYDGS LGDC *K	C817	1.472667833	Q9BXJ9	Q9BXJ9 N-alpha-acetyltransferase 15# Nata auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
LALFNPDVC*WDR	C44	1.467533637	O00483	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 #
LAALALASSESSSTPEEC*E EMSEKPK	C472	1.46671	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
TSC*KDDEAVVQAPR	C993;C1003;C992; C1004;C992	1.465286667	P35658 P35658 P35658 P35658 P35658	P35658-4 Isoform 4 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658 Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 # P35658-2 Isoform 2 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658-3 Isoform 3 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658-5 Isoform 5 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 #
RVETNQDWSLMCPNEC*PGL DEVWGEEFEK	C356	1.463205256	P23921	P23921 Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 #
C*ALGWDHQEK	C246	1.462547058	Q14247	Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 #
ELELMFGC*QVEGDAAETPP RPR	C277;C251	1.460097202	Q02750 Q02750	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 #
KIDQSEFEGFEYINPLLSAE EC*V	C595	1.459302856	P41743	P41743 Protein kinase C iota type OS=Homo sapiens GN=PRKCI PE=1 SV=2 #
C*AGNEDIITLR	C81	1.455473324	P12004	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 #
GLYDGPVC*EVSVTPK	C468;C504	1.453217673	Q16555 Q16555	Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
NDPPMEAAGFTAQVILNHPG QISAGYAPVLDC*	C363;M314 C342 C342;M314	1.449560765	P68104 A0A087W VQ9 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #

TAGPQSQVLC*GVVMDR	C556	1.449535	P35611 P35611 E7ENY0 P35611 E7EV99 P35611 P35611	P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 # E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 # E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-6 Isoform 6 of Alpha- adducin OS=Homo sapiens GN=ADD1 # P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 #
FSFC*CSPEPEAEAEAAAGP GPCER	C26	1.449005139	Q13501	Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # P04049-2 Isoform 2 of RAF proto-oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 # P04049 RAF proto- oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 PE=1 SV=1 # M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
DAVFDGSSC*ISPTIVQQFGY QR	C27;C27	1.447287577	P04049 P04049	
QPAIMPQSYGLEDGSC*SY KDFSESR	C413;C472	1.441191059	M0QXS5 P14866	
SDC*ESQECVTK	C169	1.439491521	Q9NS86	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 # Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 # Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-3 Isoform APCR-3 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-2 Isoform APCR-1 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ #
C*GESMLCVVDPDISAFR	C384	1.433887636	Q06330 Q06330 Q06330 Q06330 Q06330 Q06330	
VGVGTC*GIADKPMYQYQDT SK	C214	1.4315432	O75940	O75940 Survival of motor neuron-related- splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 # P35610-3 Isoform 3 of Sterol O- acyltransferase 1 OS=Homo sapiens GN=SOAT1 # P35610-2 Isoform 2 of Sterol O- acyltransferase 1 OS=Homo sapiens GN=SOAT1 # P35610 Sterol O- acyltransferase 1 OS=Homo sapiens GN=SOAT1 PE=1 SV=3 # Q16555-2 Isoform 2 of Dihydropyrimidinase- related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase- related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
SASLDNGGC*ALTTFSVLEGE K	C27;C34;C92	1.430805809	P35610 P35610 P35610	
FQLTDC*QIYEVLSVIR	C143;C179	1.425102508	Q16555 Q16555	
GTWEELCNCS*EMENEVLK	C652	1.424725341	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # Q8NB90 Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3 #
GVLLYGPPGC*SK	C672	1.424469847	Q8NB90	

EFC*SYLQYLEYLSQNRPPN AYELFAK	C278;C261	1.424355332	O14744 O14744	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 # O14744-2 Isoform 2 of Protein arginine N- methyltransferase 5 OS=Homo sapiens GN=PRMT5 #
FASGGC*DNLIK	C233;C173;C17 3;C190;C187	1.42382	P55735 A8MXL6 P55735 A0A0C4D FR6 P55735	P55735-3 Isoform 3 of Protein SEC13 homolog OS=Homo sapiens GN=SEC13 # A8MXL6 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=1 # P55735-2 Isoform 2 of Protein SEC13 homolog OS=Homo sapiens GN=SEC13 # A0A0C4DFR6 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=1 # P55735 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3 # Q96T76-8 Isoform 5 of MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 # Q96T76 MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 # P23381 Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 # P23381-2 Isoform 2 of Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS #
LMGLLSDPELGPAAADGFSL MSDC*TDVLR	C869;M825 C848	1.4235	Q96T76 Q96T76	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # H0Y9D8 Inorganic pyrophosphatase 2# mitochondrial (Fragment) OS=Homo sapiens GN=PPA2 PE=1 SV=1 # Q9H2U2 Inorganic pyrophosphatase 2# mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2 # Q9H2U2-2 Isoform 2 of Inorganic pyrophosphatase 2# mitochondrial OS=Homo sapiens GN=PPA2 # Q13162 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 #
TDIQC*LIPCAIDQDPYFR	C305;C264	1.41763	P23381 P23381	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 # P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
LEGDLTGPSVDVEVPDVELE C*PDAK	C2162	1.41729328	Q09666	Q5JTH9 RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 # Q9Y3A3-2 Isoform 2 of MOB-like protein phocein OS=Homo sapiens GN=MOB4 # S4R3N1 Protein HSPE1-MOB4 OS=Homo sapiens GN=HSPE1-MOB4 PE=3 SV=1 # Q9Y3A3-3 Isoform 3 of MOB-like protein phocein OS=Homo sapiens GN=MOB4 # Q9Y3A3 MOB-like protein phocein OS=Homo sapiens GN=MOB4 PE=1 SV=1 # Q9Y4P1-2 Isoform 2 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B # Q9Y4P1 Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B PE=1 SV=2 # Q9Y4P1-6 Isoform 6 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B #
STNC*FGDNDPIDVCEIGSK	C140;C161;C17 6	1.415945	H0Y9D8 Q9H2U2 Q9H2U2	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 #
TREEEC*HFYAGGQVYPGEA SR	C51	1.415649647	Q13162	
ALANVNIGSLIC*NVGAGGPA PAAGAAPAGGPAPSTAAAPA EEK	C36;C61	1.415598391	P05386 P05386	
LEFSIYPAPQVSTAVVEPYNSI LTTHTTLEHSDCAFMDNEAI YDIC*R	C213;M203 C213	1.415248826	P68363 Q71U36 P68366	
GHSSDSNPAIC*R	C31	1.415083241	Q5JTH9	
HTLDGAAC*LLNSNK	C102;C170;C11 3;C134	1.413364185	Q9Y3A3 S4R3N1 Q9Y3A3 Q9Y3A3	
TSVPC*AGATAFPADSDR	C277;C189;C18 9	1.412225514	Q9Y4P1 Q9Y4P1 Q9Y4P1	
LVAFC*PFASSQVALENANAV SEGVVHEDLR	C52	1.409399564	O00567	
SGGLQTPEC*LSR	C439	1.409004194	P85037	



YKDLEQQDC*EIAQEIQEK	C85;C85	1.405970299	Q8IVM0 Q8IVM0	Q8IVM0-2 Isoform 2 of Coiled-coil domain-containing protein 50 OS=Homo sapiens GN=CCDC50 # Q8IVM0 Coiled-coil domain-containing protein 50 OS=Homo sapiens GN=CCDC50 PE=1 SV=1 #
RQSDSLVQC*GVTSPSSAEA TGK	C261	1.405649151	Q9HC52	Q9HC52 Chromobox protein homolog 8 OS=Homo sapiens GN=CBX8 PE=1 SV=3 # Q9Y4P1-2 Isoform 2 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B #
NFPAIGGTGPTSDTGWGC*M LR	C162	1.400519587	Q9Y4P1 Q9Y4P1 Q9Y4P1	Q9Y4P1 Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B PE=1 SV=2 # Q9Y4P1-6 Isoform 6 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B #
YC*AAPTEPVIHNGSQGTGTN GSEISDSYQAEYPDEYHGE YQDDYPR	C273	1.400455418	Q15417	Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 #
AQQAC*IEAK	C105;C180;C199; C127;C66	1.399464378	H3BUD0 H3BS86 Q9UNE7 Q9UNE7 H3BTA3	H3BUD0 E3 ubiquitin-protein ligase CHIP (Fragment) OS=Homo sapiens GN=STUB1 PE=1 SV=2 # H3BS86 E3 ubiquitin-protein ligase CHIP (Fragment) OS=Homo sapiens GN=STUB1 PE=1 SV=7 # Q9UNE7 E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2 # Q9UNE7-2 Isoform 2 of E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 # H3BTA3 E3 ubiquitin-protein ligase CHIP (Fragment) OS=Homo sapiens GN=STUB1 PE=1 SV=1 # Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
SC*NGPVLVGSPQGGVDIEE VAASNPELIFK	C162;C162;C162	1.398277676	Q96I99 E9PDQ8 Q96I99	O75348 V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 # P34896 Serine hydroxymethyltransferase# cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 # P34896-2 Isoform 2 of Serine hydroxymethyltransferase# cytosolic OS=Homo sapiens GN=SHMT1 # Q8TDD1 ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 # Q8TDD1-2 Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 #
GSC*STEVEKETQEK	C69	1.397786646	O75348	O75348 V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 #
LDPQC*WGVNVQPYSGSPAN FAVYTALVEPHGR	C110;C110	1.395990231	P34896 P34896	P34896 Serine hydroxymethyltransferase# cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 # P34896-2 Isoform 2 of Serine hydroxymethyltransferase# cytosolic OS=Homo sapiens GN=SHMT1 # Q8TDD1 ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 # Q8TDD1-2 Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 #
LGPGRPLPTFPTSEC*TSDVE PDTR	C73;C73	1.395451013	Q8TDD1 Q8TDD1	Q8TDD1 ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 # Q8TDD1-2 Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 #
AAQLC*GAGMAAVVDK	C838;C834;C822; C833	1.395387056	P19367 P19367 P19367 P19367	P19367-3 Isoform 3 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367 Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 # P19367-4 Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367-2 Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1 #
ENVLQYC*R	C261;C261	1.394985129	A0A087W V66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
AFQHLSEAVQAAAAEQPPS WSC*GPAAGVIDAYMTLADF CDQQLR	C3403	1.393862846	P78527	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #
NDAPEEAGEGC*VAAILGETE VQQFLR	C57	1.393460169	Q96DC7	Q96DC7 Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 PE=1 SV=2 #

C*SPTVAFVEFPSSPQLK	C1054;C669;C669;C669;C657;C1054	1.389018649	G5EA03 Q9UPQ0 Q9UPQ0 Q9UPQ0 D6RD46 Q9UPQ0 Q9UPQ0	G5EA03 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=1 # Q9UPQ0-10 Isoform 10 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0-2 Isoform 2 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=4 # D6RD46 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=1 # Q9UPQ0-4 Isoform 4 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0-3 Isoform 3 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 #
LPTDLTAC*DNR	C111;C82	1.380347275	Q96RS6 Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # Q96RS6-2 Isoform 2 of NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 #
SLHDALC*VVK	C397	1.379128491	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
AAAGELQEDSGLC*VLAR	C172	1.37747459	Q96C19	Q96C19 EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1 #
C*SWLVPSPK	C265	1.371049224	Q3SXM5	Q3SXM5 Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens GN=HSDL1 PE=1 SV=3 #
AINILLEGNSDTTTSWETVGC*K	C104	1.370668089	Q5T6F2	Q5T6F2 Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBAP2 PE=1 SV=1 #
C*TPACISFGPK	C34	1.367211092	P34932	P34932 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 #
LNNLIC*DESDVKDLAFK	C362;C361	1.36627881	Q96EB1 Q96EB1	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 #
SLC*NLEESITSAGR	C63	1.365668599	Q52LJ0	Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #
TGC*TFPEKPDFH	C353	1.36371827	P55263	P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 #
AGLGEGVPPGNYGNYGYAN SGYSAC*EEENER	C28;C28;C28;C28	1.360710896	Q68DU7 C9JTT8 O15155 O15155	Q68DU7 BET1 homolog OS=Homo sapiens GN=DKFZp781C0425 PE=1 SV=1 # C9JTT8 BET1 homolog OS=Homo sapiens GN=BET1 PE=1 SV=1 # O15155 BET1 homolog OS=Homo sapiens GN=BET1 PE=1 SV=1 # O15155-2 Isoform 2 of BET1 homolog OS=Homo sapiens GN=BET1 #



LANTC*FNEIEK	C241	1.357233497	Q9NP61	Q9NP61 ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens GN=ARFGAP3 PE=1 SV=1 #
EEADQPPSC*GPEDDAQLQL ALSLSR	C205	1.356449135	Q9Y6I3	Q9Y6I3 Epsin-1 OS=Homo sapiens GN=EPN1 PE=1 SV=2 #
C*GVPFTDLLDAAK	C230;C201;C14 9	1.355795	Q01433 H0Y360 Q01433	Q01433 AMP deaminase 2 OS=Homo sapiens GN=AMPD2 PE=1 SV=2 # H0Y360 AMP deaminase 2 (Fragment) OS=Homo sapiens GN=AMPD2 PE=1 SV=1 # Q01433-2 Isoform Ex1A-2-3 of AMP deaminase 2 OS=Homo sapiens GN=AMPD2 #
ETNDDNYGPGPSLRPPNVAC *WR	C177;C177;C17 7;C177;C177;C1 79;C179	1.351923389	Q9Y520 Q9Y520 Q9Y520 Q9Y520 Q9Y520 E7EPN9	Q9Y520-4 Isoform 4 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C # Q9Y520-6 Isoform 6 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C # Q9Y520-5 Isoform 5 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C # Q9Y520-3 Isoform 3 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C # Q9Y520 Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=4 # Q9Y520-7 Isoform 7 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C # E7EPN9 Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=1 #
SESGGLGVSMVEYVLS SSPG DSC*LR	C251;M221 C270;M221 C234;M257 C234;M238 C234 C234;M221	1.351643746	Q14671 Q14671 H0YEH2 Q14671 Q5T1Z8 Q5T1Z4	Q14671-2 Isoform 2 of Pumilio homolog 1 OS=Homo sapiens GN=PUM1 # Q14671 Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=3 # H0YEH2 Pumilio homolog 1 (Fragment) OS=Homo sapiens GN=PUM1 PE=1 SV=1 # Q14671-3 Isoform 3 of Pumilio homolog 1 OS=Homo sapiens GN=PUM1 # Q5T1Z8 Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=1 # Q5T1Z4 Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=1 #
AFVNPFPDYAAAAGALLASG AAEETGC*VRPPATTTDEPGLP FHQDGK	C49	1.351372066	Q9NS86	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 #
VIGIEC*SSISDYAVK	C73;C119;C101; C109;C95;C91	1.348874644	E9PKG1 H7C211 Q99873 Q99873 Q99873 Q99873	E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # H7C211 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 # Q99873-2 Isoform 2 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
PSASC*DTLLDDIEDIVSQEDS KPQDR	C6	1.346665345	Q5VV42	Q5VV42 Threonylcarbamoyladenosine tRNA methylthiotransferase OS=Homo sapiens GN=CDKAL1 PE=1 SV=1 #
FIC*EQDHQNFLR	C658;C614	1.346367803	Q92598 Q92598	Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 # Q9Y4P8-2 Isoform 2 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 # Q9Y4P8 WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 PE=1 SV=1 # Q9Y4P8-4 Isoform 4 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 # Q9Y4P8-6 Isoform 6 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 #
LDGSLETTNEILDSASHDC*PL VTQTYGAAAGK	C375;C393;C37 5;C393	1.344963213	Q9Y4P8 Q9Y4P8 Q9Y4P8 Q9Y4P8	Q9Y4P8-2 Isoform 2 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 PE=1 SV=1 # Q9Y4P8-4 Isoform 4 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 # Q9Y4P8-6 Isoform 6 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 #

NDTPC*GTTIGPILASR	C431;C413	1.344877779	E7ETB3 Q9ULA0	E7ETB3 Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=1 SV=2 # Q9ULA0 Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=1 SV=1 #
EALAEASAWC*YLYGTGSVA GVYLPGSR	C3821	1.343560102	Q15149	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # I3L0M9 Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # Q15370
ADDTFEALC*IEPFSSPPELPD VMKPQDSGSSANEQAVQ	C111	1.33965994	I3L0M9 Q15370 B8ZZU8	Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # B8ZZU8 Transcription elongation factor B (SIII)# polypeptide 2 (18kDa# elongin B)# isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # Q96IJ6 Mannose-1-phosphate guanylyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 # Q96IJ6-2 Isoform 2 of Mannose-1-phosphate guanylyltransferase alpha OS=Homo sapiens GN=GMPPA #
LLPAITILGC*R	C389;C442	1.337414234	Q96IJ6 Q96IJ6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 # Q01970 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 PE=1 SV=2 # Q01970-2 Isoform 2 of 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 #
FDPTQFQDC*IIQGLTETGTDL EAVAK	C35;C67;C39	1.335952654	Q7L1Q6 Q7L1Q6 Q7L1Q6	P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 # Q12982-2 Isoform 2 of BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 # Q12982 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # H7C096 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 (Fragment) OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # J3KN59 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # O00487 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 # P40763 Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 # P40763-2 Isoform Del-701 of Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 # P40763-3 Isoform 3 of Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 # P08237-3 Isoform 3 of ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM # P08237 ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 # P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
VC*TLAIIDPGDSDIIR	C92;C92	1.335819913	P62888 E5RI99	
NEANQPLC*LPALLIYTEASDY IPDDHQDYAEALINPIK	C834;C767	1.331115898	Q01970 Q01970	
NC*GCLGASPNEQLQEENL K	C32	1.331041023	P54136	
YVFNLAEALVPMYVYGIPE C*IK	C416 C295;M165 C357;M287 C173;M408	1.330262469	Q12982 Q12982 H7C096 J3KN59	
SWMEGLTLQDYSEHC*K	C238	1.328336667	O00487	
ANC*DASLIVTEELHLITFETE VYHQGLK	C426;C426;C426	1.327739209	P40763 P40763 P40763	
SSYLNIVGLVGSIDNDFC*GT DMTIGTDSALHR	C241;C170	1.327335118	P08237 P08237	
VVMALGDYMGASCHAC*IGG TNVR	C134	1.326323067	P60842	

AYHEQLSVAEITNAC*FEPAN QMVK	C295	1.320159647	Q13748 P68363 Q71U36 P68366	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
SLPSAVYC*IEDK	C674	1.319971716	O43290	O43290 U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 #
ISEVFDC*WFESGSMPLYAQV HYPFENKR	C526	1.319917181	A0A0A0M SX9 P41252	A0A0A0MSX9 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # P41252 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 #
LDINLLDNVNC*LYHGEGAQ QR	C34	1.317084152	O14980	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 #
SC*GPASQSTLGLK	C232;C115;C255;C254;C240;C256;C241;C255	1.316813131	Q9BXS6 HOYMD2 Q9BXS6 Q9BXS6 Q9BXS6 Q9BXS6 Q9BXS6	Q9BXS6-7 Isoform 7 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 # HOYMD2 Nucleolar and spindle-associated protein 1 (Fragment) OS=Homo sapiens GN=NUSAP1 PE=1 SV=1 # Q9BXS6-2 Isoform 2 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 # Q9BXS6-3 Isoform 3 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 # Q9BXS6-4 Isoform 4 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 # Q9BXS6 Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 PE=1 SV=1 # Q9BXS6-6 Isoform 6 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 # Q9BXS6-5 Isoform 5 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 #
AVC*MLSNTTAIAEAWAR	C376;C376;C310;C400;C376;C376;C376	1.315767527	Q13748 P68363 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
VLTC*TDLEQGNFFLDFENA QPTESEKEIYNQVNVVLK	C10	1.31354275	Q9NUQ9	Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 #
TIQFVDWC*PTGFK	C347;C347;C281;C417;C371;C347;C347	1.313434666	Q13748 Q9BQE3 Q9NY65 F5H5D3 C9J2C0 Q71U36 Q9NY65	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #

VEQNSEPC*AGSSSESDLQT VFK	C184;C260	1.311812982	E9PCJ7 Q8N806	E9PCJ7 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 # Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 #
IINDNATYC*R	C211	1.31077964	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 #
VELC*SFSGYK	C6;C6;C6	1.309083024	C9JNW5 C9JXB8 P83731	C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # K7EP90 RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=1 SV=1 # Q9BTD8-4 Isoform 4 of RNA-binding protein 42 OS=Homo sapiens GN=RBM42 # Q9BTD8-2 Isoform 2 of RNA-binding protein 42 OS=Homo sapiens GN=RBM42 # Q9BTD8-3 Isoform 3 of RNA-binding protein 42 OS=Homo sapiens GN=RBM42 # K7EQ03 RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=1 SV=1 # Q9BTD8 RNA- binding protein 42 OS=Homo sapiens GN=RBM42 PE=1 SV=1 #
IFC*GDLGNEVNDILAR	C363;C351;C35 5;C356;C331;C3 85	1.30801774	K7EP90 Q9BTD8 Q9BTD8 Q9BTD8 K7EQ03 Q9BTD8	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # P23381 Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 # P23381-2 Isoform 2 of Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS # P21980 Protein-glutamine gamma- glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 # P49915 GMP synthase [glutamine- hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 # O95801 Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 # P31153 S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 # P49756 RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3 # Q14116-2 Isoform 2 of Interleukin-18 OS=Homo sapiens GN=IL18 # Q14116 Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1 # Q9H6R3 Acyl-CoA synthetase short-chain family member 3# mitochondrial OS=Homo sapiens GN=ACSS3 PE=1 SV=1 # A0A0B4J1R2 Acyl-CoA synthetase short- chain family member 3# mitochondrial OS=Homo sapiens GN=ACSS3 PE=1 SV=1 # Q15022 Polycomb protein SUZ12 OS=Homo sapiens GN=SUZ12 PE=1 SV=3 #
FIC*TTSAIQNR	C20	1.306186185	P53396	
IALESEGRPEEQMESDNC*S GGDDDWTHLSSK	C331	1.3032525	Q13501	
C*ESAFLSK	C36;C36;C36	1.30324	C9JNW5 C9JXB8 P83731	
TDIQCLIPC*AIDQDPYFR	C309;C268	1.303	P23381 P23381	
C*DLELETNGR	C10	1.300879438	P21980	
TVGVQGDC*R	C523	1.298541196	P49915	
LSEAAC*EEDSASEGLGELF LDGLSTENPHGAR	C238	1.298167418	O95801	
TC*NVLVALEQQSPDIAQGVH LDR	C104	1.295014945	P31153	
ENDENC*GPTTTFVGNISEK	C83	1.294823426	P49756	
NLNDQVLFIDQGNRPLFEDM TSDSC*R	C70;M69 C74	1.293613333	Q14116 Q14116	
C*DVETLEWSK	C428;C427	1.292942703	Q9H6R3 A0A0B4J1 R2	
LQLLDGEYEVAMQEMEEC*PI SK	C325	1.29242	Q15022	

EPFDLGEPEQSNNGGFPC*TT APK	C213;C277;C22 9	1.292182904	Q99961 Q99961 Q99961	Q99961-3 Isoform 3 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 # Q99961 Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 # Q99961-2 Isoform 2 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 #
HPSIIFIDELDALC*PK	C459	1.290149983	Q8NB90	Q8NB90 Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3 #
SEVEEVDFAGWLC*K	C287;C384	1.289804165	G5E9C7 P36507	G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 #
VTDGALVVVDCVSGVC*VQT ETVLR	C136	1.289233204	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
NGLQSC*PIKEDSFLQR	C1058	1.28918641	P00533	P00533 Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 #
SEGTYC*CGPVPVR	C370	1.288718775	P21980	P21980 Protein-glutamine gamma- glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 #
AVC*MLSNTTAVAEAWAR		1.288421102		Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
VASMAQSAPSEAPSC*SPFG K	C212;M185 C196;M231 C139 C116;M128 C242;M105	1.287786808	Q00013 A8MTH1 Q00013 C9J9J4 C9JB34	Q00013-2 Isoform 2 of 55 kDa erythrocyte membrane protein OS=Homo sapiens GN=MPP1 # A8MTH1 55 kDa erythrocyte membrane protein (Fragment) OS=Homo sapiens GN=MPP1 PE=1 SV=1 # Q00013 55 kDa erythrocyte membrane protein OS=Homo sapiens GN=MPP1 PE=1 SV=2 # C9J9J4 55 kDa erythrocyte membrane protein (Fragment) OS=Homo sapiens GN=MPP1 PE=1 SV=1 # C9JB34 55 kDa erythrocyte membrane protein (Fragment) OS=Homo sapiens GN=MPP1 PE=1 SV=1 #
HISPTAPDTLGC*YPFYK	C419;C384	1.285261085	A0A087W WF6 P49005	A0A087WWF6 DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1 # P49005 DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1 # Q5R363 SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 # Q96SB4-3 Isoform 1 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 # H3BLV9 SRSF protein kinase 1 (Fragment) OS=Homo sapiens GN=SRPK1 PE=1 SV=1 # Q96SB4 SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 # Q96SB4-4 Isoform 3 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 #
AEIPC*EDEQEQEHNGLDKNK	C626;C626;C47 1;C455;C439	1.284763128	Q5R363 Q96SB4 H3BLV9 Q96SB4 Q96SB4	Q96SB4-3 Isoform 1 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 # H3BLV9 SRSF protein kinase 1 (Fragment) OS=Homo sapiens GN=SRPK1 PE=1 SV=1 # Q96SB4 SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 # Q96SB4-4 Isoform 3 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 #
DPC*AAPNEGFCASAGVQTEA GVADLTWVGER	C65	1.283211743	Q9BQA1	Q9BQA1 Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1 #
EEHLC*TQR	C270	1.280348951	J3KN67	J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 #
SSPGLSDTIFC*R	C27	1.277383248	Q9H8M7	Q9H8M7 Protein FAM188A OS=Homo sapiens GN=FAM188A PE=1 SV=1 #
SIQFVDWC*PTGFK	C347	1.276226636	P68366	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
NC*SSPEFSK	C58;C53	1.273865	B0QZ18 Q99829	B0QZ18 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # Q99829 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 #



NIDPKPC*TPR	C85;C85;C85;C85	1.272839058	K7EQ55 Q96EP5 Q96EP5 K7EK33	K7EQ55 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=2 # Q96EP5-2 Isoform 2 of DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 # Q96EP5 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=1 # K7EK33 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=2 #
LC*CPATAPQEAPAEGR	C114;C147	1.270704778	Q96B54 M0QXZ5	Q96B54 Zinc finger protein 428 OS=Homo sapiens GN=ZNF428 PE=1 SV=2 # M0QXZ5 Zinc finger protein 428 (Fragment) OS=Homo sapiens GN=ZNF428 PE=1 SV=1 #
IEEDVVVTDSGIELLTC*VPR	C403;C467	1.270103031	P12955 P12955	P12955-3 Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
HAELIASTFVDQC*K	C283	1.269466848	Q9UBB4	Q9UBB4 Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1 #
C*MPTFQFFK	C73	1.268148359	P10599	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 #
AAAPAPVSEAVC*R	C456;C491;C367;C450;C394;C290;C131;C454;C336;C373;C469;C151;C166;C160;C131;C395;C408;C394;C123;C472;C408;C386	1.267604304	P20810 P20810 P20810 P20810 E7EVY3 P20810 E7EQA0 A0A0C4D GB5 E9PDE4 E9PCH5 P20810 H0YD33 H0Y9H6 H0Y7F0 A0A0A0M R45 P20810 P20810 B7Z574 E7EQ12 P20810 E7ES10 P20810	P20810-5 Isoform 5 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-3 Isoform 3 of Calpastatin OS=Homo sapiens GN=CAST # E7EQA0 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PDE4 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PCH5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # H0YD33 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y9H6 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y7F0 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0A0MR45 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-2 Isoform 2 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E7EQ12 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # E7ES10 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST #
AGMAAVASPTGNC*DLER	C560	1.266467564	Q6P1M0	Q6P1M0 Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1 #
IHESAGLPFFEIVDAPLNIC*ESR	C155;C155	1.265170186	O95340 O95340	O95340 Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2 # O95340-2 Isoform B of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 #
SSTETC*YSAIPK	C2477	1.264748142	O75369	O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB #

IGFPETEEEELEEIASNSDC* FPSAPDVK	C353;C340	1.263121381	Q9Y3F4 Q9Y3F4	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP # Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 # Q9BX40 Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B PE=1 SV=1 # Q9BX40-2 Isoform 2 of Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B # Q5TBP9 Protein LSM14 homolog B (Fragment) OS=Homo sapiens GN=LSM14B PE=1 SV=1 #
DLAVVTQSAEAPAEEDLLGP NC*YYDK	C310;C310;C230	1.261687796	Q9BX40 Q9BX40 Q5TBP9	Q9UET6 Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens GN=FTSJ1 PE=1 SV=2 # P33316-2 Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase# mitochondrial OS=Homo sapiens GN=DUT # X6RA14 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=1 # P10768 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 # Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 # D6RD67 Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial (Fragment) OS=Homo sapiens GN=MCCC2 PE=1 SV=2 # Q9HCC0-2 Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial OS=Homo sapiens GN=MCCC2 # Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 #
IIVPFVTC*GDLSSYSDSR	C238	1.260530984	Q9UET6	Q8NF37 Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 # P32321 Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1 SV=2 # P32321-2 Isoform 2 of Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD # C9JXG8 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=2 # P43487 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # C9JJ34 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # F6WQW2 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # C9JGV6 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=7 # P43487-2 Isoform 2 of Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 #
PC*SEETPAISPSKR	C3	1.260054711	P33316	Q5T7C4 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=1 # P09429 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 # P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 # A0AVT1 Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1 #
CPALYWLSGLTC*TEQNFISK	C27;C56	1.260034903	X6RA14 P10768	
LC*SGPGIVGNLVDPSAR	C245;C245	1.258557947	Q9Y5P6 Q9Y5P6	
AATGEEVSAEDLGGADLHC* R	C42;C229;C267	1.253621979	D6RD67 Q9HCC0 Q9HCC0	
VMAEALGVSVTDYTFEDC*QL ALAEGQLR	C314	1.252778474	Q8NF37	
IVGIGYNGMPNGC*SDDVLP WR	C71 C60;M67	1.250458175	P32321 P32321	
AWVWNTHADFADEC*PKPEL LAIR	C82;C132;C132; C209;C82;C132	1.248322097	C9JXG8 P43487 C9JJ34 F6WQW2 C9JGV6 P43487	
MSSYAFFVQTC*R	C23;M13 C23	1.248136067	Q5T7C4 P09429	
HGFC*GIPITDTR	C140	1.247876153	P12268	
FSPLCQWLYLEAADIVESLGK PEC*EEFLPR	C433	1.246893333	A0AVT1	

DCIGGC*SDLVSLQQSGELLT R	C83	1.245331545	P35754	P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
DSYGMSPC*NTAVVPQGWS VEALNSPHSESFVSPEAVAE PPQPTAVPLELAK	C198;M178 C181	1.24376	E7EVA0 P27816	E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 # Q9H0C8 Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 #
C*GVTSVPDIR	C301	1.24314	Q9H0C8	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
YSYVC*PDLVK	C235	1.24254	P61158	B1AKU2 E3 ubiquitin-protein ligase XIAP (Fragment) OS=Homo sapiens GN=XIAP PE=1 SV=1 # P98170 E3 ubiquitin-protein ligase XIAP OS=Homo sapiens GN=XIAP PE=1 SV=2 #
TC*VPADINKEEEFVEEFNR	C12;C12	1.237976822	B1AKU2 P98170	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
STLTDSLVC*K	C41	1.235686744	P13639	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 #
NIC*FTVWDVGGQDR	C62	1.235396221	P18085	B7Z5P7 Leupaxin OS=Homo sapiens GN=LPXN PE=1 SV=1 # O60711-2 Isoform 2 of Leupaxin OS=Homo sapiens GN=LPXN # O60711 Leupaxin OS=Homo sapiens GN=LPXN PE=1 SV=1 #
SGLAYC*PNDYHQLFSPR	C179;C204;C19 9	1.234816449	B7Z5P7 O60711 O60711	Q13155 Aminoacyl tRNA synthase complex- interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 #
SPWLAGNELTVADVVLWSVL QQIGGC*SVTVPANVQR	C291	1.231514092	Q13155	P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 #
ISGADINSIC*QESGMLAVR	C379	1.230745288	P43686	E9PJN1 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA4 PE=1 SV=1 # O75676-2 Isoform 2 of Ribosomal protein S6 kinase alpha-4 OS=Homo sapiens GN=RPS6KA4 # O75676 Ribosomal protein S6 kinase alpha-4 OS=Homo sapiens GN=RPS6KA4 PE=1 SV=1 # A0A0A6YYC0 Ribosomal protein S6 kinase alpha-4 (Fragment) OS=Homo sapiens GN=RPS6KA4 PE=1 SV=4 #
TFSFC*GTIEYMAPEIIR	C198;C198;C19 8;C182	1.229130229	E9PJN1 O75676 O75676 A0A0A6Y YC0	O75694-2 Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 # O75694 Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 #
DNAAVDGLSLHLQDICPLLYS TDDAIC*SK	C815;C874	1.227981129	O75694 O75694	Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 #
ESESCDC*LQGFQLTHSLGG GTGSGMGTLLISK	C129	1.224624333	Q9BVA1	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 #
FQSSAVMALQEASEAYLVGL FEDTNLC*A	C111	1.224304293	Q71DI3	Q9UBS0 Ribosomal protein S6 kinase beta-2 OS=Homo sapiens GN=RPS6KB2 PE=1 SV=2 #
VDPPFRPC*LQSEEDVSQFD TR	C348	1.223461625	Q9UBS0	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB # MQQY67 Electron transfer flavoprotein subunit beta (Fragment) OS=Homo sapiens GN=ETFB PE=1 SV=1 #
FMTPVIQDNPSGWGPC*AVP EQFR	C19 C19;M5	1.219939005	O15371 O15371 O15371	P38117 P38117 MQQY67
HSMNPFCEIAVEEAVR	C133;M38 C42;M129 C42	1.21816313	P38117 P38117 MQQY67	

AHVVPC*FDASK	C1157;C1130;C1157	1.217885734	P21333 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
YFNPTGAHASGC*IGEDPQGI PNNLMPYVSQVAIGR	C196	1.217335	Q14376	Q14376 UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 # P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB # P45954 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 #
VGSFC*LSEAGAGSDSFALK	C73;C175	1.216260152	P45954 P45954	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 # P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
GNLYSFGC*PEYGQLGHNSD GK	C280	1.215936611	Q9P258	O15355 Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 # Q13418-2 Isoform 2 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK # Q13418 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 # A0A0A0MTH3 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1 # Q13418-3 Isoform 3 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK # P82932 28S ribosomal protein S6# mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 #
QLFALSC*TAEQGVLPDDL S GVIR	C96;C60;C112;C75;C112;C96	1.215848578	P04899 P04899 P04899 P04899 P04899	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # Q9Y512 Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3 #
C*SGDGVGAPR	C13	1.213386094	O15355	P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # Q9BTX1-2 Isoform 2 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 # Q9BTX1 Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 PE=1 SV=2 # Q9BTX1-5 Isoform 5 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 #
DFNEEC*PR	C178;C239;C270;C105	1.21263	Q13418 Q13418 A0A0A0MTH3 Q13418	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q92616 eIF-2-alpha kinase activator GCN1 OS=Homo sapiens GN=GCN1 PE=1 SV=6 #
EC*EGIVPVPLAEK	C105	1.210878274	P82932	
LGTLAPFC*CPWEQLTQDWE SR	C705	1.20935802	Q99575	
LVVPATQC*GSLIGK	C109	1.208041586	Q15365	
IC*DGVMQFAGIR	C457	1.206266247	Q9Y512	
TIGGGDDSFTTFFC*ETGAGK	C54	1.206183017	P68366	
MAGIFDVNTC*YGSPQSPQLI R	C468;M419 C467;M459 C428	1.199371024	Q9BTX1 Q9BTX1 Q9BTX1	
AFC*GFEDPR	C4494	1.194857646	Q15149	
VLQEALC*VISGVPGLK	C648	1.1933	Q92616	

SDGLQWSAEQPC*NPSKPK	C193;C185;C215	1.191492177	Q9NUQ6 Q9NUQ6 Q9NUQ6	Q9NUQ6-4 Isoform 4 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L # Q9NUQ6 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 # Q9NUQ6-3 Isoform 3 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L # P52564 Dual specificity mitogen-activated protein kinase kinase 6 OS=Homo sapiens GN=MAP2K6 PE=1 SV=1 # P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 # P52564-2 Isoform 2 of Dual specificity mitogen-activated protein kinase 6 OS=Homo sapiens GN=MAP2K6 # P46734-2 Isoform 1 of Dual specificity mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAP2K3 # P46734 Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 # Q9Y6E0-2 Isoform A of Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 # B4DR80 Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 # Q9Y6E0 Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 # P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 # P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 # O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 # A0A075B736 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 # Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 # Q5SQY0 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=1 # P04350 Q5JP53 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # J3KTA4 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # Q8IZ07 Ankyrin repeat domain-containing protein 13A OS=Homo sapiens GN=ANKRD13A PE=1 SV=3 #
MC*DFGISGYLVDVSAK	C178;M206 C212;M139 C196;M211 C207 C140;M177	1.190737907	P52564 P46734 P52564 P46734 P46734	
IIDLLEAAEDEIEDIQQEITVLSQ C*DSPYVTK	C77;C77;C89	1.1897051	Q9Y6E0 B4DR80 Q9Y6E0	
LPACVVDC*GTGYTK	C12	1.188306667	P61158	
THEAEIVEGENHTYC*IR	C2191;C2172;C2199	1.185725513	P21333 Q60FE5 P21333	
GTWEELC*NSCEMENEVLK	C649	1.185233584	O95573	
NMMAAC*DPR	C303;C303;C303; C266;C650;C303; C231;C303;C269; C303;C285;C303	1.185145311	Q13509 P68371 A6NNZ2 A0A075B736 36 A0A0B4J269 69 Q9BVA1 Q13509 Q3ZCM7 Q5SQY0 P04350 Q5JP53 Q9BUF5	
LIDFLEC*GK	C234;C234	1.185125514	P17844 J3KTA4	
AIQESLLTSTEGLC*PSALSET SR	C540	1.184178999	Q8IZ07	

VC*ISILHAPGDDPMGYESSA ER	C61	1.180856542	P60604 P60604	P60604-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 # P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 #
AVFPEGPC*EEPLQLR	C900;C900	1.180684143	Q96P48 Q96P48	Q96P48 Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=3 # Q96P48-3 Isoform 3 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 #
ENVPPGPEVC*ITHQEGEK	C156;C316;C316; 6;C156;C156	1.179967272	Q9UHB6 Q9UHB6 Q9UHB6 F8VQE1 Q9UHB6	Q9UHB6-2 Isoform Alpha of LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 # Q9UHB6 LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1 # Q9UHB6-4 Isoform 4 of LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 # F8VQE1 LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1 # Q9UHB6-5 Isoform 5 of LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 #
FSIQTMC*PIEGEGNIAR	C205	1.179266556	Q13155	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 #
MLPTYVC*ATPDGTEKGDFLA LDLGGTNFR	C517	1.17696	P52789	P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
VTDDLVC*LVIYK	C48	1.176824009	P49458	P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 #
METYC*SSGSTDTSVIDAVT HALTATTPYTR	C201 C288;M197	1.174646074	Q02338 E9PCG9	Q02338 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 # E9PCG9 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=1 #
MQPDQQVVINC*AIVR	C64	1.174051893	P50552	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 #
ECISIHVQQAGVQIGNAC*WE LYCLEHGIQPDGQMPSDK	C20	1.173915336	Q13748 P68363 Q71U36	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
C*ELLYEGPPDDEAAMGIK	C369	1.172997008	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
NIC*FTVWDVGGQDK	C62	1.168421968	P84085	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 #
SFGVQPC*VSTVLVEPAR	C592	1.1676	Q8TB52	Q8TB52 F-box only protein 30 OS=Homo sapiens GN=FBXO30 PE=1 SV=3 #
AAC*LLDGVVVALKK	C53	1.166284951	Q8TDX7	Q8TDX7 Serine/threonine-protein kinase Nek7 OS=Homo sapiens GN=NEK7 PE=1 SV=1 #
GEELSC*EER	C38	1.166083467	P31947	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 #

					Q8NB37-3 Isoform 3 of Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 # Q8NB37 Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 PE=1 SV=1 #
SWVFDYSYSLTGPSVC*ELVR	C118;C154;C92;C78;C154	1.16471955	Q8NB37 Q8NB37 H0YF25 H0YE25 Q8NB37		H0YF25 Parkinson disease 7 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # H0YE25 Parkinson disease 7 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # Q8NB37-2 Isoform 2 of Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # M0QYM7 Tubulin beta-4A chain (Fragment) OS=Homo sapiens GN=TUBB4A PE=1 SV=7 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDIC*FR	C193;C131 C141;C201 C211;C183 C211;C201 C211 C201	1.162574936	P68371 Q9BVA1 P04350 Q5JP53 M0QYM7 Q9BUF5		Q08J23 tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 #
YEPDSANPDALQC*PIVLCGW R	C673	1.162431752	Q08J23		Q16831 Uridine phosphorylase 1 OS=Homo sapiens GN=UPP1 PE=1 SV=1 #
IGTSGGIGLEPGTVVITEQAV DTC*FK	C162	1.162086508	Q16831		Q8WZA9 Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1 #
TDGEGEDPEC*LGEKG	C340	1.161632007	Q8WZA9		P63104 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 #
DIC*NDVLSLEK	C94	1.161358592	P63104		Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 #
VRPSTGNSASTPQSQC*LPS EIEVK	C131;C131	1.160745892	Q9UJX3 Q9UJX3		P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
IAVYSC*PFDGMITETK	C244	1.160300473	P50990		A0A0A0M QS1 Pyrraline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrraline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 # Q53H96-2 Isoform 2 of Pyrraline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL #
SDVC*TPGGTTIYGLHALEQG GLR	C247;C235;C21 5	1.159472823	A0A0A0M QS1 Q53H96 Q53H96		P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
AAAPAPEEEMDEC*EQALAA EPK	C316 C266;M313	1.159058099	P26641 P26641		O15355 Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 #
GTEAGQVGEPIPTGEAGPS C*SSASDKLPR	C241	1.1542541	O15355		P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 #
TAVC*DIPPR	C354;C354;C31 7;C354;C354;C3 20;C354;C336	1.153623333	P68371 A6NNZ2 A0A075B7 36 Q9BVA1 Q3ZCM7 Q5SQY0 P04350 Q5JP53		A0A075B736 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 # Q5SQY0 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #

HTEVPTGTC*PVDPFEAQWA ALENK	C611;C467;C60 0	1.152732504	P49757 G3V3Z8 P49757	P49757 Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=2 # G3V3Z8 Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=1 # P49757-3 Isoform 3 of Protein numb homolog OS=Homo sapiens GN=NUMB #
LVSSPCC*IVTSTYGWTANME R	C590	1.152376461	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
AIVLFTSDAC*GLSDVAHVESL QEK	C193;C326;C17 3	1.151089099	P24468 P24468 P24468	P24468-2 Isoform 2 of COUP transcription factor 2 OS=Homo sapiens GN=NR2F2 # P24468 COUP transcription factor 2 OS=Homo sapiens GN=NR2F2 PE=1 SV=1 # P24468-3 Isoform 3 of COUP transcription factor 2 OS=Homo sapiens GN=NR2F2 #
MYGISLC*QAILDETKGDYK	C324	1.150345931	P04083	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 #
AC*PRPEGLNFQDLK	C307;C227;C21 9	1.149320994	P15927 P15927 P15927	P15927-3 Isoform 3 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 # P15927-2 Isoform 2 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 # P15927 Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1 #
IEC*SDNGDGTCSVSYLPTKP GEYFVNILFEEVHIGSPFK	C1087;C1087	1.149219889	O75369 O75369	O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB #
IEC*QDNGDGGSCAVSYLPTK GEYTINILFAEAHIGSPFK	C1109	1.14921778	Q14315	Q14315 Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3 #
AAVEEGIVLGGGC*ALLR	C442	1.147630332	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
IEDIDNEDWENPQLC*SDYVK	C50;C131;C131	1.147343054	H0YMP3 O95067 H1UBN3	H0YMP3 G2/mitotic-specific cyclin-B2 OS=Homo sapiens GN=CCNB2 PE=1 SV=1 # O95067 G2/mitotic-specific cyclin-B2 OS=Homo sapiens GN=CCNB2 PE=1 SV=1 # H1UBN3 Cyclin B2 OS=Homo sapiens GN=CCNB2V PE=1 SV=1 #
PMC*VESFSDYPLGR	C390 C411;M389	1.147305929	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
SLLC*GEDEAADENPESQEM LEEQLVR	C941	1.145859456	Q9HAV4	Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 #
GYWAGLDASAQTTSHELTP NDLIGC*IIGR	C298;C302	1.14547	Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 #
AQQEQLLLQKQLQQQQQP PSQLC*TAPASSHER	C385;C296;C38 5;C527;C345;C5 27	1.141908714	Q9Y2D5 Q9Y2D5 Q9Y2D5 Q9Y2D5 C9JVY5 Q9Y2D5	Q9Y2D5 A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 PE=1 SV=3 # Q9Y2D5-7 Isoform 5 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 # Q9Y2D5-6 Isoform 4 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 # C9JVY5 A-kinase anchor protein 2 (Fragment) OS=Homo sapiens GN=AKAP2 PE=1 SV=1 # Q9Y2D5-4 Isoform 2 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 #
TDVC*VFAAQEDLETMQAF QVFNK	C96	1.141063833	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 #
VGEGPGVC*WLAPEQTAGK	C151	1.140694922	Q9H4A4	Q9H4A4 Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 #



C*DTEFPNFK	C503	1.137898448	P27694	P27694 Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2 #
CPEALFQPSFLGMESC*GIHE TTFNSIMK	C272	1.136894743	P63261	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 #
EAPDGC*PDHVLR	C98;C81;C100	1.135481859	Q9UBB6 Q9UBB6 Q9UBB6	Q9UBB6 Neurochondrin OS=Homo sapiens GN=NCDN PE=1 SV=1 # Q9UBB6-2 Isoform 2 of Neurochondrin OS=Homo sapiens GN=NCDN # Q9UBB6-3 Isoform 3 of Neurochondrin OS=Homo sapiens GN=NCDN #
STFFNVLTSQASAEENFPFC* TIDPNESRVPVPPER	C75;C55	1.135263391	J3KQ32 Q9NTK5	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 #
ADLC*SIEQELSSIGSGNSK	C94;C94	1.134113393	C9K0J5 Q70E73	C9K0J5 Ras association (RalGDS/AF-6) and pleckstrin homology domains 1# isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1 # Q70E73 Ras-associated and pleckstrin homology domains-containing protein 1 OS=Homo sapiens GN=RAPH1 PE=1 SV=3 #
LSC*QPMLSLDDFQLQPPVTF R	C105	1.130988974	O75607	O75607 Nucleoplasmin-3 OS=Homo sapiens GN=NPM3 PE=1 SV=3 #
AFQYVETHGEVC*PANWTPD SPTIKPSAASK	C229	1.130181597	P30048	P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 #
C*AAVDVEPPSK	C670	1.128049522	Q15020	Q15020 Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 #
ECISIHVGQAGVQIGNACWEL YC*LEHGIQPDGQMPSDK	C25	1.126438213	Q13748 P68363 Q9BQE3 F5H5D3 Q71U36	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 #
TQSPC*FGDDDDPAK	C256;C344;C32 4	1.125798742	Q12765 Q12765 Q12765	Q12765-3 Isoform 3 of Secernin-1 OS=Homo sapiens GN=SCRN1 # Q12765-2 Isoform 2 of Secernin-1 OS=Homo sapiens GN=SCRN1 # Q12765 Secernin-1 OS=Homo sapiens GN=SCRN1 PE=1 SV=2 #

				Q5VWV2 Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 PE=1 SV=1 # Q8TEW0-3 Isoform 3 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-8 Isoform 8 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # F5GZI3 Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 PE=1 SV=1 # Q5VWU8 Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 PE=1 SV=1 # Q8TEW0 Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 PE=1 SV=2 # Q8TEW0-4 Isoform 4 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-7 Isoform 7 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-10 Isoform 10 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-2 Isoform 2 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-5 Isoform 5 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-11 Isoform 11 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-6 Isoform 6 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q8TEW0-9 Isoform 9 of Partitioning defective 3 homolog OS=Homo sapiens GN=PAR3 # Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 # P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 # O60763 General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2 # Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 # E9PQS1 Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # E9PJU8 Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # E9PPB5 Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # Q9H0W9 Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # Q9H0W9-2 Isoform 2 of Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 # Q9H0W9- 4 Isoform 4 of Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 # A0A087WT99 Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 # P23919 Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 #
AAISDSADC*SLSPDVPVLA FQR	C746;C746;C80 3;C520;C803;C8 06;C806;C790;C 803;C803;C746; C790;C790;C79 0	1.123670977	Q5VWV2 Q8TEW0 Q8TEW0 F5GZI3 Q5VWU8 Q8TEW0 Q8TEW0 Q8TEW0 Q8TEW0 Q8TEW0 Q8TEW0 Q8TEW0 Q8TEW0 Q8TEW0	
FFACAPNYSYAALCEC*LR	C513	1.122877046	Q96RS6	
GLAPLHWADDDGNPTEQYPL NPNNGSPGGVAGICSC*DGR	C1287	1.122701433	O15067	
SGQGAFGNMC*R	C96	1.122689326	P36578	
C*QNEQLQTAVTQQVSIQQ HK	C678	1.122049714	O60763	
NEC*DPALALLSDYVLHNSNT MR	C459	1.121527889	Q13200	
SHIMPAEFSSC*PLNSDEEVN K	C207;M108 C167 C115;M160 C226;M200 C167;M219	1.12148381	E9PQS1 E9PJU8 E9PPB5 Q9H0W9 Q9H0W9 Q9H0W9 A0A087W T99	
ELDSLNNC*LGDAGILQLVES VR	C409	1.11943509	P13489	
ENFSLDWC*K	C117	1.114368859	P23919	

INEIVYFLPFC*HSELIQLVNK	C572;C527;C542;C371;C513;C577	1.113738712	Q9H078 Q9H078 Q9H078 Q9H078 Q9H078 H0YGM0	Q9H078 Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1 # Q9H078-4 Isoform 4 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-2 Isoform 2 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-5 Isoform 5 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-3 Isoform 3 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # H0YGM0 Caseinolytic peptidase B protein homolog (Fragment) OS=Homo sapiens GN=CLPB PE=1 SV=1 #
VFFVESVC*DDPDVIAANILEVK	C158;C158	1.113406506	O60825 O60825	O60825-2 Isoform 2 of 6-phosphofructo-2-kinase/fructose-2#6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 # O60825 6-phosphofructo-2-kinase/fructose-2#6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 PE=1 SV=2 # P49748-3 Isoform 3 of Very long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADVL # P49748 Very long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 # P49748-2 Isoform 2 of Very long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADVL #
ELGAFGLQVPSELGGVGLC*NTQYAR	C179;C156;C134	1.112906921	P49748 P49748 P49748	Q15646-2 Isoform p30 of 2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL # Q15646 2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL PE=1 SV=2 # Q15646-3 Isoform 3 of 2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL #
ACGGPGNFC*PSFSELQR	C188;C188;C188	1.110458409	Q15646 Q15646 Q15646	Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 #
SC*DPGLEDPCGLNR	C706	1.109285656	Q9HAV4	P04150-11 Isoform Alpha-C1 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-12 Isoform Alpha-C2 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-3 Isoform Alpha-2 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-13 Isoform Alpha-C3 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-8 Isoform Alpha-B of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150 Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 PE=1 SV=1 # G5E972 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 # P42167 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 #
QSSANLLC*FAPDLIINEQR	C537;C533;C623;C525;C596;C622	1.108062509	P04150 P04150 P04150 P04150 P04150	Q32MZ4-3 Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # Q32MZ4 Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 # Q32MZ4-2 Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 #
EMFPYEASTPTGISASC*R	C323;M348 C363	1.107391132	G5E972 P42167	O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # M0QXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 #
EIDC*LSPEAQK	C14;C14;C14	1.103291388	Q32MZ4 Q32MZ4 Q32MZ4	
QMFEPVSC*TFTYLLGDR	C34 C34;M28	1.10106948	O95571 M0QXB5	

VSDTVVEPYNATLSIHQLVEN TDETYC*IDNEALYDICFR	C201;C548;C12 9	1.100081744	Q13509 A0A0B4J2 69 Q13509	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 #
AYHEQLTVAEITNAC*FEPAN QMVK		1.099981024		Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
DTC*YSPKPSVYLSTPSSASK	C540	1.091365144	Q9Y5K6	Q9Y5K6 CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 # P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
SYC*NDQSTGDIK	C106	1.091099616	P00492	Q96L21 60S ribosomal protein L10-like OS=Homo sapiens GN=RPL10L PE=1 SV=3 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 # R4GND3 Pleckstrin homology-like domain family A member 1 OS=Homo sapiens GN=PHLDA1 PE=1 SV=1 # Q8WV24 Pleckstrin homology-like domain family A member 1 OS=Homo sapiens GN=PHLDA1 PE=1 SV=4 #
MLSC*AGADR	C105;C105	1.090864987	Q96L21 P27635	M0QZ22 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # Q9UPU9 Protein Smaug homolog 1 OS=Homo sapiens GN=SAMD4A PE=1 SV=3 # A0A087WUK6 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # A0A087WZT0 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # Q9UPU9-3 Isoform 3 of Protein Smaug homolog 1 OS=Homo sapiens GN=SAMD4A # Q5PRF9 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 #
C*CILTEEGLLIPPK	C30;C171	1.090829673	R4GND3 Q8WV24	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 # Q14738-2 Isoform Delta-2 of Serine/threonine- protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D # E9PFR3 Serine/threonine- protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D PE=1 SV=1 # Q14738 Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D PE=1 SV=1 #
GWNEC*EQTVALLSLK	C20;C20;C20;C2 0;C20;C20	1.088637871	M0QZ22 Q9UPU9 A0A087W UK6 A0A087W ZT0 Q9UPU9 Q5PRF9	Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 # O95373 Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 #
DIDFLKEEEHDC*FLEEIMTK	C173	1.087434968	P12268	
C*TAKPSSSGK	C17;C17;C17	1.082961864	Q14738 E9PFR3 Q14738	
VQYPQSQAC*K	C633	1.082384393	Q14204	
GIDQC*IPLFVEAALER	C757	1.080213555	O95373	

					Q8IWZ3 Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 # O75179-2 Isoform 2 of Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 # O75179 Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 PE=1 SV=3 # O75179-7 Isoform 7 of Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 # Q8IWZ3-4 Isoform 4 of Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 # H0YM23 Ankyrin repeat domain-containing protein 17 (Fragment) OS=Homo sapiens GN=ANKRD17 PE=1 SV=1 # E9PDP5 Ankyrin repeat and KH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 # Q8IWZ3-6 Isoform 6 of Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 # O75179-6 Isoform 6 of Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 # Q96S55 ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 PE=1 SV=2 # Q96S55-3 Isoform 3 of ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 # Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 # Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8IY67 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 # Q8IY67-2 Isoform 2 of Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 # A0A087WZ13 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 # E9PAU2 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 # P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 # P30566 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 # P37198 Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=3 # P09110 3-ketoacyl-CoA thiolase# peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 # H0Y4D4 3-ketoacyl-CoA thiolase# peroxisomal (Fragment) OS=Homo sapiens GN=ACAA1 PE=1 SV=1 # C9JDE9 3-ketoacyl-CoA thiolase# peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=1 # P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 # P48147 Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 # Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 # Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 #
LTSSVSC*ALDEAAAALTR	C181;C210;C210;C97;C181;C95;C181;C181;C210	1.079893576	Q8IWZ3 O75179 O75179 O75179 Q8IWZ3 H0YM23 E9PDP5 Q8IWZ3 O75179		
SLLETNEIPSLILWGPPGC*GK	C272;C52	1.078254512	Q96S55 Q96S55		
PGHLQEGFGC*VVTNRFDQL FDDESDPFEVLK	C11;C11;C11;C11	1.078027186	Q8NC51 Q8NC51 Q8NC51 Q8NC51		
ALSAVHSPTFCQLAC*GQDGLK	C255;C255;C255;C272	1.077928202	Q8IY67 Q8IY67 A0A087WZ13 E9PAU2		
YSNVIFLEVDVDDC*QDVASE CEVK	C62	1.077325064	P10599		
IC*LAEAFLTADTILNTLQNI SEGLVVYPK	C340	1.076840002	P30566		
DIIEHLNTSGAPADTSDPLQ QIC*K	C475	1.075925268	P37198		
DC*LIPMGITSENVAER	C177	1.075917695	P09110 H0Y4D4 C9JDE9		
AYGGS*AK	C83	1.075823333	P49207		
IC*DPYAWLEDPDSEQTK	C25	1.075361781	P48147		
NVTQIEPFC*LETDRR	C630;C594	1.071256243	Q9ULW0 Q9ULW0		

GDLNDCFIPC*TPK	C147;C203	1.070015416	P11586 F5H2F4	P11586 C-1-tetrahydrofolate synthase# cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 # F5H2F4 C-1-tetrahydrofolate synthase# cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=1 #
GC*LLYGPPGTGK	C184;C170	1.068212214	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
LFTESC*SISPK	C68;C68;C68	1.067545854	C9JXQ7 Q9Y6I9 C9JHH5	C9JXQ7 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 # Q9Y6I9 Testis- expressed sequence 264 protein OS=Homo sapiens GN=TEX264 PE=1 SV=1 # C9JHH5 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 #
FEQSDLEAFYNVITVC*GTNE VR	C306;C308	1.066801708	Q5JPI3 Q5JPI3	Q5JPI3-2 Isoform 2 of Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 # Q5JPI3 Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 PE=1 SV=1 #
MAYQEYPNSQNWPEDTNFC* FQPEQVVDPIQTDPFK	C126 C143;M108	1.064656225	E7EVA0 P27816	E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 #
C*CSGAIIVLTK	C423	1.059032846	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2
NQSFC*PTVNLDKLWTLVSE QTR	C70;C70	1.058856558	P46776 E9PLL6	# E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 #
LVDPLGEMPLAPSWEHATC* LANAEEQDMQR	C93	1.055103826	O95394 O95394 O95394	O95394-3 Isoform 2 of Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 # O95394 Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1 # O95394-4 Isoform 3 of Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 #
VWQIQSCSALTGEGVQDGM NWVC*K	C174	1.051585	P36405	P36405 ADP-ribosylation factor-like protein 3 OS=Homo sapiens GN=ARL3 PE=1 SV=2 # Q86UP2 Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1 # Q86UP2-4 Isoform 4 of Kinectin OS=Homo sapiens GN=KTN1 # B7Z6P3 Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1 # Q86UP2-3 Isoform 3 of Kinectin OS=Homo sapiens GN=KTN1 #
DC*NGDTPNLSFYR	C87	1.047914097	A0A087X0 28	A0A087X028 Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=1 # A0A0A0MR02 Voltage-dependent anion- selective channel protein 2 (Fragment)
SC*SGVEFSTSGSSNTDTGK	C47;C47	1.047881772	A0A0A0M R02 P45880	OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
EC*ELYVQK	C18	1.046625631	P10644	P10644 cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1 #
AHEILPNLVCC*SAK	C149	1.043629363	P50990	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 # A0A024R571 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=1 #
FMC*AQLPNPVLDSISIIDTPGI LSGEK	C152;M137 C138;M151 C152	1.043475928	A0A024R5 71 Q9H4M9 C9JC03	Q9H4M9 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 # C9JC03 EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=1 SV=1 #
KAEGDLGPSWVC*GFSNLES QVLEK	C184	1.043183978	Q15814	Q15814 Tubulin-specific chaperone C OS=Homo sapiens GN=TBCC PE=1 SV=2 #

LMC*PQEIVDYIADKK	C95 C140;M94	1.0426325	O14561 H3BNK3	O14561 Acyl carrier protein# mitochondrial OS=Homo sapiens GN=NDUFAB1 PE=1 SV=3 # H3BNK3 Acyl carrier protein (Fragment) OS=Homo sapiens GN=NDUFAB1 PE=1 SV=1 #
QVQSLTC*EVDALKGTNESLE R	C328	1.042452249	P08670	P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 #
ALVDGPC*TQVR	C42;C42	1.041622264	E7EPB3 P50914	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 #
EDIGVGSYSVC*K	C436	1.041068464	P51812	P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 #
AGAIAPC*EVTVPAQNTGLGP EK	C119;C99;C119	1.039645385	P05388 F8VW21 F8VU65	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # F8VW21 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # F8VU65 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #
YKDEDGDLITIFDSSDLSFAIQ C*SR	C80;C80;C80;C80; 0;C80;C80;C80; C80	1.039297996	Q05BK6 C9JUE0 Q92734 Q92734 C9JJP5 Q92734 Q92734 C9JTY3	Q05BK6 Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=1 # C9JUE0 Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=1 SV=1 # Q92734 Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2 # Q92734-3 Isoform 3 of Protein TFG OS=Homo sapiens GN=TFG # C9JJP5 Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=1 SV=1 # Q92734-2 Isoform 2 of Protein TFG OS=Homo sapiens GN=TFG # Q92734-4 Isoform 4 of Protein TFG OS=Homo sapiens GN=TFG # C9JTY3 Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=1 SV=1 #
LVVPASQC*GSLIGK	C109;C109	1.039062272	Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 #
QASLFPDEKEDNLLGTTCLIA TAVITLTFNEPSAEDSK	C651;C651	1.038030822	Q01780 Q01780	Q01780-2 Isoform 2 of Exosome component 10 OS=Homo sapiens GN=EXOSC10 # Q01780 Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 #
QALVEFEDVLGAC*NAVNYAA DNQIYIAGHPAFVNYSTSQK	C92;C151	1.037716664	M0QXS5 P14866	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
GQNGDDSSAGGDFPPPAEV EPTPEAELLAQPC*HDSEASK	C122	1.03688321	O94992	O94992 Protein HEXIM1 OS=Homo sapiens GN=HEXIM1 PE=1 SV=1 #
EENVGLHQTLTDLNELNC*I	C283;C109;C24 7	1.033114767	P67936 K7EPB9 P67936	P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 #
VAASC*GAIQYIPTELDQVR	C134	1.029662968	Q7L2H7	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #

				J3KRX5 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621-2 Isoform 2 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 # J3QLC8 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=1 # A0A087WXM6 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # A0A0A0MRF8 Protein RPL17-C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 # A0A0A6YYL6 Protein RPL17-C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 # P18621 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 # J3QQT2 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621-3 Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 #
INPYMSSPC*HIEMILTEK	C144 C144;M102 C144;M140 C134;M140 C106;M140 C106;M130	1.029652001	J3KRX5 P18621 J3QLC8 A0A087WXM6 A0A0A0MRF8 A0A0A6YYL6 P18621 J3QQT2 P18621	
VFIMDSC*DELIPEYLNfir	C366	1.027840982	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
PC*FYDIDLDTETEQVK	C896;C961;C962	1.02733	A0A087WVM4 Q6UB35 B7ZM99	A0A087WVM4 Monofunctional C1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # Q6UB35 Monofunctional C1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # B7ZM99 MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 #
IGSSLYALGTQDSTDC*K	C148;C276;C264	1.026913651	Q9UNH7 A0A0A0MRI2 Q9UNH7	Q9UNH7-2 Isoform 2 of Sorting nexin-6 OS=Homo sapiens GN=SNX6 # A0A0A0MRI2 Sorting nexin 6# isoform CRA_b OS=Homo sapiens GN=SNX6 PE=1 SV=1 # Q9UNH7 Sorting nexin-6 OS=Homo sapiens GN=SNX6 PE=1 SV=1 #
AIVDALPPPC*ESACTVPTDV DK	C270	1.026791966	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 #
LHDAIVEVVC*LLR	C483;C470;C470;C483;C483;C470	1.026442291	O00429 O00429 O00429 O00429 O00429 G8JLD5 O00429	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 # O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 # O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L #
SLHDALC*VLAQTVK	C395	1.025354327	P78371	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 #
VQTDAFVSNELDDPDDLQC* K	C486;C465	1.021078196	E7ERK9 Q9U110	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9U110 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
TC*ATDLQTK	C42	1.020801224	O95861	O95861 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1 #



SQEATEAAPSC*VGDMADTP R	C84	1.019617799	Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8	Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 #
ASFENNCEIGC*FAK	C15	1.019355784	P56537	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 #
LNPPAQLPNSEGLC*EFLEYV AESLEPPSPFELLEPPPTSGGF LR	C182;C208	1.018613675	Q66K74 Q66K74	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 #
VVNEINIEDLC*LTK	C92	1.01809589	Q8N5K1	Q8N5K1 CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 #
EQVPSLGSNVAC*GLAYTDY HK	C568	1.016599532	A1L0T0	A1L0T0 Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 #
AFAFVTFADDQIAQSLC*GED LIIK	C244;C244;C244; 4;C244;C244	1.014908648	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
IDPENAEFLTALC*ELR	C476;C428	1.014172972	Q13325 Q13325	Q13325 Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 PE=1 SV=1 # Q13325-2 Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 #
LWNTLGVK*K	C138	1.013974008	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
ISPVYHFVFTNESNETDYVPL PIIDSVEC*NK	C384;C342;C25 4	1.012719258	E9PJD7 Q6ZMK1 Q6ZMK1	E9PJD7 Cysteine and histidine-rich protein 1 OS=Homo sapiens GN=CYHR1 PE=1 SV=1 # Q6ZMK1 Cysteine and histidine-rich protein 1 OS=Homo sapiens GN=CYHR1 PE=1 SV=2 # Q6ZMK1-2 Isoform 2 of Cysteine and histidine-rich protein 1 OS=Homo sapiens GN=CYHR1 #
VAC*ITEQVLTLVNKR	C477	1.01224	P04843	P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 #
C*ANLFEALVGTK	C39	1.010698974	Q9P1F3	Q9P1F3 Costars family protein ABRACL OS=Homo sapiens GN=ABRACL PE=1 SV=1 #
SC*SGVEFSTSGHAYTDTGK	C36	1.007056504	Q9Y277	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #
SSSVTTSETQPC*TPSSSDY SDLQR	C334	1.006893716	P50552	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 #
LC*WFLDEAAAR	C237	1.004808197	O95336	O95336 6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2 #
IC*DQWDALGSLTHSR	C499	1.004678986	O43707	O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 #
C*EFQDAYVLLSEK	C237	1.00339365	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
FMADC*PHTIGVEFGTR	C40	1.002730713	P61106	P61106 Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 #
IC*DDELILIK	C357	1.000448996	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #

LC*LISTFLEDGIR	C32;C32;C32	0.996545	O15260 Q5T8U5 O15260	O15260 Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3 # Q5T8U5 Surfeit 4 OS=Homo sapiens GN=SURF4 PE=1 SV=1 # O15260-2 Isoform 2 of Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 #
AHEILPNLVC*CSAK	C148	0.989455715	P50990	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
FC*DNVWTFVLNDVEFR	C68	0.989071113	P52657	P52657 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 #
KPTDGASSNC*VTDISHLVR	C369;C710;C708	0.985798977	P49321 P49321 P49321	P49321-2 Isoform 2 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321-3 Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 #
EVYEGEVTELTTPC*ETENPM GGYGK	C141	0.985685024	Q9Y265	Q9Y265 RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 #
GAEPETGSAVSAAQC*QVGP TR	C90;C69	0.982269623	E7ERK9 Q9U110	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9U110 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
KC*GETAFIAPQCEMPIEWW CR	C81	0.982207741	E9PBS1 P22234	E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
ASC*LYGQLPK	C48	0.979725168	P09211	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 #
LSSC*DSFTSTINELNHCLSLR	C92	0.979166473	P07814	P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 #
YAGLSTC*FR	C300;C300	0.977509377	Q5T5C7 P49591	Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 #
LAPILC*DGTATFVDLVPGFR	C568	0.97594213	O43264	O43264 Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 #
NTVLC*NVVEQFLQADLAR	C70	0.974290607	Q14258	Q14258 E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 #
DTGTVHLNELGNTQNFMLLC* PR	C126	0.970951656	Q2NL82	Q2NL82 Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 #
ALNALC*DGLIDELNQALK	C62	0.969474299	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
IDLGNC*QDEK	C1247;C862;C863;C863;C786;C875;C1247	0.968533134	G5EA03 Q9UPQ0 Q9UPQ0 Q9UPQ0 D6RD46 Q9UPQ0 Q9UPQ0	G5EA03 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=1 # Q9UPQ0-10 Isoform 10 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0-2 Isoform 2 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=4 # D6RD46 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=1 # Q9UPQ0-4 Isoform 4 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0-3 Isoform 3 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 #

SGANVLICGPNGC*GK	C477	0.96835	P28288	P28288 ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1 #
IIC*SAGLSLLAEER	C195;C107	0.961433799	Q9BV86 S4R338	Q9BV86 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #
EGLLLWC*QR	C154;C154;C173;C154;C154;C161	0.961306656	P12814 P12814 O43707 P12814 P12814 P35609	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # P12814-3 Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-4 Isoform 4 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P35609 Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1 # Q06210-2 Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 # Q06210
GYDSAGVGFDDGGNDKDWEA NAC*K	C55;C55	0.95938488	Q06210 Q06210	Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 #
GPSGC*VESLEVTCT	C657	0.959000281	P47897	P47897 Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1 #
AYPVSGC*FDYLSLDPDTIHI GGR	C1079	0.95857	Q9BTC0	Q9BTC0 Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5 #
VGLPIGQGGFGC*IYLADMNS SESVGSDAPCVVK	C50	0.958546896	Q99986	Q99986 Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 # E9PKU4 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 # E9PKZ0 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 # G3V1A1 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=1 # P62917 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 #
AQLNIGNVLPVGTMPPEGTIVC *CLEEKPGDR	C114;M107 C114	0.955467288	E9PKU4 E9PKZ0 G3V1A1 P62917	Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 #
VQEAPIDEHWIIEC*NDGVFQ R	C91	0.955217956	Q14353	P63151-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A # P63151 Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1 #
SFNIVDIKPANMEELTEVITAA EFHPNSC*NTFVYSSSK	C239 C249;M222	0.954324	P63151 P63151	P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 #
C*DISLQFFLPPFSLGK	C157	0.95377732	P13010	P31946-2 Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB # P31946 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 #
IEAELQDIC*NDVLELLDKYLIP NATQPESK	C94;C96	0.953546882	P31946 P31946	P56192 Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
AEVLIVGPEDC*VVPFLTRP K	C38	0.953390357	P56192	Q00577 Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2 #
YKWC*EYGLTFTEK	C76;C76	0.951686482	A0A0A0M R02 P45880	P63208 S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2 #
AAC*EQLHQQQQQQEETAA ATLLQGEEEGEED	C292	0.951552905	Q00577	
ENQWC*EEK	C160	0.951099048	P63208	

TDVLVLSCL*DLITDVALHEVVD LFR	C106;C106;C106 6	0.951006119	Q9NR50 Q9NR50 Q9NR50	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 #
YTQQGFGNLPIC*MAK	;C841	0.944560912	P01767 A0A087W VM4 B7ZM99	P01767 Ig heavy chain V-III region BUT OS=Homo sapiens PE=1 SV=1 # A0A087WVM4 Monofunctional C-1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # B7ZM99 MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 #
IISNASC*TTNCLAPLAK	C152	0.943526579	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
LGTDESC*FNMILATR	C363;C341	0.94297607	P20073 P20073	P20073 Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 # P20073-2 Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7 #
EEDLEDKNNFGAEPHQNGE C*YPNEK	C845;C801	0.942890892	Q92598 Q92598	Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 #
TDC*SPIQFESAWALTNIASG TSEQTK	C133	0.942713116	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
SC*SPSPVSPQVQQAADTIS DSVAVPASLLGMR	C96	0.942136458	Q9NQW6	Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 #
EIFEDVIDAANC*SSADR	C379	0.941019936	A0A087X2 11	A0A087X211 Protein CIP2A OS=Homo sapiens GN=KIAA1524 PE=1 SV=1 # Q14697 Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 #
TRDGS DYEGWC*WPGSAGY PDFTNPTMR	C502	0.939880021	Q14697 Q14697	Q14697-2 Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB #
SQSPAASDC*SSSSSSASLPS SGR	C179	0.937364818	O95817	O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 #
ENSTLNC*ASFTAGIVEAVLTH SGFPAK	C139	0.935016188	Q8IUR0	Q8IUR0 Trafficking protein particle complex subunit 5 OS=Homo sapiens GN=TRAPPC5 PE=1 SV=1 #
SYESSEDC*SEAAAGSPAR	C378;C367	0.934917122	Q6P6C2 Q6P6C2	Q6P6C2 RNA demethylase ALKBH5 OS=Homo sapiens GN=ALKBH5 PE=1 SV=2 # Q6P6C2-3 Isoform 3 of RNA demethylase ALKBH5 OS=Homo sapiens GN=ALKBH5 #
VDVFREDLC*TK	C22	0.932335029	Q06323	Q06323 Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 #
LEKPNEGYLEFFVDC*SASAT PEFEGR	C85	0.932097387	Q15024	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 #
ENKPSIIFIDEIDSLC*GSR	C240	0.929015	O75351	O75351 Vacuolar protein sorting-associated protein 4B OS=Homo sapiens GN=VPS4B PE=1 SV=2 #
FGVIC*LEDLIEIAFP GK	C184	0.928760088	Q6DKI1	Q6DKI1 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 #
VTEDENDEPIEIPSEDDGTVL LSTVTAQFPGAC*GLR	C39;C39;C39;C39 9;C39	0.927414675	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #

STGVVNIPAAEC*LDEYEDDE AGQK	C173;C119	0.925981636	Q96IZ0 H0Y116	Q96IZ0 PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 # H0Y116 PRKC apoptosis WT1 regulator protein (Fragment) OS=Homo sapiens GN=PAWR PE=1 SV=1 #
INTQEPEETLDFDFC*STNVIN K	C112;C148	0.924834541	O60671 O60671	O60671-2 Isoform 2 of Cell cycle checkpoint protein RAD1 OS=Homo sapiens GN=RAD1 # O60671 Cell cycle checkpoint protein RAD1 OS=Homo sapiens GN=RAD1 PE=1 SV=1 #
SVPC*ESNEANEANEANK	C16	0.923126478	Q9NS25	Q9NS25 Sperm protein associated with the nucleus on the X chromosome B1 OS=Homo sapiens GN=SPANXB1 PE=2 SV=2 #
YGAVDPLLALLAVPDMSSLAC *GYLR	C223	0.922013432	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
WLSDEC*TNVAVNFLSR	C345;C350;C38 0	0.921777208	O75521 A0A0C4D GA2 O75521	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 #
LC*YVALDFENEMATAASSSS LEK	C219	0.921021128	P68133 P68032	P68133 Actin# alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 # P68032 Actin# alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 #
THEDLYIIPINC*DR	C104;C204	0.920487382	P22692 P22692	P22692-2 Isoform 2 of Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 # P22692 Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2 #
WTQTLSELDLAVPFC*VNFR	C188	0.919285157	Q9Y266	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 #
LNEC*VDHTPK	C192	0.918988397	P78417	P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
AEEDVEPEC*IMEK	C127	0.918923848	Q9UJU6 Q9UJU6 Q9UJU6	Q9UJU6-3 Isoform 3 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6-2 Isoform 2 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6 Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 #
VIGSGC*NLDSAR	C192;C164;C16 3	0.918638863	P00338 P07195 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
MC*LFAGFQR	C594;C575	0.9157575	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #

					H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
LC*EPEVLNSLEETYSPPFR	C177;C261;C261;C106;C224;C261;C261;C227;C261;C261;C242	0.911590759		H0YJA2 Q6PJT7 Q6PJT7 G3V5I6 Q6PJT7 G3V256 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7	
IIDINYYPVPEAC*LSNKR	C492	0.910756667	P23921		P23921 Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RPM1 PE=1 SV=1 # D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 #
NC*LTNFHGMDLTR	C59	0.909332564		D6RB09 D6RAT0 P61247 D6RG13	
YLAEVAC*GDDRK	C134	0.907912688	P27348		P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #
VDLNSNGFIC*DYELHELK	C33	0.907243004	P13797		P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
MPC*ESSPPESADTPTSTR	C1372;M1371 C1373	0.906275	A0A087W V66 P46013		A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
ICDGCIIIVDAVEGVC*PQTQA VLR	C124;C73	0.905853985		Q7Z2Z2 Q7Z2Z2	Q7Z2Z2 Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2 # Q7Z2Z2-2 Isoform 2 of Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 #
HLSSC*AAPAPLTAER	C141	0.905315039	Q6IBS0		Q6IBS0 Twinfilin-2 OS=Homo sapiens GN=TFW2 PE=1 SV=2 #
GFTDADNTWEPEENLDC*PE LIEAFLNSQK	C69	0.90376463	Q13185		Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 #
TVLCGTC*GQPADK	C479;C492;C187;C591;C591;C561	0.900540154		P02545 P02545 A0A0C4D GC5 P02545 P02545 P02545	P02545-4 Isoform 4 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-5 Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA # A0A0C4DGC5 Prelamin-A/C (Fragment) OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545-6 Isoform 6 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545-3 Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA #

YMACC*LLYR	C316;C283;C316;C316	0.897539533	P68363 A6NHL2 Q71U36 P68366	P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # Q9P0W2-2 Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B # C9J8X5 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related (Fragment) OS=Homo sapiens GN=HMG20B PE=1 SV=1 # Q9P0W2 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B PE=1 SV=1 # Q9P0W2-3 Isoform 3 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B # B5MDG7 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related (Fragment) OS=Homo sapiens GN=HMG20B PE=1 SV=2 #
GGDC*DGFSFDVPIFTEEFL DQNK	C75;C177;C177;C153;C194	0.895995245	Q9P0W2 C9J8X5 Q9P0W2 Q9P0W2 B5MDG7	Q9P0W2 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B PE=1 SV=1 # Q9P0W2-3 Isoform 3 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B # B5MDG7 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related (Fragment) OS=Homo sapiens GN=HMG20B PE=1 SV=2 #
IC*PVEFNPNFVAR	C33;C33;C33	0.895180106	Q9UI30 Q9UI30 F5GX77	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q9UI30-2 Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # G3V2E7 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # E7EVH7 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 # Q07866-8 Isoform S of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-6 Isoform N of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-5 Isoform K of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # F8W6L3 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # Q07866 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=2 # Q07866-2 Isoform C of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-7 Isoform P of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # G3V5R9 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # Q07866-10 Isoform D of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-3 Isoform G of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # G3V3H3 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # Q07866-9 Isoform I of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-4 Isoform J of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 #
LC*QENQWLRDELANTQQK	C114;C286;C114;C114;C114;C114;C114;C114;C114;C114	0.89099894	G3V2E7 E7EVH7 Q07866 Q07866 Q07866 F8W6L3 Q07866 Q07866 Q07866 G3V5R9 Q07866 Q07866 G3V3H3 Q07866 Q07866	

ASTASPC*NNNINAATAVALQ EPR	C528;C599;C60 5;C598	0.889306256	Q71RC2 Q71RC2 Q71RC2 Q71RC2	Q71RC2-6 Isoform 6 of La-related protein 4 OS=Homo sapiens GN=LARP4 # Q71RC2 La- related protein 4 OS=Homo sapiens GN=LARP4 PE=1 SV=3 # Q71RC2-4 Isoform 4 of La-related protein 4 OS=Homo sapiens GN=LARP4 # Q71RC2-3 Isoform 3 of La- related protein 4 OS=Homo sapiens GN=LARP4 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2- 2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # Q9BPZ3 Polyadenylate-binding protein- interacting protein 2 OS=Homo sapiens GN=PAIP2 PE=1 SV=1 # D6RA77 Polyadenylate-binding protein-interacting protein 2 (Fragment) OS=Homo sapiens GN=PAIP2 PE=1 SV=1 # P55884 Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 # P55884-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B # Q9UHB9 Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU # Q9UIQ6-3 Isoform 3 of Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP # Q9UIQ6-2 Isoform 2 of Leucyl- cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP # Q9UIQ6 Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP PE=1 SV=3 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # Q16643-2 Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643-3 Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643 Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 # P57772 Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC PE=1 SV=4 # P57772-2 Isoform 2 of Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC # C9J8T0 Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC PE=1 SV=1 # Q16643-2 Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643-3 Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643 Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 # Q9NQW6-2 Isoform 2 of Actin-binding protein anillin OS=Homo sapiens GN=ANLN # Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 #
YMAC*CLLYR	C315 C315;M320 C322;M313 C282;M313 C315;M280	0.887876169	Q9BQE3 A6NHL2 Q71U36 A6NHL2 P68366	
C*FQEMLEEEEEHEWFIPAR	C60	0.88526	Q9BPZ3 D6RA77	
FSHQGVQLIDFSPC*ER	C384;C384	0.883795107	P55884 P55884	
C*SLQAAAILDANDAHQTETS SSQVK	C525	0.883563981	Q9UHB9	
KAVVVC*PK	C588	0.88043091	Q00839	
EPC*LHPLEPDEVEYEPR	C16;C21;C35	0.878785	Q9UIQ6 Q9UIQ6 Q9UIQ6	
IWC*FGPDGTGPNILTDITK	C651	0.876796458	P13639	
EGTQASEGYFSQSQEEFFAQ SEELC*AK	C615;C659;C61 3	0.87605079	Q16643 Q16643 Q16643	
SSLPEFQAAPAEPEPGEPLL QVTLVDC*PGHASLIR	C93;C66;C93	0.87354	P57772 P57772 C9J8T0	
APPPVFYKNPPEIDITC*WDA DPVPEEEEGFEGGD	C634;C678;C63 2	0.87108	Q16643 Q16643 Q16643	
NNAFPC*QVNIK	C675;C712	0.870962689	Q9NQW6 Q9NQW6	



QMEKDETVSDC*SPHIANIGR	C206;C206	0.865843865	P47756 P47756	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # E5KLJ9 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # E5KLJ6 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # E5KLK1 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # E5KLJ5 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # J3KND1 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=1 # E9PRZ1 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=1 # Q96ER3 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=2 #
EGC*TVSPETISLNVK	C394;C393;C376;C430	0.86411763	E5KLJ9 E5KLJ6 E5KLK1 E5KLJ5	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 # E7ERJ7 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 # Q13310 Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1 # P11940 Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 # Q13310-3 Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 # E7EQV3 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 #
DKEEEEEVAGGDC*IGSTVYSK	C25;C25;C25	0.857629209	J3KND1 E9PRZ1 Q96ER3	Q9H223 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 # A0A087WUA5 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 # J9JIC5 Protein Njmu-R1 OS=Homo sapiens GN=C17orf75 PE=1 SV=1 # Q9HAS0 Protein Njmu-R1 OS=Homo sapiens GN=C17orf75 PE=1 SV=2 #
YWLC*AATGPSIK	C249	0.856612056	P63244	P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 # P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
GFGFVC*FSSPEEATK	C307;C339;C339;C294	0.854460889	E7ERJ7 Q13310 P11940 Q13310 E7EQV3	P59998 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 # F8WCF6 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4-TTLL3 PE=3 SV=1 # P59998-3 Isoform 3 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 #
GYDFC*QVLQWFAER	C175;C175	0.853193819	Q9H223 A0A087WUA5	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 # P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
NNMNC*EAR	C182;C182	0.853071217	J9JIC5 Q9HAS0	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
VDEFPLC*GHMVSDEYEQLS SEALEAAR	C49	0.852700586	P27635	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
WEALHAAECP*GPSLIR	C178	0.851182134	P53701	
IQFNDLQSLLC*ATLQNVLR	C585;C440	0.850952329	Q14974 Q14974	
ATLQAALC*LENFSSQVVER	C21;C21;C40	0.850692207	P59998 F8WCF6 P59998	
LVSSPC*CIVTSTYGWTANMER	C589	0.85056896	P08238	
HGLEVIYMIPIDEYC*VQQLK	C651;M521 C529	0.850177196	P07900 P07900	
TDVNKIEEFLEEVLC*PPK	C100	0.848466282	Q9Y696	
RPTEIC*ADPQFIIGGATR	C82	0.847418945	P17655	

IC*DQWDNLGALTQK	C480;C480;C480;C480	0.844869231	P12814 P12814 P12814 P12814	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-3 Isoform 3 of Alpha- actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-4 Isoform 4 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 # Q9BYG3 MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 # P17676 CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB PE=1 SV=2 # P17676-2 Isoform 2 of CCAAT/enhancer- binding protein beta OS=Homo sapiens GN=CEBPB # Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 # Q9BW85 Coiled-coil domain-containing protein 94 OS=Homo sapiens GN=CCDC94 PE=1 SV=1 # P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 # P07814 Bifunctional glutamate-proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 # P19367-3 Isoform 3 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367 Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 # P19367-4 Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367-2 Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1 # Q01813 ATP-dependent 6- phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 # Q8IYU8 Calcium uptake protein 2# mitochondrial OS=Homo sapiens GN=MICU2 PE=1 SV=2 # Q9Y2Q3-3 Isoform 3 of Glutathione S- transferase kappa 1 OS=Homo sapiens GN=GSTK1 # Q9Y2Q3 Glutathione S- transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3 # Q9Y2Q3-2 Isoform 2 of Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 # Q96T76-8 Isoform 5 of MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 # Q96T76 MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 # P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 # Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
C*LSAAEEK	C207	0.844525458	J3KN67	
TVDSQGPTPVC*TPTFLER	C237	0.843699356	Q9BYG3	
APPTAC*YAGAAPAPSQVK	C248;C225	0.84253764	P17676 P17676	
QVLMGPYNPDC*PEVGFFD VLGNDR	C129	0.838575847	Q9H3P7	
ADPDC*SNGQPQAAPTPGAP QNR	C275	0.838021351	Q9BW85	
QYDADLEQILIQWITTQC*R	C38;C59;C38	0.83710485	P37802 P37802 X6RJP6	
ERPTPSLNNNC*TTSEDSLVL YNR	C744	0.836587029	P07814	
AILQLGLNSTC*DDSILVK	C817;C813;C80 1;C812	0.834229034	P19367 P19367 P19367 P19367	
YAYLNVVGMVGSIDNDFC*GT DMTIGTDSALHR	C179	0.83312008	Q01813	
DGTVLC*ELINALYPEGQAPV KK	C63;C84;C63	0.828735	P37802 P37802 X6RJP6	
DIEDTLSGIQTAGC*GSTFFR	C144	0.828227605	Q8IYU8	
ETTEAAC*R	C164;C176;C23 2	0.828171547	Q9Y2Q3 Q9Y2Q3 Q9Y2Q3	
ELLESCCHSC*PFSSTAAAK	C771;C750	0.827202655	Q96T76 Q96T76	
GLC*AIAQAESLR	C97	0.825440454	P23396	
ADIDVSGPKVDVEC*PDVNIE GPEGK	C2806	0.824775993	Q09666	

C*TPSVISFGSK	C34;C34	0.823345678	Q92598 Q92598	Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 # E9PIR7 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 # A0A087WSY9 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=2 # Q16881 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3 # E2QRB9 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=2 # Q16881-3 Isoform 3 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-4 Isoform 4 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-6 Isoform 6 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-5 Isoform 5 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-7 Isoform 7 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-2 Isoform 2 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # F8W809 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 # A0A087WSW9 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 #
YLGIPGDKEYCISSDDLFLSLP YC*PGK	C189;C339;C339; C151;C288;C2 41;C304;C189;C 151;C233;C189; C239	0.822125	E9PIR7 A0A087W SY9 Q16881 E2QRB9 Q16881 Q16881 Q16881 Q16881 F8W809 A0A087W SW9	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 # P83881 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 # Q969Q0 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 # J3KQN4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=1 # H7BZ11 Protein RPL36A-HNRNPH2 OS=Homo sapiens GN=RPL36A-HNRNPH2 PE=3 SV=2 # HOY5B4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=2 # Q9Y2Z0-2 Isoform 2 of Protein SGT1 homolog OS=Homo sapiens GN=SUGT1 # Q9Y2Z0 Protein SGT1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3 # P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 # Q5T9A4-3 Isoform 3 of ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B # Q5T9A4 ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1 # M0QZF4 SH3KBP1-binding protein 1 (Fragment) OS=Homo sapiens GN=SHKBP1 PE=1 SV=1 # Q8TBC3 SH3KBP1-binding protein 1 OS=Homo sapiens GN=SHKBP1 PE=1 SV=2 # M0R2P6 SH3KBP1 binding protein 1# isoform CRA_c OS=Homo sapiens GN=SHKBP1 PE=1 SV=1 # M0R0S2 SH3KBP1-binding protein 1 (Fragment) OS=Homo sapiens GN=SHKBP1 PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
NC*NDFQYESK	C112	0.820872745	Q04917	
LECEVPNC*R	C77;C77;C113;C 77;C77	0.819353367	P83881 Q969Q0 J3KQN4 H7BZ11 HOY5B4	
ALEQKPDDAQYYC*QR	C49;C49	0.819300864	Q9Y2Z0 Q9Y2Z0	
SC*GSSTPDEFPTDIPGTK	C105	0.818650561	P41091	
FMLVLASNLPEQFDC*AINSR	C415;M448 C461	0.81606	Q5T9A4 Q5T9A4	
SVDGSPPTAFTVLEC*EGSR	C151;C550;C52 5;C121	0.813581947	M0QZF4 Q8TBC3 M0R2P6 M0R0S2	
SNGLGPVMSGNTAYPVISC*P PLTPDWGVQDVWSSLR	C350	0.813329215	P22234	

EQSIC*AAEEQPAEDGQGET NK	C490	0.812067083	Q9UGP8	Q9UGP8 Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2 #
AVSTGVQAGIPMPC*FTTALS FYDGYR	C409 C422;M407	0.812017228	P52209 P52209	P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6- phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
NTGIIC*TIGPASR	C49;C49	0.812015585	P14618 P14618	P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
EDLNC*QEEEDPMNK	C139	0.811768816	O75821 K7ENA8	O75821 Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 # K7ENA8 Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=1 SV=1 # Q9H6T3-2 Isoform 2 of RNA polymerase II- associated protein 3 OS=Homo sapiens GN=RPAP3 # Q9H6T3-3 Isoform 3 of RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 # Q9H6T3 RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 PE=1 SV=2 #
QDVC*QSYSEK	C485;C360;C51 9	0.807636667	Q9H6T3 Q9H6T3 Q9H6T3	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
LMWLFGC*PLLLDDVAR	C66	0.807549578	O15067	Q01813-2 Isoform 2 of ATP-dependent 6- phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP # Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # Q02809-2 Isoform 2 of Procollagen-lysine#2- oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 # Q02809 Procollagen- lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 #
EEFC*VPMVMVPATVSNNVP GSDFSIGADTALNTITDTCDR	C521;C529	0.80753	Q01813 Q01813	P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 # P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 #
VGVDYEGGGC*R	C727;C680	0.80662785	Q02809 Q02809	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
LC*ASGAGATPDTAIEEIKEK	C31;C31	0.804777724	P53384 P53384	Q9Y3Z3 Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2 #
SNELGDVGVHC*VLQGLQTP SCK	C75	0.804508058	P13489	Q9UG63-2 Isoform 2 of ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 # Q9UG63 ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2 #
ENEITGALLPC*LDESRFENL GVSSLGER	C80	0.804006667	Q9Y3Z3	Q14240-2 Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 # Q14240 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2 # E7EQG2 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=1 #
DGPC*IYNNLEFGIDLDR	C411;C411	0.802902609	Q9UG63 Q9UG63	P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha- aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 #
VILALGDYMGATCHAC*IGGT NVR	C135 C135;M128 C136;M128	0.801664488	Q14240 Q14240 E7EQG2	Q96KR1 Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 #
GSDC*GIVNVNIPTSGAEIGG AFGGEK	C450;C478	0.800387185	P49419 P49419	
AEDIKGTGC*VK	C525	0.800202322	Q96KR1	

SELEC*VTNITLANVIR	C27;C27	0.798115357	Q9Y6W5 Q9Y6W5	Q9Y6W5-2 Isoform 2 of Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 # Q9Y6W5 Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3 #
ALSGYC*GFMAANLYAR	C888	0.79802107	P53618	P53618 Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3 #
ESLNASIVDAINQAADC*WGI R	C121;C167	0.796191	A0A087W YB4 Q9UJZ1	A0A087WYB4 Stomatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 # Q9UJZ1 Stomatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 #
LHIVQVVC*K	C191	0.794947722	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
GTVLLADNVIC*PGAPDFLAH VR	C173;C223	0.792469056	P21964 P21964	P21964-2 Isoform Soluble of Catechol O-methyltransferase OS=Homo sapiens GN=COMT # P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 #
VFIMDNC*EELIPEYLNfir	C496;M371 C374	0.792416887	P07900 P07900	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
SEHGPIFFPESGQPEC*LK	C295;C324;C24 7;C323	0.788086131	Q96ME7 Q96ME7 Q96ME7 G3XAG1	Q96ME7-3 Isoform 3 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # Q96ME7 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=2 # Q96ME7-2 Isoform 2 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # G3XAG1 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=1 #
SYIEGYVPSQADVAVFEAVSS PPPADLC*HALR	C50;C50;C50	0.787643512	P24534 F2Z2G2 C9JZW3	P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 # F2Z2G2 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 # C9JZW3 Elongation factor 1-beta (Fragment) OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 #
AADC*ISEPVNR	C45	0.78713	P43304	P43304 Glycerol-3-phosphate dehydrogenase# mitochondrial OS=Homo sapiens GN=GPD2 PE=1 SV=3 #
ANC*IDSTASAEAVFASEVK	C268	0.785755056	P22087	P22087 rRNA 2'-O-methyltransferase fibrillar OS=Homo sapiens GN=FBL PE=1 SV=2 #
MLPDKDC*R	C118;C63;C80;C 80	0.78442	E9PK25 G3V1A4 P23528 E9PP50	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
YFAGNLAGGAAGATSLC*FV YPLDFAR	C129;C129;C12 9;C129	0.781787207	P12236 P12235 P05141 V9GYG0	P12236 ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 # P12235 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 # P05141 ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 # V9GYG0 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=1 #

GEFYVIEYAAC*DATYNEIVTF ER	C99;C86;C50;C1 4;C14;C99	0.780972797	P51114 B4DXZ6 E9PFF5 E7EU85 P51114 P51114	P51114-2 Isoform 2 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # B4DXZ6 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # E9PFF5 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # E7EU85 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # P51114-3 Isoform 3 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # P51114 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3 # B7Z4D2 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-4 Isoform 4 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95-3 Isoform 3 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=2 # B3KRD1 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-2 Isoform 2 of Syntabulin OS=Homo sapiens GN=SYBU # A0A0C4DG86 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-5 Isoform 5 of Syntabulin OS=Homo sapiens GN=SYBU # Q99700 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=2 # Q99700-2 Isoform 2 of Ataxin-2 OS=Homo sapiens GN=ATXN2 # Q99700-4 Isoform 4 of Ataxin-2 OS=Homo sapiens GN=ATXN2 # F8WB06 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # F8VQP2 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # V9GY86 Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # H0YH87 Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=1 SV=1 # Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 # E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # H7C2I1 Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 # Q99873-2 Isoform 2 of Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
LESLQSMEMAHSGSLRDEL C*LDFPCDSPEK	C259;C386;C38 8;C389;C183;C3 21;C394;C270	0.780086026	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	
RGPEVTSQGVQTSSPAC*K	C892;C892;C89 2;C627;C627;C7 32;C813	0.777693936	Q99700 Q99700 Q99700 F8WB06 F8VQP2 V9GY86 H0YH87	
YKVC*NYGLTFTQK	C65	0.777600368	Q9Y277	
GQLC*ELSCSTDYR	C314;C360;C34 2;C350;C336;C3 32	0.776869266	E9PKG1 H7C2I1 Q99873 Q99873 Q99873	

				E9PLU1 Mitochondrial fission regulator 1-like (Fragment) OS=Homo sapiens GN=MTFR1L PE=1 SV=1 # Q9H019-3 Isoform 3 of Mitochondrial fission regulator 1-like OS=Homo sapiens GN=MTFR1L # Q9H019-2 Isoform 2 of Mitochondrial fission regulator 1-like OS=Homo sapiens GN=MTFR1L # E9PLU1 Q9H019 Q9H019 E9PSD6 Q9H019 C9JF50 E9PRK5 E9PRW1	E9PLU1 Mitochondrial fission regulator 1-like (Fragment) OS=Homo sapiens GN=MTFR1L PE=1 SV=1 # Q9H019 Mitochondrial fission regulator 1-like OS=Homo sapiens GN=MTFR1L PE=1 SV=2 # C9JF50 Mitochondrial fission regulator 1-like (Fragment) OS=Homo sapiens GN=MTFR1L PE=1 SV=1 # E9PRK5 Mitochondrial fission regulator 1-like OS=Homo sapiens GN=MTFR1L PE=1 SV=1 # E9PRW1 Mitochondrial fission regulator 1-like (Fragment) OS=Homo sapiens GN=MTFR1L PE=1 SV=1 #
ASFETLPNISDLC*LR	C52;C52;C52;C52;C52;C52;C52;C52	0.776366031			
FLGPEIFFHPEFANPDFTQPIS EVDVEIQNC*PIDVR	C256;C307	0.775171839	B4DXW1 P61158	B4DXW1 P61158	B4DXW1 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=1 # P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
GRDDC*GTFEDTGPLLQFDY K	C268;C286	0.774744518	Q14684 Q14684	Q14684 Q14684	Q14684-2 Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B # Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 # E7EMZ9 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3 # O95359-6 Isoform 6 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # H0Y911 Transforming acidic coiled-coil-containing protein 2 (Fragment) OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359-2 Isoform 2 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # Q4VXL4 HCG41426# isoform CRA_c OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E9PBC6 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # H0YA73 Transforming acidic coiled-coil-containing protein 2 (Fragment) OS=Homo sapiens GN=TACC2 PE=1 SV=1 # D6RAA5 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359-1 Isoform 1 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # Q4VXL8 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E9PGB3 Transforming acidic coiled-coil-containing protein 2 (Fragment) OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359-3 Isoform 3 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # O95359-5 Isoform 5 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 #
LPQQSYNFDPTC*DESVPD FK	C2329;C2374;C452;C113;C78;C78;C2378;C102;C452;C452;C452;C469;C2374;C520	0.774510182		E7EMZ9 O95359 O95359 H0Y911 O95359 Q4VXL4 E9PBC6 H0YA73 D6RAA5 O95359 Q4VXL8 E9PGB3 O95359 O95359	
GNFTLPEVAEC*FDEITYVEL QKEEAQK	C629	0.772874779	Q00839	Q00839	Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #

IC*PVETLVEEAIQCAEK	C213	0.772219242	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
LLAIC*QPLTYSTR	C136;C136	0.772159788	P47893 P47888	P47893 Olfactory receptor 3A2 OS=Homo sapiens GN=OR3A2 PE=2 SV=3 # P47888 Olfactory receptor 3A3 OS=Homo sapiens GN=OR3A3 PE=2 SV=3 #
AVAGASAMFAGLQDLGVANG EDLKETLTNC*TEPLK	C71	0.771294465	A0A0X1K G71	A0A0X1KG71 Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1 #
GC*TPSGEGADSEPR	C137	0.76731	Q92917	Q92917 G patch domain and KOW motifs-containing protein OS=Homo sapiens GN=GPKOW PE=1 SV=2 #
FSNPYSIEYSELDC*EEGWTQ LK	C140	0.766837179	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
ATELFVQC*LATYSYR	C55	0.766725145	Q9NRG0	Q9NRG0 Chromatin accessibility complex protein 1 OS=Homo sapiens GN=CHRAC1 PE=1 SV=1 #
VC*NVAPIAGETK	C188;C336	0.76568	H0YG10 Q13823	H0YG10 Nucleolar GTP-binding protein 2 (Fragment) OS=Homo sapiens GN=GNL2 PE=1 SV=2 # Q13823 Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 #
VLLSICSLLC*DPNPDDPLVPE IAR	C113;C111;C111; C105;C82;C82; C111;C82;C112 ;C111	0.763242254	P61077 P61077 P61077 H9KV45 P62837 D6RAH7 A0A0A0M QU3 D6RFM0 A0A087W Y85 P62837	P61077-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # H9KV45 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 # D6RAH7 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # A0A0A0MQU3 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # D6RFM0 Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=3 SV=1 # A0A087WY85 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 #
HEC*QANGPEDLNR	C118;C135	0.76289613	P60981 P60981	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
FNLPHYEQGISQDQLIC*SLQ R	C170	0.762601238	Q96M11	Q96M11 Hydrolethal syndrome protein 1 OS=Homo sapiens GN=HYLS1 PE=1 SV=1 #
HCGYLALVTSLSC*GADWVFI PECPPDDDWEEHLR	C294;C223	0.761097722	P08237 P08237	P08237-3 Isoform 3 of ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM # P08237 ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 #
GTLTLC*PYHSDR	C779	0.760899839	Q13200	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 #
LEFSIYPAPQVSTAVVEPYNSI LTTHTTLEHSDC*AFMVDNEA IYD	C200	0.757386543	P68363 Q9BQE3 F5H5D3 Q71U36 P68366	P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #



FNPIETFLLGSC*ASDR	C367;C215	0.754655959	A0A087W T20 Q9NV06	A0A087WT20 DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13 PE=1 SV=1 # Q9NV06 DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13 PE=1 SV=2 #
LLYEALVDC*K	C175	0.753846046	Q7L2H7	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #
AKC*ELSSSVQTDINLPYLTM DSSGPK	C317	0.748228745	P38646	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 #
VPAFEGDDGFC*VFESNAIAY YVSNEELR	C68;C118	0.747030815	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
NPVSQC*MR	C50;C50;C50;C50; C50	0.746445277	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
NYLPAINGIVFLVDC*ADHSR	C102	0.743535	Q9NR31	Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 # M0R0Z6 Egl nine homolog 2 (Fragment) OS=Homo sapiens GN=EGLN2 PE=1 SV=1 # Q96KS0 Egl nine homolog 2 OS=Homo sapiens GN=EGLN2 PE=1 SV=1 # M0R035 Egl nine homolog 2 (Fragment) OS=Homo sapiens GN=EGLN2 PE=4 SV=7 # M0QXR0 Egl nine homolog 2 (Fragment) OS=Homo sapiens GN=EGLN2 PE=4 SV=1 # Q96KS0-2 Isoform p40 of Egl nine homolog 2 OS=Homo sapiens GN=EGLN2 # M0R110 Egl nine homolog 2 (Fragment) OS=Homo sapiens GN=EGLN2 PE=4 SV=1 # M0QXM8 Egl nine homolog 2 (Fragment) OS=Homo sapiens GN=EGLN2 PE=4 SV=1 # M0R1W4 Egl nine homolog 2 (Fragment) OS=Homo sapiens GN=EGLN2 PE=4 SV=1 # M0R2X9 Egl nine homolog 2 (Fragment) OS=Homo sapiens GN=EGLN2 PE=4 SV=1 #
MGVESYLPC*PLLPSYHC*PG VPSEASAGSGTTPR	C17;C42 C50 C50;C9 C42 C50;C42	0.736411147	M0R0Z6 Q96KS0 M0R035 M0QXR0 Q96KS0 M0R110 M0QXM8 M0R1W4 M0R2X9	K7EJR3 26S proteasome non-ATPase regulatory subunit 8 (Fragment) OS=Homo sapiens GN=PSMD8 PE=1 SV=7 # P48556 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2 # R4GMR5 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=1 #
GNIPAESYFFIDILLDIRDEI AGC*IEK	C211;C274;C21 1	0.734970433	K7EJR3 P48556 R4GMR5	P21796 Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 #
EHINLGC*DMDFDIAGPSIR	C127	0.734657992	P21796	P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 # P30050-2 Isoform 2 of 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 #
C*TGGEVGATSALAPK	C17;C17	0.73413935	P30050 P30050	P26196 Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 #
GNEFEDYC*LKR	C102	0.733179275	P26196	H0YMV8 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=1 SV=1 # Q71UM5 40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3 # P42677 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 #
LTEGC*SFR	C93;C77;C77	0.730086672	H0YMV8 Q71UM5 P42677	

NLSDLIDLVPVSLC*EDLLSSVD QPLK	C36;C36	0.727443255	P47756 P47756	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # P67775 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 # P62714 Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 # E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-3 Isoform 3 of Alpha- actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-4 Isoform 4 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 #
LQEVPHGPMC*DLLWSDPD DR	C196;M195 C196	0.725951437	P67775 P62714	
AC*GNFGIPCELR	C288;C288	0.72529375	E9PBS1 P22234	
MVSDINNAWGC*LEQVEKGY EEWLLNEIR	C370;M360 C370	0.724744979	P12814 P12814 P12814 P12814	
AC*ANPAAGSVILLENLR	C108	0.723991807	P00558	P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
YFTQGN*VNLTEALSLYEEQ LGR	C318	0.723563527	P52788	P52788 Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 # Q96PK6-2 Isoform 2 of RNA-binding protein 14 OS=Homo sapiens GN=RBM14 # Q96PK6 RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 # Q96PK6-5 Isoform 5 of RNA-binding protein 14 OS=Homo sapiens GN=RBM14 #
IFVGNVSAAC*TSQELR	C90;C90;C90	0.721721578	Q96PK6 Q96PK6 Q96PK6	
NIELIC*QENEGENDPVLQR	C228	0.72031348	Q15691	Q15691 Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3 # A0A087WW35 Methyltransferase-like protein 2A OS=Homo sapiens GN=METTLL2A PE=1 SV=1 # Q6P1Q9 Methyltransferase-like protein 2B OS=Homo sapiens GN=METTLL2B PE=1 SV=3 # Q6P1Q9-2 Isoform 2 of Methyltransferase-like protein 2B OS=Homo sapiens GN=METTLL2B # Q96IZ6 Methyltransferase-like protein 2A OS=Homo sapiens GN=METTLL2A PE=1 SV=5 # P51553 Isocitrate dehydrogenase [NAD] subunit gamma# mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 #
ISDLEIC*ADEFPGSSATYR	C106;C171;C10 6;C171	0.719951549	A0A087W W35 Q6P1Q9 Q6P1Q9 Q96IZ6	
HAC*VPVDFEEVHVSSNADE EDIR	C81	0.716624702	P51553	
LGVENC*YFPMFVSQSALEK	C1076	0.71643	P07814	P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 #
EALC*DPTVASR	C258	0.714720535	Q9BRX2	Q9BRX2 Protein pelota homolog OS=Homo sapiens GN=PELO PE=1 SV=2 #
ATGHSGGGC*ISQGR	C24	0.713042946	Q9HA64	Q9HA64 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 #

EGITGPPADSSKPIGPDDAID ALSSDFTC*GSPTAAGK	C302;C324;C20 0;C227;C283;C2 41;C227;C287;C 305;C241;C219	0.71058	P20810 P20810 P20810 E7EVY3 P20810 P20810 B7Z574 A0A0C4D GB5 P20810 E7ES10 P20810	P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # E7ES10 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST # P62195 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 # P62195-2 Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 # P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 # P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 # E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 # A0A0A0MTN3 Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=1 # P21266 Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3 # M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 # Q9BTT0-2 Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E # Q9BTT0 Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1 # Q9BTT0-3 Isoform 3 of Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E # O43572 A-kinase anchor protein 10# mitochondrial OS=Homo sapiens GN=AKAP10 PE=1 SV=2 # O43252 Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2 # P51858-3 Isoform 3 of Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF # P51858-2 Isoform 2 of Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF # P51858 Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1 #
FVVDVDKNIDINDVTPNC*R	C112;C104	0.710304076	P62195 P62195	
VPTANVSVVDLTC*R	C247	0.709771065	P04406	
GC*TATLGNFAK	C229	0.708418969	P15880	
ITSC*IFQLLQEAGIK	C63;C63	0.706075576	E9PBS1 P22234	
CENC*DCLQGFQLTHSLGGG TGSGMGTLLISK	C127	0.701336946	Q13509 A0A0B4J2 69 Q13509	
YTC*GEAPDYDR	C39;C39	0.700937195	A0A0A0M TN3 P21266	
LC*FSTAQHAS	C522;C581	0.70081	M0QXS5 P14866	
SLDLFNC*EITNLEDYR	C82;C123;C75	0.698916114	Q9BTT0 Q9BTT0 Q9BTT0	
SC*LDYQTQETK	C110	0.698818036	O43572	
TDSCDVNDC*VQQVVELLQE R	C212	0.698605956	O43252	
SC*VEEPEPEPEAAEGDGDK K	C124;C101;C10 8	0.697443909	P51858 P51858 P51858	

KPASFMTSIC*DER	C845	0.69610829	P53396	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 #
ISGPNPLSC*LK	C207	0.694402245	Q9BRU9	Q9BRU9 rRNA-processing protein UTP23 homolog OS=Homo sapiens GN=UTP23 PE=1 SV=2 #
C*SEGSFLLTTFPRPVTVEPM DQLDDEEGLPEK	C208	0.694280876	Q15233	Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 #
C*LEELVFGDVENDEDEDALLR	C90	0.692962658	Q9Y5J1	Q9Y5J1 U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 #
TSAPITC*ELLNK	C1999	0.691538988	Q14204	Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 #
GMYGIENEVFLSLPC*ILNAR	C294	0.691232502	P07195	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 #
ASVGFGGSC*FQK	C276	0.690883381	O60701	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 #
SVNSLDGLASVLYPGC*DTLD K	C85	0.690697607	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 #
ADTSQEIC*SPR	C1010;C1027;C1027;C66	0.690648135	P52948 P52948 P52948 H7C3P6	P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
GLC*ESVVEADLVEALEK	C84	0.686266769	B7WPG3	B7WPG3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 #
VYQPVSC*PLSDLSENVESVV NEEK	C566;C506;C251;C374	0.684864954	Q99590 A0A0A0M TP7 Q99590 F8VXG7	Q99590 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 # A0A0A0MTP7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 # Q99590-2 Isoform 2 of Protein SCAF11 OS=Homo sapiens GN=SCAF11 # F8VXG7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 #
AQNTWGC*GNSLR	C423;C410;C148;C522;C522;C522;C441	0.68319404	P02545 P02545 A0A0C4D GC5 P02545 P02545 P02545 P02545 Q5TCI8	P02545-5 Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-4 Isoform 4 of Prelamin-A/C OS=Homo sapiens GN=LMNA # A0A0C4DGC5 Prelamin-A/C (Fragment) OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545-6 Isoform 6 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-2 Isoform C of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545-3 Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA # Q5TCI8 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 #
ELEAVC*QDVLSLLDNYLIK	C97	0.681818784	P61981	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 #
VAWSPC*GNYLASASFDATT CIWK	C72	0.680767863	O76071	O76071 Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens GN=CIAO1 PE=1 SV=1 #
HEASDFPC*R	C32	0.676666269	P18031	P18031 Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 #
LC*YVALDFEQEMATAASSSS LEK	C217	0.673919743	P63261 Q6S8J3	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 #
IYGETPEAC*R	C282	0.672687479	P51116	P51116 Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 #

GNHEC*ASINR	C138;C126;C127	0.670738448	P62136 P62140 P62136	P62136-2 Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA # P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 # G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 #
LC*DFGVSGQLIDSMANSFVG TR	C114	0.670204254	G5E9C7 Q02750 Q02750 P36507	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 # O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 # O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L #
YIETSELC*GGAR	C374;C361;C361;C361;C374;C361	0.668848627	O00429 O00429 O00429 O00429 O00429 G8JLD5 O00429	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 # P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 # A0A0G2JL1 WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=1 SV=1 # H0Y6G3 WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=1 SV=1 # O15213 WD repeat-containing protein 46 OS=Homo sapiens GN=WDR46 PE=1 SV=3 # A0A140T9L0 WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=1 SV=1 #
GVLLYGPPGC*GK	C137	0.667757826	Q8NBU5	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 #
ETVYC*LNDDDETEVLKEDIQ GFR	C296	0.666422676	P13010	
IC*QADIVEAVDIASAAK	C107;C107;C172;C107	0.666335546	A0A0G2JJ L1 H0Y6G3 O15213 A0A140T9 L0	
ISSINSISALC*EATGADVEEV ATAIGMDQR C*SDNTEVEVSNLENKQPVE STSAK	C241  C71	0.666224979  0.66415	O60701  Q9NQW6	

AEPYC*SVLPGFTFIQHLPLSER	C291;C391;C291;C302;C240;C291;C391	0.657664557	M0QYZ0 Q9BUJ2 Q9BUJ2 B7Z4B8 M0R3F1 A0A0A0MRA5 Q9BUJ2	M0QYZ0 Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Fragment) OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=1 # Q9BUJ2 Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2 # Q9BUJ2-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=1 # B7Z4B8 Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=1 # M0R3F1 Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Fragment) OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=1 # A0A0A0MRA5 Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=1 # Q9BUJ2-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 #
SPGVVISDDEPGYDLDFC*IPNHYAEDLER	C23	0.656765396	P00492	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
TC*FISCVASGQRPHLCCISHGLASFLESVWFHC*LS	C185 C154	0.654414108	B4DVA9	B4DVA9 Protein O-glucosyltransferase 1 OS=Homo sapiens GN=POGLUT1 PE=1 SV=1 #
NHLLPDIVTC*VQSSR	C184	0.650315227	Q9BSD7	Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 #
C*PFTGNVSIR	C60	0.650284043	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
LICC*DILDVLDKHLIPAANTGESK	C98	0.648989892	P62258	P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 #
QYVDGDQCESNPCLNGGSC	C117	0.64624	P00740	P00740 Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2 #
KDDINSYEC*WCPFGFEGK	C283	0.64501725	Q96A49	Q96A49 Synapse-associated protein 1 OS=Homo sapiens GN=SYAP1 PE=1 SV=1 #
TQEDEEEISTSPGVSEFVSDA	C358	0.643878682	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
FDAC*NLNQEDLR				O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 #
AEQSDVANAVLDGADC*IMLSGETAK				Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 #
C*YVQPQWVFDVSVNAR	C391;C386	0.642331225	O00541 O00541	
AHTVLAASC*AR	C104	0.640264534	Q8WUY1	Q8WUY1 Protein THEM6 OS=Homo sapiens GN=THEM6 PE=1 SV=2 #
C*LAQEVNIPDWIVDLR	C140;C140	0.638455654	Q9Y4W2 Q9Y4W2	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 # Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L #
IYHPNINSNGSIC*LDILR	C85	0.638256232	P62837	P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 #
VPLASQGLGPGSTVLLVVDK	C78;C70;C70	0.637711947	P05161 A0A096LNZ9 A0A096LPJ4	P05161 Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5 # A0A096LNZ9 Ubiquitin-like protein ISG15 (Fragment) OS=Homo sapiens GN=ISG15 PE=1 SV=5 # A0A096LPJ4 Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=1 #
C*DEPLSILVR				
TYSHLNIAGLVGSIDNDFC*GTDMTIGTDSALHR	C170	0.632925274	P17858	P17858 ATP-dependent 6-phosphofructokinase# liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 #
SIKDTIC*NQDER	C462;C456;C509	0.632313465	Q9ULV4 Q9ULV4 Q9ULV4	Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C #

GYEVIYLTEPVDEYC*IQUALPE FDGKR	C576	0.631316667	P14625	P14625 Endoplasmic OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 #
EGTDSSQGIPQLVSNISAC*Q VIAEAVR	C29	0.626170559	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
LTESPC*ALVASQYGWSGNM ER	C645	0.62224861	P14625	P14625 Endoplasmic OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 #
ETGANLAIC*QWGFDEANH LLLQNNLPAVR	C281;C264;C30 2	0.618066176	E9PCA1 B7ZAR1 P48643	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 #
VADSSPFALELLISDDC*FVLD NGLCGK	C37;C267;C282	0.615133871	H7C0X8 P40121 P40121	H7C0X8 Macrophage-capping protein (Fragment) OS=Homo sapiens GN=CAPG PE=1 SV=1 # P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage- capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 #
EQHGVAASC*LEDLR	C38;C38;C38	0.61271	O00273 K7ERT1 O00273	O00273-2 Isoform DFF35 of DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA # K7ERT1 DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1 # O00273 DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1 #
FSGDLDDQTC*R	C245	0.610334446	P05455	P05455 Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 #
LC*SLLDSEYNTCEGAFGAL QK	C142;C134	0.609406095	Q92973 Q92973	Q92973 Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 # Q92973-2 Isoform 2 of Transportin-1 OS=Homo sapiens GN=TNPO1 #
LNGGLGTSMGC*K	C112;C132;C12 3;C123	0.606195114	Q16851 E7EUC7 A0A087W YS1 Q16851	Q16851-2 Isoform 2 of UTP--glucose-1- phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 # E7EUC7 UTP--glucose- 1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=1 # A0A087WYS1 UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=1 # Q16851 UTP-- glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 #
IPDIVLWPTC*HDDVVK	C214	0.60619037	O00116	O00116 Alkylidihydroxyacetonephosphate synthase# peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1 #
FPEELTQTFMSC*NLITGMFQ R	C389 C339;M387	0.605096224	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
IGEGLDQALPC*LTELILTNS LVELGDLPLASLK	C89;C89	0.603930496	P09661 H0YKK0	P09661 U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 # H0YKK0 Small nuclear ribonucleoprotein polypeptide A# isoform CRA_a OS=Homo sapiens GN=SNRPA1 PE=1 SV=1 #
LNISFPATGC*QK	C12	0.603764319	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
LNLSGVNLPGLVQQGC*VSA K	C1097;C1045	0.601829495	C9K0J5 Q70E73	C9K0J5 Ras association (RalGDS/AF-6) and pleckstrin homology domains 1# isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1 # Q70E73 Ras-associated and pleckstrin homology domains-containing protein 1 OS=Homo sapiens GN=RAPH1 PE=1 SV=3 #
EAVFPFQPGSVAEVC*ITFDQ ANLTVK	C89	0.599258714	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 #
AVDGEGAPAPSSGEPAEDE GPTDTAEAGSDPQAEQLLEE QVPC*GTAHEK	C631	0.596173999	O43823	O43823 A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1 #

WNTDNTLGTEIAIEDQIC*QGLK	C103;C103	0.591823645	A0A0A0MR02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
LVTSPCC*IVTSTYGWTANMER	C720	0.59062	P07900 P07900	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
DVAWAPSIGLPTSTIASC*SQDGR	C280;C220;C237;C234	0.587257992	P55735 P55735 A0A0C4DFR6 P55735	P55735-3 Isoform 3 of Protein SEC13 homolog OS=Homo sapiens GN=SEC13 # P55735-2 Isoform 2 of Protein SEC13 homolog OS=Homo sapiens GN=SEC13 # A0A0C4DFR6 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=1 # P55735 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3 #
QGAESDQAEPIIC*SSGAEAPANSLPSK	C283	0.584473089	Q7Z434	Q7Z434 Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2 #
VC*NFLASQVFPFSR	C205;C214	0.584433169	Q99714 Q99714	Q99714-2 Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 # Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 #
IEYNDQNDGSC*DVK	C604	0.5816	O75369	O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB #
GNSPPSSGEAC*R	C194	0.578491996	P41227	P41227 N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1 #
NTPSFLIAC*NK	C179	0.577946878	Q9Y5M8	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 #
NAEDC*LYELPENIR	C70;C145	0.576488225	A0A087X2F5 Q9NZ63	A0A087X2F5 Uncharacterized protein C9orf78 OS=Homo sapiens GN=C9orf78 PE=1 SV=1 # Q9NZ63 Uncharacterized protein C9orf78 OS=Homo sapiens GN=C9orf78 PE=1 SV=1 #
GFEVVMTEPIDEYC*VQQLK	C521	0.576070001	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
IIPGFMC*QGGDFTR	C62 C62;M61	0.574194073	F8WE65 C9J5S7 P62937	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 # C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 # P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #
NESC*SENYTTDFIYQLYSEEK	C641	0.573769408	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
DINAYNC*EEPTEK	C91	0.571068177	P30041	P30041 Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 #
WAELLPLLQQC*QVVR	C30	0.570751194	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
NFEATLGWLQEHAC*SR	C519;C573	0.56905875	Q9P2J5 Q9P2J5	Q9P2J5-2 Isoform 2 of Leucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=LARS # Q9P2J5 Leucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 #
VNQAIWLLC*TGAR	C155;C176;C155	0.567571956	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
LQEALDAEMLEDEAGGGGAGPGGAC*K	C57	0.55581923	Q1KMD3	Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #
LIC*CDILDVLDKHLIPAANTGESK	C97	0.546998892	P62258	P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 #



FRWDFAAEPEDC*APVVVEL PEGIEMG	C370	0.544142142	Q9Y312	Q9Y312 Protein AAR2 homolog OS=Homo sapiens GN=AAR2 PE=1 SV=2 #
C*PEALFQPSFLGMESCGIHE TTFNSIMK	C257	0.543623443	P63261 P60709	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #
DVQIGDIVTVGEC*RPLSK	C131	0.542739632	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
YADLTEDQLPSC*ESLKDTIA R	C153	0.54070076	P18669	P18669 Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 #
ATDYPC*LLILDQPNEFETLR	C145	0.540404679	Q9NVG8	Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
TATAVAHC*K	C25;C25	0.540275864	M0R210 P62249	M0R210 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 # P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 #
LLC*GLLAER	C81	0.53913	P14174	P14174 Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 #
YLLQYQEPIPCQLVTALC*DI K	C115;C115;C115 5	0.538776484	H0YL69 P25789 H0YMZ1	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
GLYGIKDDVFLSVPC*ILGQN GISDLVK	C322;C293	0.538618749	P00338 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
VGTGEPC*DWVGDEGAGH FVK	C171;C158	0.538544943	P52209 P52209	P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
KAQC*PIVER	C66;C87;C66	0.536426667	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
DTIVLLC*KPEPELNAAIPSAN PAK	C529;C524	0.535712953	Q8WUM4 Q8WUM4	Q8WUM4-2 Isoform 2 of Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP # Q8WUM4 Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 #
IIDLEEADEIEDIQQEITVLSQ C*DSSYVTK	C77;C77;C77;C7 7	0.534047346	B4E0Y9 Q9P289 Q8NBY1 Q9P289	B4E0Y9 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 # Q9P289-3 Isoform 3 of Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 # Q8NBY1 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 # Q9P289 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=2 #
DTC*SYVNVEDVSGAISHLSL GEIPAMAQPFVSSEER	C271	0.532946399	P46976	P46976-2 Isoform GN-1 of Glycogenin-1 OS=Homo sapiens GN=GYG1 #
C*QPKPSEEAPK	C116	0.532555	Q9H6F5	Q9H6F5 Coiled-coil domain-containing protein 86 OS=Homo sapiens GN=CCDC86 PE=1 SV=1 #

STSQGFC*FNILCVGETGIGK	C33;C41;C51;C41;C41	0.531611595	D6RDU5 D6RGI3 Q9NVA2 Q9NVA2 D6RER5	D6RDU5 Septin-11 (Fragment) OS=Homo sapiens GN=SEPT11 PE=1 SV=1 # D6RGI3 Septin 11# isoform CRA_b OS=Homo sapiens GN=SEPT11 PE=1 SV=1 # Q9NVA2-2 Isoform 2 of Septin-11 OS=Homo sapiens GN=SEPT11 # Q9NVA2 Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 # D6RER5 Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=1 #
IC*ELLPEAAINDVYLAPLLQC LIEGLSAEPR	C436;C291	0.530701622	Q14974 Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
VGIGPGSVC*TTR	C186;C204;C204	0.528438997	Q9P2T1 H0YNJ6 Q9P2T1	Q9P2T1 GMP reductase 2 OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # H0YNJ6 GMP reductase OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # Q9P2T1-2 Isoform 2 of GMP reductase 2 OS=Homo sapiens GN=GMMPR2 #
ADIIHAC*DIVEDAAIAYGYNNI QMTLPK	C362	0.523052125	Q9NSD9	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 #
VFDPSC*GLPYWYWNADTDLV SWLSPHDPNSVVTK	C60;C60;C49;C60;C60;C60;C60	0.522686707	O60828 O60828 H7C053 O60828 C9JQA1 O60828 O60828 O60828	O60828-2 Isoform 2 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828 Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # H7C053 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # O60828-3 Isoform 3 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # C9JQA1 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # O60828-7 Isoform 7 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828-6 Isoform 6 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828-4 Isoform 4 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 #
EC*LPLIIFLR	C41	0.514614957	P62701	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 #
ECEHCDC*LQGFQLTHSLGG GTGSGMGTLISK	C129	0.51387	Q9BUF5	Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
EKIEAELQDIC*NDVLELLDK	C94;C96	0.509283078	P31946 P31946	P31946-2 Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB # P31946 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 #
LLDLVQQSC*NYK	C34;C30	0.50731139	B1AHD1 P55769	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #
TGQATVASGIPAGWMGLDC* GPSSKK	C316	0.506605	P00558	P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
IEGC*IIGFDEYMNLVLDAAEEI HSK	C6	0.502275861	A6NHK2 P62304	A6NHK2 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P62304 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 #
C*SLPAEEDSVLEK	C652;C635	0.50041	E7EVA0 P27816	E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 #
VIEINPYLLGTMAGGAADC*S FWER	C111	0.498092364	P28074	P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #
NAFAC*FDEEATGTIQEDYLR	C108;C114;C109	0.495992608	P19105 J3QRS3 O14950	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 # J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 # O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 #

KITAFVPNDGC*LNFIENDEV LVAGFGR	C90	0.495499091	P62266	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 #
SGETEDTFIADLVVGLC*TGQIK	C389	0.494497733	P06733	P06733 Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 #
APPPSLTDC*IGTVDSR	C20;C20	0.49371818	Q9NZZ3 Q9NZZ3	Q9NZZ3 Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1 # Q9NZZ3-2 Isoform 2 of Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 #
YSEEANLIEEC*EQAER	C131	0.493373602	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 #
DEFTNTC*PSDKEVEIAYSDV AK	C234	0.491053153	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
GC*IVDANLSVLNLVIVK	C100	0.483816354	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
YAEYFLRPMLQYVC*DNSPE VR	C915 C933;M910	0.482375	O00410 O00410	O00410-3 Isoform 3 of Importin-5 OS=Homo sapiens GN=IPO5 # O00410 Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 #
GIFPVLC*KDPVQEAWAEDVD LR	C474	0.479263183	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
FQYEC*GNYSGAELYFFR	C141	0.477853377	P60228	P60228 Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 #
TDDYLDQPC*YETINR	C202	0.467926277	P50395	P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 #
VETELQGVC*DTVLGLLDSHLIK	C96	0.465576365	P31947	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 #
EAGVGNGTC*APVR	C37	0.463312274	Q96C86	Q96C86 m7GpppX diphosphatase OS=Homo sapiens GN=DCPS PE=1 SV=2 #
FSPNSSNPIIVSC*GWDK	C168	0.453543333	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
AEPQPC*TSLAWSADGQTLF AGYTDNLVR	C286	0.451945272	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
DFTPVC*TTTELGR	C47	0.45179656	P30041	P30041 Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 #
LADQC*TGLQGFLVFHSGGG GTGSGFTSLLMER	C129	0.450501857	Q9BQE3 Q71U36	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 #
TEGGGSEAPLC*PGPPAGEE PAISEAAPEAGAPTSASGLNG HPTLSGGGDQR	C2243;C1098	0.44992644	E7EVA0 P27816	E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 #
NVC*LPPEMEVALTEDQVPAL K	C552;C535	0.441014829	E7EVA0 P27816	E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 #
ALANSLAC*QGK	C339;C393	0.437032637	P04075 P04075	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA #
NC*IVLIDSTPYR	C100;C80	0.430190417	P62241 Q5JR95	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 # Q5JR95 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=1 #
AC*YLSINPQKDETELEK	C222;C222	0.4286	P61163 R4GMT0	P61163 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 # R4GMT0 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 #

IAAESSENVDC*PENPK	C588;C644;C620	0.424264439	Q32MZ4 Q32MZ4 Q32MZ4	Q32MZ4-3 Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # Q32MZ4 Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 # Q32MZ4-2 Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # P60484-2 Isoform alpha of Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN # P60484 Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # A0A0U1RR63 Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # Q8TE73 Dynein heavy chain 5# axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3 # Q969U6 F-box/WD repeat-containing protein 5 OS=Homo sapiens GN=FBXW5 PE=1 SV=1 # Q969U6-2 Isoform 2 of F-box/WD repeat-containing protein 5 OS=Homo sapiens GN=FBXW5 # A0A096LNM2 F-box/WD repeat-containing protein 5 (Fragment) OS=Homo sapiens GN=FBXW5 PE=1 SV=1 # O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
PFC*EDLDQWLSEDDNHVAAI HC*KAGK	C124;C278 C297 C297;C105 C278	0.423300197	P60484 P60484 A0A0U1R R63	
EPTDYLTLANNPETLGKIEDC* MK	C256	0.423273362	Q8TE73	
FDSPDLLLEAGDPATSPC*R	C277;C277;C93	0.418473861	Q969U6 Q969U6 A0A096LNM M2	
EEFASTC*PDDEEIELAYEQV AK	C223	0.417651215	O00299	
LCLNIC*VGESGDR	C25;C23;C24	0.41752	P62913 Q5VVC8 P62913	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 # Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 # P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 # E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 # A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 # Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL #
AVLFC*LSEDKK	C77;C22;C39;C39	0.416829956	E9PK25 G3V1A4 P23528 E9PP50	
AATMSAVEAATC*R	C278;M258 C246 C266;M238	0.415288088	A0A0A0M QS1 Q53H96 Q53H96	
C*DENILWLDYK	C152;C152	0.414261022	P14618 P14618	P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
FTLDC*THPVEDGIMDAANFE QFLQER	C25	0.407	P35268	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 # H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
YLLQYQEPIPC*EQLVTALCDI K	C107;C107;C107	0.400020312	H0YL69 P25789 H0YMZ1	
LNC*FLEQLDK	C911	0.3971	P52732	P52732 Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2 #

KTPC*GEGSK	C70;C70	0.394305881	P60866 P60866	P60866 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 # P60866-2 Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 #
EDPTVSALLTSEKDWQGFLE LYLQNSPEAC*DYGL	C237	0.391926844	P78417	P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
HTGCC*GDNDPIDVCEIGSK	C114	0.379892336	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 #
ALLVTASQC*QQPAENK	C93;C92	0.379130851	Q01518 Q01518	Q01518 Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 # Q01518-2 Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 #
C*GNQAAIMELDDTLK	C269	0.377815	P67775 P62714	P67775 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 # P62714 Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 #
ILYSQC*GDVMR	C33	0.377108715	G8JLA2 P60660	G8JLA2 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660-2 Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 #
SEPAEPC*IGSK	C105;C155;C145;C155	0.376075	Q96F24 Q96F24 Q96F24 A0A087W UL7	Q96F24 Nuclear receptor-binding factor 2 OS=Homo sapiens GN=NRBF2 # Q96F24 Nuclear receptor-binding factor 2 OS=Homo sapiens GN=NRBF2 PE=1 SV=1 # Q96F24-3 Isoform 3 of Nuclear receptor-binding factor 2 OS=Homo sapiens GN=NRBF2 # A0A087WUL7 Nuclear receptor-binding factor 2 OS=Homo sapiens GN=NRBF2 PE=1 SV=1 #
VLNEEC*DQNWYK	C32;C32	0.375587806	P62993 P62993	P62993 Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1 # P62993-2 Isoform 2 of Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 #
C*HDYYTTEFLYNLYSSEGK	C630	0.370689444	P17858	P17858 ATP-dependent 6-phosphofructokinase# liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 #
TLPTLQELHLSDNLLGDAGLQ LLCEGLDPQC*R	C142	0.366584076	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
TIAEC*LADELINAAK	C172;C193;C172	0.361790029	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
LEQVMAGATLNQMLWC*R	C310	0.360003705	Q9UL42	Q9UL42 Paraneoplastic antigen Ma2 OS=Homo sapiens GN=PNMA2 PE=1 SV=2 #
AVLLVGLC*DSGK	C73	0.358355109	Q9Y5M8	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 #
LNEDMAC*SVAGITSDANVLT NELR	C74;M72 C74	0.355642843	H0YL69 P25789 H0YMZ1	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
VLSNVNLPADLDLVC*NAEWW STK	C320;C289	0.353735215	Q8N159 K7EK11	Q8N159 N-acetylglutamate synthase# mitochondrial OS=Homo sapiens GN=NAGS PE=1 SV=1 # K7EK11 N-acetylglutamate synthase# mitochondrial (Fragment) OS=Homo sapiens GN=NAGS PE=1 SV=1 #

C*SEGVFLLTTTPRPVIVEPLE QLDDEDGLPEK	C431;C431	0.34717	P23246 P23246	P23246-2 Isoform Short of Splicing factor# proline- and glutamine-rich OS=Homo sapiens GN=SFPQ # P23246 Splicing factor# proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 #
YVLC*TAPR	C370	0.345999831	J3KQ69	J3KQ69 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=2 #
FLDGNELTLADC*NLLPK	C178	0.320564505	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
VTVAGLAGKDPVQC*SR	C46;C46	0.318545424	Q99497 K7ELW0	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 # K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 #
YEAAFPLSPC*GR	C143;C98	0.318466745	H0YF29 Q6P1X6	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 # Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 #
GDLENAFLNLVQC*IQNKPLY FADR	C262	0.318043873	P07355	P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 #
LVTSPC*CIVTSTYGW TANME R	C719	0.315952954	P07900 P07900	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
LNLPIIIGLAPLC*ENMPGSK	C335	0.314270084	P28838 P28838	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 #
LC*PGGQLPFLLYGTEVHTDT NK	C59	0.309830722	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
GLGTDEDSLIEIC*SR	C151;C133	0.30093129	P07355 P07355	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 #
MGMAC*LTMTMEGTTSTSSI YQNGDISGNANSMK	C5	0.298010662	O60674	O60674 Tyrosine-protein kinase JAK2 OS=Homo sapiens GN=JAK2 PE=1 SV=2 #
LGTVYC*QASFPGANIIGNK	C217;C213;C30 2;C205;C276;C3 02	0.296885228	P04150 P04150 P04150 P04150 P04150 P04150	P04150-11 Isoform Alpha-C1 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-12 Isoform Alpha-C2 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-3 Isoform Alpha-2 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-13 Isoform Alpha-C3 of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150-8 Isoform Alpha-B of Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 # P04150 Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 PE=1 SV=1 #
KNPFGLVPVLENSQGQLIYES AITC*EYLDEAYPGK	C62;C90	0.291057499	P78417 P78417	P78417-3 Isoform 3 of Glutathione S- transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S- transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
DPRVLILDEATSALDVQC*EQ AK	C641;C641	0.288474666	Q03519 A0A140T9 S0	Q03519-2 Isoform 2 of Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 # A0A140T9S0 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 #
C*QPVFSFGNSEQTKDENSS K	C1129;C1087;C 1160	0.280937707	P49790 P49790 P49790	P49790 Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2 # P49790-2 Isoform 2 of Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 # P49790-3 Isoform 3 of Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 #
NIFLVAATLRPETMFGQTNC* WVR	C305	0.26032	Q9P2J5	Q9P2J5 Leucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 #

LILADALC*YAHTFNPK	C376;C345	0.257806611	P28838 P28838	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 #
NADMSEEMQQDSVEC*ATQA LEK	C24	0.256462836	P63167	P63167 Dynein light chain 1# cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 # Q9BVJ6-2 Isoform 2 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A # Q9BVJ6
VQTLLEELEELGKEEC*FQNK	C354;C522;C47 0	0.251310323	Q9BVJ6 Q9BVJ6 Q9BVJ6	U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1 # Q9BVJ6-3 Isoform 3 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A # Q4KWH8-2 Isoform 2 of 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1 # Q4KWH8 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1 #
LPYHLGDDAEEGEVSDSDSA DEIEDEC*KFK	C454;C472;C47 2;C472	0.244915457	Q4KWH8 Q4KWH8 Q4KWH8 Q4KWH8	Q4KWH8-4 Isoform 4 of 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1 # Q4KWH8-3 Isoform 3 of 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1 #
APVAGTC*YQAEWDDYVPK	C168	0.241384899	P30086	P30086 Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 #
QSEMQMKGAVTCEVC*MNV VQK	C297	0.24085406	Q6NUJ1	Q6NUJ1 Proactivator polypeptide-like 1 OS=Homo sapiens GN=PSAPL1 PE=2 SV=2 #
ADHQPLTEASYVNLPTIALC* NTDSPLR	C153;C148;C14 8	0.240816897	A0A0C4D G17 C9J9K3 P08865	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #
HLYTLGGDIINALC*FSPNR	C240	0.230760737	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
FLLADNLYC*K	C108;C113	0.224750051	B4DWR3 P61758	B4DWR3 Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=1 # P61758 Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=3 #
DSGYGDIWC*PER	C137;C213;C17 6;C228;C228;C2 28;C228;C176	0.211932571	E9PMS6 J3KP06 F8WD26 Q8WWI1 Q8WWI1 Q8WWI1 Q8WWI1 E9PMP7	E9PMS6 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=1 # J3KP06 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 # F8WD26 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 # Q8WWI1-4 Isoform 4 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # Q8WWI1 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 # Q8WWI1-3 Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # Q8WWI1-2 Isoform 2 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # E9PMP7 LIM domain only protein 7 (Fragment) OS=Homo sapiens GN=LMO7 PE=1 SV=7 #
SGDAAIVEMVPGKPMC*VES FSQYPLGR	C411	0.211089264	Q05639	Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
PFELSPLVC*AKYGWVTVEC DMLK	C102	0.199161439	Q86WB0 Q86WB0	Q86WB0 Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 # Q86WB0-2 Isoform 2 of Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 #

SDLYSSC*DR	C338	0.195278242	Q96E39	Q96E39 RNA binding motif protein# X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 # Q969T9 WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1 # A6NG10 WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=2 # K7EMC9 WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1 # K7EIJ0 WW domain-binding protein 2 (Fragment) OS=Homo sapiens GN=WBP2 PE=1 SV=1 # K7ENL2 WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1 # B4DFG2 WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1 #
DC*EIKQPVFGANYIK	C80;C58;C80;C58;C80;C80	0.19025058	Q969T9 A6NG10 K7EMC9 K7EIJ0 K7ENL2 B4DFG2	Q9HCF6-6 Isoform 6 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-5 Isoform 5 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-2 Isoform 2 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-11 Isoform 11 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-3 Isoform 3 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # E9PBI7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # A2A3F3 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # Q9HCF6 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=2 SV=4 # Q9HCF6-7 Isoform 7 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F4 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # G5E9G1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # H7BYP1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=2 # Q9HCF6-4 Isoform 4 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # Q9HCF6-8 Isoform 8 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 #
AAFPGGLGDKVEDLTC*CHPER	C1593;C1583;C1581;C1608;C1593;C1453;C1440;C1606;C1596;C1443;C1440;C1430;C1571;C1585;C1553	0.18359824	Q9HCF6 Q9HCF6 Q9HCF6 Q9HCF6 E9PBI7 A2A3F3 Q9HCF6 Q9HCF6 A2A3F4 G5E9G1 H7BYP1 Q9HCF6 A2A3F7 Q9HCF6	Q6NYC8 Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1 # A0A0G2JHC2 Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1 #
QDYSEEC*GR	C276;C276	0.17919909	Q6NYC8 A0A0G2JHC2	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
ETVSEESNVLC*LSK	C591	0.168922148	P13639	O76003 Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 #
ELEASEELDTIC*PK	C229	0.155993603	O76003	



VIVVGNPANTNC*LTASK	C137;C155	0.133754445	P40925 P40925	P40925 Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 # P40925-3 Isoform 3 of Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 #
KC*PFYAAEQDK	C319;C265;C236	0.12781	A0A087WT44 T44 P30519 P30519	A0A087WT44 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=1 # P30519 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2 # P30519-2 Isoform 2 of Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 #
ATVAPEDVSEVIFGHVLAAGC *GQNPVR	C65;C94	0.127069786	Q9BWD1 Q9BWD1	Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # Q9BWD1-2 Isoform 2 of Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 #
NCHC*EAHWAPPFC*DKFGF GGSTDSGPIR	C687;C675 C678 C684;C678 C684	0.11818688	O43184 O43184 O43184 O43184	O43184 Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 PE=1 SV=3 # O43184-3 Isoform 3 of Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 # O43184-2 Isoform 2 of Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 # O43184-4 Isoform 4 of Disintegrin and metalloproteinase domain-containing protein 12 OS=Homo sapiens GN=ADAM12 #

				Q9HCF6-6 Isoform 6 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-5 Isoform 5 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-2 Isoform 2 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-11 Isoform 11 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-3 Isoform 3 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # E9PBI7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # A2A3F3 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # Q9HCF6 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=2 SV=4 # Q9HCF6-7 Isoform 7 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F4 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # G5E9G1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # H7BYP1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=2 # Q9HCF6-4 Isoform 4 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # Q9HCF6-8 Isoform 8 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q8TBB5-2 Isoform 2 of Kelch domain-containing protein 4 OS=Homo sapiens GN=KLHDC4 # Q8TBB5 Kelch domain-containing protein 4 OS=Homo sapiens GN=KLHDC4 PE=1 SV=1 # Q8TBB5-3 Isoform 3 of Kelch domain-containing protein 4 OS=Homo sapiens GN=KLHDC4 # Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P21291 Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSR1 PE=1 SV=3 # Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 #
AAFPGGLGDKVEDLTCC*HP ER	C1594;C1584;C1582;C1609;C1594;C1454;C1441;C1607;C1597;C1444;C1441;C1431;C1572;C1586;C1554	0.116108265	Q9HCF6 Q9HCF6 Q9HCF6 Q9HCF6 E9PBI7 A2A3F3 Q9HCF6 Q9HCF6 A2A3F4 G5E9G1 H7BYP1 Q9HCF6 A2A3F7 Q9HCF6	
HGVLYVYGGMFEAGDRQVTL SDLHC*LDLHR	C408;M450 C434 C465;M419	0.115082864	Q8TBB5 Q8TBB5 Q8TBB5	
NDQC*YDDIR	C29;C23;C76	0.108266104	Q9ULV4 Q9ULV4 Q9ULV4	
AYHEQLSVAEITSSC*FEPNS QMVK	C229;C319;C295	0.10393	Q9NY65 C9J2C0 Q9NY65	
C*SQAVYAAEK	C122	0.082433422	P21291	
SAC*DTVDTWLDDTAK	C4216	0.05581	Q14204	

LQQGLVTSSAEQMLQRLC*GR	C113;C693	0.02182959	Q8ND23 Q8ND23	Q8ND23-3 Isoform 3 of Leucine-rich repeat-containing protein 16B OS=Homo sapiens GN=LRRRC16B # Q8ND23 Leucine-rich repeat-containing protein 16B OS=Homo sapiens GN=LRRRC16B PE=2 SV=2 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 #
NC*DC*LQGFQLTHSLGGGT GSGMGTLISK	C57 C476;C55 C129;C474 C127	0.016944775	Q13509 A0A0B4J2 69 Q13509	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 #
KQC*QQLQTAIAEAEQR	C383	0.006229767	Q5XKE5	Q5XKE5 Keratin# type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 #
QSRTC*STQVC*R	C3687 C3692;C3688 C3693	0.001131017	A2VEC9 A0A096LN W2	A2VEC9 SCO-spondin OS=Homo sapiens GN=SSPO PE=2 SV=1 # A0A096LNW2 SCO-spondin OS=Homo sapiens GN=SSPO PE=4 SV=1 #
FFAFWGQDINNLTPLEC*GR ESR	C635;C735	0.001009883	A8MT40 Q8NCN5	A8MT40 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # Q8NCN5 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 #

**Table A3.5**

IsoTOP-ABPP analysis of JNS 140 (100 µM) in vitro in 231MFP proteomes.

Peptide	Modified residue	Average area ratio	Uniprot ID	Protein
DNTIEHLLPLFLAQLKDEC*PEVR	C198;C377	21.47309398	B3KQV6 P30153	B3KQV6 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=1 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
GLC*AIAQAESLR	C97	4.925447319	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #
KAQC*PIVER	C66;C87;C66	4.922512991	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
YFASRMFC*LR	C240	4.887501637	C9JZ99	C9JZ99 Serum paraoxonase/lactonase 3 OS=Homo sapiens GN=PON3 PE=1 SV=1 #
AQILVLTYPILIGNYGIPDDEMD EFGLC*K	C73 C73;M67	4.832060112	F8VPD4 P27708	F8VPD4 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 # P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
MVAAVAC*AQVPK	C431 C393;M425	4.265820398	Q9HCC0 Q9HCC0	Q9HCC0 Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial OS=Homo sapiens GN=MCCC2 # Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 #
NAGNC*LSPAVIVGLLK	C369;C335	4.249244818	O43175 Q5SZU1	O43175 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 # Q5SZU1 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 #
QYPWGVAEVENGEHC*DFTILR	C244;C279;C280;C280;C260	3.961826681	G3V1Q4 Q16181 Q16181 E7EPK1 E7ES33	G3V1Q4 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 #
AVEEYSC*EFGSAK	C56	3.902800116	Q00325	Q00325-2 Isoform B of Phosphate carrier protein# mitochondrial OS=Homo sapiens GN=SLC25A3 #
MGVEAVIALLEATPDTPAC*V VSLNGNHAVR	C343	3.863111218	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFBP PE=1 SV=2 #
AYHEQLSVAEITSSC*FEPNS QMVK	C53;C229;C319;C295	3.650775	V9GZ17 Q9NY65 C9J2C0 Q9NY65	V9GZ17 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
VC*NFLASQVPPFSR	C205;C214	3.539568352	Q99714 Q99714	Q99714-2 Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 # Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 #
VC*TLAIIDPGDSDIIR	C92;C92	3.525819837	P62888 E5RI99	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #

C*EHRIMESLAWLSDSPLFDLIK	C553	3.4000315	P06400	P06400 Retinoblastoma-associated protein OS=Homo sapiens GN=RB1 PE=1 SV=2 #
DLIMDNC*EELIPEYLNFIK	C178	3.33201	Q58FG1	Q58FG1 Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1 #
C*FIVGADNVGSK	C27	3.153531811	P05388	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #
SNLGPVMSGNTAYPVISC*P	C350	3.151222541	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
PLTPDWGVQDVWSSLR				O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 # O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 # O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 # O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 #
TGNPMSVC*GR	C574;C493;C499;C490;C491	2.985111312	O95793 O95793 O95793 A0A087X1A5 Q5JW30	Q9NR30 Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 # Q9NR30-2 Isoform 2 of Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 #
DSEDNPQTLIFSATC*PHWVFNVAK	C378;C310	2.957134675	Q9NR30 Q9NR30	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
VMTIPYQPMPASSPVIC*AGGQDR	C194	2.894097961	Q15365	A5A3E0 POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 # Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 # P0CG39 POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 #
C*PEALFQPCFLGMESCGIHE TTFNSIMK	C957	2.891866193	A5A3E0 Q6S8J3 P0CG39	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 #
C*AGPTPEAELQALAR	C52	2.693538283	Q15050	Q96KB5 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 # Q96KB5-2 Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK #
INPIC*NDHYR	C70;C70	2.545061648	Q96KB5 Q96KB5	Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 # A0A087WXX9 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=1 # Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 #
TSC*GSPNYAAPEVISGR	C185;C174;C200;C174	2.534994107	Q13131 A0A087WXX9 Q13131 P54646	P54646 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=2 #

DC*GGAAQLAGPAAEADPLGR	C8;C8;C8;C8;C8;C8;C8	2.469884445	Q9Y508 A0A096LNV3 A0A096LNT1 A0A096LP02 Q9Y508 A0A096LNN8 A0A096LPF9	Q9Y508 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNV3 E3 ubiquitin-protein ligase RNF114 (Fragment) OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNT1 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 # A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 #
AVQDLC*GWR	C428	2.364221929	Q9P258	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 # C9J938 Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=1 SV=1 # Q15019-2 Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2 # C9JB25 Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=1 SV=1 # Q15019 Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 #
LTVVDTPGYGDAINC*R	C111;C146;C111;C111	2.33409	C9J938 Q15019 C9JB25 Q15019	H3BRV9 Nuclear transport factor 2 (Fragment) OS=Homo sapiens GN=NUTF2 PE=1 SV=1 # P61970 Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1 #
TQLGAIYDASC*LTWEGQQFQ GK	C38;C38	2.328792161	H3BRV9 P61970	P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
LQDAFSSIGQSC*HLDLPQIAIVGGQSAGK	C27;C27	2.30402891	P50570 P50570	P10826-2 Isoform Beta-2 of Retinoic acid receptor beta OS=Homo sapiens GN=RARB # Q5TON5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L PE=1 SV=1 # Q5TON5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L # Q5TON5 Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L PE=1 SV=3 # Q5TON5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L # Q5TON5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L #
VIGIEC*SSISDYAVK	C101	2.284902284	Q99873	Q12923-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-4 Isoform 4 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923-3 Isoform 3 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 # Q12923 Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2 #
ALKAC*FSGLTQTEWQHR	C36	2.283394446	P10826	Q9NQ88 Fructose-2#6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 # A0A0U1RQD1 Chromosome 12 open reading frame 5# isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 #
FTSC*VAFFNILNELNDYAGQR	C69;C69;C69;C69;C69;C69	2.282026832	Q5TON5 S4R347 Q5TON5 Q5TON5 Q5TON5 Q5TON5	
KSQTGILLGVC*SK	C798;C798;C798;C798	2.270401827	Q12923 Q12923 Q12923 Q12923	
EQFSQGSNSNC*LETSLAEIFPLGK	C161;C102	2.231652347	Q9NQ88 A0A0U1RQD1	

AVC*MLSNTTAAIEAWAR	C361;C376;C310;C400;C376;C376;C376	2.203751774	P68366 P68363 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
IINDNATYC*R	C211	2.167390454	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # P09914 Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 # P09914-2 Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 #
MEC*PEIDCEEGWALLK	C138;M105 C107	2.142495381	P09914 P09914	Q5VST9-2 Isoform 2 of Obscurin OS=Homo sapiens GN=OBSCN # H3BPX2 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=2 # Q5VST9 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3 # Q5VST9-6 Isoform 5 of Obscurin OS=Homo sapiens GN=OBSCN # A6NGQ3 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=4 #
APEVTILEPLQDVQLSEGGQDA SFQC*R	C4271;C5228;C4271;C4786;C5228	2.127025034	Q5VST9 H3BPX2 Q5VST9 Q5VST9 A6NGQ3	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 # E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 #
NMITGTSQADC*AVLIVAAGV GEFEAGISK	C111;C111;C111	2.098637738	P68104 Q05639 P68104	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 # P41252 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 # J3KR24 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # Q12955 Ankyrin-3 OS=Homo sapiens GN=ANK3 PE=1 SV=3 # O95373 Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 #
ALVDGPC*TQVR	C42;C42	2.095900529	E7EPB3 P50914	P37235 Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3 # H3BRG4 Cytochrome b-c1 complex subunit 2# mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=1 # H3BSJ9 Cytochrome b-c1 complex subunit 2# mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=1 # P22695 Cytochrome b-c1 complex subunit 2# mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 # Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # H0YMV8 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=1 SV=1 # Q71UM5 40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3 # P42677 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 #
GC*STVLSPEGSAQFAAQIFG LSNHLVWSK	C374	2.068057764	P22234	
VMPFSTAC*NTPLSNFESHQ NYK	C75 C185;M69	2.046995	P41252 J3KR24	
ELC*KMADSFSGTDTILESPD DFSQHDQDK	C2096	2.002791529	Q12955	
GIDQC*IPLFVEAALER	C757	1.979142406	O95373	
LLQC*DPSSASQF	C185	1.97742281	P37235	
NALANPLYC*PDYR	C192;C192;C192	1.918716033	H3BRG4 H3BSJ9 P22695	
LPLMEC*VQMTQDVQK	C360	1.915406667	Q01813	
LTEGC*SFR	C93;C77;C77	1.913268736	H0YMV8 Q71UM5 P42677	

LPTDLTAC*DNR	C111	1.888082017	Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 #
VAAALENTHLLEVVNQC*LSA R	C158	1.870448405	Q9Y3D0	Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 #
C*QNALQQVVAR	C602;C620	1.840799507	Q06210 Q06210	Q06210-2 Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 # Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 #
YAIC*SALAASALPALVMSK	C125	1.840422941	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 # Q9Y6E0-2 Isoform A of Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 # B4DR80 Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 # Q9Y6E0
IIDLEEADEIEDIQQEITVLSQ C*DSPYVTK	C77;C77;C89	1.836116875	Q9Y6E0 B4DR80 Q9Y6E0	Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 # P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 # F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 # P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN # P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN #
TSSVSNPQDSVSGSPC*SR	C108;C106;C108; C108	1.79013	P49023 F5GZ78 P49023 P49023	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
LVAFC*PFASSQVALENANAV SEGVVHEDLR	C52	1.784260783	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
SGDAAIVEMVPGKPMC*VES FSQYPPLGR	C411	1.776285	Q05639	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
IHESAGLPFFEIVDAPLNIC*E SR	C155;C155	1.751467714	O95340 O95340	O95340 Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2 # O95340-2 Isoform B of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 #
LALFNPDVC*WDR	C44	1.731739306	O00483	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 #
NHPVPVIAMVNLAAAAGC* QLVASCDIAVASDK	C155;C208	1.725079503	Q96DC8 Q5W0J8	Q96DC8 Enoyl-CoA hydratase domain-containing protein 3# mitochondrial OS=Homo sapiens GN=ECHDC3 PE=1 SV=2 # Q5W0J8 Enoyl-CoA hydratase domain-containing protein 3# mitochondrial (Fragment) OS=Homo sapiens GN=ECHDC3 PE=1 SV=1 #
SGQGAFGNMC*R	C96	1.719992922	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
DTGTVHLNELGNTQNFMLLC* PR	C126	1.692198992	Q2NL82	Q2NL82 Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 #
APLAVTSQVINC*R	C330	1.68409	P42695	P42695 Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=1 SV=2 #
AVASQLDC*NFLK	C207;C193	1.674461813	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
YGIIC*MEDLIHEIYTVGK	C186;C146	1.648124898	P18124 A8MUD9	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 # A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 #
GC*LLYGPPGTGK	C184;C170	1.646409713	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #



AVC*MLSNNTTAVAEAWAR	C376;C446	1.628448639	Q9BQE3 F5H5D3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
LC*WFLDEAAAR	C237	1.57900385	O95336	O95336 6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2 # A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 # Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL #
SDVC*TPGGTTIYGLHALEQG GLR	C247;C235;C215	1.563557094	A0A0A0M QS1 Q53H96 Q53H96	M0QZS6 SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1 # Q9UBE0 SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # K7EJH8 Alpha-actinin-4 (Fragment) OS=Homo sapiens GN=ACTN4 PE=1 SV=1 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 #
YCFSEMAPVC*AVVGGILAQE IVK	C222;M299 C303	1.548599272	M0QZS6 Q9UBE0	
C*QLEINFNTLQTK	C332;C152;C351	1.528908927	P12814 K7EJH8 O43707	
AFC*EPGNVENNGVLSFIK	C250;C250	1.482206191	A0A0C4D GZ5 P54577	A0A0C4DGZ5 Tyrosine--tRNA ligase OS=Homo sapiens GN=YARS PE=1 SV=1 # P54577 Tyrosine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB #
VAVTEGC*QPSR	C1326	1.478304021	O75369	
RGPC*IIYNEDNGIIK	C208	1.4711625	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # P25705 ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 # P25705-3 Isoform 3 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 # P25705-2 Isoform 2 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 #
QC*TGLQGFLVFHSGGGTG SGFTSLLMER	C114	1.469475574	P68366 P68363 Q9BQE3 F5H5D3 Q71U36 P68366	
YTIVVSATASDAAPLQYLAPY SGC*SMGEYFR	C294	1.468829824	P25705 P25705 P25705	
TIYAGNALC*TVK	C155;C106;C155	1.459927089	P13804 P13804 HOYLU7	P13804 Electron transfer flavoprotein subunit alpha# mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 # P13804-2 Isoform 2 of Electron transfer flavoprotein subunit alpha# mitochondrial OS=Homo sapiens GN=ETFA # HOYLU7 Electron transfer flavoprotein subunit alpha# mitochondrial (Fragment) OS=Homo sapiens GN=ETFA PE=1 SV=1 # Q8WUM4-2 Isoform 2 of Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP # Q8WUM4 Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 # G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 #
SCVLFNC*AALASQIAAEQNL DNDEGLK	C127;C127	1.44767708	Q8WUM4 Q8WUM4	
C*LHNFLTDGVPAGEAFTEDF QGLR	C316;C268	1.44278107	G3V1A6 P57764	

C*PGESLINPGFK	C180	1.440479482	Q9BUH6	Q9BUH6 Protein PAXX OS=Homo sapiens GN=C9orf142 PE=1 SV=2 # B3KSI3 Branched-chain-amino-acid aminotransferase OS=Homo sapiens GN=BCAT2 PE=1 SV=1 # M0QZP4 Branched-chain-amino-acid aminotransferase OS=Homo sapiens GN=BCAT2 PE=1 SV=1 # M0QXF9 Branched-chain-amino-acid aminotransferase (Fragment) OS=Homo sapiens GN=BCAT2 PE=1 SV=1 # O15382 Branched-chain-amino-acid aminotransferase# mitochondrial OS=Homo sapiens GN=BCAT2 PE=1 SV=2 # M0QZ10 Branched-chain-amino-acid aminotransferase OS=Homo sapiens GN=BCAT2 PE=1 SV=1 # O15382-2 Isoform B of Branched-chain- amino-acid aminotransferase# mitochondrial OS=Homo sapiens GN=BCAT2 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 # B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 # P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # P78347 General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 # P78347-4 Isoform 4 of General transcription factor II-I OS=Homo sapiens GN=GTF2I # P78347-3 Isoform 3 of General transcription factor II-I OS=Homo sapiens GN=GTF2I # P78347-2 Isoform 2 of General transcription factor II-I OS=Homo sapiens GN=GTF2I # P40939 Trifunctional enzyme subunit alpha# mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 # P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A # P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 # A0A0C4DGR2 Prostate tumor overexpressed gene 1# isoform CRA_d OS=Homo sapiens GN=PTOV1 PE=1 SV=1 # M0QY25 Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 PE=1 SV=1 # Q86YD1 Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 PE=1 SV=1 # Q86YD1-2 Isoform 2 of Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 # Q9NY15 Stabilin-1 OS=Homo sapiens GN=STAB1 PE=1 SV=3 # O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 #
EVFGSGTAC*QVCPVHR	C302;C250;C33 4;C342;C342;C2 50	1.436562299	B3KSI3 M0QZP4 M0QXF9 O15382 M0QZ10 O15382	
AC*LISLGYDIGNDPQGEAEF AR	C774	1.424119054	P12814	
TLIQNC*GASTIR	C417;C410;C45 5	1.42343744	P49368 B4DUR8 P49368	
IQFNDLQSLLC*ATLQNVLR	C585	1.421130597	Q14974	
SILSPGGSC*GPIK	C215;C215;C21 5;C215	1.397502168	P78347 P78347 P78347 P78347	
TGIEQGS DAGYLC*ESQK	C322	1.389357297	P40939	
VLDALFPCVQGGTTAIPGAFG C*GK	C221;C254	1.367961468	P38606 P38606	
DLETLKSLC*R	C308;C308;C34 0;C308	1.356606177	A0A0C4D GR2 M0QY25 Q86YD1 Q86YD1	
AGNGGC*HGLATCRAVGGG QR	C958	1.340627675	Q9NY15	
ISSINSISALC*EATGADVEEV ATAIGMDQR	C241	1.33879206	O60701	
HLNEIDL FHC*IDPNDSK	C62;C58;C58	1.336569382	A0A087W YT3 Q15185 Q15185	
ITVVGVGQVGMAC*AISILGK	C36	1.329487863	P07195	

TDVC*VFAAQEDLETMQAF QVFNK	C96	1.315696601	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # J3KTF8 Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDI PE=1 SV=7 # P52565 Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI PE=1 SV=3 # J3QQX2 Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI PE=1 SV=1 # P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB # P45954 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 #
VAVSADPNVNVVVTGLTLV C*SSAPGPLELDLTGDLESFK K	C79;C79;C79	1.30504381	J3KTF8 P52565 J3QQX2	Q9UBF2-2 Isoform 2 of Coatmer subunit gamma-2 OS=Homo sapiens GN=COPG2 # Q9UBF2 Coatmer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 # P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 # P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
VGSFC*LSEAGAGSDSFALK	C73;C175	1.302685	P45954 P45954	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
HPSAVTAC*NLDLENLITDSN R	C325;C325	1.296930593	Q9UBF2 Q9UBF2	P31150 Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 #
DSNNLC*LHFNPR	C43	1.275265845	P09382	P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #
C*AGNEDIITLR	C81	1.249824128	P12004	P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 #
AYHEQLSVAEITNAC*FEPAN QMVK	C280	1.226345392	P68366 P68363 Q71U36 P68366	
QAVLGAGLPSTPC*TTINK	C119	1.216175137	P24752	
TDDYLDQPC*LETVNR	C202	1.208983071	P31150	
VIEINPYLLGTMAGGAADC*S FWER	C111	1.187962264	P28074	
ISGADINSIC*QESGMLAVR	C348	1.181914278	P43686 P43686	

					Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 # D6R927 Recombining-binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=1 # Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-3 Isoform 3 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-2 Isoform 2 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ #
IIQFQATPC*PK	C300;C313;C299;C298;C224;C299;C278;C238	1.177385302	Q06330 Q06330 D6R927 Q06330 Q06330 Q06330 Q06330		
C*QNEQLQTAVTQQVSIQQHK	C678	1.148454737	O60763	O60763	O60763 General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2 #
GEETPVIVGSALC*ALEGR	C222	1.136996886	P49411	P49411	P49411 Elongation factor Tu# mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 # I3L3Q4 Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=1 SV=1 # Q9HC38-2 Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 # Q9HC38-3 Isoform 3 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 # F6TLX2 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 # I3L1F4 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 #
HEEFEEGC*K	C41;C41;C41;C245;C41	1.127535713	I3L3Q4 Q9HC38 Q9HC38 F6TLX2 I3L1F4		
SIQFVDWC*PTGFK	C332;C347;C347	1.123813427	P68366 P68363 P68366	P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
LSLEPLPC*YQLELDAVAEVK	C32	1.11694926	Q96RS6	Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 #
TATAVAHC*K	C25	1.115882197	P62249	P62249	P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 #
EKLC*YVALDFENEMATAASSLEK	C219	1.106120674	P68032	P68032	P68032 Actin# alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 # Q8NCM8 Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4 # Q8NCM8-2 Isoform 2 of Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 # H0YDE0 Cytoplasmic dynein 2 heavy chain 1 (Fragment) OS=Homo sapiens GN=DYNC2H1 PE=1 SV=1 #
LQSAMALFAC*KTLGLK	C3702;M83 C88 C3695;M3697	1.105864998	Q8NCM8 Q8NCM8 H0YDE0		
SFC*PGGTDSVSPPPSVITQENLGR	C314	1.094696387	Q9C0C9	Q9C0C9	Q9C0C9 (E3-independent) E2 ubiquitin-conjugating enzyme OS=Homo sapiens GN=UBE2O PE=1 SV=3 #
NPLC*PLGQTVQSELEFR	C115	1.085454748	Q9Y5R8	Q9Y5R8	Q9Y5R8 Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 #
AITIAGVPQSVTEC*VK	C158	1.0845	Q15365	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
SVVC*QESDLPDELLYGR	C187	1.080566459	Q9NS86	Q9NS86	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 #

HSDRQDC*R	C103	1.059252324	Q86X51	Q86X51 Uncharacterized protein CXorf67 OS=Homo sapiens GN=CXorf67 PE=2 SV=1 #
LNISFPATGC*QK	C12	1.05214852	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
DLC*FSPGLMEASHVVNDVN EAVQLVFR	C392	1.049000278	Q9BXW7 Q9BXW7	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 # Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 #
SELEC*VTNITLANVIR	C27;C27	1.04614834	Q9Y6W5 Q9Y6W5	Q9Y6W5-2 Isoform 2 of Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 # Q9Y6W5 Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3 #
WC*EYGLTFTEK	C76;C76	1.04045373	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
VMQPQILEVNFNPDC*ER	C612	1.03067973	Q14166	Q14166 Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2 #
C*SSFMAPPVTDLGELR	C127	1.028438744	P36551	P36551 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 #
LQDPKDDEC*PVVNAYATLIE NDSNPEVR	C177	1.02588	Q9BPX3	Q9BPX3 Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1 #
DC*IGGCSDLVSLQQSGELLT R	C79	1.025271948	P35754	P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
LTPGC*EAEAETEAIFFVQQ FTDMEHNR	C2359	1.024873534	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
FQSSAVMALQEASEAYLVGL FEDTNLC*AIHAK	C111	1.021564392	Q71DI3	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 #
LGMLSPEGTC*K	C212	1.019636657	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
IDATQVEVNPFGGETPEGQVV C*FDAK	C255;C255;C255 5	1.015534097	Q96199 E9PDQ8 Q96199	Q96199 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96199-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
FMYC*TPFTLDGR	C1933;M1933 C1904;M1931 C1902;M1931 C1944;M1911 C1913 C1935;M1942 C1933;M1900	1.006993382	Q96N67 Q96N67 Q96N67 H0Y7L2 Q96N67 Q96N67 Q96N67	Q96N67-3 Isoform 3 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67-2 Isoform 2 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67-4 Isoform 4 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # H0Y7L2 Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=2 # Q96N67-6 Isoform 6 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67 Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4 # Q96N67-5 Isoform 5 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 #
AEPQC*TSLAWSADGQTLF AGYTDNLVR	C286	1.002120432	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
IHEGC*EEPATHNALAK	C874;C870;C870	1.001294059	A0A087W VQ6 Q00610 Q00610	A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #

AQDIEAGDGTTSVVIIAGSLLD SC*TK	C90;C120	0.997598071	P50991 P50991	P50991-2 Isoform 2 of T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 # P50991 T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NRG0 Chromatin accessibility complex protein 1 OS=Homo sapiens GN=CHRAC1 PE=1 SV=1 #
ECISIHVQAGVQIGNACWEL YC*LEHGIQPDGQMPSDK	C25	0.992629027	P68363 Q9BQE3 F5H5D3 Q71U36	
ATELFVQC*LATYSYR	C55	0.985325478	Q9NRG0	
DC*GATWVVLGHSER	C87;C124	0.979088573	P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 # P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 # # E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 #
NQSFC*PTVNLDKLWTLVSE QTR	C70;C13	0.978365265	P46776 E9PJD9	
PSPGAAMLVC*EETLELGAQ GCWGSTSPR	C210	0.975945395	Q86SQ6	Q86SQ6-1 Isoform 1 of Adhesion G protein-coupled receptor A1 OS=Homo sapiens GN=ADGRA1 #
LPLC*SLPGEPGNPDQQLQ R	C75	0.966197223	Q96GX2	Q96GX2 Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 #
VLC*ELADLQDK	C76	0.947755	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # E9PLZ8 Multivesicular body subunit 12A (Fragment) OS=Homo sapiens GN=MVB12A PE=1 SV=7 # Q96EY5-2 Isoform 2 of
SC*SPLAFSAFGDLTIK	C92;C191;C231	0.939954759	E9PLZ8 Q96EY5 Q96EY5	Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A # Q96EY5 Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A PE=1 SV=1 # P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
AAVEEGIVLGGGC*ALLR	C442	0.93811388	P10809	
DFNEEC*PR	C178;C239;C270;C105	0.922563333	Q13418 Q13418 A0A0A0MTH3 Q13418	Q13418-2 Isoform 2 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK # Q13418 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 # A0A0A0MTH3 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1 # Q13418-3 Isoform 3 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK #
ELAPAVSVLQLFC*SSPK	C296;C296;C296	0.919767258	Q9Y678 Q9UBF2 Q9UBF2	Q9Y678 Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 # Q9UBF2-2 Isoform 2 of Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 # Q9UBF2 Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 # Q9NQW6-2 Isoform 2 of Actin-binding protein anillin OS=Homo sapiens GN=ANLN # Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 # Q9Y570-4 Isoform 4 of Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 # Q9Y570-2 Isoform 2 of Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 # Q9Y570 Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 #
NNAFPC*QVNIK	C675;C712	0.919233055	Q9NQW6 Q9NQW6	
QC*EGITSPGSK	C238;C51;C238	0.917979591	Q9Y570 Q9Y570 Q9Y570	
GTEAGQVGEPIPTGEAGPS C*SSASDK	C241	0.917667186	O15355	O15355 Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 #

				Q9BQE3 Q9NY65 F5H5D3 C9J2C0 Q71U36 Q9NY65	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
TIQFVDWC*PTGFK	C347;C281;C417;C371;C347;C347	0.91730669			
YLAEVAC*GDDR	C134	0.915674928	P27348		P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 # B4E0Y9 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 # Q9P289-3 Isoform 3 of Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 # Q8NBY1 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 # Q9P289 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=2 #
IIDLEEADEIEDIQQEITVLSQ C*DSSYVTK	C77;C77;C77;C77	0.911598543	B4E0Y9 Q9P289 Q8NBY1 Q9P289		Q15459-2 Isoform 2 of Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 # Q15459 Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
EVLDDQVC*YR	C179;C244	0.910875	Q15459 Q15459		
NMMAAC*DPR	C303;M299 C303;M646 C303;M281 C285;M299 C650;M299 C303	0.89570779	Q13509 P68371 A0A0B4J269 Q9BVA1 P04350 Q5JP53 Q9BUF5		
CPEALFQPSFLGMESC*GIHE TTFNSIMK	C272	0.893212345	P60709		P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
LTTPTYGDLNHLVLSATMSGV TTC*LR	C239;C239;C239;C221	0.892100718	P68371 Q9BVA1 P04350 Q5JP53		P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
YMAC*CLLYR	C385;M313 C315 C300;M313 C315;M320 C282;M383 C322;M313 C315;M313 C315;M280	0.891137287	P68366 P68363 Q9BQE3 A6NHL2 F5H5D3 Q71U36 A6NHL2 P68366		

LC*VQNSPQEAR	C150;C150;C150; 0;C150;C141	0.889163328	P33240 P33240 E7EWR4 E9PID8 A0A0A0M T56	P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 # P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
EC*LPLIIFLR	C41	0.887856943	P62701	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 #
VWNLANC*K	C182	0.877367412	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
LWNTLGVK*K	C138	0.876798132	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
C*EFQDAYVLLSEK	C237	0.876452936	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
EQNYC*ESR	C160;C107	0.862420169	Q7L5D6 Q7L5D6	Q7L5D6 Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1 # Q7L5D6-2 Isoform 2 of Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 #
YMACC*LLYR	C316;M280 C316;M313 C301;M313 C316;M320 C316 C323;M313 C283;M383 C386;M313	0.85852565	P68366 P68363 Q9BQE3 A6NHL2 F5H5D3 Q71U36 A6NHL2 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
ITAFVPNDGC*LNFIEENDEVL VAGFGR	C90	0.855129862	P62266	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 #
YDC*GEEILITVLSAMTEEA AV AIK	C159	0.852209033	P63241 P63241 Q6IS14	P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 # Q6IS14 Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=2 SV=2 #
SMVSPVPSPTGTISV PNSC*P ASPR	C254	0.852075571	P85037	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOKK1 PE=1 SV=1 #
SWAWAPSGNLLATC*SR	C123	0.850562933	O76071	O76071 Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens GN=CIAO1 PE=1 SV=1 #
TGC*TFPEKPDFH	C318;C353;C33 6	0.847649165	P55263 P55263 P55263	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK # P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 # P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK #
EEC*PVFTPPGGETLDQVK	C114;C55	0.846727739	Q9NQ88 A0A0U1R QD1	Q9NQ88 Fructose-2#6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 # A0A0U1RQD1 Chromosome 12 open reading frame 5# isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 #



AC*YLSINPQKDETELETK	C222	0.846058867	P61163	P61163 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # M0QYM7 Tubulin beta-4A chain (Fragment) OS=Homo sapiens GN=TUBB4A PE=1 SV=7 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # Q9Y678 Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 # Q08J23-3 Isoform 3 of tRNA (cytosine(34)- C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 # Q08J23 tRNA (cytosine(34)- C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 # Q08J23-2 Isoform 2 of tRNA (cytosine(34)-C(5))- methyltransferase OS=Homo sapiens GN=NSUN2 # Q96L21 60S ribosomal protein L10-like OS=Homo sapiens GN=RPL10L PE=1 SV=3 # X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 #
VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDICFR	C201;C201;C20 1;C183;C131;C2 01	0.842287988	P68371 Q9BVA1 P04350 Q5JP53 M0QYM7 Q9BUF5	
NTPLC*DSFVFR	C429	0.832315916	O95573	
HPSAVTAC*NLDLENLVTD SNR	C325	0.82074786	Q9Y678	
MVYSTC*SLNPIEDEAVIASLL EK	C85;M316 C321;M281 C286	0.818912893	Q08J23 Q08J23 Q08J23	
MLSC*AGADR	C105;C105;C10 5	0.815345	Q96L21 X1WI28 P27635	
EAGVGNGTC*APVR	C37	0.812709123	Q96C86	
IKSGEEDFESLASQFSDC*SS AK	C40;C113;C113	0.808896493	K7EN45 K7EMU7 Q13526	
DHQPC*IIFMDEIDAIGGR	C242;C228	0.805349937	A0A087X2 I1 P62333	
VVSGMVNC*NDDQGVLGR	C230	0.805197277	P21980	
GLNPLNAYSDLAEFLETEC*Y QTPFNK	C343	0.802460259	O14879	
GDSEPTPGC*SGLGPGGVR	C13;C13;C12;C1 3;C13	0.797880224	Q8WW01 Q8WW01 HOYCV5 E9PPN1 F2Z3M0	
TVEEIEACMAGC*DK	C418;C482	0.796613004	P12955 P12955	

AENGLLMTPC*YTANFVAPEV LKR	C579	0.794771717	P51812	P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 #
C*ASQAGMTAYGTR	C132	0.794065105	E9PDU6 Q15417 Q15417 Q15417	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417-3 Isoform 3 of Calponin-3 OS=Homo sapiens GN=CNN3 # Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 #
LSSC*DSFTSTINELNHCLSLR	C92	0.791010038	P07814	P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 #
TMVNLALENAC*DEATYQLGL DMEELEEIEEDAGLNGGLG R	C109	0.790755944	P11217	P11217 Glycogen phosphorylase# muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 #
YWLC*AATGPSIK	C249	0.78831517	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
LQEVPHGPMC*DLLWSDPD DR	C196;M195 C196	0.788125	P67775 P62714	P67775 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 # P62714 Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 #
WC*NVQSTQDEFEELTMSQK	C59;C59	0.78767	P27707 D6RFG8	P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
LTVIDTPGFGDHINNENC*WQ PIMK	C211	0.787147301	Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8	Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 #
YDQDLC*YTDILFTEQER	C156;C131;C16 6	0.782780969	Q15029 Q15029 Q15029	Q15029-3 Isoform 3 of 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 # Q15029-2 Isoform 2 of 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 # Q15029 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 #
VNLQMVYDSPLC*R	C533 C493;M526 C462;M486	0.779224199	Q9Y285 Q9Y285 K7ER00	Q9Y285-2 Isoform 2 of Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA # Q9Y285 Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 # K7ER00 Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=1 #
GC*TATLGNAK	C229	0.778911699	P15880	P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 #
TC*NVLVALEQQSPDIAQGVH LDR	C104	0.776001261	P31153	P31153 S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 #
GNHEC*ASINR	C138;C126;C12 7	0.774015219	P62136 P62140 P62136	P62136-2 Isoform 2 of Serine/threonine- protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA # P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # P62136 Serine/threonine-protein phosphatase PP1- alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 #
VLHDAQQC*R	C608	0.767559442	A1L0T0	A1L0T0 Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 #

C*DYMDEVTYGELEKEEAQPI VTK	C602	0.766747857	H3BQZ7 Q1KMD3	H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 # P20073 Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 # P20073-2 Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7 #
LGTDESC*FNMILATR	C363;C341	0.766105852	P20073 P20073	P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 # G5E9W3 Cleavage and polyadenylation specific factor 3# 73kDa# isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 # B7Z4L4 Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 # P04843 Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 # Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=7 # C9JX21 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # C9JNR4 Transforming protein RhoA (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOA PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 # P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 # B7Z4D2 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-4 Isoform 4 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95-3 Isoform 3 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=2 # B3KRD1 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-2 Isoform 2 of Syntabulin OS=Homo sapiens GN=SYBU # A0A0C4DG86 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-5 Isoform 5 of Syntabulin OS=Homo sapiens GN=SYBU # P49327 Fatty acid synthase OS=Homo sapiens GN=FSN PE=1 SV=3 # O43252 Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2 #
C*PEALFQPSFLGMESCGIHE TTFNSIMK	C257	0.763693675	P60709	
DVQIGDIVTVGEC*RPLSK	C131	0.761796906	P62280	
NFNHYHILSPC*DLSNYTDLAM STVK	C461	0.761017622	G5E9W3 Q9UKF6	
VDEFPLC*GHMVSDEYEQLS SEALEAAR	C49;C49	0.759833815	X1WI28 P27635	
VAC*ITEQVLTLVNKR	C305;C477	0.757309985	B7Z4L4 P04843	
LVIVGDGAC*GK	C16;C16;C16;C1 6;C16;C16	0.756729837	Q5JR08 C9JX21 C9JNR4 P61586 P08134 E9PQH6	
C*TPSVISFGSK	C34;C34	0.748102439	Q92598 Q92598	
C*FGTGAAGNR	C1312	0.744721812	P78527	
LESLQSMEMAHSGSLRDEL C*LDFPCDSPEK	C259;C386;C38 8;C389;C183;C3 21;C394;C270	0.744047248	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	
AFDTAGNGYC*R	C223	0.74330996	P49327	
TDSC*DVNDCVQQVVELLQE R	C207	0.740930988	O43252	

IHMGC*AENTAK	C196	0.740153156	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
LEVDAIVNAANSSLLGGGGV DGC*IHR	C186	0.729994079	Q9BQ69	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #
FFACAPNYSYAALCEC*LR	C513	0.729263539	Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 #
NIC*FTVWDVGGQDR	C62;C35	0.728107716	P18085 C9JAK5	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 # C9JAK5 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=1 #
GDGQFFAVSVVC*PETGAR	C213	0.724724168	O95163	O95163 Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3 #
VQEAPIDEHWIIEC*NDGVFQ R	C91;C91	0.721900227	Q14353 Q14353	Q14353-2 Isoform 2 of Guanidinoacetate N- methyltransferase OS=Homo sapiens GN=GAMT # Q14353 Guanidinoacetate N- methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 #
EEFASTC*PDDEEIELAYEQV AK	C223	0.720560588	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
TSGNVEDDLIIFPDDC*EFK	C80	0.714253698	Q16186	Q16186 Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 #
KPVTDC*VISVPSFFTAER	C140;C140	0.712214384	Q92598 Q92598	Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 #
HTGCC*GDNDPIDVCEIGSK	C114	0.710515	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 # Q9H4L5-2 Isoform 1b of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5-3 Isoform 1c of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5 Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1 # Q9H4L5-4 Isoform 1d of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 #
LDINLLDNVVNC*LYHGEGAQ QR	C34	0.700903056	O14980	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 # Q96SI9-2 Isoform 2 of Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP # Q96SI9 Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1 #
GLLIKDDMDLELVLMC*K	C95;M108 C109	0.697747783	Q96SI9 Q96SI9	Q96SI9 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TP11 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3 #
DPETLVGYSMVGC*QR	C135	0.695982957	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TP11 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3 #
VPADTEVVC*APPTAYIDFAR	C42;C79	0.695858938	P60174 P60174	P60174 Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3 #

AAAPAPVSEAVC*R	C456;C491;C367;C450;C394;C290;C131;C454;C336;C373;C469;C151;C166;C160;C131;C395;C408;C394;C123;C472;C386	0.694793866	P20810 P20810 P20810 P20810 E7EVY3 P20810 E7EQA0 E7EQA0 A0A0A0M GB5 E9PDE4 E9PCH5 P20810 H0YD33 H0Y9H6 H0Y7F0 A0A0A0M R45 P20810 P20810 B7Z574 E7EQ12 P20810 P20810	P20810-5 Isoform 5 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-3 Isoform 3 of Calpastatin OS=Homo sapiens GN=CAST # E7EQA0 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PDE4 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PCH5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # H0YD33 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y9H6 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y7F0 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0A0MR45 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-2 Isoform 2 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E7EQ12 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST # Q96TA1 Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 # Q96TA1-2 Isoform 2 of Niban-like protein 1 OS=Homo sapiens GN=FAM129B # J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 # Q07020 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 # Q07020-2 Isoform 2 of 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 # H0YHA7 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # H0YLV5 GMP reductase OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # Q9P2T1 GMP reductase 2 OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # H0YNJ6 GMP reductase OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # H0YNH0 GMP reductase 2 (Fragment) OS=Homo sapiens GN=GMMPR2 PE=1 SV=7 # Q9P2T1-2 Isoform 2 of GMP reductase 2 OS=Homo sapiens GN=GMMPR2 # H0YMB3 GMP reductase OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # F8WAN9 GMP reductase OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # A0A087WWM4 GMP reductase OS=Homo sapiens GN=GMMPR2 PE=1 SV=1 # Q9Y4K4 Mitogen-activated protein kinase kinase kinase 5 OS=Homo sapiens GN=MAP4K5 PE=1 SV=1 # A0A0A0MQR1 Mitogen-activated protein kinase kinase kinase OS=Homo sapiens GN=MAP4K5 PE=1 SV=1 #
GPTKEELC*K	C466;C453	0.687935	Q96TA1 Q96TA1	
GC*GTVLLSGPR	C136;C134;C134;C105;C113	0.679893837	J3QQ67 G3V203 Q07020 Q07020 H0YHA7	
VGIGPGSVC*TTR	C171;C186;C204;C229;C204;C153;C187;C186	0.67558379	H0YLV5 Q9P2T1 H0YNJ6 H0YNH0 Q9P2T1 H0YMB3 F8WAN9 A0A087W WM4	
HC*PDSESR	C418;C418	0.674818934	Q9Y4K4 A0A0A0M QR1	

NESC*SENYTTDFIYQLYSEE GK	C641	0.673212688	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
LLQPDFQPVC*ASQLYPR	C258;C201;C265	0.67314641	Q9UJW0 Q9UJW0 Q9UJW0	Q9UJW0 Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1 # Q9UJW0-2 Isoform 2 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # Q9UJW0-3 Isoform 3 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 #
KC*DLISIPK	C426;C420;C473	0.665186007	Q9ULV4 Q9ULV4 Q9ULV4	Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C #
TIGGGDDSFSTFFFC*ETGAGK	C39;C54	0.665074852	P68366 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
GAFC*DLVWSDPEDVDTWAI SPR	C192;C229;C170	0.660549849	O00743 O00743 O00743	O00743 Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1 # O00743-3 Isoform 3 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C # O00743-2 Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C #
VVMALGDYMGASCHAC*IGG TNVR	C134 C134;M121	0.659112197	P60842 P60842	P60842-2 Isoform 2 of Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 # P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
QEPLGSDSEGVNC*LAYDEAI MAQQDR	C23	0.65888311	F5H6Q1 F5H3F0 J3KR44 Q96FW1	F5H6Q1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # F5H3F0 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # J3KR44 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 # Q96FW1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 #
ATVAPEDVSEVIFGHVLAAGC *GQNPVR	C65	0.651750738	Q9BWD1	Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 #
VLQEALC*VISGVPGLK	C648	0.651016891	Q92616	Q92616 eIF-2-alpha kinase activator GCN1 OS=Homo sapiens GN=GCN1 PE=1 SV=6 #
LNEDMAC*SVAGITSDANVLT NELR	C74;C43;C74;C74;C74;C50	0.643697988	H0YL69 H0YN18 P25789 H0YMZ1 H0YMA1 H0YKT8	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 # H0YMA1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YKT8 Proteasome subunit beta type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
LDTNSDGQLDFSEFLNLIGGL AMAC*HDSFLK	C91	0.635773701	P31949	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 #
WLSDEC*TNAAVFNLSR	C345;C350;C380	0.63090193	O75521 A0A0C4D GA2 O75521	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 #
SIC*TTVLELLDKYLIANATNPE SK	C94	0.62788665	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #

VGVGPGSVC*TTR	C186	0.627335	P36959	P36959 GMP reductase 1 OS=Homo sapiens GN=GMPPR PE=1 SV=1 #
IAVYSC*PFDGMITETK	C244	0.620773344	P50990	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
SQAAPGSSPC*R	C713;C797	0.617870442	Q8N556 Q8N556	Q8N556 Actin filament-associated protein 1 OS=Homo sapiens GN=AFAP1 PE=1 SV=2 # Q8N556-2 Isoform 2 of Actin filament- associated protein 1 OS=Homo sapiens GN=AFAP1 #
ENEITGALLPC*LDESR	C80	0.617774968	Q9Y3Z3	Q9Y3Z3 Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2 # Q9BZG1 Ras-related protein Rab-34 OS=Homo sapiens GN=RAB34 PE=1 SV=1 #
VLAELPQC*LR	C19;C19;C19	0.617025	Q9BZG1 Q9BZG1 A8MYQ9	Q9BZG1-2 Isoform 2 of Ras-related protein Rab-34 OS=Homo sapiens GN=RAB34 # A8MYQ9 Ras-related protein Rab-34# isoform NARR OS=Homo sapiens GN=RAB34 PE=1 SV=2 #
INISEGNC*PER	C54;C54;C54;C5 4;C54	0.616519695	Q15366 Q15366 Q15366 Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
AFVNPFPDYAAAAGALLASG AAEETGC*VRPPATTDEPGLP FHQDGK	C49	0.611604581	Q9NS86	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 #
GEVPC*TVTSASPLEEATLSE LK	C37;C141	0.61108	H7C068 P48047	H7C068 ATP synthase subunit O# mitochondrial (Fragment) OS=Homo sapiens GN=ATP5O PE=1 SV=1 # P48047 ATP synthase subunit O# mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 # Q4VXL4 HCG41426# isoform CRA_c OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E9PBC6 Transforming acidic coiled-coil- containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E7EMZ9 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # D6RAA5 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359-1 Isoform 1 of Transforming acidic coiled-coil- containing protein 2 OS=Homo sapiens GN=TACC2 # Q4VXL8 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3 # O95359-3 Isoform 3 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # O95359-6 Isoform 6 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # O95359-5 Isoform 5 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # H0Y911 Transforming acidic coiled-coil- containing protein 2 (Fragment) OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359-2 Isoform 2 of Transforming acidic coiled-coil- containing protein 2 OS=Homo sapiens GN=TACC2 #
MSESPTPC*SGSSFEETEALV NTAAK	C2573;M2566 C277;M2570 C2573;M644 C2528;M656 C651;M656 C2577;M2521 C663;M2566 C308;M266 C651;M712 C663;M644 C719;M301 C273	0.605853316	Q4VXL4 E9PBC6 E7EMZ9 D6RAA5 O95359 Q4VXL8 O95359 O95359 O95359 O95359 H0Y911 O95359	

VC*EEIAIIPSKK	C35;C35;C35	0.605585299	H0YN88 A0A075B7 16 P08708	H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 #
TVPFC*STFAAFFTR	C386	0.6040875	P29401	P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 # Q9P0V9-2 Isoform 2 of Septin-10 OS=Homo sapiens GN=SEPT10 # Q9P0V9 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EW69 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 # B5ME97 Septin 10# isoform CRA_c OS=Homo sapiens GN=SEPT10 PE=1 SV=2 # E7EX04 Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=1 #
STLIDTLFNTNFEDYESSHFC* PNVK	C100;C100;C10 0;C100;C85	0.60393272	Q9P0V9 Q9P0V9 E7EW69 B5ME97 E7EX04	P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 # Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN # Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 # Q14247-2 Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN #
QIPAITC*IQSQWR	C781	0.603765	P46940	P51116 Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 # Q5SQT8 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 # Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 # P31749 RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2 # P31751 RAC-beta serine/threonine- protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 # P31749-2 Isoform 2 of RAC- alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 # Q9Y243-2 Isoform 2 of RAC-gamma serine/threonine- protein kinase OS=Homo sapiens GN=AKT3 # Q9Y243 RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 PE=1 SV=1 # M0R0P9 RAC-beta serine/threonine- protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=1 #
AYHEQLTVAEITNAC*FEPAN QMVK	C295	0.601314579	Q9BQE3 F5H5D3	Q53GS7 Nucleoporin GLE1 OS=Homo sapiens GN=GLE1 PE=1 SV=2 # P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 # Q96AC1-2 Isoform 2 of Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 # H0YJ34 Fermitin family homolog 2 (Fragment) OS=Homo sapiens GN=FERMT2 PE=1 SV=1 # Q96AC1-3 Isoform 3 of Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 # Q96AC1 Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1 #
SCYDLSC*HAR	C471	0.601116453	P41250	
HC*SQVDSVR	C112;C112;C11 2	0.599309472	Q14247 Q14247 Q14247	
IYGETPEAC*R	C282	0.599071698	P51116	
NYLPAINGIVFLVDC*ADHSR	C102;C102	0.598959764	Q5SQT8 Q9NR31	
TFC*GTPEYLAPEVLEDNDYGR	C310;C311;C24 8;C307;C307;C2 49	0.597965864	P31749 P31751 P31749 Q9Y243 Q9Y243 M0R0P9	
VQDITMQWYQQLQDASMQC *VLTFEGLTNSK ELDLSNNC*LG DAGILQLVES VR	C400  C409	0.597469707  0.596578504	Q53GS7  P13489	
MQHLNPDQPQLIPEQITTDITPE C*LVSPR	C520;M498 C520;M451 C473;M498 C520	0.596374505	Q96AC1 H0YJ34 Q96AC1 Q96AC1	



AVLFC*LSEDKK	C77;C22;C39;C39	0.589861417	E9PK25 G3V1A4 P23528 E9PP50	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 # O95671-3 Isoform 3 of N-acetylserotonin O- methyltransferase-like protein OS=Homo sapiens GN=ASMTL # O95671-2 Isoform 2 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL # O95671 N-acetylserotonin O- methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3 # A5A3E0 POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 #
AEAGEAGQATAEAEAC*HR	C216;C258;C274	0.589591277	O95671 O95671 O95671	P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 # A0A087X1Z3 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1 # Q9UL46 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 # P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 # C9JAK5 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=1 # Q96EY8 Cob(I)yrinic acid a#-c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # S4R3P5 Cob(I)yrinic acid a#-c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # F5H4Z7 Cob(I)yrinic acid a#-c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 # P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6- phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
LC*YVALDFEQEMATVASSSS LEK	C917	0.589348111	A5A3E0	
DAFEHIVTQFSSVPVSVVSDS YDIYNAC*EK	C287	0.58445128	P43490	
C*GFLPGNEK	C106;C91	0.584313878	A0A087X1 Z3 Q9UL46	
TWYVQATC*ATQGTGLYEGL DWLSNELSK	C159;C132	0.582842527	P18085 C9JAK5	
IQCTLQDVGSALATPC*SSAR	C132;C80;C132	0.582770959	Q96EY8 S4R3P5 F5H4Z7	
SGIQPLC*PER	C341	0.581320762	P42166	
AVSTGVQAGIPMPC*FTTALS FYDGYR	C409 C422;M407	0.578751016	P52209 P52209	
THEAEIVEGENHTYC*IR	C2191;C2172;C2199	0.576945039	P21333 Q60FE5 P21333	
FTSGAFLSPSVSQEC*R	C1051;C1068;C1068;C107	0.572856661	P52948 P52948 P52948 H7C3P6	
C*SPIGVYTS GK	C354;C397	0.571920863	B1AHB1 P33992	

AQLNIGNVLPVGTMPGIVC C*LEEKPGDR	C115 C115;M107	0.57127	E9PKU4 E9PKZ0 G3V1A1 P62917	E9PKU4 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 # E9PKZ0 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 # G3V1A1 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=1 # P62917 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 #
VSLDPELEEALTSASDTELC* DLAAILGMHNLITNTK	C132	0.569628384	Q9NYL9	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 # O14929 Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1 # A0A0A0MR02 Voltage-dependent anion- selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 # P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 # P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # P21281 V-type proton ATPase subunit B# brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 # Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # A8MU58 Aminoacyl tRNA synthase complex- interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 # Q8IU81 Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens GN=IRF2BP1 PE=1 SV=1 # Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 # P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha- aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 # A0FGR8-2 Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 # H7BX11 Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # Q9BXJ9 N-alpha-acetyltransferase 15# NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 # P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 #
VDFNFC*VEADVEGK	C101	0.569517233	O14929	
PMC*IPPSYADLGK	C13;C13	0.568422791	A0A0A0M R02 P45880	
VDDEILGFISEATPLGGIQAAS TESC*NQQLDLALCR	C561	0.566663532	P42166	
GC*WDSIHVVEVQEK	C147;C147;C17 6;C135;C173	0.565985161	P47756 P47756 B1AK88 B1AK87 B1AK85	
VNQAIWLLC*TGAR	C155;C176;C15 5	0.565274356	P46782 M0R0R2 M0R0F0	
GPVLAEDFLDIMGQPINPQC *R	C162	0.563716942	P21281	
RPLNPLASGQGTSEENTFY S WLEGLC*VEK	C241	0.563557683	Q96HE7	
FSIQTMC*PIEGEGNIAR	C127	0.562990564	A8MU58	
LFTEYPC*GSGNVYAGVLAV A R	C280	0.562534514	Q8IU81	
ADIIHAC*DIVEDAAIAYGYNNI QMTLPK	C362	0.559716787	Q9NSD9	
GSDC*GIVNVNIPTSGAEIGG AFGGEK	C450;C478	0.559298595	P49419 P49419	
AC*DLPAAVHFPDTER	C153;C123	0.558097643	A0FGR8 H7BX11	
LFNTAVC*ESK	C721	0.5559029	Q9BXJ9	
LGEWVGLC*K	C92	0.555277017	P25398	

DASALLDPMEC*TDTAEEQR	C287 C114;M285 C287;M112	0.55334725	Q9BTE3 Q9BTE3 Q9BTE3	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 # Q9BTE3-3 Isoform 3 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP # Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP # P61077-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # H9KV45 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 # D6RAH7 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # A0A0A0MQU3 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # D6RFM0 Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=3 SV=1 # A0A087WY85 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-5 Isoform 5 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 # E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 # E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 # A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 # Q9UFC0 Leucine-rich repeat and WD repeat-containing protein 1 OS=Homo sapiens GN=LRWD1 PE=1 SV=2 # P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 # P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 # Q9Y5P4 Collagen type IV alpha-3-binding protein OS=Homo sapiens GN=COL4A3BP PE=1 SV=1 # Q9Y5P4-3 Isoform 3 of Collagen type IV alpha-3-binding protein OS=Homo sapiens GN=COL4A3BP # Q9Y5P4-2 Isoform 2 of Collagen type IV alpha-3-binding protein OS=Homo sapiens GN=COL4A3BP #
VLLSICSLLC*DPNPDDPLVPE IAR	C113;C111;C111; C105;C82;C82 ;C111;C82;C112 ;C111	0.553057911	P61077 P61077 P61077 H9KV45 P62837 D6RAH7 A0A0A0MQU3 QU3 D6RFM0 A0A087WY85 P62837	
YSDVEVPASVTGYSFASDGD SGTC*SPLR	C430;C430;C430; C430;C430;C430; C430;C430	0.546331308	P35611 P35611 P35611 E7ENY0 P35611 E7EV99 P35611 P35611	
SVPTTQC*LDNSK	C226;C226	0.542241489	A0A087WV66 V66 P46013	
AC*ASPSAQVEGSPVAGSDG SQPAVK	C249	0.541908938	Q9UFC0	
VIGSGC*NLDSAR	C192;C164;C163	0.540951138	P00338 P07195 P00338	
ISLGLPVGAVINC*ADNTGAK	C28	0.540419123	P62829	
SEDETEYGC*R	C65;C193;C65	0.538417628	Q9Y5P4 Q9Y5P4 Q9Y5P4	

NC*SSPEFSK	C58;C53;C53	0.535213393	B0QZ18 Q99829 F2Z2V0	B0QZ18 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # Q99829 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # F2Z2V0 Copine-1 (Fragment) OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # P50213-2 Isoform 2 of Isocitrate dehydrogenase [NAD] subunit alpha#
C*SDFTEEICR	C273;C351	0.534683092	P50213 P50213	mitochondrial OS=Homo sapiens GN=IDH3A # P50213 Isocitrate dehydrogenase [NAD] subunit alpha# mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 # Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine- protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
QGFWEFETLQQQEC*K	C259;C259	0.532733127	Q06124 Q06124	A0A024R571 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=1 # Q9H4M9 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 # C9JC03 EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=1 SV=1 #
FMC*AQLPNPVLDISIIIDTPGI LSGEK	C152;M137 C138;M151 C152	0.532049519	A0A024R5 71 Q9H4M9 C9JC03	Q96EY5-2 Isoform 2 of Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A # Q96EY5 Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A PE=1 SV=1 #
SPLPLGFSPVC*DPMSDK	C90	0.53172294	Q96EY5 Q96EY5	Q06210-2 Isoform 2 of Glutamine--fructose-6- phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 # Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 #
VDSTTC*LFPVEEK	C246;C264	0.529734243	Q06210 Q06210	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 #
YIYDQC*PAVAGYGPIQLPD YNR	C453	0.527036248	P31930	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
FSPNSSNPIIVSC*GWDK	C168	0.526152047	P63244	Q16555-2 Isoform 2 of Dihydropyrimidinase- related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase- related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
FQLTDC*QIYEVLSVIR	C143;C179	0.52070371	Q16555 Q16555	P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 #
NCGC*LGASPNLEQLQEENL K	C34	0.519923887	P54136	

				Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EUU4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 # F2Z2G2 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 # C9JZW3 Elongation factor 1-beta (Fragment) OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 #
EAVQC*VQELASPSLLFIVR	C1265;C1225;C1179;C1266;C1178;C1069;C1226;C1101;C1272;C1102;C1070	0.517846247	Q04637 Q04637 E9PGM1 Q04637 Q04637 E7EUU4 Q04637 Q04637 E7EX73 Q04637	
SYIEGYVPSQADVAVFEAVSS PPPADLC*HALR	C50;C50;C50	0.516203529	P24534 F2Z2G2 C9JZW3	
VAC*AEEWQESR	C87	0.514722564	O75663	
VGESNLNGDEPTQC*SR	C570;C549	0.514064871	Q96T76 Q96T76	
GFEVVMTEPIDEYC*VQQLK	C521	0.512965128	P08238	
DSAQC*AAIAER	C376	0.51083721	Q96RS6	
RPTEIC*ADPQFIIGGATR	C82	0.510324567	P17655	
MLPDKDC*R	C118;C63;C80;C80	0.509028629	E9PK25 G3V1A4 P23528 E9PP50	
ISAFGYLEC*SAK	C159;C159;C159	0.506484261	Q5JR08 P08134 E9PQH6	
ELETVC*NDVLSLLDK	C97	0.504671961	Q04917	
SSTETC*YSAIPK	C2477	0.504258869	O75369	
FTLDC*THPVEDGIMDAANFE QFLQER	C25	0.503927773	P35268	

IISNASC*TTNCLAPLAK	C152	0.503789344	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
NC*LNPQFSK	C54	0.501370452	O75131	O75131 Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 #
AHEILPNLVCC*SAK	C149	0.500546392	P50990	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
FSFC*CSPEPEAEAEAAAGP GPCER	C26;C26	0.498521982	E7EMC7 Q13501	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
DLNC*VPEIADTLGAVAK	C22	0.498274093	O14744	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 #
ALANVNIGSLIC*NVGAGGPA PAAGAAPAGGPAPSTAAAPA EEK	C36;C61	0.496744238	P05386 P05386	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 # P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 #
QVLMGYPNPDTC*PEVGFFD VLGNDR	C129	0.495659502	Q9H3P7	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 #
LNQVC*FDDDGTSPPQDR	C422;C299	0.494075987	Q8N1F7 Q8N1F7	Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 # Q8N1F7-2 Isoform 2 of Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 #
VC*NYGLTFTQK	C66;C65	0.493432963	Q9Y277 Q9Y277	Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 # Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #
LMDLDVEQLGIPEQEYSC*VV K	C135	0.493063867	P12004	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 #
HGSQDC*GSR	C148;C148	0.492315631	C9JRJ5 Q9UGP4	C9JRJ5 LIM domain-containing protein 1 OS=Homo sapiens GN=LIMD1 PE=1 SV=1 # Q9UGP4 LIM domain-containing protein 1 OS=Homo sapiens GN=LIMD1 PE=1 SV=1 #
QVQSLTC*EVDALK	C328;C328	0.492257745	B0YJC4 P08670	B0YJC4 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=1 # P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 #
EEHLC*TQR	C270;C233;C212; C208;C217	0.490184162	J3KN67 P06753 A0A087W WU8 Q5VU61 Q5HYB6	J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 # P06753-2 Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 # A0A087WWU8 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 # Q5VU61 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 # Q5HYB6 Epididymis luminal protein 189 OS=Homo sapiens GN=DKFZp686J1372 PE=1 SV=1 #
LEEEDEDEEDGESGC*TFLV GLIQK	C405	0.48642709	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
FPEELTQTFMSC*NLITGMFQ R	C389 C339;M387	0.485816669	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
TYAIC*GAIR	C56;C56;C56	0.482879954	Q8WVC2 Q9BYK1 P63220	Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # Q9BYK1 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # P63220 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 #
LGGSLIVAFEGC*PV	C146;C163	0.481396193	P60981 P60981	P60981-2 Isoform 2 of Dextrin OS=Homo sapiens GN=DSTN # P60981 Dextrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
LC*YVALDFEQEMAMVASSS SLEK	;C880	0.48041508	P01615 P0CG39	P01615 Ig kappa chain V-II region FR OS=Homo sapiens PE=1 SV=1 # P0CG39 POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 #

VDLNSNGFIC*DYELHELK	C33	0.478471254	P13797	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 # Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC # Q15149 OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
EALAEASAWC*YLYGTGSVA GVYLPGSR	C3652;C3670;C3662;C3821;C3684;C3707;C3711;C3688;C3684	0.478019457	Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149 Q15149	
SGETEDTFIADLVVGLC*TGQIK	C389	0.477711301	P06733	P06733 Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 # Q86TX2 Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 # A0A087X0W7 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # P49753-2 Isoform 2 of Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 # P49753 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 # A0A087WT95 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # G3V4F2 Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 # P53621-2 Isoform 2 of Coatomer subunit alpha OS=Homo sapiens GN=COPA # P53621 Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 # I3L0K2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # I3L3M7 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 #
SEFYANEAC*KR	C339;C339;C219;C401;C381;C313	0.477046351	Q86TX2 A0A087X0W7 P49753 P49753 A0A087WT95 G3V4F2	
TTYQALPC*LPSMYGYPNR	C984	0.47662424	P53621 P53621	
SWC*PDCVQAEPVVR	C43;C43;C43	0.476462611	I3L0K2 I3L3M7 Q9BRA2	
TLQNTMNLGLQNAC*DEAIY QLGLDLEEEIEEDAGLNG GLGR	C109	0.476188886	P11216	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 # Q8NBF2 NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 # P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 # Q9NZM1-2 Isoform 2 of Myoferlin OS=Homo sapiens GN=MYOF # Q9NZM1 Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 # P49321-3 Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 # P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 # P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
AILFSQPLQITDTQQGC*IAPV ELR	C716	0.475953812	Q8NBF2	
EMQNLSFQDC*YSSK	C111	0.475384628	P30084	
ASLLSAPPC*R	C1383;C1425	0.474553685	Q9NZM1 Q9NZM1	
KPTDGASSNC*VTDISHLVR	C710;C708	0.473463344	P49321 P49321	
EENVGLHQTLQTLNELNC*I	C283;C109;C247	0.473373178	P67936 K7EPB9 P67936	
ADEASELAC*PTPK	C2202	0.47324235	P49327	

NNIDVFYFSC*LIPLNVLVVED GK	C761;C832;C81 8	0.473209051	P63010 P63010 P63010	P63010-3 Isoform 3 of AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 # P63010-2 Isoform 2 of AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 # P63010 AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 #
YFTQGNC*VNLTEALSLYEEQ LGR	C318;C265	0.471195431	P52788 P52788	P52788 Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 # P52788-2 Isoform 2 of Spermine synthase OS=Homo sapiens GN=SMS #
STLTDSLVC*K	C41	0.470511812	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
GEELSC*EER	C38;C38	0.46881161	P31947 P31947	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 # P31947-2 Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN #
LHDAIVEVWTC*LLR	C483;C470;C47 0;C470;C470;C4 83;C483;C470	0.46763985	O00429 O00429 O00429 O00429 O00429 G8JLD5 O00429	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 # O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 # O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L #
ELEVLLMC*NK	C109;M90 C91 C91;M108	0.466543333	P62910 F8W727 D3YTB1	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #



				G3V2E7 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # E7EVH7 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 # Q07866-8 Isoform S of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-6 Isoform N of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q9NSK0 Kinesin light chain 4 OS=Homo sapiens GN=KLC4 PE=1 SV=3 # C9J8T5 Kinesin light chain 4 (Fragment) OS=Homo sapiens GN=KLC4 PE=1 SV=2 # Q07866-5 Isoform K of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # F8W6L3 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # Q9NSK0-4 Isoform 4 of Kinesin light chain 4 OS=Homo sapiens GN=KLC4 # Q07866 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=2 # Q07866-2 Isoform C of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-7 Isoform P of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # G3V5R9 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # Q9NSK0-3 Isoform 3 of Kinesin light chain 4 OS=Homo sapiens GN=KLC4 # Q07866-10 Isoform D of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-3 Isoform G of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # G3V3H3 Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=1 # Q07866-9 Isoform I of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-4 Isoform J of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 #
LC*QENQWLR	C114;C286;C114;C114;C113;C91;C114;C114;C113;C114;C114;C114;C114;C131;C114;C114;C114;C114	0.466063577	G3V2E7 E7EVH7 Q07866 Q07866 Q9NSK0 C9J8T5 Q07866 F8W6L3 Q9NSK0 Q07866 Q07866 Q07866 G3V5R9 Q9NSK0 Q07866 Q07866 G3V3H3 Q07866 Q07866	
QAFTDVATGSLGQGLGAAC* GMAITGK	C133	0.46600936	P29401	P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 #
LTWHSC*PEDEAQ	C177	0.465821415	Q13185	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 #
SVLC*STPTINIPASPFMQK	C22	0.465593034	Q96KB5 Q96KB5	Q96KB5 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 # Q96KB5-2 Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK #
AALEALGSC*LNNK	C91;C70	0.465528184	P34897 P34897	P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 # P34897-3 Isoform 3 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 #
AGC*AVTSLLESELTK	C1218;C1203;C1218;C1227;C1183;C1227	0.464304517	O60610 O60610 A0A140T8Z0 A0A0G2JH68 H9KV28 O60610	O60610-3 Isoform 3 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # O60610-2 Isoform 2 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # A0A140T8Z0 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # A0A0G2JH68 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # H9KV28 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 # O60610 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 #

YDSYESC*DSR	C67;C128;C117; C147;C94;C66	0.464112165	Q9ULX6 Q9ULX6 M0QYT7 M0R010 V9GZ50 M0R1Y5	Q9ULX6-2 Isoform 2 of A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L # Q9ULX6 A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3 # M0QYT7 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 # M0R010 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 # V9GZ50 A kinase (PRKA) anchor protein 8-like# isoform CRA_c OS=Homo sapiens GN=AKAP8L PE=1 SV=1 # M0R1Y5 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=2 #
FMPV IQDNPSGWGPC*AVP EQFR	C19 C19;M5	0.463137356	O15371 O15371 O15371	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D #
GTPEQPQC*GFSNAVQILR	C67	0.463091557	Q86SX6	Q86SX6 Glutaredoxin-related protein 5# mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 #
AFAFVTFADDQIAQSLC*GED LIIK	C244;C244;C244; C244;C244	0.462542697	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
LQGINC*GPDFTSPFANLGR	C662;C622;C57 5;C662;C575;C4 66;C622;C498;C 669;C498;C466	0.461957448	Q04637 Q04637 E9PGM1 Q04637 Q04637 Q04637 E7EUU4 Q04637 Q04637 E7EX73 Q04637	Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EUU4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 #
LLEGDGGPNTGGMGAYC*PA PQVSNLLLLK	C237	0.458377584	P22102	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 #
VAASC*GAIQYIPTELDQVRK	C134	0.457835549	Q7L2H7	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #
WTQTLSELDAVPFC*VNFR	C188	0.455711794	Q9Y266	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 #

LLLC*GGAPLSATTQR	C450	0.451548842	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # Q9BTT0 Acidic leucine-rich nuclear phosphoprotein 32 family member E
C*PNLTYLNLSGNK	C87;C39	0.451382014	Q9BTT0 Q9BTT0	OS=Homo sapiens GN=ANP32E PE=1 SV=1 # Q9BTT0-3 Isoform 3 of Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E # P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 # P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
SC*GSSTPDEFPTDIPGTK	C105	0.450184977	P41091	
FLGPEIFFHPEFANPDFTQPIS EVDVEVIQNC*PIDVR	C307	0.449502147	P61158	
IAEDLGGPYVWGQYDLLVLP PSFPYGGMENPC*LTFVTPTL LAGDK	C275	0.449021193	P09960	P09960 Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 #
KITIADC*GQLE	C161	0.448665	P62937	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 # Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
KDC*EVMMIGLPGAGK	C497	0.44802	Q00839 Q00839	
FSFCC*SPEPEAEAEAAAGP GPCER	C27;C27	0.445653611	E7EMC7 Q13501	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q9BV86 N-terminal Xaa-Pro-Lys N- methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 # Q9NQZ2 Something about silencing protein 10 OS=Homo sapiens GN=UTP3 PE=1 SV=1 #
IIC*SAGLSLLAEER	C195;C107	0.44521	Q9BV86 S4R338	
TSAAAC*AVTDLSDSDSDFDEK	C359	0.445034342	Q9NQZ2	
TVDSQGPTPVC*TPTFLER	C237	0.444492547	Q9BYG3	Q9BYG3 MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 # P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 # P31153 S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 # P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 # G3V1V0 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # G8JLA2 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660-2 Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 # B7Z6Z4 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 # J3KND3 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # F8W1R7 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 #
SGDAAIVDMVPGKPMC*VES FSDYPLGR	C411;C390	0.444090492	P68104 P68104	
IC*DQISDAVLDAHLQQDPDA K	C34	0.443017032	P31153	
AGAIAPC*EVTVPAQNTGLGP EK	C119	0.442084961	P05388	
ATDYPC*LLILDQPNEFETLR	C145	0.441241135	Q9NVG8	
ILYSQC*GDVMR	C32	0.440960873	G3V1V0 G8JLA2 P60660 B7Z6Z4 P60660 J3KND3 F8W1R7	
VGEGPGVC*WLAPEQTAGK	C151	0.440519824	Q9H4A4	Q9H4A4 Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 #

NPVSQC*MR	C50;C50;C50;C50;C50	0.439766961	A0A087X260 A0A087X260 A0A087WYY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
VTDGALVVVDCVSGVC*VQT ETVLR	C136	0.439232782	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # P61289-3 Isoform 3 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 # B3KQ25 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 # P61289 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 # K7ESG5 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 # P61289-2 Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 # P59998 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 # A0A0A6YYG9 Protein ARPC4-TLL3 OS=Homo sapiens GN=ARPC4-TLL3 PE=4 SV=1 # P59998-2 Isoform 2 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 # F8WCF6 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4-TLL3 PE=3 SV=1 # P59998-3 Isoform 3 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 # F8WDD7 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=4 SV=1 # P08559 Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 # P08559-4 Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 # P08559-2 Isoform 2 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 # G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # H3BRW9 Dual-specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=1 # Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 # Q96JB2 Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3 #
LDEC*EEAFQGTK	C103;C31;C92;C36;C92	0.4378561	P61289 B3KQ25 P61289 K7ESG5 P61289	
ATLQAALC*LENFSSQVVER	C21;C21;C21;C21;C40;C21	0.437447999	P59998 A0A0A6YYG9 P59998 F8WCF6 P59998 F8WDD7	
NFYGGNGIVGAQVPLGAGIAL AC*K	C181;C219;C188	0.437065687	P08559 P08559 P08559	
LC*DFGVSGQLIDSMANSFVG TR	C114;C31;C207;C181;C211	0.436890843	G5E9C7 H3BRW9 Q02750 Q02750 P36507	
SLHDALC*VLAQTVK	C395	0.434958869	P78371	
AAAENLPVPAELPIEDLC*SLT SQSLPIELTSVVPESTEDILLK	C65	0.433809005	Q96JB2	

AVFPEGPC*EEPLQLR	C900;C900;C655;C660;C660;C655	0.43371	Q96P48 Q96P48 E7EU13 Q96P48 Q96P48 Q96P48	Q96P48 Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=3 # Q96P48-3 Isoform 3 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # E7EU13 Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=1 # Q96P48-2 Isoform 2 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # Q96P48-1 Isoform 1 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # Q96P48-4 Isoform 4 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 #
NC*IVLIDSTPYR	C100	0.433621623	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 # D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
SC*PSFSASSEGTR	C9;C9;C9	0.432960909	D6RCP9 P27707 D6RFG8	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 # P51878-3 Isoform 3 of Caspase-5 OS=Homo sapiens GN=CASP5 # P49662-4 Isoform 4 of Caspase-4 OS=Homo sapiens GN=CASP4 # P51878-6 Isoform 6 of Caspase-5 OS=Homo sapiens GN=CASP5 # P51878-5 Isoform 5 of Caspase-5 OS=Homo sapiens GN=CASP5 # P51878-2 Isoform 2 of Caspase-5 OS=Homo sapiens GN=CASP5 # P49662 Caspase-4 OS=Homo sapiens GN=CASP4 PE=1 SV=1 # P51878 Caspase-5 OS=Homo sapiens GN=CASP5 PE=1 SV=3 # P49662-2 Isoform 2 of Caspase-4 OS=Homo sapiens GN=CASP4 # A0A087WZP8 Caspase OS=Homo sapiens GN=CASP4 PE=1 SV=1 # O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
AHEILPNLVC*CSAK	C148	0.431171494	P50990	
VIIVQAC*R	C173;C258;C245;C328;C257;C258;C315;C202;C211	0.43108	P51878 P49662 P51878 P51878 P51878 P49662 P51878 P49662 A0A087WZP8	
LMWLFGC*PLLLDDVAR	C66	0.430125767	O15067	
AVDGE GAPAPESSGEP AEDE GPTDTAEAGSDPQAEQLLEE QVPC*GTAHEK	C631	0.429472817	O43823	O43823 A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1 #
SEGGFIWAC*K	C269	0.428981226	O75874	O75874 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 #
QMFEPVSC*TFTYLLGDR	C34;C34	0.426245536	O95571 M0QXB5	O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # M0QXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 #
ALLVTASQC*QQPAENK	C93;C92	0.425283334	Q01518 Q01518	Q01518 Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 # Q01518-2 Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 #
NAFAC*FDEEATGTIQEDYLR	C108;C114;C109	0.424402883	P19105 J3QRS3 O14950	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 # J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 # O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 #

IPC*DSPQSDPVDTPSTK	C891;C1250;C1251	0.423896554	P46013 A0A087WV66 V66 P46013	P46013-2 Isoform Short of Antigen KI-67 OS=Homo sapiens GN=MKI67 # A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
IIPLEEGLQLPSPTATSQLPL ESDAVEC*LNYQHVK	C132;C132	0.421889618	P61978 P61978	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK #
ECENCDC*LQGFQLTHSLGG GTGSGMGTLLISK	C476	0.419563574	A0A0B4J269 69	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 #
VQENSAYIC*SR	C585	0.418971076	Q9Y3T9	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 #
VADSSPFALELLISDDC*FVLD NGLCGK	C267;C282	0.418765436	P40121 P40121	P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 #
CPALYWLSGLTC*TEQNFISK	C56	0.417805	P10768	P10768 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 #
NTVLC*NVVEQFLQADLAR	C70	0.417107755	Q14258	Q14258 E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 #
LTESPC*ALVASQYGWSGNM ER	C645	0.416867071	P14625	P14625 Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 #
FIC*TTSIQNR	C20;C20	0.416479775	P53396 P53396	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 # P53396-2 Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY #
LQEALDAEMLEDEAGGGGA GPGGAC*K	C57;C57	0.416426654	H3BQZ7 Q1KMD3	H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #
FLSQIESDC*LALLQVR	C794	0.415481123	P52789	P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
VGVDYEGGGC*R	C727;C680	0.413926574	Q02809 Q02809	Q02809-2 Isoform 2 of Procollagen-lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 # Q02809 Procollagen-lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 #
TDC*SPIQFESAWALTNIASG TSEQTK	C133	0.413581846	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
SQSPAASDC*SSSSSSASLPS SGR	C179;C121	0.41292302	O95817 C9JFK9	O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 # C9JFK9 BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=1 SV=1 #
C*DSSPDSAEDVRK	C132	0.411615334	P02765	P02765 Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 #
MYGISLC*QAILDETKGDYK	C324	0.411480347	P04083	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 #

					H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
LC*EPEVLNSLEETYSPPFR	C177;C261;C261;C106;C224;C261;C261;C227;C261;C261;C242	0.410989482	H0YJA2 Q6PJT7 Q6PJT7 G3V5I6 Q6PJT7 G3V256 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7		
GYDFC*QVLQWFAER	C175;C175	0.410462136	Q9H223 A0A087W UA5	Q9H223 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 # A0A087WUA5 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 # H0YJA0 Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 # G3V2G3 Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 # G3V253 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=1 # G3V336 Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 # Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 #	
QSELEPVVSLVDVLEEDDEELE NEAC*AVLGGSDSEK	C35;C35;C35;C35;C35	0.409679209	H0YJA0 G3V2G3 G3V253 G3V336 Q8N806	P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 # A0A0A0MRN5 Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=1 # Q9NZN2 Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3 # Q9NZN2-2 Isoform 2 of Opioid growth factor receptor OS=Homo sapiens GN=OGFR #	
VADSSPFALELLISDDCFVLD NGLC*GK	C275;C290	0.406071158	P40121 P40121	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #	
TGTQEVGQDPGEAVQPC*R	C391;C443;C443	0.405559139	A0A0A0M RN5 Q9NZN2 Q9NZN2	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #	
VC*NQIEFLNTEFK	C39	0.403155	O14879		
VTEDENDEPIEPSDDGTVL LSTVTAQFPGAC*GLR	C39;C39;C39;C39;C39	0.401602994	A0A087X 60 A0A087W YY0 B1AKP7 Q13148 G3V162		

AESPEEVAC*R	C1401;C1401;C1392	0.400619778	Q7Z6Z7 Q7Z6Z7 Q7Z6Z7	Q7Z6Z7 E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 # Q7Z6Z7-2 Isoform 2 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 # Q7Z6Z7-3 Isoform 3 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 #
NTLANSC*GTGIR	C393;C416	0.399405932	Q96BF6 Q96RE7	Q96BF6 Nucleus accumbens-associated protein 2 OS=Homo sapiens GN=NACC2 PE=1 SV=1 # Q96RE7 Nucleus accumbens-associated protein 1 OS=Homo sapiens GN=NACC1 PE=1 SV=1 #
EPFDLGEPEQSNNGGFPC*TT APK	C213;C277;C229	0.398541486	Q99961 Q99961 Q99961	Q99961-3 Isoform 3 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 # Q99961 Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 # Q99961-2 Isoform 2 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 #
SC*NGPVLVGGSPQGGVDIEE VAASNPELIFK	C162;C162;C162	0.398320038	Q96I99 E9PDQ8 Q96I99	Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
VAEPELMGTPDGTC*YPPPP VPR	C1889 C1826;M1882	0.397996211	F8VPD4 P27708	F8VPD4 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 # P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
DLTTAGAVTQC*YR	C80;C109;C80;C109	0.397715113	M0R3D6 M0R117 M0R1A7 Q02543	M0R3D6 60S ribosomal protein L18a (Fragment) OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R117 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R1A7 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 #
TYLLDGSC*MVEESGTLESQLEATK	C2238;C2233;C2213;C2218	0.397485563	Q13813 Q13813 Q13813 A0A0D9SF54	Q13813-2 Isoform 2 of Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 # Q13813 Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 # Q13813-3 Isoform 3 of Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 # A0A0D9SF54 Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=1 #
NWYVQPSC*ATSGDGLYEGL TWLTSNYK	C155	0.396439137	P62330	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 #
GISC*MNTTLESSEPFK	C242	0.396434389	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 #
FSHQGVQLIDFSPC*ER	C384;C384	0.395354808	P55884 P55884	P55884 Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 # P55884-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B #
GNSPPSSGEAC*R	C179;C194	0.392689014	P41227 P41227	P41227-2 Isoform 2 of N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 # P41227 N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1 #
TDDYLDQPC*YETINR	C202	0.392427968	P50395	P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 #
VLFPGCTPPAC*LLDGLVR	C414;C440	0.391968834	Q66K74 Q66K74	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 #



STFFNVLTNQASAENFPFC* TIDPNESR	C75;C55	0.389872635	J3KQ32 Q9NTK5	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 #
LC*PGGQLPFLLYGTEVHTDT NK	C59	0.389729332	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
NWYIQATC*ATSGDGLYEGL DWLSNQLR	C159	0.388304807	P84077	P84077 ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2 #
VPAFEGDDGFC*VFESNAIAY YVSNEELR	C68;C118	0.388138147	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
IC*DPYAWLEDPDSEQTK	C25	0.387766103	P48147	P48147 Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 #
VGVGTC*GIADKPMQYQDT SK	C214	0.387689967	O75940	O75940 Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 #
GAEPETGSAVSAAQC*QVGP TR	C90;C69	0.385687915	E7ERK9 Q9U110	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9U110 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
EKIEAELQDIC*NDVLELLDK	C94;C96	0.384729588	P31946 P31946	P31946-2 Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB # P31946 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 #
YEAAPFLSPC*GR	C143;C98	0.384045348	H0YF29 Q6P1X6	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 # Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 #
TIIP LISQC*TPK	C212	0.383256517	P40926	P40926 Malate dehydrogenase# mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 #
C*LEELVFGDVENDE DALLR	C90	0.381132372	Q9Y5J1	Q9Y5J1 U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 #
DIC*NDVLSLEK	C94	0.381103214	P63104	P63104 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 #
VFIMDNC*EELIPEYLN FIR	C496;M371 C374	0.380124649	P07900 P07900	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
LC*YVALDFEQEMATAASSSS LEK	C217	0.380054872	P60709 Q6S8J3	P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 #
GMYGIENEVFLSLPC*ILNAR	C294	0.377188618	P07195	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 #
YADLTEDQLPSC*ESLK	C153	0.375015315	P18669	P18669 Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 #
C*DISLQFFLPFSLGK	C157	0.374544529	P13010	P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 #
C*ELSSSVQTDINLPYL T MDS SGPK	C317	0.373744901	P38646	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 #
IEEDVVVTD SGIELLTC*VPR	C403;C426;C46 7	0.372875012	P12955 P12955 P12955	P12955-3 Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955-2 Isoform 2 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
SYC*NDQSTGDIK	C106	0.371121404	P00492	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #

SC*SGVEFSTSGSSNTDTGK	C47;C47	0.370446639	A0A0A0MR02 R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 # P02545-5 Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-4 Isoform 4 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-6 Isoform 6 of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545-2 Isoform C of Prelamin-A/C OS=Homo sapiens GN=LMNA # P02545 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 # P02545-3 Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA # Q5TCI8 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 #
AQNTWGC*GNSLR	C423;C410;C522;C522;C522;C441	0.370351996	P02545 P02545 P02545 P02545 P02545 Q5TCI8	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 # P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # Q5T280 Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 #
LEGDLTGPSVGVVEVPDVELE C*PDAK	C1900	0.368977574	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
C*SEGSFLLTFFPRPVTVEPM DQLDDEEGLPEK	C119	0.368239211	Q15233 Q15233	Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 # P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # Q5T280 Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 #
TIAEC*LADELINAAK	C172;C193;C172	0.368167205	P46782 M0R0R2 M0R0F0	Q5T280 Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 #
LNQQQHPDC*K	C239	0.368083051	Q5T280	Q5T280 Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 #
ICPVETLVEEAIQC*AEK	C225	0.367151458	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
EVFSSC*SSEVVLSGDDEEY QR	C108	0.367039716	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
TDGEGEDPEC*LGE GK	C340	0.366714947	Q8WZA9	Q8WZA9 Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1 #
AC*ANPAAGSVILLENLR	C80;C108	0.366206111	P00558 P00558	P00558-2 Isoform 2 of Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 # P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
LGYAGNTEPQFIIPSC*IAIK	C34	0.36568	P61158	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
FC*DNVWTFVLNDVEFR	C68	0.364131175	P52657	P52657 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 #
AAAGELQEDSGLC*VLAR	C172	0.36372234	Q96C19	Q96C19 EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1 #
IKADPDGPEAQAEAC*SGER	C18;C18;C18	0.363644125	D6RCB9 D6RC52 Q9NX24	D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # D6RC52 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 # Q92688-2 Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B # Q92688 Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 #
SLDLFNC*EVTNLNDYR	C123;C123	0.363608084	Q92688 Q92688	Q92688-2 Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B # Q92688 Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 #

QMEKDETVSDC*SPHIANIGR	C206;C206;C235;C194;C232	0.362146929	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 #
AEGSDEVANAVLDGADC*IMLSGETAK	C358;C358	0.361697954	P14618 P14618	Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 # P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # H7C2S8 Procollagen-lysine#2-oxoglutarate 5-dioxygenase 3 (Fragment) OS=Homo sapiens GN=PLOD3 PE=1 SV=1 # O60568 Procollagen-lysine#2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 # O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 # P55072 Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 # E7ERF2 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # Q16630-2 Isoform 2 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 # Q16630-3 Isoform 3 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 # F8WJN3 Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=1 # Q16630 Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
LEDVENLGC*R	C329;C329	0.361390116	Q9UJX3 Q9UJX3	
NLSDLIDLVPVSLC*EDLLSSVDQPLK	C36;C36;C65;C24;C62	0.361027535	P47756 P47756 B1AK88 B1AK87 B1AK85	
GLDYEGGGC*R	C217;C691	0.360555	H7C2S8 O60568	
HFVLDEC*DK	C197	0.360216439	O00148	
EDEEESLNEVGYDDIGGC*RK	C209	0.360156294	P55072	
SLHDALC*VVK	C397;C397	0.356639851	E7ERF2 P17987	
ELHGQNPVVTPC*NK	C159;C159;C159;C159	0.356350913	Q16630 Q16630 F8WJN3 Q16630	
YSTGSDSASFHTTPSMC*LN PDLEGPPELAYTIQQQYAIPIQ PDLTK	C217 C217;M212 C213;M216	0.354595009	Q15366 Q15366 Q15366 Q15366	

AGSDGESIGNC*PFSQR	C35	0.353845538	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
VLTC*TDLEQGNFFLDLFENA QPTESEKEIYNQVNVVLK	C10	0.353566367	Q9NUQ9	Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 #
ALANSLAC*QGK	C339;C393	0.353177706	P04075 P04075	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA #
LC*SGPGIVGNVLDPSAR	C245;C245	0.3527	Q9Y5P6 Q9Y5P6	Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 # Q12982-2 Isoform 2 of BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 # Q12982
YVFNLAEELVPMYVGIPE C*IK	C416 C295;M165 C357;M287 C173;M408	0.352036495	Q12982 Q12982 H7C096 J3KN59	BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # H7C096 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 (Fragment) OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # J3KN59 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 #
SYC*AEIAHNVSSK	C96;C114;C96	0.351832756	P62910 F8W727 D3YTB1	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
AAAPAPEEEMDEC*EQALAA EPK	C316 C266;M313	0.351668642	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
YAGLSTC*FR	C300;C300	0.349505	Q5T5C7 P49591	Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 #
NIELIC*QENEGENDPVLQR	C228	0.34944236	Q15691	Q15691 Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3 #
FDPTQFQDC*IIQGLTETGTDL EAVAK	C35;C67;C39	0.348564704	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 #
QYDADLEQILIQWITTQC*R	C38;C59;C38	0.347630204	P37802 P37802 X6RJP6	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
SQEATEAAPSC*VGDMADTP R	C84	0.347521299	Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8	Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 #

EGGVQLLLTIVDTPGFGDAVD NSNC*WQPVIDYIDSK	C90;C125;C126; C126;C106	0.347047234	G3V1Q4 Q16181 Q16181 E7EPK1 E7ES33	G3V1Q4 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 #
DGTVLC*ELINALYPEGQAPV KK	C63;C84;C63	0.346212394	P37802 P37802 X6RJP6	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
HELQANC*YEEVKDR	C177;C122;C13 9;C139	0.344928786	E9PK25 G3V1A4 P23528 E9PP50	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
C*SVLPLSQNQEFMPFVK	C616	0.34425	P41250	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 #
ILATGANVILTTGGIDDMC*LK	C296 C296;M295	0.343309063	E7ERF2 P17987	E7ERF2 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # Q16555-2 Isoform 2 of Dihydropyrimidinase- related protein 2 OS=Homo sapiens
GLYDGPVC*EVSVTPK	C468;C504	0.342512086	Q16555 Q16555	GN=DPYSL2 # Q16555 Dihydropyrimidinase- related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
SAC*SLESNLEGLAGVLEADL PNYK	C44	0.342422989	Q09161	Q09161 Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 #
LGPQSDPTEANLESADPEL C*IR	C38;C38	0.342341727	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
DAPAPAASQPSGC*GK	C22;C22;C30;C2 2;C13;C23;C30; C22	0.342016954	F8WBU3 F8WCL3 C9JNL5 Q96115 H7C2M1 H7C4A1 A0A0A0M QU4 Q96115	F8WBU3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # F8WCL3 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # C9JNL5 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=8 # Q96115-2 Isoform 2 of Selenocysteine lyase OS=Homo sapiens GN=SCLY # H7C2M1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=1 # H7C4A1 Selenocysteine lyase (Fragment) OS=Homo sapiens GN=SCLY PE=1 SV=7 # A0A0A0MQU4 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=1 # Q96115 Selenocysteine lyase OS=Homo sapiens GN=SCLY PE=1 SV=4 #
VLGAHILGPGAGEMVNEAAL ALEYGASC*EDIAR	C454;C477;C37 8;C429	0.339476267	E9PEX6 P09622 P09622 P09622	E9PEX6 Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=1 SV=1 # P09622 Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 # P09622-2 Isoform 2 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD # P09622-3 Isoform 3 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD #

DADANAGLTSC*PR	C721;C749;C556;C676	0.338380968	Q5TCZ1 Q5TCZ1 Q5TCZ1 H0Y507	Q5TCZ1-3 Isoform 3 of SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A # Q5TCZ1 SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A PE=1 SV=1 # Q5TCZ1-2 Isoform 2 of SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A # H0Y507 SH3 and PX domain-containing protein 2A (Fragment) OS=Homo sapiens GN=SH3PXD2A PE=1 SV=1 #
SNELGDVGVHC*VLQGLQTP SCK	C75	0.338366652	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
SSGGFWAC*K	C308	0.338112612	P48735	P48735 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 # M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866
QPAIMPQSYGLEDGSC*SY KDFSESR	C413;M460 C472	0.338031428	M0QXS5 P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
GDLENAFLNLVQC*IQNKPLY FADR	C280;C262	0.337923994	P07355 P07355	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 #
LVSSPC*CIVTSTYGWTANME R	C589	0.336533657	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
NSNVDSYLESLYQSC*PR	C106;C767;C645	0.33627469	Q7Z2W4 C9J6P4 Q7Z2W4	Q7Z2W4-4 Isoform 4 of Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 # C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
LNIIISNLDC*VNEVIGIR	C402;C402;C390	0.335170364	P30154 P30154 P30153	P30154-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B # P30154 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
ELELMFGC*QVEGDAAETPP RPR	C251 C277;M248	0.332245	Q02750 Q02750	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 #
KDLNC*QEEEDPMNK	C104	0.330740888	K7ER90	K7ER90 Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=1 SV=1 #
ELEAVC*QDVLSLLDNYLIK	C97	0.328720058	P61981	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 #
FC*DNSSAIQ GK	C270	0.32701	O15067	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
SVNSLDGLASVLYPGC*DTLD K	C85	0.325557265	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 #
DWQGFLELYLQNSPEAC*DY GL	C209;C237	0.324792329	P78417 P78417	P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
IIPGFMC*QGGDFTR	C62	0.324429947	P62937	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #

LLAPDC*EIIQEVGK	C215	0.324382394	Q9NQ75	Q9NQ75 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 #
QASC*SGDEYR	C119;C200;C200;C228;C119	0.321814551	A0A087WT27 O95394 O95394 O95394 J3KN95	A0A087WT27 Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1 # O95394-3 Isoform 2 of Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 # O95394 Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1 # O95394-4 Isoform 3 of Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 # J3KN95 Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1 #
GMENLLEVQVPEDVEQQLQ QLDC*R	C368	0.321146417	Q9BTY7	Q9BTY7 Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1 #
LSEAAC*EEDSASEGLGELF LDGLSTENPHGAR	C238	0.320814354	O95801	O95801 Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 #
HEC*QANGPEDLNR	C118;C135	0.319994584	P60981 P60981	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
AIVDALPPPC*ESACTVPTDV DK	C270	0.318939816	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 #
APPPSLTDC*IGTVDSR	C20;C20	0.318830171	Q9NZZ3 Q9NZZ3	Q9NZZ3 Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1 # Q9NZZ3-2 Isoform 2 of Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 #
EGILNDDIYC*PPETAVLLASY AVQSK	C117	0.318710155	P26038	P26038 Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 #
DGSDYEGWC*WPGSAGYPD FTNPTMR	C502;C524	0.318565299	Q14697 Q14697	Q14697 Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 # Q14697-2 Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB #
LAAAQGQAPLEPTQDGSAIET C*PK	C474;C423	0.317138161	Q7Z2Z2 Q7Z2Z2	Q7Z2Z2 Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2 # Q7Z2Z2-2 Isoform 2 of Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 #
C*GETAFIAPQCEMPIEWVC R	C81	0.317041899	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
STGVVNIPAAEC*LDEYEDDE AGQKER	C173;C119	0.316361279	Q96I20 H0Y116	Q96I20 PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 # H0Y116 PRKC apoptosis WT1 regulator protein (Fragment) OS=Homo sapiens GN=PAWR PE=1 SV=1 #
IEAELQDIC*NDVLELLDKYLIP NATQPESK	C94;C96	0.315946826	P31946 P31946	P31946-2 Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB # P31946 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 #
IGFPETTEEELEEIASNSDC*I FPSAPDVK	C353;C340	0.314942566	Q9Y3F4 Q9Y3F4	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP # Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 #
LVSSPCC*IVTSTYGWTANME R	C590	0.313586748	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
GAVEC*CPNCR	C149;C149	0.313519806	P31689 P31689	P31689 DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 # P31689-2 Isoform 2 of DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 #
HLYTLGGDIINALC*FSPNR	C240	0.310334667	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #

FLENTPSSLNIEDIEDLFLSLAQ YYC*SK	C283;C146;C28 3	0.310330447	Q9NUY8 E9PGE5 Q9NUY8	Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 # E9PGE5 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=1 # Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 #
ALNALC*DGLIDELNQAALK	C62	0.310215873	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
IC*ELLPEAAINDVYLAPLLQC LIEGLSAEPR	C436	0.309043646	Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 #
IVGIGYNGMPNGC*SDDVLP WR	C71 C60;M67	0.308967695	P32321 P32321	P32321 Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1 SV=2 # P32321-2 Isoform 2 of Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD #
LSEEAEC*PNPSTPSK	C947	0.30864	O94804	O94804 Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1 #
TDSCDVNDC*VQQVVELLQ R	C212	0.308252296	O43252	O43252 Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2 #
ADHQPLTEASYVNLPTIALC* NTDSPLR	C153;C148;C14 8	0.308122439	A0A0C4D G17 C9J9K3 P08865	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #
AILQQLGLNSTC*DDSILVK	C817	0.308112997	P19367	P19367-3 Isoform 3 of Hexokinase-1 OS=Homo sapiens GN=HK1 #
NTGIIC*TIGPASR	C49;C49	0.307285245	P14618 P14618	P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
LQEVEC*EEQR	C318;C318;C10 0;C253	0.307199412	Q13596 Q13596 H0YK42 Q13596	Q13596 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3 # Q13596-3 Isoform 3 of Sorting nexin-1 OS=Homo sapiens GN=SNX1 # H0YK42 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=1 # Q13596-2 Isoform 1A of Sorting nexin-1 OS=Homo sapiens GN=SNX1 #
WNDNC*PSWNTIDPEER	C301;C223	0.303864431	P17655 P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P17655-2 Isoform 2 of Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 #
APPSSGAPPASTAQAPC*GQ AAYGQFGQGDVQNGPSSTV QMQR	C78	0.303529506	P53992	P53992 Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3 #
DGNASGTTLLEALDC*ILPPT R	C234;C213	0.301402713	P68104 P68104	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
IEGC*IIGFDEYMNLVLDAAEEI HSK	C6	0.301355893	A6NHK2 P62304	A6NHK2 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P62304 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 #



				J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # A0A087WZU8 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A087WT22 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-8 Isoform 8 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A087X1Q1 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # E7ESS1 Cellular tumor antigen p53 (Fragment) OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-7 Isoform 7 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A087WXZ1 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-9 Isoform 9 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A087WXZ1 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # Q32MZ4-3 Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # Q32MZ4 Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 # Q32MZ4-2 Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 # Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 # P27816-2 Isoform 2 of Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 # E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 # P27816-5 Isoform 5 of Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # P12814-3 Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P35609 Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1 # P35609-2 Isoform 2 of Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 # Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
C*SDSDGLAPPQHLIR	C182;C171;C182;C23;C50;C143;C182;C143;C50;C143;C143;C50;C23	0.300791093	J3KP33 A0A087WZU8 P04637 A0A087WT22 T22 P04637 P04637 A0A087X1Q1 Q1 P04637 E7ESS1 P04637 P04637 P04637 A0A0U1RQC9 QC9 P04637 P04637 A0A087WXZ1 XZ1	
C*EMSEHPSQTVR	C694	0.30061711	Q32MZ4 Q32MZ4 Q32MZ4	
VPTANVSVVDLTC*R	C247	0.300254151	P04406	
DAANC*WTSLLESEYAADPWVQDQMQR	C99	0.299989131	Q8WVJ2	
TEGGGSEAPLC*PGPPAGEEPAISEAAPEAGAPTSASGLNGHPTLSGGGDQR	C925;C2243;C1098;C756	0.299829752	P27816 E7EVA0 P27816 P27816	
EGLLLWC*QR	C154;C173;C154;C161;C161	0.299231296	P12814 O43707 P12814 P35609 P35609	
GPFVEAEVPDVLLEC*PDAK	C1833	0.297465782	Q09666	

ADDTFEALC*IEPFSSPELDP VMKPDQSGSSANEQAVQ	C111	0.297157847	I3L0M9 Q15370 B8ZZU8	I3L0M9 Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # Q15370 Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # B8ZZU8 Transcription elongation factor B (SIII)# polypeptide 2 (18kDa# elongin B)# isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 #
TDICQGALGDC*WLLAAIASLT LNEEILAR	C105;C27	0.296751877	P17655 P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P17655-2 Isoform 2 of Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 #
ICDGCIIIVDAVEGVC*PQTQA VLR	C124;C73	0.296154569	Q7Z2Z2 Q7Z2Z2	Q7Z2Z2 Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2 # Q7Z2Z2-2 Isoform 2 of Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 #
AETSDVANAVLDGADC*IMLS GETAK	C401;C370	0.293887802	P30613 P30613	P30613 Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR PE=1 SV=2 # P30613-2 Isoform L-type of Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR #
MC*DLVSDFDGFSER	C182	0.293640182	P30520	P30520 Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3 #
YGGAEVVDIEILLC*QR	C119;C98	0.292436033	P34897 P34897	P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 # P34897-3 Isoform 3 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 #
TVGVQGDC*R	C523;C424	0.292186049	P49915 P49915	P49915 GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 # P49915-2 Isoform 2 of GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS #
VCENIPIVLC*GNK	C120;C138;C137;C116	0.290847042	P62826 J3KQE5 B5MDF5 F5H018	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 # J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 # B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 # F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 #
DIDFLKEEEHDC*FLEEIMTK	C173	0.289659667	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
VAHALAEGLGVIAC*IGEK	C127;C164	0.289234495	P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 #
SDGLQWSAEQPC*NPSKPK	C125;C193;C102;C185;C215	0.288952493	B8ZZZ7 Q9NUQ6 A0A0A0M SG5 Q9NUQ6 Q9NUQ6	B8ZZZ7 DNA polymerase-transactivated protein 6# isoform CRA_b OS=Homo sapiens GN=SPATS2L PE=1 SV=1 # Q9NUQ6-4 Isoform 4 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L # A0A0A0MSG5 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=1 # Q9NUQ6 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 # Q9NUQ6-3 Isoform 3 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L #
AEQFYC*GDTEGK	C395;C395	0.286405307	Q02218 A0A0D9S FS3	Q02218 2-oxoglutarate dehydrogenase# mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3 # A0A0D9SFS3 2-oxoglutarate dehydrogenase# mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=1 #
AVLLASDAQEC*TLEEVVER	C332;C332	0.286223027	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #

IWC*FGPDGTGPNILTDITK	C651	0.286124846	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
DQELYFFHELSPGSC*FFLPK	C343;C376	0.283254742	P26639 P26639	P26639 Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 # P26639-2 Isoform 2 of Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS #
LEGLTGPSVDVEVPDVELE C*PDAK	C2162	0.28252811	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
EDLNC*QEEEDPMNK	C139	0.281303678	O75821 K7ENA8	O75821 Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 # K7ENA8 Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=1 SV=1 #
NC*NDFQYESK	C112	0.280154943	Q04917	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 # Q32MZ4-3 Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # Q32MZ4 Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 #
IAAESSENVDC*PENPK	C588;C644;C620	0.276509496	Q32MZ4 Q32MZ4 Q32MZ4	# Q32MZ4-2 Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 #
GGC*PGGEATLSQPPPR	C22	0.276236185	P20290	P20290 Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1 #
YGAVDLLALLAVPDMSSLAC *GYLR	C223	0.275895	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 # Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
YSLADQTSGDQSPLPPCTPT PPC*AEMR	C569	0.275620787	Q06124 Q06124	#
NIC*FTVWDVGGQDK	C62;C62	0.275081688	P84085 C9J1Z8	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 # C9J1Z8 ADP-ribosylation factor 5 (Fragment) OS=Homo sapiens GN=ARF5 PE=1 SV=1 #
LVVPATQC*GSLIGK	C109	0.274296057	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
LNLPINIIGLAPLC*ENMPGSK	C335	0.272926715	P28838 P28838	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 #
GIFPVLK*KDPVQEAWAEDVD LR	C474;C474	0.272804769	P14618 P14618	P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
SC*VEEPEPEPEAAEGDGDK K	C101	0.271831145	P51858	P51858-2 Isoform 2 of Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF # I3L0Z8 Segment polarity protein dishevelled homolog DVL-2 (Fragment) OS=Homo sapiens GN=DVL2 PE=1 SV=1 # O14641 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 # I3L2N2 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 #
C*WDPSQAYFTLPR	C32;C354;C348	0.271485158	I3L0Z8 O14641 I3L2N2	Q96DC7 Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 PE=1 SV=2 # Q96DC7-2 Isoform 2 of Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 #
NDAPEEAGEGC*VAAILGETE VQQFLR	C57;C57	0.269641299	Q96DC7 Q96DC7	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
ICELLPEAAINDVYLAPLLQC* LIEGLSAEPR	C455;C310	0.26922	Q14974 Q14974	



IAQLIC*ER	C91;C111;C134; C222;C137;C19 9	0.260561557	H0YMP1 A0A0C4D GL3 P33316 P33316 H0YNW5 H0YKC5	H0YMP1 Deoxyuridine 5'-triphosphate nucleotidohydrolase# mitochondrial (Fragment) OS=Homo sapiens GN=DUT PE=1 SV=1 # A0A0C4DGL3 DUTP pyrophosphatase# isoform CRA_c OS=Homo sapiens GN=DUT PE=1 SV=1 # P33316-2 Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase# mitochondrial OS=Homo sapiens GN=DUT # P33316 Deoxyuridine 5'-triphosphate nucleotidohydrolase# mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=4 # H0YNW5 Deoxyuridine 5'-triphosphate nucleotidohydrolase# mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=1 # H0YKC5 Deoxyuridine 5'-triphosphate nucleotidohydrolase# mitochondrial (Fragment) OS=Homo sapiens GN=DUT PE=1 SV=1 #
SSLQYSSPAPDGC*GDQTLG DLLLTPTR	C646	0.259157925	P22102	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 #
TDVNKIEEFLEEVLC*PPK	C100	0.258591484	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
GLYGIKDDVFLSVPC*ILGQN GISDLVK	C322;C293	0.257790616	P00338 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
VEQNSEPC*AGSSSESDLQT VFK	C260	0.257101805	Q8N806	Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 #
GLGTDEDSLIEIIC*SR	C151;C133	0.257045984	P07355 P07355	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # H0YEB6 Sjogren syndrome/scleroderma autoantigen 1 (Fragment) OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # O60232 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # G3V1B8 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 #
AAQGPPAPAVPPNTDVMAC* TQTALLQK	C146;M150 C115 C152;M113	0.25613	H0YEB6 O60232 G3V1B8	C9K0J5 Ras association (RalGDS/AF-6) and pleckstrin homology domains 1# isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1 # Q70E73 Ras-associated and pleckstrin homology domains-containing protein 1 OS=Homo sapiens GN=RAPH1 PE=1 SV=3 #
LNLSGVNLPGVLQQGC*VSA K	C1097;C1045	0.255505584	C9K0J5 Q70E73	F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 #
VC*ENIPIVLCGNK	C108	0.254102942	F5H018	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
AHVVPC*FDASK	C1157;C1130;C 1157	0.254090143	P21333 Q60FE5 P21333	Q8WVV9-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # C9IYN3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=2 # D6W592 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # Q8WVV9 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 #
GLC*ESVVEADLVEALEK	C79;C79;C84;C8 4	0.254033664	Q8WVV9 C9IYN3 D6W592 Q8WVV9	

LICC*DILDVLDK	C76	0.253562511	P62258	P62258-2 Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE #
IC*DQWDALGSLTHSR	C499	0.252262493	O43707	O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 #
C*YVQPQWVFDVSVNAR	C391;C386;C374	0.251652873	O00541 O00541 B5MCF9	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 # O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 # B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 #
VRPSTGNSASTPQSQC*LPS EIEVK	C131;C131	0.251529868	Q9UJX3 Q9UJX3	Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 #
DINAYNC*EEPTEK	C91	0.251227083	P30041	P30041 Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 #
DKEEEEEVAGGDC*IGSTVYS K	C25	0.250640172	Q96ER3	Q96ER3 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=2 #
TQSPC*FGDDDDPAK	C256;C344;C324	0.248553779	Q12765 Q12765 Q12765	Q12765-3 Isoform 3 of Secernin-1 OS=Homo sapiens GN=SCRN1 # Q12765-2 Isoform 2 of Secernin-1 OS=Homo sapiens GN=SCRN1 # Q12765 Secernin-1 OS=Homo sapiens GN=SCRN1 PE=1 SV=2 #
VILITPTPLC*ETAWEEQCIQG CK	C117	0.246868711	H7C5G1	H7C5G1 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 #
EITSLDTENIDEILNNADVALV NFYADWC*R	C58	0.244274193	Q9BS26	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 #
YLLQYQEPIPCQLVTALC*DI K	C115;C84;C115;C115;C115;C91	0.244171382	H0YL69 H0YN18 P25789 H0YMZ1 H0YMA1 H0YKT8	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 # H0YMA1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YKT8 Proteasome subunit beta type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
C*DENILWLDYK	C152	0.24327379	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
EPAPAEALPQQYPEPAPAAL C*GPPPR	C363	0.242436649	Q8IU81	Q8IU81 Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens GN=IRF2BP1 PE=1 SV=1 #
SDC*ESQECVTK	C169	0.241752598	Q9NS86	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 #
AEEDVEPEC*IMEK	C24;C127;C127;C127;C32;C56;C102	0.240663873	Q9UJU6 Q9UJU6 Q9UJU6 Q9UJU6 Q9UJU6 H0Y5J4 B4DDD6	Q9UJU6-5 Isoform 5 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6-3 Isoform 3 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6-2 Isoform 2 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6 Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 # Q9UJU6-4 Isoform 4 of Drebrin-like protein OS=Homo sapiens GN=DBNL # H0Y5J4 Drebrin-like protein (Fragment) OS=Homo sapiens GN=DBNL PE=1 SV=1 # B4DDD6 Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 #
AINC*ATSGVVGLVNCLR	C1448	0.237258192	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
SSPGLSDTIFC*R	C27	0.237246687	Q9H8M7	Q9H8M7 Protein FAM188A OS=Homo sapiens GN=FAM188A PE=1 SV=1 #

SSSSVTTSETQPC*TPSSSDY SDLQR	C334	0.232277237	P50552	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 # A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 #
APVPSTC*SSTFPEELSPPSH QAK	C160;C160;C16 0	0.231448937	A0A087W Y61 Q14980 Q14980	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 # E9PQS1 Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # E9PJU8 Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # E9PPB5 Ester hydrolase C11orf54 (Fragment) OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # Q9H0W9 Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 # Q9H0W9-2 Isoform 2 of Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 # Q9H0W9- 4 Isoform 4 of Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 # A0A087WT99 Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 #
IC*PVETLVEEAIQCAEK	C213	0.230191411	P30084	
SHIMPAEFSSC*PLNSDEEVN K	C207;M108 C167 C115;M160 C226;M200 C167;M219	0.227452372	E9PQS1 E9PJU8 E9PPB5 Q9H0W9 Q9H0W9 Q9H0W9 A0A087W T99	
TAFQEALDAAGDKLVVDFD ATWC*GPCK	C32	0.227246954	P10599	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 # P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 # Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q9UI30- 2 Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 #
LVTSPC*CIVTSTYGWTANME R	C719	0.226942281	P07900 P07900	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
IC*PVEFNPNFVAR	C33;C33;C33	0.225990341	Q9UI30 Q9UI30 F5GX77	P00558-2 Isoform 2 of Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 # P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 # P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 # P30086 Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 #
VDVEC*PDVNIIEGPEGK	C2806	0.225721417	Q09666	
C*PASEPGLDATTASESR	C1029;C1029	0.22478162	Q27J81 Q27J81	
TGQATVASGIPAGWMGLDC* GPSSKK	C288;M312 C316	0.224107403	P00558 P00558	
ETVYC*LNDDDETEVLKEDIQ GFR	C296	0.222447673	P13010	
APVAGTC*YQAEWDDYVPK	C168	0.221625	P30086	

YLLQYQEPIPC*EQLVTALCDI K	C107;C76;C107; C107;C107;C83	0.221239927	H0YL69 H0YN18 P25789 H0YMZ1 HOYMA1 HOYKT8	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 # HOYMA1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YKT8 Proteasome subunit beta type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
FQYEC*GNYSGAAEYLYFFR	C141	0.22065	P60228	P60228 Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 #
GFGFVC*FSSPEEATK	C339;C339;C30 7;C339;C339;C3 14;C339;C339	0.216663113	B1ANR0 Q13310 E7ERJ7 Q13310 P11940 A0A087W TT1 Q13310 P11940	B1ANR0 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC4 PE=1 SV=1 # Q13310 Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1 # E7ERJ7 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 # Q13310-2 Isoform 2 of Polyadenylate- binding protein 4 OS=Homo sapiens GN=PABPC4 # P11940 Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 # A0A087WTT1 Polyadenylate- binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 # Q13310-3 Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 # P11940-2 Isoform 2 of Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 #
IYGGSVTGATC*K	C218;C255	0.215457611	P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 #
LNNLIC*DESDVK	C362	0.214802795	Q96EB1	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 #
AQVPGSSPGLLSLSLNQPPA APEC*K	C314	0.214695	Q86W42	Q86W42 THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1 #
LAPILC*DGTATFVDLVPGFR	C568	0.214450419	O43264	O43264 Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 #
INALTAASEAAC*LIVSVDETIK NPR	C511	0.212494264	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #



LPQQSYNFDPTDC*DESVD FK	C78;C2378;C23 29;C452;C452;C 452;C2374;C237 4;C452;C520;C1 13;C78	0.211708954	Q4VXL4 E9PBC6 E7EMZ9 D6RAA5 O95359 Q4VXL8 O95359 O95359 O95359 O95359 H0Y911 O95359	Q4VXL4 HCG41426# isoform CRA_c OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E9PBC6 Transforming acidic coiled-coil- containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E7EMZ9 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # D6RAA5 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359-1 Isoform 1 of Transforming acidic coiled-coil- containing protein 2 OS=Homo sapiens GN=TACC2 # Q4VXL8 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3 # O95359-3 Isoform 3 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # O95359-6 Isoform 6 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # O95359-5 Isoform 5 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 # H0Y911 Transforming acidic coiled-coil- containing protein 2 (Fragment) OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359-2 Isoform 2 of Transforming acidic coiled-coil- containing protein 2 OS=Homo sapiens GN=TACC2 # O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 # P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
FLDGNELTLADC*NLLPK	C178	0.20915	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 # P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
ADTSQEIC*SPR	C1010;C1027;C 1027;C66	0.208611499	P52948 P52948 P52948 H7C3P6	P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
DEFTNTC*PSDKEVEIAYSDV AK	C234	0.20612846	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 # Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=2 SV=1 # F8WDZ3 CKLF-like MARVEL transmembrane domain- containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 # Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 #
TTC*SSGSALGPGAGAAQPS ASPLEGLLDLSYPR	C12;C12;C12	0.205174624	Q96FZ5 F8WDZ3 Q96FZ5	Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 # Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 #
ETTQNALQTPC*YTPYYVAPE VLGPEK	C203;C203	0.204523488	C9J8E1 Q16644	C9J8E1 MAP kinase-activated protein kinase 3 (Fragment) OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 # Q16644 MAP kinase-activated protein kinase 3 OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 #
VIVVGNPANTNC*LTASK	C137;C155	0.202203077	P40925 P40925	P40925 Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 # P40925-3 Isoform 3 of Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 #

MTGESEC*LNPSTQSR	C1212;C1181	0.200813027	Q9H2G2 Q9H2G2	Q9H2G2 STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 # Q9H2G2-2 Isoform 2 of STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK # P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sG12 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
QLFALSC*TAESEQVLPDDL GVIR	C96;C60;C112;C75;C112;C96	0.19981632	P04899 P04899 P04899 P04899 P04899	Q9ULW3 Activator of basal transcription 1 OS=Homo sapiens GN=ABT1 PE=1 SV=1 # P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 # Q16851-2 Isoform 2 of UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 # E7EUC7 UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=1 # A0A087WYS1 UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=1 # Q16851 UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 # Q86VP6 Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 # P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 # Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 # Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 # Q10567-3 Isoform C of AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 # Q10567-2 Isoform B of AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 # P63010-3 Isoform 3 of AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 # P63010-2 Isoform 2 of AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 # P63010 AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 # Q10567 AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2 # Q16643-2 Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643-3 Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643 Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 #
AATEQEPLGTEQTLDAEEE QEESEEAAC*GSK DNLTWTSDSAGEEC*DAAE GAEN	C37 C237	0.199192798 0.195803113	Q9ULW3 P27348	
LNGGLGTSMGC*K	C112;C132;C123;C123	0.194648849	Q16851 E7EUC7 A0A087WYS1 Q16851	
HCEC*AEEGTR	C942	0.19447494	Q86VP6	
LVTSPCC*IVTSTYGWTANME R	C720	0.193284509	P07900 P07900	
MGFPSKTDSPSC*EYSR	C419	0.192909051	Q9HAV4	
GC*QDFGWDPFCQPDGYEQ TYAEMPK	C146	0.192452157	Q9BY32	
DC*EDPNPLIR	C95;C95;C38;C95;C95;C95	0.19003	Q10567 Q10567 P63010 P63010 P63010 Q10567	
APPPVFYNKPPEIDITC*WDA DPVPEEEEGFEGGD	C634;C678;C632	0.188683476	Q16643 Q16643 Q16643	

EIDC*LSPEAQK	C14;C14;C14	0.18771005	Q32MZ4 Q32MZ4 Q32MZ4	Q32MZ4-3 Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # Q32MZ4 Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 # Q32MZ4-2 Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 #
YC*TDTVLFR	C58;C58	0.18411	P12955 P12955	P12955-3 Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
LC*SLLDSEDYNTCEGAFGAL QK	C142;C134	0.180392452	Q92973 Q92973	Q92973 Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 # Q92973-2 Isoform 2 of Transportin-1 OS=Homo sapiens GN=TNPO1 #
LGGTIDDC*ELVEGLVLTQK	C191;C221	0.1786287	P50991 P50991	P50991-2 Isoform 2 of T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 # P50991 T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 # Q8TDP1 Ribonuclease H2 subunit C OS=Homo sapiens GN=RNASEH2C PE=1 SV=1 # E9PN81 Ribonuclease H2 subunit C OS=Homo sapiens GN=RNASEH2C PE=1 SV=1 # Q8TDP1-2 Isoform 2 of Ribonuclease H2 subunit C OS=Homo sapiens GN=RNASEH2C # H0YEF3 Ribonuclease H2 subunit C (Fragment) OS=Homo sapiens GN=RNASEH2C PE=1 SV=1 #
DAVPATLHLLPC*EVAVDGPA PVGR	C34;C34;C34;C2 8	0.173955907	Q8TDP1 E9PN81 Q8TDP1 H0YEF3	Q8TDP1 Ribonuclease H2 subunit C OS=Homo sapiens GN=RNASEH2C PE=1 SV=1 # Q8TDP1-2 Isoform 2 of Ribonuclease H2 subunit C OS=Homo sapiens GN=RNASEH2C # H0YEF3 Ribonuclease H2 subunit C (Fragment) OS=Homo sapiens GN=RNASEH2C PE=1 SV=1 #
GFTDADNTWEPEENLDC*PE LIEAFLNSQK	C69	0.172003367	Q13185	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 # F5H039 Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1 # Q9NQX3-2 Isoform 2 of Gephyrin OS=Homo sapiens GN=GPHN # Q9NQX3 Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1 #
VTTGAPIPC*GADAVVQVEDT ELIR	C465;C452;C41 9	0.171570746	F5H039 Q9NQX3 Q9NQX3	F5H039 Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1 # Q9NQX3-2 Isoform 2 of Gephyrin OS=Homo sapiens GN=GPHN # Q9NQX3 Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1 #
LMEPIYLVEIQC*PEQVGGIY GVLNR	C751	0.171286689	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
GQLC*ELSCSTDYR	C342	0.170932263	Q99873	Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
NPFGLVPVLENSQGQLIYESA ITC*EYLDEAYPGKK	C90	0.168655911	P78417	P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
GC*DVVVIPAGVPR	C93	0.166326293	P40926	P40926 Malate dehydrogenase# mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 #
AAEEEEEEEEVDLAC*TPTD VR	C285	0.166004831	P24385	P24385 G1/S-specific cyclin-D1 OS=Homo sapiens GN=CCND1 PE=1 SV=1 #
EQSIC*AAEEQPAEDGQGET NK	C490	0.163955758	Q9UGP8	Q9UGP8 Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2 #
EVYEGEVTETPC*ETENPM GGYGK	C141	0.160619751	Q9Y265	Q9Y265 RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 #
AC*GNFGIPCELR	C288	0.160055381	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 # G3V1Q4 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 #
ADTLTPEEC*QQFK	C168;C203;C20 4;C204;C184	0.159891492	G3V1Q4 Q16181 Q16181 E7EPK1 E7ES33	G3V1Q4 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 #
GVSLPLGFTFSFPC*QQNSLD ESILLK	C578;C606	0.157684965	E9PB90 P52789	E9PB90 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=1 # P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
STDWEDDGGWAWEENEPQ EPEEEGNTC*K	C67	0.157415272	Q9H2M9	Q9H2M9 Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1 #

LAC*LSEEGNEIESGK	C213	0.157408383	Q9Y2L1	Q9Y2L1 Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2 #
GNFTLPEVAEC*FDEITYVEL QK	C648;C629	0.156564729	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
VSGPDPKPGSNC*SPAQSVL SEVPSVPTNGMAK	C23	0.15469575	P22314	P22314 Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 #
DGFYEAELC*PDR	C105;C105;C92; C116;C105;C105;C105	0.154306572	A0A087X0 W8 Q04206 Q04206 E9PKH5 Q2TAM5 Q04206 Q04206	A0A087X0W8 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206-4 Isoform 4 of Transcription factor p65 OS=Homo sapiens GN=RELA # Q04206-2 Isoform 2 of Transcription factor p65 OS=Homo sapiens GN=RELA # E9PKH5 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # Q2TAM5 RELA protein OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206-3 Isoform 3 of Transcription factor p65 OS=Homo sapiens GN=RELA # Q04206 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=2 # H3BQH0 Calponin-2 (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=2 # Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # Q99439-2 Isoform 2 of Calponin-2 OS=Homo sapiens GN=CNN2 # U3KPS3 Calponin-2 (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 # H3BVI6 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X1X5 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #
C*ASQSGMTAYGTR	C73;C175;C136; C18;C164;C196; C166;C132;C112	0.150005133	H3BQH0 Q99439 Q99439 U3KPS3 B4DDF4 B4DUT8 A0A087X271 H3BVI6 A0A087X1X5	P26583 High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 # Q5T7C4 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=1 # B2RPK0 Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 # D6R9A6 High mobility group protein B2 (Fragment) OS=Homo sapiens GN=HMGB2 PE=1 SV=1 # P09429 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 #
MSSYAFFVQTC*R	C23;M13 C23	0.149859576	P26583 Q5T7C4 B2RPK0 D6R9A6 P09429	O75083 WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 # P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
LATGSDDNC*AFFEGPPFK	C170	0.144432389	O75083	Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 #
GGTLFGGEVC*K	C684	0.140722975	P42166	Q16643-2 Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643-3 Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643 Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 #
SLLC*GEDEAADENPESQEM LEEQLVR	C941	0.140418223	Q9HAV4	P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
EGTQASEGYFSQSQEEFAQ SEELC*AK	C615;C659;C613	0.138227323	Q16643 Q16643 Q16643	P40222 Alpha-taxilin OS=Homo sapiens GN=TXLNA PE=1 SV=3 #
EFCENLSADC*R	C317	0.137472157	P30153	
VTEAPC*YPGAPSTEASGQT GPQEPTSAR	C523	0.136363941	P40222	

ELEASEELDTIC*PK	C229	0.135956461	O76003	O76003 Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 #
MLQPC*GPPADKPEEN	C76	0.134896431	Q9BWJ5	Q9BWJ5 Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1 #
C*GEDDETIPSEYR	C376;C411;C28 7;C370;C314;C2 10;C51;C374;C2 56;C293;C389;C 71;C86;C80;C51 ;C315;C328;C31 4;C43;C392;C30 6	0.13417906	P20810 P20810 P20810 E7EVY3 P20810 E7EQA0 A0A0C4D GB5 E9PDE4 E9PCH5 P20810 H0YD33 H0Y9H6 H0Y7F0 A0A0A0M R45 P20810 P20810 B7Z574 E7EQ12 P20810 P20810	P20810-5 Isoform 5 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-3 Isoform 3 of Calpastatin OS=Homo sapiens GN=CAST # E7EQA0 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PDE4 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PCH5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # H0YD33 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y9H6 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y7F0 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0A0MR45 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-2 Isoform 2 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E7EQ12 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST # P60891-2 Isoform 2 of Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 # P11908-2 Isoform 2 of Ribose- phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 # P60891 Ribose- phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 # P11908 Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2 # P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
VTAVIPC*FPYAR	C24;C91;C91;C9 1	0.13349623	P60891 P11908 P60891 P11908	P60891-2 Isoform 2 of Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 # P60891 Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 # P11908 Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2 # P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
DCIGGC*SDLVSLQQSGELLT R	C83	0.132960105	P35754	P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
EAVFPFQPGSVAEVC*ITFDQ ANLTVK	C89	0.132190663	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 #
AITIAGIPQSIIEC*VK	C158;C158;C15 8;C158	0.129487166	Q15366 Q15366 Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
EGILSDEIYC*PPETAULLGSY AVQAK	C117;C117	0.126560725	P15311 E7EQR4	P15311 Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 # E7EQR4 Ezrin OS=Homo sapiens GN=EZR PE=1 SV=3 # E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 #
MAYQEYPNSQNWPEDTNFC* FQPEQVVDPIQTDPFK	C126 C143;M108	0.120892314	E7EVA0 P27816	E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 #

LLSALC*PEEPPVHSSAQIVSK	C334;C334;C334 4	0.119699998	Q9NR50 Q9NR50 Q9NR50	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 #
SGGLQTPEC*LSR	C276;C439	0.109832762	P85037 P85037	P85037-2 Isoform 2 of Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 # P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 #
SVSGTDVQEEC*R	C256;C254	0.102271109	P49321 P49321	P49321-3 Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 #
INGC*YEALSGGATTEGFEDF TGGIAEWYELK	C191	0.088590934	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
VDCTANTNTC*NK	C92	0.077343499	P30101	P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 #
VETNQDWSLMC*PNECPGLD EVWGEEFEK	C352	0.068443334	P23921	P23921 Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 #
GQVC*LPVISAENWKPATK	C86;C54;C144	0.067231998	P68036 P68036 P68036	P68036 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 # P68036-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 # P68036-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 #
C*EDLETQTQSEK	C344;C312	0.054230799	O00592 O00592	O00592 Podocalyxin OS=Homo sapiens GN=PODXL PE=1 SV=2 # O00592-2 Isoform 2 of Podocalyxin OS=Homo sapiens GN=PODXL #
INTQEPEETLDFDFC*STNVIN K	C112;C148	0.048609486	O60671 O60671	O60671-2 Isoform 2 of Cell cycle checkpoint protein RAD1 OS=Homo sapiens GN=RAD1 # O60671 Cell cycle checkpoint protein RAD1 OS=Homo sapiens GN=RAD1 PE=1 SV=1 #
GSDASDFLLETQSAC*SDTS ESSAAGGQNSR	C7548;C7511	0.04860928	H3BQK9 H3BPE1	H3BQK9 Microtubule-actin cross-linking factor 1# isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=1 # H3BPE1 Microtubule-actin cross-linking factor 1# isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=1 #
ELEQVC*NPIISGLYQGAGGP GPGGFGAQGPK	C604;C603;C54 8;C603	0.048128599	A0A0G2JI W1 P0DMV8 P0DMV8 P0DMV9	A0A0G2JIW1 Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1 # P0DMV8 Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1 # P0DMV8-2 Isoform 2 of Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A # P0DMV9 Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1 #
SNPENNVGLITLANDC*EVLT TLTPDTGR	C58;C58;C43;C5 8	0.047427313	P55036 Q5VWC4 A6PVX3 P55036	P55036-2 Isoform Rpn10E of 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 # Q5VWC4 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 # A6PVX3 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=1 SV=1 # P55036 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 #
LVILANNC*PALR	C52;C52	0.041210697	P62888 E5R199	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5R199 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #

YMPQNPC*IIATK	C138;M133 C137;M133 C138	0.036728321	Q09028 Q09028 Q09028	Q09028-2 Isoform 2 of Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 # Q09028-3 Isoform 3 of Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 # Q09028 Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3 # Q9HCC9-4 Isoform 4 of Lateral signaling target protein 2 homolog OS=Homo sapiens GN=ZFYVE28 # Q9HCC9-3 Isoform 3 of Lateral signaling target protein 2 homolog OS=Homo sapiens GN=ZFYVE28 # Q9HCC9-2 Isoform 2 of Lateral signaling target protein 2 homolog OS=Homo sapiens GN=ZFYVE28 # Q9HCC9 Lateral signaling target protein 2 homolog OS=Homo sapiens GN=ZFYVE28 PE=1 SV=3 # Q9HCC9-5 Isoform 5 of Lateral signaling target protein 2 homolog OS=Homo sapiens GN=ZFYVE28 #
DPDAELAC*SMQYDDQELEQ LSR	C233	0.022215306	Q9HCC9 Q9HCC9 Q9HCC9 Q9HCC9 Q9HCC9	O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # Q02790 Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # E9PHA2 Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=1 SV=1 # Q15003 Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=1 SV=3 # H7C557 Multiple epidermal growth factor-like domains protein 6 OS=Homo sapiens GN=MEGF6 PE=1 SV=2 # O75095 Multiple epidermal growth factor-like domains protein 6 OS=Homo sapiens GN=MEGF6 PE=1 SV=4 # O75095-2 Isoform 2 of Multiple epidermal growth factor-like domains protein 6 OS=Homo sapiens GN=MEGF6 # P08559 Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 # P08559-4 Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 # P08559-2 Isoform 2 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 #
VGEAGLLSVDC*SEAGPGAL GLEAVSDSGTK	C1158	0.020892095	O75369	
TQLAVC*QQR	C396	0.018785	Q02790	
LVPASQC*GSLIGK	C109;C109;C109; C109	0.017832555	Q15366 Q15366 Q15366 Q15366	
SELLFPSDVQTLSTGEPLP ELGC*VEMTDLK	C285	0.015127128	E9PHA2 Q15003	
LHTDSRTC*LAINSCALGNGG CQHHCVQLTITR	C207;C200;C95	0.008660041	H7C557 O75095 O75095	
LPCIFIC*ENNR	C222;C260;C222 9	0.008591996	P08559 P08559 P08559	
AESHNDC*PVR	C17	0.008415147	Q16831	
FFAFWGQDINNLTPLEC*GR ESR	C635;C735	0.005874075	A8MT40 Q8NCN5	
QSRTC*STQVC*R	C3687 C3692;C3688 C3693	0.00487877	A2VEC9 A0A096LN W2	A2VEC9 SCO-spondin OS=Homo sapiens GN=SSPO PE=2 SV=1 # A0A096LNW2 SCO-spondin OS=Homo sapiens GN=SSPO PE=4 SV=1 #
PFSC*PECNLQFARLDNLK	C492	0.002219865	O43167	O43167 Zinc finger and BTB domain-containing protein 24 OS=Homo sapiens GN=ZBTB24 PE=1 SV=2 #

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IYEGQVEVTGDEYNVESIDGQ PGAFTC*YLDAGLAR	C144;C94	0.001	P46777 Q5T7N0	P46777 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 # Q5T7N0 60S ribosomal protein L5 (Fragment) OS=Homo sapiens GN=RPL5 PE=1 SV=2 #
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**Table A3.6**IsoTOP-ABPP analysis of JNS 1-40 (100  $\mu$ M) in situ in 231MFP proteomes.

Peptide	Modified residue	Average area ratio	Uniprot ID	Protein
DNTIEHLLPLFLAQLKDEC*PEVR	C198;C377	24.78878098	B3KQV6 P30153	B3KQV6 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=1 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
FEQSDLEAFYNVITVC*GTNEVR	C306;C308	4.957554892	Q5JPI3 Q5JPI3	Q5JPI3-2 Isoform 2 of Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 # Q5JPI3 Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 PE=1 SV=1 # Q00325-2 Isoform B of Phosphate carrier protein# mitochondrial OS=Homo sapiens GN=SLC25A3 #
AVEEYSC*EFGSAK	C56	4.735849142	Q00325	Q00325-2 Isoform B of Phosphate carrier protein# mitochondrial OS=Homo sapiens GN=SLC25A3 #
SCSSSC*AVHDLIFWR	C46	4.21067	O95197	O95197-3 Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3 #
TC*LPGFPGAPCAIK	C1817;C1886;C1930;C1931	4.130220133	P51610 P51610 P51610 A6NEM2	P51610-2 Isoform 2 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 # P51610 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 # P51610-4 Isoform 4 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 # A6NEM2 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 # Q96FV9 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # A0A087WWS1 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # J3KT14 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # A0A087WY84 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # Q96FV9-2 Isoform 2 of THO complex subunit 1 OS=Homo sapiens GN=THOC1 # J3QQZ3 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # J3KRD7 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 #
KC*TLDQAFR	C49;C49;C49;C32;C49;C49;C49	4.11965	Q96FV9 A0A087WWS1 J3KT14 A0A087WY84 Y84 Q96FV9 J3QQZ3 J3KRD7	Q96FV9 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # A0A087WWS1 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # J3KT14 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # A0A087WY84 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # Q96FV9-2 Isoform 2 of THO complex subunit 1 OS=Homo sapiens GN=THOC1 # J3QQZ3 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 # J3KRD7 THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 #
AYHEQLSVAEITSSC*FEPNSQMVK	C319	4.03307731	C9J2C0	C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
ACFC*IDNEALYDICFR	C201	3.994758766	Q9H4B7	Q9H4B7 Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 #
FC*ACPEEAHALELR	C64;C64;C64	3.959089789	Q9NP81 Q9NP81 M0QWZ7	Q9NP81 Serine--tRNA ligase# mitochondrial OS=Homo sapiens GN=SARS2 PE=1 SV=1 # Q9NP81-2 Isoform 2 of Serine--tRNA ligase# mitochondrial OS=Homo sapiens GN=SARS2 # M0QWZ7 Serine--tRNA ligase# mitochondrial OS=Homo sapiens GN=SARS2 PE=1 SV=1 #
NQC*LFTNTQCK	C68;C68;C68;C93;C68;C68	3.803765871	B7Z6B6 Q9UL40 B7Z6Q2 Q9UL40 D6RJ07 Q9UL40	B7Z6B6 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 # Q9UL40 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 # B7Z6Q2 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 # Q9UL40-2 Isoform 2 of Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 # D6RJ07 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 # Q9UL40-3 Isoform 3 of Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 #

ALADAQIPYSAVDQACVGYV FGDSTC*GQR	C71;C71	3.781674565	E9PLD1 P22307	E9PLD1 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=1 # P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 #
VAASC*GAIQYIPTELDQVR	C134	3.709300108	Q7L2H7	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 # H7BZT7 S-formylglutathione hydrolase (Fragment) OS=Homo sapiens GN=ESD PE=1 SV=1 # U3KQT1 S-formylglutathione hydrolase (Fragment) OS=Homo sapiens GN=ESD PE=1 SV=1 # X6RA14 S- formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=1 # P10768 S- formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 #
SVSAFAPICNPVLC*PWGK	C129;C39;C152; C181	3.613108845	H7BZT7 U3KQT1 X6RA14 P10768	
MC*DCFHMLPTWPGTPGSV SGRQLQPGEPGAETEDDHS VTEGPADEGIR	C2	3.326065	Q8IVF2	Q8IVF2 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 # M0QYH6 Prostate tumor-overexpressed gene 1 protein (Fragment) OS=Homo sapiens GN=PTOV1 PE=1 SV=1 # A0A0C4DGR2 Prostate tumor overexpressed gene 1# isoform CRA_d OS=Homo sapiens GN=PTOV1 PE=1 SV=1 # M0QY25 Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 PE=1 SV=1 # Q86YD1 Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 PE=1 SV=1 # Q86YD1-3 Isoform 3 of Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 # Q86YD1-2 Isoform 2 of Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 #
DLETLKSLC*R	C71;C308;C308; C340;C151;C30 8	3.305295491	M0QYH6 A0A0C4D GR2 M0QY25 Q86YD1 Q86YD1 Q86YD1	
SGLTPNDIDVIELHDC*FSTNE LLTYEALGLCPEGQGATLVD RGDNTYGGK	C307;C307	3.280716448	E9PLD1 P22307	E9PLD1 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=1 # P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 #

SESELIDELSEDFDRSEC*K	C429;C464;C340;C423;C367;C263;C104;C427;C309;C346;C442;C124;C139;C133;C104;C368;C381;C367;C96;C445;C381;C359	3.262500233	P20810 P20810 P20810 E7EVY3 P20810 E7EQA0 A0A0C4D GB5 E9PDE4 E9PCH5 P20810 H0YD33 H0Y9H6 H0Y7F0 A0A0A0M R45 P20810 P20810 B7Z574 E7EQ12 P20810 E7ES10 P20810	P20810-5 Isoform 5 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-3 Isoform 3 of Calpastatin OS=Homo sapiens GN=CAST # E7EQA0 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PDE4 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # H0YD33 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y9H6 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y7F0 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0A0MR45 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-2 Isoform 2 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E7EQ12 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # E7ES10 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST # Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q96GL9 Protein FAM163A OS=Homo sapiens GN=FAM163A PE=2 SV=1 # B0QZ18 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # Q99829 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # F2Z2V0 Copine-1 (Fragment) OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # Q13162 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 # P52701 DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2 # O43159 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 # E9PPP6 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=1 # A2A299 Protein-glutamine gamma-glutamyltransferase 2 (Fragment) OS=Homo sapiens GN=TGM2 PE=1 SV=7 # P21980 Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 # P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 # P30048-2 Isoform 2 of Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 #
PGENC*SPAWGAAPAYDAA DTHLR	C16	3.22017	Q14353	
SNIIFPC*DEVMLLLENLGN NVHR	C689	3.1983682	Q14974	
GPTCNAC*SSQALDGRGSLA PLTSEPCSQPCGVAASHCTT CSPYSSPFYIR	C65	3.192529788	Q96GL9	
SDPLC*VLLQDVGGSWAEL GR	C35;C30;C30	3.09915	B0QZ18 Q99829 F2Z2V0	
EEEC*HFYAGGQVYPGEASR	C51	3.084989229	Q13162	
SSLSC*SLQEGLIPGSQFWDA SK	C615	3.063958035	P52701	
AQLSGLQLQPC*LYK	C451;C135	2.972962728	O43159 E9PPP6	
VVSGMVC*NDDQGVLLGR	C230;M227 C230	2.922595094	A2A299 P21980	
HDVNC*EVVAVSVDHSHSL AWINTPR	C127;C109	2.884514673	P30048 P30048	

YSDESGNMDFDNFISC*LVR	C232;C232	2.846139459	A0A0C4D GQ5 P04632	A0A0C4DQG5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #
AC*FCIDNEALYDICFR	C199	2.830884927	Q9H4B7	Q9H4B7 Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 # Q03405 Urokinase plasminogen activator surface receptor OS=Homo sapiens GN=PLAUR PE=1 SV=1 # M0R383 Urokinase plasminogen activator surface receptor (Fragment) OS=Homo sapiens GN=PLAUR PE=1 SV=1 # M0QYR6 Urokinase plasminogen activator surface receptor (Fragment) OS=Homo sapiens GN=PLAUR PE=1 SV=1 # M0R0Y4 Urokinase plasminogen activator surface receptor (Fragment) OS=Homo sapiens GN=PLAUR PE=1 SV=1 # Q03405-2 Isoform 2 of Urokinase plasminogen activator surface receptor OS=Homo sapiens GN=PLAUR # M0QYS6 Urokinase plasminogen activator surface receptor (Fragment) OS=Homo sapiens GN=PLAUR PE=1 SV=1 #
C*NEGPILELENLQNGR	C198;C73;C173; C132;C198;C87	2.81701666	Q03405 M0R383 M0QYR6 M0R0Y4 Q03405 M0QYS6	Q6IQ22 Ras-related protein Rab-12 OS=Homo sapiens GN=RAB12 PE=1 SV=3 # A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 # P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A # P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 # Q92796-3 Isoform 3 of Disks large homolog 3 OS=Homo sapiens GN=DLG3 # Q5JUW8 Discs# large homolog 3 (Neuroendocrine-dlg# Drosophila)# isoform CRA_b OS=Homo sapiens GN=DLG3 PE=1 SV=1 # Q92796 Disks large homolog 3 OS=Homo sapiens GN=DLG3 PE=1 SV=2 # Q92796-2 Isoform 2 of Disks large homolog 3 OS=Homo sapiens GN=DLG3 # E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 # P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 # P54136 Arginine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 # Q06481-3 Isoform 3 of Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 # Q06481-4 Isoform 4 of Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 # Q06481 Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2 # Q06481-6 Isoform 6 of Amyloid- like protein 2 OS=Homo sapiens GN=APLP2 # E9PQS3 Amyloid-like protein 2 (Fragment) OS=Homo sapiens GN=APLP2 PE=1 SV=1 # Q06481-2 Isoform 2 of Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 # P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 # F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 # P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN # P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN #
FTDDTFC*EACK	C68	2.81585578	Q6IQ22	
C*MPAPEEIVEELPASK	C3013	2.811812703	A0A087W V66 P46013	
VLDALFPCVQGGTTAIPGAFG C*GK	C221;C254	2.809748467	P38606 P38606	
DSC*LPSQGLSFSYGDILHVIN ASDDEWWQAR	C36;C537;C519; C182	2.800772689	Q92796 Q5JUW8 Q92796 Q92796	
GC*STVLSPEGSAQFAAQIFG LSNHLVWSK	C374;C374	2.734057761	E9PBS1 P22234	
YGIC*MEDLIHEYTVGK	C186	2.663931193	P18124	
NCGC*LGASPNLEQLQEENL K	C34	2.663839171	P54136	
C*LVGEFVSDVLLVPEK	C133;C133;C133; C143;C118;C133	2.657793931	Q06481 Q06481 Q06481 Q06481 E9PQS3 Q06481	
TSSVSNPQDSVSGSPC*SR	C108;C106;C108; C108	2.644969327	P49023 F5GZ78 P49023 P49023	

VNLQMVYDPLC*R	C533 C493;M526 C462;M486	2.620059619	Q9Y285 Q9Y285 K7ER00	Q9Y285-2 Isoform 2 of Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA # Q9Y285 Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 # K7ER00 Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 # Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # Q5VTE0 Putative elongation factor 1-alpha- like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 # P68104 Elongation factor 1- alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # A0A087WV01 Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 #
ECEHCDC*LQGFQLTHSLGG GTGSGMGTLLISK	C129	2.594726667	Q9BUF5	
C*MPTFQFFK	C73	2.564045351	P10599	
KESESC*DCLQGFQLTHSLG GGTSGMGTLLISK	C127;C127	2.56329	Q13885 Q9BVA1	
GNVAGDSKNDPPMEAGFT AQVIILNHPGQISAGYAPVLD C*	C363;C363;C34 2;C361	2.55784262	Q5VTE0 P68104 A0A087W VQ9 A0A087W V01	
GEETPVIVGSALC*ALEGR	C222	2.50805637	P49411	P49411 Elongation factor Tu# mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 # P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 # A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 # A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 # J3KNF4 Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1 # O14618 Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1 # E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 # O95197-3 Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3 # P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 #
ISGADINSIC*QESGMLAVR	C348;C379	2.499077337	P43686 P43686	
LGTTAGQMC*SGLPGLSSVDI NNFGDSINESEGIPLKR	C475 C475;M474	2.482449892	A0A087W V66 P46013	
VLPNLPC*VVQEGAIVMAR	C141	2.477113261	A0A0A0M QS1 Q53H96	
QICSC*DGLTIWEER	C227;C246	2.443215	J3KNF4 O14618	
ALVDGPC*TQVR	C42;C42	2.433857367	E7EPB3 P50914	
SC*SSSCAVHDLIFWR	C42	2.410278692	O95197	
CCLTYC*FNKPEDK	C149	2.39	P62979	
DEYSIDNEALYDIC*FR	C211	2.3789475	Q13885	
IVNLAC*K	C226	2.354930707	O00116	O00116 Alkylidihydroxyacetonephosphate synthase# peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1 # Q8IXH6 Tumor protein p53-inducible nuclear protein 2 OS=Homo sapiens GN=TP53INP2 PE=1 SV=2 # Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 # O75663 TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 # O75663-2 Isoform 2 of TIP41-like protein OS=Homo sapiens GN=TIPRL #
NQSSFIYQPC*QR	C214	2.326896712	Q8IXH6	
AVQDLC*GWR	C428	2.250885606	Q9P258	
VAC*AEEWQESR	C87;C87	2.238805207	O75663 O75663	

TC*FISCVASGQRPHLCCISH GLASFLESVWFHC*LS	C185 C154	2.224440687	B4DVA9	B4DVA9 Protein O-glucosyltransferase 1 OS=Homo sapiens GN=POGLUT1 PE=1 SV=1 #
AGIDGESIGNC*PFSQR	C191;C32;C32	2.20755	Q9NZA1 Q9NZA1 Q9NZA1	Q9NZA1 Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3 # Q9NZA1-3 Isoform 3 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 # Q9NZA1-2 Isoform 1 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 #
TFVDFFSQC*LHEEYR	C215	2.160356278	Q53GQ0	Q53GQ0 Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 #
LEAIETQDPSLGC*GLPLNCT PIK	C172;C113	2.150274605	Q9NVP2 K7ES22	Q9NVP2 Histone chaperone ASF1B OS=Homo sapiens GN=ASF1B PE=1 SV=1 # K7ES22 Histone chaperone ASF1B OS=Homo sapiens GN=ASF1B PE=1 SV=1 #
ELQIC*PATAGSGPAATQDFS K	C1119;C1100	2.145974814	P00519 P00519	P00519-2 Isoform IB of Tyrosine-protein kinase ABL1 OS=Homo sapiens GN=ABL1 # P00519 Tyrosine-protein kinase ABL1 OS=Homo sapiens GN=ABL1 PE=1 SV=4 #
KADVIVLAGTVC*DFR	C354	2.141875	A1L0T0	A1L0T0 Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 # E9PQA7 BSD domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BSDC1 PE=1 SV=7 # Q9NW68-3 Isoform 3 of BSD domain-containing protein 1 OS=Homo sapiens GN=BSDC1 # Q9NW68-2 Isoform 2 of BSD domain-containing protein 1 OS=Homo sapiens GN=BSDC1 # Q9NW68 BSD domain-containing protein 1 OS=Homo sapiens GN=BSDC1 PE=1 SV=1 # E9PS77 BSD domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BSDC1 PE=1 SV=1 # Q9NW68-7 Isoform 7 of BSD domain- containing protein 1 OS=Homo sapiens GN=BSDC1 # Q9NW68-5 Isoform 5 of BSD domain-containing protein 1 OS=Homo sapiens GN=BSDC1 #
TIDC*DVITLMGTPSGTAEPYD GTK	C33;C116;C99;C 99;C60;C116;C9 9	2.138764099	E9PQA7 Q9NW68 Q9NW68 Q9NW68 E9PS77 Q9NW68 Q9NW68	Q96EY5-2 Isoform 2 of Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A # Q96EY5 Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A PE=1 SV=1 #
SC*SPLAFSAFGDLTIK	C191;C231	2.068190153	Q96EY5 Q96EY5	O14556 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 # K7EP73 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific (Fragment) OS=Homo sapiens GN=GAPDHS PE=1 SV=1 # B0QZ18 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # Q99829 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 # A6PVH9 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 #
YNP GSMNIVSNASC*TTNCLA PLAK	C156 C224;M148	2.055649863	O14556 K7EP73	P31153 S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 # P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 # Q9Y6I3 Epsin-1 OS=Homo sapiens GN=EPN1 PE=1 SV=2 #
VRNC*SSPEFSK	C58;C53;C53	2.054465	B0QZ18 Q99829 A6PVH9	
TC*NVLVALEQQSPDIAQGVH LDR	C104	2.021868927	P31153	
ELEVLLMC*NK	C109;M90 C91 C91;M108	1.996183186	P62910 F8W727 D3YTB1	
EEADQPPSC*GPEDDAQLQL ALSLSR	C205	1.992724273	Q9Y6I3	

NSCNNFIYGGC*R	C109;C116;C166	1.99113843	O43291 K7EM91 O43291	O43291-2 Isoform 2 of Kunitz-type protease inhibitor 2 OS=Homo sapiens GN=SPINT2 # K7EM91 Kunitz-type protease inhibitor 2 OS=Homo sapiens GN=SPINT2 PE=1 SV=1 # O43291 Kunitz-type protease inhibitor 2 OS=Homo sapiens GN=SPINT2 PE=1 SV=2 #
GPC*IIYNEDNGIIK	C208	1.9737375	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
SLHDALC*VVK	C397	1.961415961	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
YSYVC*PDLVK	C235	1.947390274	P61158	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
LLEQAEAEGC*QR	C326	1.945674466	Q9UBN6	Q9UBN6 Tumor necrosis factor receptor superfamily member 10D OS=Homo sapiens GN=TNFRSF10D PE=1 SV=1 #
VTELQQQPLC*TSVNTIYDNA VQGLR	C277	1.937706135	Q96AG4	Q96AG4 Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 #
SFFDNISC*DDNR	C311;C375;C50; C375;C334;C54	1.931755713	A0A140TA 76 Q8ND56 A0A0G2J Q95 Q8ND56 Q8ND56 A0A096LP 11	A0A140TA76 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 # Q8ND56-2 Isoform 2 of Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A # A0A0G2JQ95 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 # Q8ND56 Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A PE=1 SV=3 # Q8ND56-3 Isoform 3 of Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A # A0A096LP11 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 #
KAC*GDSTLTQITAGLDPVGR	C25	1.928037313	P62879	P62879 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 #
LCLNIC*VGESGDR	C25;C23;C24	1.924678121	P62913 Q5VVC8 P62913	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 # Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 # P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 # E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
HELQANC*YEEVK	C177;C122;C139; C139	1.915489699	E9PK25 G3V1A4 P23528 E9PP50	O95620 tRNA-dihydrouridine(20a/20b) synthase [NAD(P)+]-like OS=Homo sapiens GN=DUS4L PE=2 SV=2 # F8WEL2 tRNA-dihydrouridine(20a/20b) synthase [NAD(P)+]-like OS=Homo sapiens GN=DUS4L PE=1 SV=1 #
DSEFTTNQGDC*PLIVQFAAN DAR	C82;C82	1.898597423	O95620 F8WEL2	Q7Z5K2 Wings apart-like protein homolog OS=Homo sapiens GN=WAPL PE=1 SV=1 # Q7Z5K2-3 Isoform 3 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL # Q7Z5K2-2 Isoform 2 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL #
C*SSYSESSEAAQLEEVTSVL EANSK	C94;C179;C137	1.888253154	Q7Z5K2 Q7Z5K2 Q7Z5K2	Q92878 DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 # Q92878-3 Isoform 3 of DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 # Q92878-2 Isoform 2 of DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 #
NIDQC*SEIVK	C1296;C1157;C 1302	1.885579555	Q92878 Q92878 Q92878	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #
LPLMEC*VQMTQDVQK	C360	1.88464	Q01813	

C*ILTTVDPDTGVDR	C272	1.882595	Q969Z3	Q969Z3 Mitochondrial amidoxime reducing component 2 OS=Homo sapiens GN=MARC2 PE=1 SV=1 #
SQMYSTDYDQILPDC*YSWP EEVQK	C481 C556;M469	1.872442852	P48163 P48163	P48163 NADP-dependent malic enzyme OS=Homo sapiens GN=ME1 PE=1 SV=1 # P48163-2 Isoform 2 of NADP-dependent malic enzyme OS=Homo sapiens GN=ME1 #
C*SWLVPSPK	C265;C210	1.868573333	Q3SXM5 Q3SXM5	Q3SXM5 Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens GN=HSDL1 PE=1 SV=3 # Q3SXM5-2 Isoform 2 of Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens GN=HSDL1 #
FC*NIMGSSNGVDQEHFSNV VK	C150	1.862236905	Q9NYL9	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 # Q8WVV9-5 Isoform 5 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # Q8WVV9-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL #
NIIQPPSCVLHYYNVPLC*VTE ETFTK	C430;C459;C45 9;C464;C464;C4 30	1.8534475	Q8WVV9 Q8WVV9 C9IYN3 D6W592 Q8WVV9 B7WPG3	C9IYN3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=2 # D6W592 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # Q8WVV9 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # B7WPG3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 #
VGVGTC*GIADKPMQYQDT SK	C214	1.847843333	O75940	O75940 Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 # D6RER6 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=1 #
C*SSFMAPPVTDLGELR	C127	1.830551153	D6RER6 P36551 P36551	P36551-2 Isoform 2 of Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX # P36551 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 # P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB # P45954 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 #
VGSFC*LSEAGAGSDFSALK	C73;C175	1.827131848	P45954 P45954	Q6YP21 Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens GN=CCBL2 PE=1 SV=1 # Q6YP21-3 Isoform 3 of Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens GN=CCBL2 #
MDDPEC*YFNLSLK	C337;M298 C303	1.813212889	Q6YP21 Q6YP21	O75083 WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 # O75083-3 Isoform 2 of WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 #
MTVDESGQLISC*SMDDTV R	C242 C382;M231	1.80732	O75083 O75083	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # Q9BYK1 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # P63220 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 #
TGGAYGEDLGADYNLSQVC* DGK	C2468	1.806755	P49327	contaminant_INT-STD1 BSA # Q9Y287 Integral membrane protein 2B OS=Homo sapiens GN=ITM2B PE=1 SV=1 #
TYAIC*GAIR	C56;C56;C56	1.80562558	Q8WVC2 Q9BYK1 P63220	
MPC*TEDYLSLILNR SGEELIIPDAVAVDC*KDPD DVVPVGQR	C471 C38	1.804512188 1.801318377	Q9Y287	



SVLC*STPTINIPASPFMQK	C22	1.797412225	Q96KB5 Q96KB5	Q96KB5 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 # Q96KB5-2 Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK #
LVIVGDGAC*GK	C16	1.789781119	P61586	P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 #
DFIKNMITGTSQADC*AVLIVA AGVGEFEAGISK	C111;C111;C111; 1;C111;C111	1.782807317	Q5VTE0 P68104 Q05639 A0A087W VQ9 A0A087W V01	Q5VTE0 Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 # P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 # A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # A0A087WV01 Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 #
VTDTQEAE*AGPPVPDPK	C28	1.78179	Q99614	Q99614 Tetratricopeptide repeat protein 1 OS=Homo sapiens GN=TTC1 PE=1 SV=1 #
YIETSELC*GGAR	C361	1.779629375	O00429	O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L #
C*TDGIIYVDSVDVDRLEEAK	C85;C85	1.774386956	P56559 P56559	P56559 ADP-ribosylation factor-like protein 4C OS=Homo sapiens GN=ARL4C PE=1 SV=1 # P56559-2 Isoform 2 of ADP-ribosylation factor-like protein 4C OS=Homo sapiens GN=ARL4C #
YGSQC*MQPNNIMGIENICEL AAR	C182	1.758584203	F1DAL9 P10589	F1DAL9 COUP transcription factor 1 OS=Homo sapiens GN=NR2F1 PE=1 SV=1 # P10589 COUP transcription factor 1 OS=Homo sapiens GN=NR2F1 PE=1 SV=1 #
NEC*LWTDMLSNFGYPGYQS K	C163	1.750619008	P35625	P35625 Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2 #
ANASIC*FAVPDPLMPDPSKQ PK	C95;C106;C81	1.744779958	O75569 O75569 O75569	O75569-2 Isoform 2 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA # O75569 Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=1 SV=1 # O75569-3 Isoform 3 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA #
AGC*AVTSLLESELTK	C1218;C1203;C1218; C1227;C1183;C1227	1.738786271	O60610 O60610 A0A140T8 Z0 A0A0G2J H68 H9KV28 O60610	O60610-3 Isoform 3 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # O60610-2 Isoform 2 of Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 # A0A140T8Z0 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # A0A0G2JH68 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=1 # H9KV28 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 # O60610 Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 #
LGPQSDPTEANLESADPEL C*IR	C38;C38	1.735107369	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
SFC*PGGTDSVSPPPSVITQE NLGR	C314;C99	1.733245723	Q9C0C9 K7EQ12	Q9C0C9 (E3-independent) E2 ubiquitin-conjugating enzyme OS=Homo sapiens GN=UBE2O PE=1 SV=3 # K7EQ12 (E3-independent) E2 ubiquitin-conjugating enzyme (Fragment) OS=Homo sapiens GN=UBE2O PE=1 SV=1 #

NVVTIFSAPNYC*YR	C266;C266	1.730016824	P67775 P62714	P67775 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 # P62714 Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 # B4DWR3 Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=1 # P61758 Prefoldin subunit 3 OS=Homo sapiens GN=VBP1 PE=1 SV=3 # Q99757 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 # F8WDN2 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 # Q9Y5R8 Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 #
FLLADNLYC*K	C108;C113	1.722671856	B4DWR3 P61758	Q99757 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 # F8WDN2 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 # Q9Y5R8 Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 #
VVNSETPVVDFHAQWC*GP CK	C90;C90	1.718173212	Q99757 F8WDN2	Q99757 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 # F8WDN2 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 # Q9Y5R8 Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 #
NPLC*PLGQTVQSELFR	C115	1.714841868	Q9Y5R8	Q9Y5R8 Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 #
TTGLVGLAVC*NTPHER	C17;C13;C17;C17; 7;C27	1.714403977	Q16718 H7BYD0 F8WAS3 Q16718 C9IZN5	Q16718-2 Isoform 2 of NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 # H7BYD0 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (Fragment) OS=Homo sapiens GN=NDUFA5 PE=1 SV=1 # F8WAS3 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=1 # Q16718 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3 # C9IZN5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (Fragment) OS=Homo sapiens GN=NDUFA5 PE=1 SV=1 #
LLGPTVMLGGC*EFSR	C667	1.700351226	Q8N9T8	Q8N9T8 Protein KRI1 homolog OS=Homo sapiens GN=KRI1 PE=1 SV=3 #
LQDLSSC*ITQGK	C389	1.697988248	P29590	P29590-9 Isoform PML-3 of Protein PML OS=Homo sapiens GN=PML # P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK #
KIIPTLEEGQLPSPTATSQLP LESDAVEC*LNYQHVK	C132;C132	1.69563052	P61978 P61978	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK #
SWMEGLTLQDYSEHC*K	C238	1.693710875	O00487	O00487 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 #
DIVENIC*GR	C330	1.690968527	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
YC*AAPTEPVIHNGSQGTGTN GSEISDSYQAEYPDEYHGE YQDDYPR	C273;C232	1.682359665	Q15417 Q15417	Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 #
TWYVQATC*ATQGTGLYDGL DWLSHELK	C159	1.668232985	P84085	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 #
VPTANVSVVDLTC*R	C247	1.664900078	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #

					Q01518 Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 # Q5T0R1 Adenylyl cyclase-associated protein (Fragment) OS=Homo sapiens GN=CAP1 PE=1 SV=1 # Q01518-2 Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 # Q5T0R7 Adenylyl cyclase-associated protein (Fragment)
ALLVTASQC*QQPAENK	C93;C93;C92;C93; 3;C93;C93;C93; C93;C93;C92	1.66172	Q01518 Q5T0R1 Q01518 Q5T0R7 Q5T0R6 Q5T0R3 Q5T0R2 Q5T0R4 Q5T0R5 Q5T0R9		OS=Homo sapiens GN=CAP1 PE=1 SV=1 # Q5T0R6 Adenylyl cyclase-associated protein (Fragment) OS=Homo sapiens GN=CAP1 PE=1 SV=1 # Q5T0R3 Adenylyl cyclase- associated protein (Fragment) OS=Homo sapiens GN=CAP1 PE=1 SV=1 # Q5T0R2 Adenylyl cyclase-associated protein (Fragment) OS=Homo sapiens GN=CAP1 PE=1 SV=1 # Q5T0R4 Adenylyl cyclase- associated protein (Fragment) OS=Homo sapiens GN=CAP1 PE=1 SV=7 # Q5T0R5 Adenylyl cyclase-associated protein (Fragment) OS=Homo sapiens GN=CAP1 PE=1 SV=7 # Q5T0R9 Adenylyl cyclase- associated protein (Fragment) OS=Homo sapiens GN=CAP1 PE=1 SV=7 #
QMFEPVSC*TFTYLLGDR	C34 C34;M28	1.660762157	O95571 M0QXB5 M0QY80		O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # M0QXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 # M0QY80 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 #
GALMANFLTQGQVC*CNGTR	C288;C218	1.659247917	P49189 P49189		P49189 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 # P49189-2 Isoform 2 of 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 #
STDTSC*QMAGLR	C27;C27	1.656468968	C9JW94 Q9HBM1		C9JW94 Kinetochore protein Spc25 (Fragment) OS=Homo sapiens GN=SPC25 PE=1 SV=1 # Q9HBM1 Kinetochore protein Spc25 OS=Homo sapiens GN=SPC25 PE=1 SV=1 #
AQC*PIVER	C66;C87;C66	1.6553925	P46782 M0R0R2 M0R0F0		P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
LLDLVQQSC*NYK	C34;C30	1.652020857	B1AHD1 P55769		B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #
TASISSPSEGTPVGSYGC* TPQSLPK	C787;C864	1.647068251	Q6PKG0 Q6PKG0		Q6PKG0-3 Isoform 2 of La-related protein 1 OS=Homo sapiens GN=LARP1 # Q6PKG0 La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 #
C*ALLASEVPQLALQLLDPE SYVR	C539	1.639861737	Q6PJG6		Q6PJG6 BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 #

IVGIGYNGMPNGC*SDDVLP WR	C60;C60;C71;C60; C60;C60;C60	1.639047095	D6RC36 P32321 P32321 D6RAR9 D6R9S0 D6RBN2 D6RBJ9	D6RC36 Deoxycytidylate deaminase (Fragment) OS=Homo sapiens GN=DCTD PE=1 SV=1 # P32321 Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1 SV=2 # P32321-2 Isoform 2 of Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD # D6RAR9 Deoxycytidylate deaminase (Fragment) OS=Homo sapiens GN=DCTD PE=1 SV=1 # D6R9S0 Deoxycytidylate deaminase (Fragment) OS=Homo sapiens GN=DCTD PE=1 SV=1 # D6RBN2 Deoxycytidylate deaminase (Fragment) OS=Homo sapiens GN=DCTD PE=1 SV=1 # D6RBJ9 Deoxycytidylate deaminase (Fragment) OS=Homo sapiens GN=DCTD PE=1 SV=1 # E5RIM7 Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 # O00244 Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 # E5RGN3 Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 # P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 # Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 # J3KT10 Nuclear pore complex protein Nup85 OS=Homo sapiens GN=NUP85 PE=1 SV=1 # Q9BW27 Nuclear pore complex protein Nup85 OS=Homo sapiens GN=NUP85 PE=1 SV=1 # A0A0A0MRG2 Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=1 # P05067-9 Isoform L-APP752 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-3 Isoform L-APP677 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-7 Isoform L-APP733 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-4 Isoform APP695 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-6 Isoform APP714 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-5 Isoform L-APP696 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-11 Isoform 11 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-2 Isoform APP305 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067-8 Isoform APP751 of Amyloid beta A4 protein OS=Homo sapiens GN=APP # P05067 Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3 # E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 # P22692 Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2 # Q14694-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 # Q14694 Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 # Q14694-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 #
VC*IESEHSMDTLLATLKK	C46;C41;C32	1.63607	E5RIM7 O00244 E5RGN3	
NWYVQPSC*ATSGDGLYEGL TWLTSNYKS	C155	1.63555943	P62330	
GVLLYGPPGC*GK	C137	1.626582311	Q8NBU5	
SEMVPSC*PFIYIIR	C51 C51;M47	1.620520759	J3KT10 Q9BW27	
EGILQYCQEVYPQLITNVVE ANQPVTIQNWC*K	C63;C98;C98;C98; C98;C98;C98;C98; C93;C98;C98;C98; 8	1.608655493	A0A0A0MRG2 RG2 P05067 P05067 P05067 P05067 P05067 P05067 P05067 P05067 P05067 P05067 P05067 P05067 P05067	
C*MQLTDFILK	C54	1.604881938	E7EPB3 P50914	
THEDLYIIPINC*DR	C204	1.603325545	P22692	
TAGQPEGGPGADFGQSC*FP AEAGR	C302;C254;C258	1.594625557	Q14694 Q14694 Q14694	

DLNC*VPEIADTLGAVAK	C22;C22	1.592512063	O14744 O14744	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 # O14744-5 Isoform 5 of Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 #
AGQC*VIGLQMGTNK	C164	1.59062	Q99439 B4DDF4 B4DUT8 A0A087X1 X5	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X1X5 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #
AC*ADATLSQITNNIDPVGR	C25;C25	1.58993	P62873 P62873	P62873-2 Isoform 2 of Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 # P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 #
SSVQEEC*VSTISSKDEDPL AATR	C78;C78	1.587821968	Q7L0Y3 C9JVB6	Q7L0Y3 Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2 # C9JVB6 Mitochondrial ribonuclease P protein 1 (Fragment) OS=Homo sapiens GN=TRMT10C PE=1 SV=1 #
VFAEC*NDESFWFR	C38;C38;C38;C38; C38;C38;C38;C38; C38;C38;C38;C38; 8;C38	1.587280848	D6R918 Q9NX40 D6RIT9 D6RF07 D6RG39 D6RBC5 D6RA54 Q9NX40 Q9NX40 D6RC55 Q9NX40 D6RDI5	D6R918 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # Q9NX40-2 Isoform 2 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 # D6RIT9 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # D6RF07 OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # D6RG39 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # D6RBC5 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # D6RA54 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # Q9NX40-4 Isoform 4 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 # Q9NX40 OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # D6RC55 OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 # Q9NX40-3 Isoform 3 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 # D6RDI5 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 #
NSC*NNFIYGGCR	C158	1.572675	O43291	O43291 Kunitz-type protease inhibitor 2 OS=Homo sapiens GN=SPINT2 PE=1 SV=2 #
VWNLANC*K	C182	1.567173191	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
YAIC*SALAASALPALVMSK	C125	1.563899615	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
STPYEC*GFDPMSPAR	C39	1.563887708	P03897	P03897 NADH-ubiquinone oxidoreductase chain 3 OS=Homo sapiens GN=MT-ND3 PE=1 SV=1 #
LPTDLTAC*DNR	C111;C82	1.561678477	Q96RS6 Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # Q96RS6-2 Isoform 2 of NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 #
C*PFTGNVSIR	C60	1.561123823	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #
C*ELLYEGPPDDEAAMGIK	C369	1.55927	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #

TWYVQATC*ATQGTGLYEGL DWLSNELSK	C159	1.555968805	P18085	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 #
VLC*ELADLQDKEVGDGTTSV VIIAAELLK	C76	1.549626297	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
APPSSGAPPASTAQAPC*GQ AAYGQFGQGDVQNGPSSTV QMQR	C78	1.548773333	P53992	P53992 Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3 #
C*KPIDVDFDFPNSDVSSIGR	C38;C9;C38;C38	1.536965785	Q71F23 D6R9S4 Q71F23 Q09GN1	Q71F23-3 Isoform 3 of Centromere protein U OS=Homo sapiens GN=CENPU # D6R9S4 Centromere protein U (Fragment) OS=Homo sapiens GN=CENPU PE=1 SV=1 # Q71F23 Centromere protein U OS=Homo sapiens GN=CENPU PE=1 SV=1 # Q09GN1 Centromere protein U OS=Homo sapiens GN=MLF1IP PE=1 SV=1 #
EVLC*PESQSPNGVR	C137;C155	1.529103837	Q14684 Q14684	Q14684-2 Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B # Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 #
MYGC*DVGS DWR	C125;M122 C125	1.528865909	P01892 A0A140T9 I0 A0A140T9 13 A0A140T9 X5	P01892 HLA class I histocompatibility antigen# A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # A0A140T9I0 HLA class I histocompatibility antigen# A-3 alpha chain (Fragment) OS=Homo sapiens GN=HLA-A PE=1 SV=1 # A0A140T913 HLA class I histocompatibility antigen# A-3 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # A0A140T9X5 HLA class I histocompatibility antigen# A-3 alpha chain (Fragment) OS=Homo sapiens GN=HLA-A PE=1 SV=1 #
ATLQAALC*LENFSSQVVER	C21;C21;C40	1.527748272	P59998 F8WCF6 P59998	P59998 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 # F8WCF6 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4-TTLL3 PE=3 SV=1 # P59998-3 Isoform 3 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 #
WAELLPLLQQC*QVVR	C30	1.51059412	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
SSSSSSASAAAAAASSSA SC*SR	C100	1.509528706	Q07065	Q07065 Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 #
TSC*GSPNYAAPEVISGR	C185;C200;C17 6	1.501919861	Q13131 Q13131 Q96E92	Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 # Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 # Q96E92 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=1 #
SGQAGYVPC*NILGEARPEDA GAPFEQAGQK	C155;C559;C54 3	1.492241969	Q9H6S3 Q9H6S3 Q9H6S3	Q9H6S3-2 Isoform 2 of Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 # Q9H6S3-3 Isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 # Q9H6S3 Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2 #
SC*SGVEFSTSGSSNTDTGK	C47;C47	1.487904888	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #

HPSAVTAC*NLDLENLITDSNR	C325;C325	1.484846751	Q9UBF2 Q9UBF2	Q9UBF2-2 Isoform 2 of Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 # Q9UBF2 Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 # Q9NZ09-4 Isoform 4 of Ubiquitin-associated protein 1 OS=Homo sapiens GN=UBAP1 # Q9NZ09-3 Isoform 3 of Ubiquitin-associated protein 1 OS=Homo sapiens GN=UBAP1 # Q9NZ09 Ubiquitin-associated protein 1 OS=Homo sapiens GN=UBAP1 PE=1 SV=1 # A0A0D9SG79 Ubiquitin-associated protein 1 (Fragment) OS=Homo sapiens GN=UBAP1 PE=1 SV=1 #
ADFNLADFEC*EEDPFDNLELK	C225;C197;C161;C187	1.475893559	Q9NZ09 Q9NZ09 Q9NZ09 A0A0D9SG79	Q9NZ09 Ubiquitin-associated protein 1 OS=Homo sapiens GN=UBAP1 # Q9NZ09 Ubiquitin-associated protein 1 OS=Homo sapiens GN=UBAP1 PE=1 SV=1 # A0A0D9SG79 Ubiquitin-associated protein 1 (Fragment) OS=Homo sapiens GN=UBAP1 PE=1 SV=1 #
AYEYVEC*PIR	C66	1.475834829	P53701	P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 # A0A024R571 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=1 # Q9H4M9 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 # C9JC03 EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=1 SV=1 #
FMC*AQLPNPVLDISISIDTPGILSGEK	C152;M137 C138;M151 C152	1.468156271	A0A024R571 Q9H4M9 C9JC03	Q9H4M9 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 # C9JC03 EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=1 SV=1 #
LPLC*SLPGEPGNPDDQLQR	C75	1.458698578	Q96GX2	Q96GX2 Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 # P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
VIGSGC*NLDSAR	C192;C164;C163	1.458277869	P00338 P07195 P00338	Q7L5Y1-5 Isoform 5 of Mitochondrial enolase superfamily member 1 OS=Homo sapiens GN=ENOSF1 # Q7L5Y1 Mitochondrial enolase superfamily member 1 OS=Homo sapiens GN=ENOSF1 PE=1 SV=1 # Q7L5Y1-4 Isoform 4 of Mitochondrial enolase superfamily member 1 OS=Homo sapiens GN=ENOSF1 #
ALQLFLQIDSC*R	C361;C330;C337	1.448660143	Q7L5Y1 Q7L5Y1 Q7L5Y1	Q7L5Y1-5 Isoform 5 of Mitochondrial enolase superfamily member 1 OS=Homo sapiens GN=ENOSF1 # Q7L5Y1 Mitochondrial enolase superfamily member 1 OS=Homo sapiens GN=ENOSF1 PE=1 SV=1 # Q7L5Y1-4 Isoform 4 of Mitochondrial enolase superfamily member 1 OS=Homo sapiens GN=ENOSF1 #
SVNSLDGLASVLYPGC*DTLDKVFTYAK	C85	1.448404453	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # Q9H8K7 Uncharacterized protein C10orf88 OS=Homo sapiens GN=C10orf88 PE=1 SV=2 #
NC*PIGEQLQSVLGNISGYK	C218	1.446592115	Q9H8K7	Q9H8K7 Uncharacterized protein C10orf88 OS=Homo sapiens GN=C10orf88 PE=1 SV=2 #
EGTDSSQGIPQLVSNISAC*QVIAEAVR	C29	1.44418716	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P78346-2 Isoform 2 of Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 # P78346 Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1 # Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 # J3QL89 ARF GTPase-activating protein GIT1 (Fragment) OS=Homo sapiens GN=GIT1 PE=1 SV=1 # J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 # Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 #
ITVVGVGQVGMAC*AISILGK	C36	1.440903333	P07195	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P78346-2 Isoform 2 of Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 # P78346 Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1 # Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 # J3QL89 ARF GTPase-activating protein GIT1 (Fragment) OS=Homo sapiens GN=GIT1 PE=1 SV=1 # J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 # Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 #
LTIIVSDPSHC*NVLR	C87;C87	1.439402889	P78346 P78346	P78346 Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 # P78346 Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1 # Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 # J3QL89 ARF GTPase-activating protein GIT1 (Fragment) OS=Homo sapiens GN=GIT1 PE=1 SV=1 # J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 # Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 #
KGVSASAVPFTSPSLLSC*SQEGSR	C576;C39;C576;C585	1.435536632	Q9Y2X7 J3QL89 J3QRU8 Q9Y2X7	Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 # J3QL89 ARF GTPase-activating protein GIT1 (Fragment) OS=Homo sapiens GN=GIT1 PE=1 SV=1 # J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 # Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 #
LGTLPSPMLLSMNEMTLVSHAC*YPLFKDQATNNGCAMASR	C163	1.429556288	Q9UJW2	Q9UJW2-2 Isoform 2 of Tubulointerstitial nephritis antigen OS=Homo sapiens GN=TINAG #

FEIINAIYEPTTEEC*EWKPDE EDEISEELK	C132;C69;C126; C132;C72;C132; C91;C91;C132	1.423052331	P55209 F8W543 H0YIV4 F8VY35 H0YH88 P55209 F8VV59 F8W118 F5H4R6	P55209-2 Isoform 2 of Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 # F8W543 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # H0YIV4 Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F8VY35 Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # H0YH88 Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # P55209 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F8VV59 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F8W118 Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F5H4R6 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 #
TVNIWQFDLETLC*QAR	C316;C316	1.421619945	Q8N9V3 B8ZZF2	Q8N9V3 WD repeat# SAM and U-box domain-containing protein 1 OS=Homo sapiens GN=WDSUB1 PE=1 SV=3 # B8ZZF2 WD repeat# SAM and U-box domain-containing protein 1 OS=Homo sapiens GN=WDSUB1 PE=1 SV=2 #
GFAGVC*GFGGPYGETVATG PYR	C920;C892	1.419651902	Q9NZB2 Q9NZB2	Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 #
KDC*EVVMMIGLPGAGK	C497;C478	1.419185	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #



				P20810-5 Isoform 5 of Calpastatin OS=Homo sapiens GN=CAST # P20810-6 Isoform 6 of Calpastatin OS=Homo sapiens GN=CAST # P20810-4 Isoform 4 of Calpastatin OS=Homo sapiens GN=CAST # P20810-9 Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST # E7EVY3 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-3 Isoform 3 of Calpastatin OS=Homo sapiens GN=CAST # E7EQA0 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0C4DGB5 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E9PDE4 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-10 Isoform 10 of Calpastatin OS=Homo sapiens GN=CAST # H0YD33 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y9H6 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # H0Y7F0 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # A0A0A0MR45 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-2 Isoform 2 of Calpastatin OS=Homo sapiens GN=CAST # P20810 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 # B7Z574 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # E7EQ12 Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-7 Isoform 7 of Calpastatin OS=Homo sapiens GN=CAST # E7ES10 Calpastatin (Fragment) OS=Homo sapiens GN=CAST PE=1 SV=1 # P20810-8 Isoform 8 of Calpastatin OS=Homo sapiens GN=CAST # O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 # Q14671-2 Isoform 2 of Pumilio homolog 1 OS=Homo sapiens GN=PUM1 # Q14671 Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=3 # H0YEH2 Pumilio homolog 1 (Fragment) OS=Homo sapiens GN=PUM1 PE=1 SV=1 # Q14671-3 Isoform 3 of Pumilio homolog 1 OS=Homo sapiens GN=PUM1 # Q5T1Z8 Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=1 # Q5T1Z4 Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=1 # Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 # Q9Y678 Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 # V9GY01 Chromosome 15 open reading frame 23# isoform CRA_d OS=Homo sapiens GN=KNSTRN PE=1 SV=1 # Q9Y448 Small kinetochore-associated protein OS=Homo sapiens GN=KNSTRN PE=1 SV=2 # Q3B7J2-2 Isoform 2 of Glucose-fructose oxidoreductase domain-containing protein 2 OS=Homo sapiens GN=GFOD2 # Q3B7J2 Glucose-fructose oxidoreductase domain-containing protein 2 OS=Homo sapiens GN=GFOD2 PE=2 SV=1 #
AAAPAPVSEAVC*R	C456;C491;C367;C450;C394;C290;C131;C454;C336;C373;C469;C151;C166;C160;C131;C395;C408;C394;C123;C472;C408;C386	1.415161741	P20810 P20810 P20810 E7EVY3 P20810 E7EQA0 A0A0C4DGB5 E9PDE4 E9PCH5 P20810 H0YD33 H0Y9H6 H0Y7F0 A0A0A0MR45 P20810 P20810 B7Z574 E7EQ12 P20810 E7ES10 P20810	
GLTDLSAC*K	C142	1.409510296	O00567	
SLLC*GEDEAADENPESQEM LEEQLVR	C941	1.404145	Q9HAV4	
SESGGLGVSMVEYVLS SSPG DSC*LR	C251;M221 C270;M221 C234;M257 C234;M238 C234 C234;M221	1.402814237	Q14671 Q14671 H0YEH2 Q14671 Q5T1Z8 Q5T1Z4	
FQLTDC*QIYEVLSVIR	C143;C179	1.40187813	Q16555 Q16555	
HPSAVTAC*NLLENLV TDSN R	C325	1.399990526	Q9Y678	
FLEQQTLC*NNQVNDLTTALK	C218;C296	1.397922057	V9GY01 Q9Y448	
SGEWEAVEVLTEPDTNQNL C*EALQR	C272;C377	1.3978	Q3B7J2 Q3B7J2	

VLVTTNVC*AR	C284;C361;C393;C302;C367;C392;C398;C393;C310;C362	1.393143125	Q9UMR2 I3L0H8 Q9UMR2 Q9NUU7 Q9UMR2 Q9NUU7 H3BQK0 F6QDS0 I3L352 Q9UMR2	Q9UMR2-3 Isoform 3 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B # I3L0H8 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 # Q9UMR2 ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 # Q9NUU7-2 Isoform 2 of ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A # Q9UMR2-4 Isoform 4 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B # Q9NUU7 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 # H3BQK0 ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 # F6QDS0 HCG2043426# isoform CRA_b OS=Homo sapiens GN=hCG_2043426 PE=1 SV=1 # I3L352 ATP-dependent RNA helicase DDX19A (Fragment) OS=Homo sapiens GN=DDX19A PE=1 SV=1 # Q9UMR2-2 Isoform 2 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B # A0A087X0R7 Protein SENP3-EIF4A1 (Fragment) OS=Homo sapiens GN=SENP3-EIF4A1 PE=4 SV=1 # Q9H4L4 Sentrin-specific protease 3 OS=Homo sapiens GN=SENP3 PE=1 SV=2 #
SPLDPDSSLSC*TLPNGFGG QSGPEGER	C173;C243	1.392008581	A0A087X0 R7 Q9H4L4	Q9H0D6-2 Isoform 2 of 5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 # Q9H0D6 5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1 #
FSLDEEAILPDQIVC*SPVPM LR	C660;C736	1.388835	Q9H0D6 Q9H0D6	P36405 ADP-ribosylation factor-like protein 3 OS=Homo sapiens GN=ARL3 PE=1 SV=2 #
VWQIQSCSALTGEGVQDGM NWVC*K	C174	1.386716717	P36405	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
QEEVC*VIDALLADIR	C971;C971	1.38609854	Q27J81 Q27J81	O00233-2 Isoform p27-S of 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 # O00233 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 #
GIGMNEPLVDC*EGYPR	C59;M52 C59	1.385648195	O00233 O00233 J3KN29 F5H7X1 F5H5V4 F5GX23	J3KN29 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H7X1 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5H5V4 26S proteasome non-ATPase regulatory subunit 9 (Fragment) OS=Homo sapiens GN=PSMD9 PE=1 SV=1 # F5GX23 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 #
SFGVQPC*VSTVLVEPAR	C592	1.384955595	Q8TB52	Q8TB52 F-box only protein 30 OS=Homo sapiens GN=FBXO30 PE=1 SV=3 #
LAC*LSEEGNEIESGK	C213;C183;C51	1.380285	Q9Y2L1 Q9Y2L1 G3V1J5	Q9Y2L1 Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2 # Q9Y2L1-2 Isoform 2 of Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 # G3V1J5 Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=1 #
GQAGGGGPGTGPGLGEAGS LATC*ELPLAK	C45	1.379817748	Q9Y3D2	Q9Y3D2 Methionine-R-sulfoxide reductase B2# mitochondrial OS=Homo sapiens GN=MSRB2 PE=1 SV=2 #
AHEILPNLVCC*SAK	C130;C149	1.368143601	P50990 P50990	P50990-2 Isoform 2 of T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 # P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #

AHVFEFC*NLESSVESIISPK	C35;C35;C35;C35;C35	1.367387977	E5RJK5 E5RJK5 E5RJV1 E5RFV8 O60216 E5RIN7	E5RJK5 Double-strand-break repair protein rad21 homolog (Fragment) OS=Homo sapiens GN=RAD21 PE=1 SV=1 # E5RJK5 Double-strand-break repair protein rad21 homolog (Fragment) OS=Homo sapiens GN=RAD21 PE=1 SV=1 # E5RFV8 Double-strand-break repair protein rad21 homolog (Fragment) OS=Homo sapiens GN=RAD21 PE=1 SV=1 # E5RIN7 Double-strand-break repair protein rad21 homolog (Fragment) OS=Homo sapiens GN=RAD21 PE=1 SV=1 #
SASLDNGGC*ALTTFSVLEGEK	C27;C34;C92	1.358632814	P35610 P35610 P35610	P35610-3 Isoform 3 of Sterol O-acyltransferase 1 OS=Homo sapiens GN=SOAT1 # P35610-2 Isoform 2 of Sterol O-acyltransferase 1 OS=Homo sapiens GN=SOAT1 # P35610 Sterol O-acyltransferase 1 OS=Homo sapiens GN=SOAT1 PE=1 SV=3 #
GLATFC*LDK	C159;C183;C129	1.35863	O15173 O15173 O00264	O15173 Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1 # O15173-2 Isoform 2 of Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 # O00264 Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 #
LYYFQYPC*YQEGLR	C130	1.357436101	Q9NRW3	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 #
DKPELQFPFLQDEDTVATLLE C*K	C29;C49	1.352932594	P09543 P09543	P09543-2 Isoform CNP1 of 2'3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP # P09543 2'3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2 #
NVQLLSQFVSPFTGC*YGR	C90	1.352804562	Q9Y3D5	Q9Y3D5 28S ribosomal protein S18c# mitochondrial OS=Homo sapiens GN=MRPS18C PE=1 SV=1 #
GC*TATLGNFAK	C229	1.351645216	P15880	P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 #
QNLFQTGSNVSFSC*GGETR	C203;C203	1.347439846	Q9H4L5 Q9H4L5	Q9H4L5-2 Isoform 1b of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5-4 Isoform 1d of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 #
ELSFSGIPC*EGGLR	C36	1.3452804	Q9NVG8	Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
TVEEIEACMAGC*DK	C418;C482	1.343155309	P12955 P12955	P12955-3 Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
ENEITGALLPC*LDESR	C80;C80;C80	1.338081993	Q9Y3Z3 Q9Y3Z3 Q9Y3Z3	Q9Y3Z3-2 Isoform 2 of Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 # Q9Y3Z3 Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2 # Q9Y3Z3-3 Isoform 3 of Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 #
VILALGDYMGATCHAC*IGGT NVR	C136;C135;C135	1.336103333	Q14240 Q14240 E7EQG2	Q14240-2 Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 # Q14240 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2 # E7EQG2 Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=1 #

SSSC*GDTELLGQATLPVGS SRPLSR	C359;C359;C10 7	1.33543539	O14523 O14523 E9PK05	O14523-2 Isoform 2 of C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L # O14523 C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3 # E9PK05 C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=1 #
AVGDGILC*NTYIDSYK	C264;C275	1.33397	Q53EL6 Q53EL6	Q53EL6-2 Isoform 2 of Programmed cell death protein 4 OS=Homo sapiens GN=PD4 # Q53EL6 Programmed cell death protein 4 OS=Homo sapiens GN=PD4 PE=1 SV=2 #
IC*QADIVEAVDIASAAK	C107;C107;C17 2;C107	1.331876695	A0A0G2JJ L1 H0Y6G3 O15213 A0A140T9 L0	A0A0G2JJL1 WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=1 SV=1 # H0Y6G3 WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=1 SV=1 # O15213 WD repeat-containing protein 46 OS=Homo sapiens GN=WDR46 PE=1 SV=3 # A0A140T9L0 WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=1 SV=1 #
LFTESC*SISPK	C68;C68;C68	1.331550602	C9JXQ7 Q9Y6I9 C9JHH5	C9JXQ7 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 # Q9Y6I9 Testis-expressed sequence 264 protein OS=Homo sapiens GN=TEX264 PE=1 SV=1 # C9JHH5 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 #
YLC*DFTYYTSLYQSHGR	C149;C72	1.330998573	Q9NXJ5 Q9NXJ5	Q9NXJ5 Pyroglutamyl-peptidase 1 OS=Homo sapiens GN=PGPEP1 PE=1 SV=1 # Q9NXJ5-2 Isoform 2 of Pyroglutamyl-peptidase 1 OS=Homo sapiens GN=PGPEP1 #
GLC*AIAQAESLR	C97	1.327143764	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #
AGYDGESIGNC*PFSQR	C469;C487	1.324541186	Q96NY7 Q96NY7	Q96NY7-2 Isoform A of Chloride intracellular channel protein 6 OS=Homo sapiens GN=CLIC6 # Q96NY7 Chloride intracellular channel protein 6 OS=Homo sapiens GN=CLIC6 PE=2 SV=3 #
LSSDATVLTPTNESSC*DLMT K	C188;C47;C155	1.323966667	Q63HQ0 H0Y8Y4 Q63HQ0	Q63HQ0 AP-1 complex-associated regulatory protein OS=Homo sapiens GN=AP1AR PE=1 SV=1 # H0Y8Y4 AP-1 complex-associated regulatory protein (Fragment) OS=Homo sapiens GN=AP1AR PE=1 SV=1 # Q63HQ0-2 Isoform 2 of AP-1 complex-associated regulatory protein OS=Homo sapiens GN=AP1AR #
LEGIPAYIVPQTAPDC*KK	C113	1.32391638	Q9GZT4	Q9GZT4 Serine racemase OS=Homo sapiens GN=SRR PE=1 SV=1 #
SVLLCGIEAQAC*ILNTTLDLL DR	C114;C114;C11 4	1.32198301	K7ENV7 K7EKW4 Q96AB3	K7ENV7 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=7 # K7EKW4 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=1 # Q96AB3 Isochorismatase domain-containing protein 2 OS=Homo sapiens GN=ISOC2 PE=1 SV=1 #
YIELFLNSC*PK	C420;C449;C41 3;C314;C476	1.320997739	F5H5I6 H0YAK1 H0Y8R1 Q12849 Q12849	F5H5I6 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=2 # H0YAK1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 # H0Y8R1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 # Q12849-5 Isoform 2 of G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 # Q12849 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=3 #

VEDMAELTC*LNEASVLHNLK	C91	1.319153395	P35579	P35579 Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 #
YADLTEDQLPSC*ESLKDTIAR	C153	1.317084587	P18669	P18669 Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 #
LC*ASGAGATPDTAIEEIKEK	C31;C31	1.313103333	P53384 P53384	P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 # P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 #
GVAQTPGSVEEDALLC*GPVSK	C79	1.311196986	Q9BQP7	Q9BQP7 Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens GN=MGME1 PE=1 SV=1 #
FSFCC*SPEPEAEAEAAAGP GPCER	C27;C27	1.304439471	E7EMC7 Q13501	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 #
ATELFVQC*LATYSYR	C55	1.300238368	Q9NRG0	Q9NRG0 Chromatin accessibility complex protein 1 OS=Homo sapiens GN=CHRAC1 PE=1 SV=1 #
LSIQC*YLSALDR	C224	1.300176118	Q01581	Q01581 Hydroxymethylglutaryl-CoA synthase# cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2 #
GSDC*GIVNVNIPTSGAEIGG AFGGEK	C450;C478;C414; 4;C414;C441	1.297514065	P49419 P49419 P49419 F8VS02 A0A140T9 V3	P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha- aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 # P49419-4 Isoform 4 of Alpha- aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # F8VS02 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=1 # A0A140T9V3 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=1 #
YTELPHGAISEDQAVGPADIP C*DSTGQTST FEETGQELAEELLEEEKLSK*V PVLIFANK	C162	1.296402666	Q9H773	Q9H773 dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1 #
	C118	1.295697047	P36405	P36405 ADP-ribosylation factor-like protein 3 OS=Homo sapiens GN=ARL3 PE=1 SV=2 #
LGC*NITISEDITPR	C38;C38	1.295368361	Q96FJ0 Q96FJ0	Q96FJ0 AMSH-like protease OS=Homo sapiens GN=STAMBPL1 PE=1 SV=2 # Q96FJ0-2 Isoform 2 of AMSH-like protease OS=Homo sapiens GN=STAMBPL1 #
LMC*PQEIVDYIADKK	C95 C140;M94	1.293145	O14561 H3BNK3	O14561 Acyl carrier protein# mitochondrial OS=Homo sapiens GN=NDUFAB1 PE=1 SV=3 # H3BNK3 Acyl carrier protein (Fragment) OS=Homo sapiens GN=NDUFAB1 PE=1 SV=1 #
AC*QEQIEALLESLR	C247	1.291751409	P24385	P24385 G1/S-specific cyclin-D1 OS=Homo sapiens GN=CCND1 PE=1 SV=1 #
LLAC*IASR	C174	1.289755	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #
LAAAQGOAPLEPTQDGSAIET C*PK	C474;C423	1.288553598	Q7Z2Z2 Q7Z2Z2	Q7Z2Z2 Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2 # Q7Z2Z2-2 Isoform 2 of Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 #
EQVPSLGSNVAC*GLAYTDY HK	C568	1.287856729	A1L0T0	A1L0T0 Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2 # Q96AC1-2 Isoform 2 of Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 # HOYJ34 Fermitin family homolog 2 (Fragment) OS=Homo sapiens GN=FERMT2 PE=1 SV=1 # Q96AC1-3 Isoform 3 of Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 # A0A0U1RRM8 Fermitin family homolog 2 (Fragment) OS=Homo sapiens GN=FERMT2 PE=1 SV=1 # Q96AC1 Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1 #
MQHLNPDQPQLIPEQITTDITPE C*LVSPR	C473;M498 C520 C520;M451 C370;M498 C520;M348	1.286348408	Q96AC1 HOYJ34 Q96AC1 A0A0U1R RM8 Q96AC1	

IIVFSAC*R	C89;C91	1.28201904	H0YE29 Q07960	H0YE29 Rho GTPase-activating protein 1 (Fragment) OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 # Q07960 Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 #
AC*ASPSAQVEGSPVAGSDG SQPAVK	C249;C97	1.281705237	Q9UFC0 F8WDB4	Q9UFC0 Leucine-rich repeat and WD repeat-containing protein 1 OS=Homo sapiens GN=LRWD1 PE=1 SV=2 # F8WDB4 Leucine-rich repeat and WD repeat-containing protein 1 (Fragment) OS=Homo sapiens GN=LRWD1 PE=1 SV=2 #
FMYC*TPFTLDGR	C1933;M1933 C1904;M1931 C1902;M1931 C1944;M1911 C1913 C1935;M1942 C1933;M1900	1.272902157	Q96N67 Q96N67 Q96N67 H0Y7L2 Q96N67 Q96N67 Q96N67	Q96N67-3 Isoform 3 of Deducator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67-2 Isoform 2 of Deducator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67-4 Isoform 4 of Deducator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # H0Y7L2 Deducator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=2 # Q96N67-6 Isoform 6 of Deducator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 # Q96N67 Deducator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4 # Q96N67-5 Isoform 5 of Deducator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 #
GIDQC*IPLFVEAALER	C757	1.270875568	O95373	O95373 Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 #
FQSSAVMALQEACEAYLVGL FEDTNLC*AIHAK	C111	1.266165901	P68431	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 #
QGEYGLASIC*NGGGGASAM LIQK	C413	1.2596865	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
TDVC*VFAAQEDLETMQAFA QVFNK	C96	1.258716812	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 #
SC*GSSTPDEFPTDIPGTK	C105	1.254337197	P41091	P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 #
KAEEATEAQEVVEATPEGAC* TEPR	C189	1.254053319	O75683	O75683 Surfeit locus protein 6 OS=Homo sapiens GN=SURF6 PE=1 SV=3 #
AWSTGDC*DNGGDEWEQEI R	C54;C54;C54	1.253482461	Q9BRF8 Q9BRF8 Q9BRF8	Q9BRF8-2 Isoform 2 of Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1 # Q9BRF8 Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3 # Q9BRF8-3 Isoform 3 of Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1 #
TVPFC*STFAAFFTR	C220;C394;C38 6	1.253175989	A0A0B4J1 R6 P29401 P29401	A0A0B4J1R6 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=1 # P29401-2 Isoform 2 of Transketolase OS=Homo sapiens GN=TKT # P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 #
MYGISLC*QAILDETKGDYEK	C324	1.252774159	P04083	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 #
AGAIAPC*EVTVPAQNTGLGP EK	C119;C119	1.251557446	P05388 F8VU65	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # F8VU65 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #

LEDVENLGC*R	C329;C329	1.250835113	Q9UJX3 Q9UJX3	Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 #
TPGAATASASGAAEDGAC*G CLPNPGTFEECHRK	C74	1.250675727	O96008	O96008 Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1 #
ECISIHVGQAGVQIGNAC*WE LYCLEHGIQPDGQMPSDK	C20	1.248278484	Q9BQE3 P68363 Q71U36	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 #
DFGYGVEEEEEEAAAAGGGV GAGAGGGC*GPGGADSSK R	C52	1.242949902	Q9HB90	Q9HB90 Ras-related GTP-binding protein C OS=Homo sapiens GN=RRAGC PE=1 SV=1 #
C*PIQLNEGVSFQDLDTAK	C179	1.24213	A6NDU8	A6NDU8 UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 #
MLGETC*ADCGTILLQDK	C53;M11 C16 C47;M48	1.241827046	H0YEB6 O60232 G3V1B8	H0YEB6 Sjogren syndrome/scleroderma autoantigen 1 (Fragment) OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # O60232 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # G3V1B8 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 #
EMQNLSFQDC*YSSK	C111	1.240727004	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
YIYDQC*PAVAGYGPIEQLPD YNR	C453	1.240330282	P31930	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 #
ADTSQEIC*SPR	C1010;C1027;C1027;C66	1.240004692	P52948 P52948 P52948 H7C3P6	P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
DLAVVTQSAEAPAEEDLLGP NC*YYDK	C310;C310;C230	1.239042712	Q9BX40 Q9BX40 Q5TBP9	Q9BX40 Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B PE=1 SV=1 # Q9BX40-2 Isoform 2 of Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B # Q5TBP9 Protein LSM14 homolog B (Fragment) OS=Homo sapiens GN=LSM14B PE=1 SV=1 #
FQDTSQYVC*AELQALEQEQ R	C1364	1.238460151	Q8N3D4	Q8N3D4 EH domain-binding protein 1-like protein 1 OS=Homo sapiens GN=EHP1L1 PE=1 SV=2 #
LWNTLGVK*K	C138	1.236449824	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
LC*YVALDFENEMATAASSSS LEK	C219	1.235345903	P68032	P68032 Actin# alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 #
VQENSAYIC*SR	C585	1.234511156	Q9Y3T9	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 #
YASPEMC*FVFSR	C27;M26 C27	1.2306225	A0A0A6Y Y92 P30566 P30566	A0A0A6Y92 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=1 # P30566 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 # P30566-2 Isoform 2 of Adenylosuccinate lyase OS=Homo sapiens GN=ADSL #
TADIC*QMLVSTVDGDLYPPV EEPVASTDPK	C92	1.230557989	Q15545	Q15545 Transcription initiation factor TFIID subunit 7 OS=Homo sapiens GN=TAF7 PE=1 SV=1 #

LSSAVTDLNIIMEPTEC*SELS EFVSR	C147 C147;M142	1.229582904	Q6IPU0 A0A087W TF1	Q6IPU0 Centromere protein P OS=Homo sapiens GN=CENPP PE=1 SV=1 # A0A087WTF1 Centromere protein P OS=Homo sapiens GN=CENPP PE=1 SV=1 # G5EA39 Anaphase-promoting complex subunit 15 OS=Homo sapiens GN=ANAPC15 PE=1 SV=1 # F8WDQ6 Anaphase-promoting complex subunit 15 (Fragment) OS=Homo sapiens GN=ANAPC15 PE=1 SV=1 # P60006-2 Isoform 2 of Anaphase-promoting complex subunit 15 OS=Homo sapiens GN=ANAPC15 # F5H3R3 Anaphase-promoting complex subunit 15 OS=Homo sapiens GN=ANAPC15 PE=1 SV=1 # F5H2T3 Anaphase-promoting complex subunit 15 (Fragment) OS=Homo sapiens GN=ANAPC15 PE=1 SV=1 # P60006 Anaphase-promoting complex subunit 15 OS=Homo sapiens GN=ANAPC15 PE=1 SV=1 # F5H6E4 Anaphase-promoting complex subunit 15 (Fragment) OS=Homo sapiens GN=ANAPC15 PE=1 SV=7 #
VTETLWFNLDRPC*VEETELQ QQEQQHQAQLQSIK	C24;C24;C24;C24; 4;C24;C24;C24	1.228821982	G5EA39 F8WDQ6 P60006 F5H3R3 F5H2T3 P60006 F5H6E4	O14497 AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3 # O14497-2 Isoform 2 of AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A # H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YLC2 Proteasome subunit alpha type OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 # H0YMA1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YKT8 Proteasome subunit beta type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
GPADMASQC*WGAAAAAAA AAAASGGAQQR	C336 C336;M332	1.228812923	O14497 O14497	
YLLQYQEPIPCQLVTALC*DI K	C115;C84;C115; C115;C115;C115; 5;C91	1.228194432	H0YL69 H0YN18 P25789 H0YLC2 H0YMZ1 H0YMA1 H0YKT8	



				<p>B1APG3 cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=1 # B1APF9 cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=1 # P22694-9 Isoform 9 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # A0A087WVC4 cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=1 # P22694-5 Isoform 5 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # K7ERP6 cAMP-dependent protein kinase catalytic subunit alpha (Fragment) OS=Homo sapiens GN=PRKACA PE=1 SV=1 # P22694 cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=2 # B1APG2 cAMP-dependent protein kinase catalytic subunit beta (Fragment) OS=Homo sapiens GN=PRKACB PE=1 SV=1 # P22694-4 Isoform 4 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # P22694-8 Isoform 8 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # P22694-2 Isoform 2 of cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA # P22694-6 Isoform 6 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # Q15136 Protein kinase A-alpha (Fragment) OS=Homo sapiens GN=KIN27 PE=1 SV=1 # B1APF8 cAMP-dependent protein kinase catalytic subunit beta (Fragment) OS=Homo sapiens GN=PRKACB PE=1 SV=1 # P22694-10 Isoform 10 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # A0A0A0MS54 cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=1 # P22612 cAMP-dependent protein kinase catalytic subunit gamma OS=Homo sapiens GN=PRKACG PE=1 SV=3 # P17612 cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2 # P22694-7 Isoform 7 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # P22694-3 Isoform 3 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # P22694-2 Isoform 2 of cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB # Q9Y3A3-2 Isoform 2 of MOB-like protein phocein OS=Homo sapiens GN=MOB4 # S4R3N1 Protein HSPE1-MOB4 OS=Homo sapiens GN=HSPE1-MOB4 PE=3 SV=1 # Q9Y3A3-3 Isoform 3 of MOB-like protein phocein OS=Homo sapiens GN=MOB4 # Q9Y3A3 MOB-like protein phocein OS=Homo sapiens GN=MOB4 PE=1 SV=1 # B4DM50 MOB-like protein phocein OS=Homo sapiens GN=MOB4 PE=1 SV=1 # Q99614 Tetratricopeptide repeat protein 1 OS=Homo sapiens GN=TTC1 PE=1 SV=1 #</p>
TWTLC*GTPEYLAPEIILSK	C206;C188;C207;C187;C203;C155;C200;C195;C187;C200;C192;C206;C183;C196;C170;C206;C200;C200;C204;C188;C247	1.224667711	<p>B1APG3 B1APF9 P22694 A0A087WVC4 VC4 P22694 K7ERP6 P22694 B1APG2 P22694 P22694 P17612 P22694 Q15136 B1APF8 P22694 A0A0A0MS54 S54 P22612 P17612 P22694 P22694 P22694</p>	
HTLDGAAC*LLNSNK	C102;C170;C113;C134;C35	1.223810879	<p>Q9Y3A3 S4R3N1 Q9Y3A3 Q9Y3A3 B4DM50</p>	
SENC*GVPEDLLNGLK	C8	1.223272071	Q99614	

NIC*FTVWDVGGQDK	C62	1.22159578	P84085	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 #
FSPNSSNPIIVSC*GWWDK	C168	1.220638125	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
PSYSSFTQGDSWGEVEDE EEGC*DQVAR	C48	1.219202317	Q8N6S5	Q8N6S5 ADP-ribosylation factor-like protein 6-interacting protein 6 OS=Homo sapiens GN=ARL6IP6 PE=1 SV=1 #
NLLC*GFYGR	C247;C247	1.217593146	B0QYD3 Q9UH17	B0QYD3 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 # Q9UH17 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 #
ECIC*VEEGQVPCPSLVPLPK	C141	1.216285674	P82663	P82663 28S ribosomal protein S25# mitochondrial OS=Homo sapiens GN=MRPS25 PE=1 SV=1 #
DIPDGATVLVGGFGLC*GIPE NLIDALLK	C67	1.215065	P55809	P55809 Succinyl-CoA:3-ketoacid coenzyme A transferase 1# mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 #
TYITDPVSAPC*APPLQPK	C342;C201;C364;C364	1.2135	A0A087W ZF1 C9JXK9 C9JUT4 Q93052	A0A087WZ1 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 # C9JXK9 Lipoma-preferred partner (Fragment) OS=Homo sapiens GN=LPP PE=1 SV=1 # C9JUT4 LIM domain containing preferred translocation partner in lipoma# isoform CRA_e OS=Homo sapiens GN=LPP PE=1 SV=1 # Q93052 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 #
SFFTASEGC*SNPLGGGR	C188;C188	1.212572311	Q9UKV8 Q9UKV8	Q9UKV8-2 Isoform 2 of Protein argonaute-2 OS=Homo sapiens GN=AGO2 # Q9UKV8 Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3 #
VETCGC*AEGYAR	C221;C96;C173;C194	1.210105	O14972 A8MY26 A8MTY9 O14972	O14972 Down syndrome critical region protein 3 OS=Homo sapiens GN=DSCR3 PE=2 SV=1 # A8MY26 Down syndrome critical region protein 3 OS=Homo sapiens GN=DSCR3 PE=1 SV=1 # A8MTY9 Down syndrome critical region protein 3 OS=Homo sapiens GN=DSCR3 PE=1 SV=1 # O14972-2 Isoform 2 of Down syndrome critical region protein 3 OS=Homo sapiens GN=DSCR3 #
STGVVNIPAAEC*LDEYEDDE AGQKER	C173;C119	1.209466474	Q96IZ0 H0Y116	Q96IZ0 PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 # H0Y116 PRKC apoptosis WT1 regulator protein (Fragment) OS=Homo sapiens GN=PAWR PE=1 SV=1 #
EVIAVSCGPAQC*QETIR	C71;C162	1.207825445	P38117 P38117	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB #
LLC*SQLQVADFLQNILAQED TAK	C54;C54	1.207065	O95229 O95229	O95229-2 Isoform 2 of ZW10 interactor OS=Homo sapiens GN=ZWINT # O95229 ZW10 interactor OS=Homo sapiens GN=ZWINT PE=1 SV=2 #
C*AGPTPEAELQALAR	C52	1.206009643	Q15050	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 #
LSC*QPMLSLDDFQLQPPVTF R	C105	1.200304545	O75607	O75607 Nucleoplasmin-3 OS=Homo sapiens GN=NPM3 PE=1 SV=3 #
ADVSFVLFFDC*NNEICIER	C122	1.200051376	P30085	P30085 UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3 #

VVNIIEGVDSNMC*CGTHVSN LSDLQVIK	C209;M103 C104;M291 C322;M382 C383 C292;M321	1.197835	Q9BTE6 L7N2F4 C9J5N1 Q9BTE6 Q9BTE6	Q9BTE6 Alanyl-tRNA editing protein Aarsd1 OS=Homo sapiens GN=AARSD1 PE=1 SV=2 # L7N2F4 Alanyl-tRNA-editing protein Aarsd1 (Fragment) OS=Homo sapiens GN=AARSD1 PE=1 SV=1 # C9J5N1 Protein PTGES3L- AARSD1 OS=Homo sapiens GN=PTGES3L- AARSD1 PE=1 SV=1 # Q9BTE6-2 Isoform 2 of Alanyl-tRNA editing protein Aarsd1 OS=Homo sapiens GN=AARSD1 # Q9BTE6-3 Isoform 3 of Alanyl-tRNA editing protein Aarsd1 OS=Homo sapiens GN=AARSD1 # HOYM70 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1 # A0A087X1Z3 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1 # Q9UL46 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 # O95758-4 Isoform 4 of Polypyrimidine tract- binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758-2 Isoform 2 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758-1 Isoform 1 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758 Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 PE=1 SV=2 # O95758-5 Isoform 5 of Polypyrimidine tract- binding protein 3 OS=Homo sapiens GN=PTBP3 # O95758-6 Isoform 6 of Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 # P21980 Protein-glutamine gamma- glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2 # Q12800-3 Isoform 3 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 # Q12800-2 Isoform 2 of Alpha- globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 # Q12800-4 Isoform 4 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 # F8VWL0 Alpha-globin transcription factor CP2 (Fragment) OS=Homo sapiens GN=TFCP2 PE=1 SV=1 # F8VX55 Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 PE=1 SV=1 # Q12800 Alpha- globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 PE=1 SV=2 # Q9Y570-4 Isoform 4 of Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 # Q9Y570-2 Isoform 2 of Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 # Q9Y570 Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 # P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 # P46734-2 Isoform 1 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 # P46734 Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 #
C*GFLPGNEK	C80;C106;C91	1.197580343	HOYM70 A0A087X1 Z3 Q9UL46	
IPC*DVTEAEIISLGLPFGK	C74;C40;C37;C6 8;C71;C40	1.1964225	O95758 O95758 O95758 O95758 O95758	
SEGTYC*CGPVPVR	C370	1.194549566	P21980	
IAQLFSISPC*QISQIYK	C402;C402;C45 3;C355;C375;C4 53	1.194147322	Q12800 Q12800 Q12800 F8VWL0 F8VX55 Q12800	
QC*EGITSPEGSK	C238;C51;C238	1.193946925	Q9Y570 Q9Y570 Q9Y570	
MC*DFGISGYLVDSVAK	C212;C178;C20 7	1.193838011	P46734 P46734 P46734	
VTDISGGC*GAMYEIK	C59	1.192828352	Q53S33	Q53S33 BoA-like protein 3 OS=Homo sapiens GN=BOLA3 PE=1 SV=1 #

DC*GGAAQLAGPAAEADPLGR	C8;C8;C8;C8;C8;C8;C8	1.18937197	Q9Y508 A0A096LNV3 A0A096LNT1 A0A096LP02 Q9Y508 A0A096LNN8 A0A096LPF9	Q9Y508 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNV3 E3 ubiquitin-protein ligase RNF114 (Fragment) OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LNT1 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 # A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 # A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 #
ICDEC*NYGSYQGR	C49	1.18553785	Q7RTV0	Q7RTV0 PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1 # P61077-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # H9KV45 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 # D6RAH7 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # A0A0A0MQU3 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # D6RFM0 Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=3 SV=1 # A0A087WY85 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 #
VLLSIC*SLLCDPNPDDPLVPEIAR	C109;C107;C107;C101;C78;C78;C107;C78;C108;C107	1.18222	P61077 P61077 H9KV45 P62837 D6RAH7 A0A0A0MQU3 D6RFM0 A0A087WY85 P62837	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 # O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 # B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 # P53602 Diphosphomevalonate decarboxylase OS=Homo sapiens GN=MVD PE=1 SV=1 # Q9UNI6 Dual specificity protein phosphatase 12 OS=Homo sapiens GN=DUSP12 PE=1 SV=1 # P15374 Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 # Q5TBK7 Ubiquitin carboxyl-terminal hydrolase isozyme L3 (Fragment) OS=Homo sapiens GN=UCHL3 PE=1 SV=1 # A0A087WTB8 Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=UCHL3 PE=1 SV=1 # contaminant_UBIQUITIN10 no description# F5H157 Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=1 SV=1 # Q15286 Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 #
C*YVQPQWVFDVSNAR	C391;C386;C374	1.181492807	O00541 O00541 B5MCF9	
DGDPLPSSLSC*K	C108	1.181193791	P53602	
VSC*AGQMLEVQPGLYFGGA AAVAEPDHLR	C23	1.179623421	Q9UNI6	
QTISNAC*GTIGLIHAIANNK	C95;C29;C59;C95	1.175358577	P15374 Q5TBK7 A0A087WTB8	
ENVNVEEMFNC*ITELVLR	C147;C163	1.174387199	F5H157 Q15286	

VHNQDPKDWPAQYC*EALAD EENR	C283	1.173301276	Q96MG7	Q96MG7 Non-structural maintenance of chromosomes element 3 homolog OS=Homo sapiens GN=NSMCE3 PE=1 SV=1 #
ADEASELAC*PTPK	C2202	1.171120659	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
VTSEALC*GVPVLVLANK	C78;C125;C125	1.169272485	Q13795 Q13795 Q13795	Q13795-3 Isoform 3 of ADP-ribosylation factor-related protein 1 OS=Homo sapiens GN=ARFRP1 # Q13795 ADP-ribosylation factor-related protein 1 OS=Homo sapiens GN=ARFRP1 PE=1 SV=1 # Q13795-2 Isoform 2 of ADP-ribosylation factor-related protein 1 OS=Homo sapiens GN=ARFRP1 #
MSSYAFFVQTC*R	C23	1.168811003	B2RPK0	B2RPK0 Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 #
YWLC*AATGPSIK	C249	1.167855879	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
IIC*SAGLSLLAEER	C195;C107	1.166223498	Q9BV86 S4R338	Q9BV86 N-terminal Xaa-Pro-Lys N- methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 # S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 #
VNQAIWLLC*TGAR	C155;C176;C15 5	1.165932264	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
VAVSADPNVNPVVVGLTLV C*SSAPGPLELDTGDLESFK K	C79;C79;C79;C7 9;C79	1.165007867	J3KTF8 P52565 P52565 J3QQX2 J3KRY1	J3KTF8 Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDIA PE=1 SV=7 # P52565 Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3 # P52565-2 Isoform 2 of Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA # J3QQX2 Rho GDP- dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=1 # J3KRY1 Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDIA PE=1 SV=1 #
YNFFTGC*PK	C364	1.164108011	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
QILLGIQELLNEPNIQDPAQAE AYTIYC*QNR	C138	1.163858411	P63279	P63279 SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1 #
LMWLFGC*PLLLDDVAR	C66	1.161830875	O15067	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
YLAEVAC*GDDR	C134	1.160954054	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #
NGIIVYLDVPLLDLIC*R	C163	1.160261196	Q8IYQ7	Q8IYQ7 Threonine synthase-like 1 OS=Homo sapiens GN=THNSL1 PE=1 SV=2 #
EPAPAEALPQQYEPAPAAL C*GPPPR	C363	1.15866	Q8IU81	Q8IU81 Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens GN=IRF2BP1 PE=1 SV=1 #
XLTCAICLGLYQDPVTLPC*G HNFC*GACIR	C19 C24	1.157054804	H0YGS7	H0YGS7 Tripartite motif-containing protein 65 (Fragment) OS=Homo sapiens GN=TRIM65 PE=1 SV=1 #
QPAIMPQSYGLEDGSC*SY KDFESR	C413;C472	1.155754041	M0QXS5 P14866	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
SIC*TTVLELLDKYLIANATNPE SK	C94	1.153877337	P27348	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 #
LTALDYHNPAGFNC*KDETEF R	C19	1.152591036	Q9Y224	Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 #

GSAVWC*QNVK	C33;C33;C33;C33	1.152415536	P07602 Q5BJH1 P07602 C9JIZ6 P07602	P07602-2 Isoform Sap-mu-6 of Prosaposin OS=Homo sapiens GN=PSAP # Q5BJH1 PSAP protein OS=Homo sapiens GN=PSAP PE=1 SV=1 # P07602-3 Isoform Sap-mu-9 of Prosaposin OS=Homo sapiens GN=PSAP # C9JIZ6 Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2 # P07602 Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2 # F1T0I1 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 # J3KNL6 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 #
ANNNAVAPTTC*PLQPVTDPAFASR	C46;C46	1.151721511	F1T0I1 J3KNL6	Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # Q5W0J0 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
TCDGVQC*AFEELVEK	C189;C160;C136;C115	1.150745283	Q9NP72 Q9NP72 A0A087X163 Q5W0J0	
LEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMDNEAIYDIC*R	C213;C283;C213;C213	1.149647016	Q9BQE3 F5H5D3 Q71U36 P68366	
HAC*VPVDFEEVHVSSNADEDIRNAIMAIR	C81	1.149434831	P51553	P51553 Isocitrate dehydrogenase [NAD] subunit gamma# mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 #
LTWHSC*PEDEAQ	C177	1.147096467	Q13185	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 # P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB # M0QY67 Electron transfer flavoprotein subunit beta (Fragment) OS=Homo sapiens GN=ETFB PE=1 SV=1 #
HSMNPF*CIAVEEAVR	C42;C133;C42	1.146930358	P38117 P38117 M0QY67	P63208 S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2 # Q9BXJ9 N-alpha-acetyltransferase 15# Nata auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
KENQWC*EEK	C160	1.145837445	P63208	O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 # C9JFK9 BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=1 SV=1 #
LFNTAVC*ESK	C721	1.145790241	Q9BXJ9	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 #
SQSPAASDC*SSSSSASLPS SGR	C179;C121	1.144537267	O95817 C9JFK9	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 #
LMDLDVEQLGIPEQEYSC*VVK	C135	1.14331	P12004	Q96SW2 Protein cereblon OS=Homo sapiens GN=CRBN PE=1 SV=1 # J3QT87 Protein cereblon (Fragment) OS=Homo sapiens GN=CRBN PE=1 SV=1 # J3QT51 Protein cereblon (Fragment) OS=Homo sapiens GN=CRBN PE=1 SV=1 # Q96SW2-2 Isoform 2 of Protein cereblon OS=Homo sapiens GN=CRBN #
LGTLAPFC*CPWEQLTQDWE SR	C705	1.140977332	Q99575	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 #
VQILPEC*VLPSTMSAVQLES LNK	C188	1.138633293	Q96SW2 J3QT87 J3QT51 Q96SW2	
VLSSSGSEAAVPSVC*FLVPP PNQEAQEAIVTR	C992	1.137194808	Q15149	

LSNVAPPC*ILR	C182;C182;C167	1.13652	C9JB30 Q9UPY8 Q9UPY8	C9JB30 Microtubule-associated protein RP/EB family member 3 (Fragment) OS=Homo sapiens GN=MAPRE3 PE=1 SV=1 # Q9UPY8 Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens GN=MAPRE3 PE=1 SV=1 # Q9UPY8-2 Isoform 2 of Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens GN=MAPRE3 #
ELADYLC*EDAQQLSLEDTFS TMK	C898;C898	1.134543333	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
DNQGILYEAAPTSTLTC*DSG PQK	C141;C191;C141;C141;C191;C141;C191;C191	1.13418	M0R073 Q8IV63 M0QX88 Q8IV63 M0QYG0 M0R200 Q8IV63 M0QYA8	M0R073 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 # Q8IV63-2 Isoform 2 of Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 # M0QX88 Inactive serine/threonine-protein kinase VRK3 (Fragment) OS=Homo sapiens GN=VRK3 PE=1 SV=7 # Q8IV63-3 Isoform 3 of Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 # M0QYG0 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 # M0R200 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 # Q8IV63 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=2 # M0QYA8 Inactive serine/threonine-protein kinase VRK3 OS=Homo sapiens GN=VRK3 PE=1 SV=1 #
WNDNC*PSWNTIDPEER	C301	1.133993463	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
NGYDYGQC*R	C80;C80	1.133102044	S4R3G0 Q13242	S4R3G0 Serine/arginine-rich-splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 # Q13242 Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 #
WLSDEC*TNAAVFNFLSR	C345;C350;C380	1.13262902	O75521 A0A0C4DGA2 O75521	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 # A0A0C4DGA2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 # O75521 Enoyl-CoA delta isomerase 2# mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 #
HPSIIFIDELDALC*PK	C459;C459;C459	1.131556484	Q8NB90 Q8NB90 Q8NB90	Q8NB90 Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3 # Q8NB90-3 Isoform 3 of Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 # Q8NB90-2 Isoform 2 of Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 #
VC*NQIEFLNTEFK	C39	1.131264045	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
GC*GTVLLSGPR	C136;C134;C134;C105;C113	1.131113333	J3QQ67 G3V203 Q07020 Q07020 H0YHA7	J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 # Q07020 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 # Q07020-2 Isoform 2 of 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 # H0YHA7 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 #
TTEEQVQASTPC*PR	C108	1.130849384	Q14137	Q14137 Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 #

FC*DNSSAIQ GK	C270	1.13026233	O15067	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
FLYEC*PWR	C622	1.130157188	P11498	P11498 Pyruvate carboxylase# mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 #
TEDSGLAAGPPEAAGENFAP C*SVAPGK	C132	1.129338731	Q96CP2	Q96CP2 FLYWCH family member 2 OS=Homo sapiens GN=FLYWCH2 PE=1 SV=1 #
ASLLSAPPC*R	C1425;C1412	1.128973778	Q9NZM1 Q9NZM1	Q9NZM1 Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 # Q9NZM1-6 Isoform 6 of Myoferlin OS=Homo sapiens GN=MYOF #
EFVQLVC*PDAGQQAGQVGF LNPNGSSQ GK	C427;C361;C404; C275;C382;C396; C449;C404;C52	1.12721785	B1AKN8 B1AKN7 Q12857 B1AKN6 B1AKN5 Q12857 Q12857 S4R3K5	B1AKN8 Nuclear factor 1 OS=Homo sapiens GN=NFIA PE=1 SV=1 # B1AKN7 Nuclear factor 1 OS=Homo sapiens GN=NFIA PE=1 SV=1 # Q12857 Nuclear factor 1 A-type OS=Homo sapiens GN=NFIA PE=1 SV=2 # B1AKN6 Nuclear factor 1 OS=Homo sapiens GN=NFIA PE=1 SV=1 # B1AKN5 Nuclear factor 1 OS=Homo sapiens GN=NFIA PE=1 SV=1 # Q12857-3 Isoform 3 of Nuclear factor 1 A-type OS=Homo sapiens GN=NFIA # Q12857-4 Isoform 4 of Nuclear factor 1 A-type OS=Homo sapiens GN=NFIA # Q12857-2 Isoform 2 of Nuclear factor 1 A-type OS=Homo sapiens GN=NFIA # S4R3K5 Nuclear factor 1 A-type OS=Homo sapiens GN=NFIA PE=1 SV=1 #
TPSYSISSTLNPQAPEFILGC* TASK	C142;C94;C98	1.126807879	Q14694 Q14694 Q14694	Q14694-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 # Q14694 Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 # Q14694-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 #
SWC*PDCVQAEPVVR	C43	1.126474102	Q9BRA2	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 #
FTSGAFLSPSVSQEC*R	C1051;C1068;C1068; C107	1.12634715	P52948 P52948 P52948 H7C3P6	P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 # P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 # H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 #
GAVEKGEELSC*EER	C38	1.124659201	P31947	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 #
KAEGDLGPSWVC*GFSNLES QVLEK	C184	1.12264768	Q15814	Q15814 Tubulin-specific chaperone C OS=Homo sapiens GN=TBCC PE=1 SV=2 #
LC*DFGISGQLVDSIAK	C257;C246	1.121856164	P45985 P45985	P45985-2 Isoform 2 of Dual specificity mitogen-activated protein kinase 4 OS=Homo sapiens GN=MAP2K4 # P45985 Dual specificity mitogen-activated protein kinase 4 OS=Homo sapiens GN=MAP2K4 PE=1 SV=1 #
VPADTEVVC*APPTAYIDFAR	C42;C79	1.121797736	P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 #
C*TPACISFGPK	C34;C34;C34	1.11850189	A0A087WTS8 A0A087WYC1 P34932	A0A087WTS8 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=1 # A0A087WYC1 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=1 # P34932 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 #



QAVLGAGLPSTPC*TTINK	C119	1.118372669	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #
IEDIDNEDWENPQLC*SDYVK DIYQYLR	C50;C131;C131	1.117661203	H0YMP3 O95067 H1UBN3	H0YMP3 G2/mitotic-specific cyclin-B2 OS=Homo sapiens GN=CCNB2 PE=1 SV=1 # O95067 G2/mitotic-specific cyclin-B2 OS=Homo sapiens GN=CCNB2 PE=1 SV=1 # H1UBN3 Cyclin B2 OS=Homo sapiens GN=CCNB2V PE=1 SV=1 #
AIQESLLTSTEGLC*PSALSET SR	C540	1.116865776	Q8IZ07	Q8IZ07 Ankyrin repeat domain-containing protein 13A OS=Homo sapiens GN=ANKRD13A PE=1 SV=3 # I3L4S6 WD repeat domain phosphoinositide- interacting protein 3 (Fragment) OS=Homo sapiens GN=WDR45B PE=1 SV=1 # Q5MNZ6
C*NYLALVGGGK	C56;C63;C63	1.116584585	I3L4S6 Q5MNZ6 I3L4L8	WD repeat domain phosphoinositide- interacting protein 3 OS=Homo sapiens GN=WDR45B PE=2 SV=2 # I3L4L8 WD repeat domain phosphoinositide-interacting protein 3 OS=Homo sapiens GN=WDR45B PE=1 SV=1 #
IAPC*PSQDSLYSPLDSTSA QAGEGVQR	C308;C169	1.114917533	Q99704 Q99704	Q99704 Docking protein 1 OS=Homo sapiens GN=DOK1 PE=1 SV=1 # Q99704-3 Isoform 3 of Docking protein 1 OS=Homo sapiens GN=DOK1 #
VGILDVDLC*GPSIPR	C54;C142;C54	1.113956146	H3BNF0 H3BNS4 Q9Y5Y2	H3BNF0 Cytosolic Fe-S cluster assembly factor NUBP2 OS=Homo sapiens GN=NUBP2 PE=1 SV=1 # H3BNS4 Cytosolic Fe-S cluster assembly factor NUBP2 (Fragment) OS=Homo sapiens GN=NUBP2 PE=1 SV=1 # Q9Y5Y2 Cytosolic Fe-S cluster assembly factor NUBP2 OS=Homo sapiens GN=NUBP2 PE=1 SV=1 #
DFSHPC*TWQVLDGAEDTLR	C109	1.110999116	Q9BSH5	Q9BSH5 Haloacid dehalogenase-like hydrolase domain-containing protein 3 OS=Homo sapiens GN=HDHD3 PE=1 SV=1 #
IC*DDELILIK	C357	1.109878222	P17987	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
NSPSLFPCAPLC*ER	C146	1.108783333	Q9UJM3	Q9UJM3 ERBB receptor feedback inhibitor 1 OS=Homo sapiens GN=ERRFI1 PE=1 SV=1 #
KYDGYTSC*PLVTGYNR	C379	1.108656667	Q9Y6N5	Q9Y6N5 Sulfide:quinone oxidoreductase# mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1 #
C*GESMLCVVDPDISAFR	C384	1.108302222	Q06330 Q06330 Q06330 Q06330 Q06330 Q06330	Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 # Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-3 Isoform APCR-3 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-2 Isoform APCR-1 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ #
AVASQLDC*NFLK	C207;C193	1.107789074	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #

C*AVVDVPFGGAK	C39;C172;C5	1.107465	P00367 P00367 P00367	P00367-3 Isoform 3 of Glutamate dehydrogenase 1# mitochondrial OS=Homo sapiens GN=GLUD1 # P00367 Glutamate dehydrogenase 1# mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2 # P00367-2 Isoform 2 of Glutamate dehydrogenase 1# mitochondrial OS=Homo sapiens GN=GLUD1 #
DVQIGDIVTVGEC*RPLSK	C131	1.107256645	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 # Q96II5 ARAF protein OS=Homo sapiens GN=ARAF PE=1 SV=1 # P10398 Serine/threonine-protein kinase A-Raf OS=Homo sapiens GN=ARAF PE=1 SV=2 #
TQADELPAC*LLSAAR	C600;C597	1.107136721	Q96II5 P10398	
TLQNTMVNLGLQNAC*DEAIY QLGLDLEEEIEEDAGLGNG GLGR	C109	1.107120676	P11216	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 #
GDSEPTPGC*SGLGPGGVR	C13;C13;C12;C1 3;C13	1.106837311	Q8WW01 Q8WW01 H0YCV5 E9PPN1 F2Z3M0	Q8WW01 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # Q8WW01-2 Isoform 2 of tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 # H0YCV5 tRNA-splicing endonuclease subunit Sen15 (Fragment) OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # E9PPN1 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 # F2Z3M0 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 #
LELYGAC*VEEEGALTGGPK	C199;C149;C18 6	1.106683036	Q9BST9 Q9BST9 Q9BST9	Q9BST9 Rhotekin OS=Homo sapiens GN=RTKN PE=1 SV=2 # Q9BST9-3 Isoform 3 of Rhotekin OS=Homo sapiens GN=RTKN # Q9BST9-2 Isoform 2 of Rhotekin OS=Homo sapiens GN=RTKN #
VAAALENTHLLEVNVQC*LSA R	C158	1.105871802	Q9Y3D0	Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 #
C*GVPFTDLLDAAK	C111;C155;C23 0;C112;C201;C1 49	1.105760248	Q01433 Q01433 Q01433 Q01433 H0Y360 Q01433	Q01433-3 Isoform Ex1A-3 of AMP deaminase 2 OS=Homo sapiens GN=AMPD2 # Q01433-4 Isoform Ex1B-3 of AMP deaminase 2 OS=Homo sapiens GN=AMPD2 # Q01433 AMP deaminase 2 OS=Homo sapiens GN=AMPD2 PE=1 SV=2 # Q01433-5 Isoform 5 of AMP deaminase 2 OS=Homo sapiens GN=AMPD2 # H0Y360 AMP deaminase 2 (Fragment) OS=Homo sapiens GN=AMPD2 PE=1 SV=1 # Q01433-2 Isoform Ex1A-2-3 of AMP deaminase 2 OS=Homo sapiens GN=AMPD2 #
AGLGEGVPPGNYGNYGYAN SGYSAC*EEENERLTESLR	C28;C28;C28;C2 8	1.10432629	Q68DU7 C9JTT8 O15155 O15155	Q68DU7 BET1 homolog OS=Homo sapiens GN=DKFZp781C0425 PE=1 SV=1 # C9JTT8 BET1 homolog OS=Homo sapiens GN=BET1 PE=1 SV=1 # O15155 BET1 homolog OS=Homo sapiens GN=BET1 PE=1 SV=1 # O15155-2 Isoform 2 of BET1 homolog OS=Homo sapiens GN=BET1 #
ENFSLDWC*K	C117	1.100581518	P23919	P23919 Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 #
C*DVETLEWSK	C110;C427	1.098540903	Q9H6R3 A0A0B4J1 R2	Q9H6R3-2 Isoform 2 of Acyl-CoA synthetase short-chain family member 3# mitochondrial OS=Homo sapiens GN=ACSS3 # A0A0B4J1R2 Acyl-CoA synthetase short-chain family member 3# mitochondrial OS=Homo sapiens GN=ACSS3 PE=1 SV=1 #

VVISGFGDPLIC*DNQVSTGDT TR	C103;C103;C103; C103;C103;C103; C103	1.097505656	O00468 O00468 O00468 O00468 O00468 O00468	O00468-3 Isoform 3 of Agrin OS=Homo sapiens GN=AGRN # O00468-6 Isoform 6 of Agrin OS=Homo sapiens GN=AGRN # O00468 Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5 # O00468-4 Isoform 4 of Agrin OS=Homo sapiens GN=AGRN # O00468-5 Isoform 5 of Agrin OS=Homo sapiens GN=AGRN # O00468-7 Isoform 7 of Agrin OS=Homo sapiens GN=AGRN # Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # HOY6T8 Ras-related protein Rab-18 (Fragment) OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 #	
TC*DGVQCAFEELVEK	C184;C155;C268; C131	1.09644	Q9NP72 Q9NP72 HOY6T8 A0A087X163	P27707 D6RFG8	P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
SC*PSFSASSEGTR	C9;C9	1.096193038	P29279 P29279	P29279 P29279	P29279 Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2 # P29279-2 Isoform 2 of Connective tissue growth factor OS=Homo sapiens GN=CTGF #
DGAPC*IFGGTVYR	C103;C103	1.094976011	P35998 P35998	P35998 P35998	P35998-2 Isoform 2 of 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 # P35998 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 #
AC*LIFFDEIDAIGGAR	C133;C270	1.092594629	Q96EB1 Q96EB1 Q96EB1 G5E9D4	Q96EB1 Q96EB1 Q96EB1 G5E9D4	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1-2 Isoform 2 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 # G5E9D4 Elongation protein 4 homolog (S. cerevisiae)# isoform CRA_b OS=Homo sapiens GN=ELP4 PE=1 SV=1 #
VEPC*SLTPGYTK	C219;C218;C218; C218	1.090982719	P62873	P62873	P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 #
LLLAGYDDFNC*NVWDALK	C294	1.090127917	P07814	P07814	P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 #
ERPTPSLNNNC*TTSEDSLVL YNR	C744	1.089921322	P62241	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #
NC*IVLIDSTPYR	C100	1.088997967	Q86YH6	Q86YH6	Q86YH6 Decaprenyl-diphosphate synthase subunit 2 OS=Homo sapiens GN=PDSS2 PE=1 SV=2 #
C*LLSDELSNIAMQVR	C71	1.08786	P35270	P35270	P35270 Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1 #
TVVNISSLC*ALQPFK	C159	1.08738	Q9Y696	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
AGSDGESIGNC*PFSQR	C35	1.086949516	A0A0A0MT58 Q86VL0 Q5JRI7 Q15560 Q15560	A0A0A0MT58 Q86VL0 Q5JRI7 Q15560 Q15560	A0A0A0MT58 Transcription elongation factor A protein 2 (Fragment) OS=Homo sapiens GN=TCEA2 PE=1 SV=1 # Q86VL0 TCEA2 protein OS=Homo sapiens GN=TCEA2 PE=1 SV=1 # Q5JRI7 Transcription elongation factor A protein 2 (Fragment) OS=Homo sapiens GN=TCEA2 PE=1 SV=1 # Q15560 Transcription elongation factor A protein 2 OS=Homo sapiens GN=TCEA2 PE=1 SV=1 # Q15560-2 Isoform 2 of Transcription elongation factor A protein 2 OS=Homo sapiens GN=TCEA2 #
ITTFPPVPVTC*DAVR	C108;C135;C108; C135;C108	1.085792371			

SEETNTEIVEC*ILK	C902;C903	1.082784936	A0A087W V66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
GTVLLADNVIC*PGAPDFLAH VR	C173;C223	1.082494975	P21964 P21964	P21964-2 Isoform Soluble of Catechol O-methyltransferase OS=Homo sapiens GN=COMT # P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 #
TYLLDGSC*MVEESGTLESQLEATK	C2238;C2233;C2213;C2218	1.0804325	Q13813 Q13813 Q13813 A0A0D9S F54	Q13813-2 Isoform 2 of Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 # Q13813 Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 # Q13813-3 Isoform 3 of Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 # A0A0D9SF54 Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=1 #
MEC*PEIDCEEGWALLK	C138;C107	1.080302518	P09914 P09914	P09914 Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 # P09914-2 Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 #
LLLC*GGAPLSATTQR	C450	1.079113231	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 #
QQSACIGGPPNAC*LDQLQNWFTIVAESLQQVR	C255;C255;C257	1.078839213	P42224 P42224 J3KPM9	P42224-2 Isoform Beta of Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 # P42224 Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 # J3KPM9 Signal transducer and activator of transcription OS=Homo sapiens GN=STAT1 PE=1 SV=1 #
LC*GSGFQSIVNGCQEICVK	C89;C92;C37	1.078165	A0A0B4J2 A4 P42765 K7EMEO	A0A0B4J2A4 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # P42765 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 # K7EMEO 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 #
ADPDGPEAQAEAC*SGER	C18;C18;C18	1.077516237	D6RCB9 D6RC52 Q9NX24	D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # D6RC52 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 #
VQGGVPAGSDEYEDEC*PHLI ALSSLNR	C449;C449	1.076816007	Q9BVS4 Q9BVS4	Q9BVS4 Serine/threonine-protein kinase RIO2 OS=Homo sapiens GN=RIOK2 PE=1 SV=2 # Q9BVS4-2 Isoform 2 of Serine/threonine-protein kinase RIO2 OS=Homo sapiens GN=RIOK2 #
GMENLLEVQVPEDVEQQLQ QLDC*R	C368	1.076745093	Q9BTY7	Q9BTY7 Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1 #
DHEKDAFEHIVTQFSSVPVSV VSDSYDIYNAC*EK	C287	1.076127386	P43490	P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 #
VTDGALVVVDCVSGVC*VQT ETVLR	C136	1.072718313	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
C*ALSSPSLAFTPIIK	C238;C255	1.071900306	Q8NFH5 Q8NFH5	Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 #

LENLNEAIEEDIVQSVLRPTN C*R	C293;C378;C33 6	1.071859204	Q7Z5K2 Q7Z5K2 Q7Z5K2	Q7Z5K2 Wings apart-like protein homolog OS=Homo sapiens GN=WAPL PE=1 SV=1 # Q7Z5K2-3 Isoform 3 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL # Q7Z5K2-2 Isoform 2 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL # E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # H7C2I1 Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 # Q99873-2 Isoform 2 of Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 # Q14690 Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 # Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # Q9NSD9-2 Isoform 2 of Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB # Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 # Q8IYU8 Calcium uptake protein 2# mitochondrial OS=Homo sapiens GN=MICU2 PE=1 SV=2 # Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # Q96RS6-2 Isoform 2 of NudC domain- containing protein 1 OS=Homo sapiens GN=NUDCD1 # P40227 T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 # P40227-2 Isoform 2 of T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A # O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 # O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 # P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 # P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 # Q06210-2 Isoform 2 of Glutamine--fructose-6- phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 # Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 # Q8NF37 Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 #
VIGIEC*SSISDYAVK	C73;C119;C101; C109;C95;C91	1.070172952	E9PKG1 H7C2I1 Q99873 Q99873 Q99873	
ESMC*STPAFPVSPETPYVK	C842	1.069925773	Q68CZ2	
LSC*QNLGAVLDDVPVQGFF KK	C361	1.069839592	Q14690	
YSEEANNLIEEC*EQAER	C131	1.069805594	Q96HE7	
EYTAC*ELMNIYK	C96;C195	1.069431876	Q9NSD9 Q9NSD9	
DIEDTLSGIQTAGC*GSTFFR	C144	1.067091418	Q8IYU8	
DSAQC*AAIAER	C376;C347	1.06550949	Q96RS6 Q96RS6	
NAIDDGC*VVPGAGAVEVAM AEALIK	C406;C361	1.06254418	P40227 P40227	
LALFNPDVC*WDR	C44	1.061684026	O00483	
EAEGEQFVEEAELEKSPC*QT DVLR	C239	1.06106	O14879	
VIEINPYLLGTMSGC*AADCQ YWER	C120 C116;M117 C120;M117	1.060529883	P28062 X5D2R7 P28062	
VTDDLVC*LVIYK	C48	1.06043167	P49458	
VDSTTC*LFPVEEK	C246;C264	1.059919951	Q06210 Q06210	
VMAEALGVSVTDYTFEDC*QL ALAEGQLR	C314	1.059609165	Q8NF37	

MPC*ESSPPESADTPTSTR	C1372;C1373	1.05943843	A0A087WV66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
DLSYC*LSGMYDHR	C267	1.058484244	P52597	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 # Q15366-8 Isoform 8 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-7 Isoform 7 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
INISEGNC*PER	C54;C54;C54;C54;C54;C54	1.058422383	Q15366 Q15366 Q15366 Q15366 Q15366 Q15366	Q9H8M7 Protein FAM188A OS=Homo sapiens GN=FAM188A PE=1 SV=1 # Q5T440 Putative transferase CAF17# mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 # P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # H7C068 ATP synthase subunit O# mitochondrial (Fragment) OS=Homo sapiens GN=ATP5O PE=1 SV=1 # P48047 ATP synthase subunit O# mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 # P67775 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 # P62714 Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 # Q9NR31-2 Isoform 2 of GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A # Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 # Q9GZS1-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens GN=POLR1E # Q9GZS1 DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens GN=POLR1E PE=1 SV=2 # Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # Q9BWD1-2 Isoform 2 of Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # P50135 Histamine N-methyltransferase OS=Homo sapiens GN=HNMT PE=1 SV=1 #
SSPGLSDTIFC*R	C27	1.055806328	Q9H8M7	Q9H8M7 Protein FAM188A OS=Homo sapiens GN=FAM188A PE=1 SV=1 # Q5T440 Putative transferase CAF17# mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 #
VWAVLPSSPEAC*GAASLQER	C170	1.055132644	Q5T440	Q5T440 Putative transferase CAF17# mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 #
LTPGC*EAEAEATEAICFFVQQFTDMEHNR	C2359	1.054606333	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # H7C068 ATP synthase subunit O# mitochondrial (Fragment) OS=Homo sapiens GN=ATP5O PE=1 SV=1 # P48047 ATP synthase subunit O# mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 #
GEVPC*TVTSASPLEEATLSE LK	C37;C141	1.054575509	H7C068 P48047	H7C068 ATP synthase subunit O# mitochondrial (Fragment) OS=Homo sapiens GN=ATP5O PE=1 SV=1 # P48047 ATP synthase subunit O# mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 #
C*GNQAAIMELDDTLK	C269	1.05314811	P67775 P62714	P67775 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 # P62714 Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 #
NYLPAINGIVFLVDC*ADHSR	C59;C102	1.052548428	Q9NR31 Q9NR31	Q9NR31-2 Isoform 2 of GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A # Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 # Q9GZS1-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens GN=POLR1E # Q9GZS1 DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens GN=POLR1E PE=1 SV=2 #
MDSC*IEAFGTTK	C138;C200	1.052493333	Q9GZS1 Q9GZS1	Q9GZS1-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens GN=POLR1E # Q9GZS1 DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens GN=POLR1E PE=1 SV=2 #
ATVAPEDVSEVIFGHVLAAGC*GQNPVR	C65;C94	1.052180785	Q9BWD1 Q9BWD1	Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # Q9BWD1-2 Isoform 2 of Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 #
LNIIINLDC*VNEVIGIR	C390	1.051276698	P30153	P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
VSDTVVEPYNATLSVHQLVE NTDETYCIDNEALYDIC*FR	C211;C211;C211;C193;C211	1.051192142	P68371 Q9BVA1 P04350 Q5JP53 Q9BUF5	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
FPQDDLC*QYITSDDLTQMLD NLGLK	C196	1.050586667	P50135	P50135 Histamine N-methyltransferase OS=Homo sapiens GN=HNMT PE=1 SV=1 #

LLQPDFQPVC*ASQLYPR	C258;C201;C265	1.050302145	Q9UJW0 Q9UJW0 Q9UJW0	Q9UJW0 Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1 # Q9UJW0-2 Isoform 2 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 # Q9UJW0-3 Isoform 3 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 #
VIGVELC*PEAVEDAR	C463;C11;C463;C481	1.049763035	Q8IZ69 H7C100 Q8IZ69 F2Z2W7	Q8IZ69-2 Isoform 2 of tRNA (uracil-5-)-methyltransferase homolog A OS=Homo sapiens GN=TRMT2A # H7C100 tRNA (uracil-5-)-methyltransferase homolog A (Fragment) OS=Homo sapiens GN=TRMT2A PE=1 SV=1 # Q8IZ69 tRNA (uracil-5-)-methyltransferase homolog A OS=Homo sapiens GN=TRMT2A PE=1 SV=2 # F2Z2W7 tRNA (uracil-5-)-methyltransferase homolog A OS=Homo sapiens GN=TRMT2A PE=1 SV=1 #
C*AGNEDIITLR	C81	1.048773382	P12004	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 # H3BVI2 Transcription factor Sp1 (Fragment) OS=Homo sapiens GN=SP1 PE=1 SV=1 #
SSSTGSSSSTGGGGQESQP SPLALLAATC*SR	C61;C61;C68	1.048652379	H3BVI2 P08047 P08047	P08047-2 Isoform 2 of Transcription factor Sp1 OS=Homo sapiens GN=SP1 # P08047 Transcription factor Sp1 OS=Homo sapiens GN=SP1 PE=1 SV=3 #
LSGSSLC*SGSWWSADGFLR	C32;C39;C39;C39	1.048570216	H0YG38 F5H578 O75400 O75400	H0YG38 Pre-mRNA-processing factor 40 homolog A (Fragment) OS=Homo sapiens GN=PRPF40A PE=1 SV=1 # F5H578 Pre-mRNA-processing factor 40 homolog A (Fragment) OS=Homo sapiens GN=PRPF40A PE=1 SV=1 # O75400-3 Isoform 3 of Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A # O75400 Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 #
EVYEGEVTELTTPC*ETENPM GGYGK	C141	1.047976651	Q9Y265	Q9Y265 RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 #
VC*TLAIIDPGDSDIIR	C92;C92	1.047922183	P62888 E5RI99	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #
AVC*MLSNTTAAIEAWAR	C376;C310;C400;C376;C376;C376	1.04691199	P68363 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
ELANSPDC*PQMCAVK	C187;C189;C187	1.046135	P48739 P48739 A0A0A0MSW4	P48739 Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2 # P48739-3 Isoform 3 of Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB # A0A0A0MSW4 Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=1 #
TENTIFSSTTLPRPGDPGAPP LPPDLQLEEEGTC*ANSSEMF LPLR	C215	1.045406847	O95999	O95999 B-cell lymphoma/leukemia 10 OS=Homo sapiens GN=BCL10 PE=1 SV=1 #
MTGESEC*LNPSTQSR	C1181 C1212;M1175	1.045387946	Q9H2G2 Q9H2G2	Q9H2G2 STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 # Q9H2G2-2 Isoform 2 of STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK #

AVLLASDAQEC*TLEEVVER	C332;C332	1.044261629	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #
KPTDGASSSNC*VTDISHLVR	C369;C644;C710;C342;C138;C708	1.041675575	P49321 P49321 P49321 Q5T624 H0YDS9 P49321	P49321-2 Isoform 2 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321-4 Isoform 4 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321-3 Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # Q5T624 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=1 # H0YDS9 Nuclear autoantigenic sperm protein (Fragment) OS=Homo sapiens GN=NASP PE=1 SV=1 # P49321 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 #
IC*DQWDNLGALTQK	C480;C480;C480;C480	1.041313389	P12814 P12814 P12814 P12814	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P12814-2 Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-3 Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 # P12814-4 Isoform 4 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 #
YC*GLCDSIITIYR	C151;C160	1.039085	E9PIE4 Q9Y6C9	E9PIE4 Mitochondrial carrier homolog 2 (Fragment) OS=Homo sapiens GN=MTCH2 PE=1 SV=7 # Q9Y6C9 Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 #
NC*MTDLLAK	C18	1.0367	Q00765	Q00765 Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3 #
ERFDPTQFQDC*IIQGLTETG TDLEAVAK	C35;C67;C39	1.03669838	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 #
IISNASC*TTNCLAPLAK	C152	1.036655811	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
GC*WDSIHVVEVQEK	C147;C147;C176;C135;C173	1.036221703	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
AYHEQLSVAEITNAC*FEPAN QMVK	C295	1.035522903	P68363 Q71U36 P68366	P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
GTWEELC*NSCEMENEVLK	C649	1.035335	O95573	O95573 Long-chain-fatty-acid-CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 #
VTQNLPMKEGC*TEVSLLR	C308;M304 C308	1.034694709	H3BQZ7 Q1KMD3	H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #



AGMAAVASPTGNC*DLER	C560	1.034442088	Q6P1M0	Q6P1M0 Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1 #
TC*ATDLQTK	C42;C42;C42;C42;C42	1.03415	O95861 A6NF51 O95861 O95861 F8W1J0	O95861-4 Isoform 4 of 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 # A6NF51 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=2 # O95861 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1 # O95861-2 Isoform 2 of 3'(2')#5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 # F8W1J0 3'(2')#5'-bisphosphate nucleotidase 1 (Fragment) OS=Homo sapiens GN=BPNT1 PE=1 SV=1 #
AIVDALPPPCESAC*TVPTDV DK	C274	1.033706142	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 # H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # H0YN73 40S ribosomal protein S17 (Fragment) OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 #
VC*EEIAIIPSK	C35;C35;C34;C35	1.033512901	H0YN88 A0A075B716 H0YN73 P08708	H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # H0YN73 40S ribosomal protein S17 (Fragment) OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 #
TDLLDSESQSGVFLPELDE PEYC*NAQNTALWELHALR	C683	1.030927789	Q8WTT2	Q8WTT2 Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1 SV=1 #
AIVDALPPPC*ESACTVPTDV DK	C270	1.030737116	Q15181	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 #
SPWLAGNELTVADVVLWSVL QQIGGC*SVTPANVQR	C291	1.028839738	Q13155	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 #
TC*AYTNHTVLPEALER	C373;C373	1.028503494	P11216 P11217	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 # P11217 Glycogen phosphorylase# muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 #
AEPPQC*TSLAWSADGQTLF AGYTDNLVR	C286	1.0268672	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
VLGLGLGC*LR	C88;C75	1.026146249	Q9BRJ7 K7EIN2	Q9BRJ7 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # K7EIN2 Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 #
DIIEHLNTSGAPADTSDPLQQI C*K	C399;C475	1.02487458	M0QXN5 P37198	M0QXN5 Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=1 # P37198 Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=3 #
ANC*IDSTASAEAVFASEVKK	C206;C183;C268;C244	1.022883416	M0QXL5 M0R299 P22087 M0R2Q4	M0QXL5 rRNA 2'-O-methyltransferase fibrillar (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 # P22087 rRNA 2'-O-methyltransferase fibrillar OS=Homo sapiens GN=FBL PE=1 SV=2 # M0R2Q4 rRNA 2'-O-methyltransferase fibrillar (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 #
IIDLEEADEIEDIQEIIVLSQ C*DSPYITR	C73;C73;C73	1.022412705	C9JN58 E7EM58 O00506	C9JN58 Serine/threonine-protein kinase 25 (Fragment) OS=Homo sapiens GN=STK25 PE=1 SV=1 # E7EM58 Serine/threonine-protein kinase 25 (Fragment) OS=Homo sapiens GN=STK25 PE=1 SV=7 # O00506 Serine/threonine-protein kinase 25 OS=Homo sapiens GN=STK25 PE=1 SV=1 #
GTEAGQVGEPGIPTGEAGPS C*SSASDKLPR	C241	1.021217183	O15355	O15355 Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 #

AEGSDVANAVLDGADC*IMLS GETAKGDYPLEAVR	C358	1.019881486	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
VQVSDPESTVAVAFPTIPHC *SMATLIGLSIK	C93	1.018287845	Q9Y3D0	Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 #
YDGSTIVPGEQGAEQHFQIQ QC*TDDVR	C52	1.01691	Q14019	Q14019 Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3 #
DLNYC*FSGMSDHR	C267	1.016756897	P31943 G8JLB6 E9PCY7	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # E9PCY7 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 #
ICDGCIIIVDAVEGVC*PQTQA VLR	C124;C73	1.016117537	Q7Z2Z2 Q7Z2Z2	Q7Z2Z2 Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2 # Q7Z2Z2-2 Isoform 2 of Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 #
TIGGGDDSFTTFFC*ETGAGK	C54	1.015843632	P68366	P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
GLNPLNAYSDLAEFLETEC*Y QTPFNK	C343	1.014657035	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
GC*LLYGPPGTGK	C184;C170	1.014519163	A0A087X2 I1 P62333	A0A087X21 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
YSDVEVPASVTGYSFASDGD SGTC*SPLR	C430;C430;C430; C430;C430;C430; C430	1.014477027	P35611 P35611 E7ENY0 P35611 E7EV99 P35611 P35611	P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 # E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 # E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 #
GTPEQPQC*GFSNAVQILR	C67	1.013417641	Q86SX6	Q86SX6 Glutaredoxin-related protein 5# mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 #
LNISFPATGC*QK	C12	1.013097192	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
CEYPAAC*NALETLIHR	C612	1.012580954	P54886	P54886 Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 #
MQPDQVVINC*AIVR	C64	1.011809904	P50552	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 #
AQAISPC*VQNFCALDSK	C513;C513;C513 3	1.009795704	Q8WTW3 A0A087W VI0 E9PBL8	Q8WTW3 Conserved oligomeric Golgi complex subunit 1 OS=Homo sapiens GN=COG1 PE=1 SV=1 # A0A087WVI0 Conserved oligomeric Golgi complex subunit 1 OS=Homo sapiens GN=COG1 PE=1 SV=1 # E9PBL8 Conserved oligomeric Golgi complex subunit 1 (Fragment) OS=Homo sapiens GN=COG1 PE=1 SV=2 #
VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDIC*FR	C211;C183 C211;C201 C193;C201 C211 C201	1.009381857	P68371 Q9BVA1 P04350 Q5JP53 Q9BUF5	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #

NMMAAC*DPR	C303;C303;C650;C303;C303;C285;C303	1.009148768	Q13885 P68371 A0A0B4J269 Q9BVA1 P04350 Q5JP53 Q9BUF5	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L # Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 # Q9Y4W2-3 Isoform 3 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L #
C*LAQEVNIPDWIVDLR	C140;C140;C98	1.008814463	Q9Y4W2 Q9Y4W2 Q9Y4W2	P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 # X6RFL8 Ras-related protein Rab-14 (Fragment) OS=Homo sapiens GN=RAB14 PE=1 SV=1 # P61106 Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 # Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
QVQSLTC*EVDALKGTNESLER	C328	1.006333289	P08670	
FMADC*PHTIGVEFGTR	C40;M37 C40	1.006262017	X6RFL8 P61106	
ETYC*IDNEALYDICFR	C201;C201;C548;C201;C201;C183;C201	1.005677062	Q13509 P68371 A0A0B4J269 Q9BVA1 P04350 Q5JP53 Q9BUF5	
TDC*SPIQFESAWALTNIASGTSEQTK	C133	1.005108574	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 # P78527-2 Isoform 2 of DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC # P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #
LVSSPC*CIVTSTYGWTANMER	C589	1.004548999	P08238	
DVLKEEGVSFLINTFEGGGC*GQPSGILAQPTLLYLR	C1229;C1229	1.004240165	P78527 P78527	
ENSTLNC*ASFTAGIVEAVLTHSGFPAK	C139	1.003735498	Q8IUR0	Q8IUR0 Trafficking protein particle complex subunit 5 OS=Homo sapiens GN=TRAPPC5 PE=1 SV=1 # O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
GLAPLHWADDDGNPTEQYPLNPNGSPGGVAGICSC*DGR	C1287	1.003505646	O15067	
DSGAASEQATAAPNPC*SSSR	C583;C671;C696	1.00281	Q9BU23 Q9BU23 Q9BU23	Q9BU23-3 Isoform 3 of Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 # Q9BU23-2 Isoform 2 of Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 # Q9BU23 Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 PE=1 SV=2 #
LVSSPCC*IVTSTYGWTANMER	C590	1.0015744	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 # P50995 Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 # P50995-2 Isoform 2 of Annexin A11 OS=Homo sapiens GN=ANXA11 #
GVGTDEAC*LIEILASR	C294;C261	1.000994535	P50995 P50995	

PKHEFSVDMTC*GGCAEAVS R	C12	0.999224443	O00244	O00244 Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 #
GFEVVMTEPIDEYC*VQQLK	C521	0.998639336	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
AVSTGVQAGIPMPC*FTTALS FYDGYR	C422;C409	0.997466667	P52209 P52209	P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6- phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
ELETVC*NDVLSLLDK	C97	0.997290587	Q04917	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 #
WC*NVQSTQDEFEELTMSQK	C59;C59;C59	0.997221931	D6RCP9 P27707 D6RFG8	D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
AC*FQVGTSEEMK	C718	0.996601261	P35658 P35658 P35658 P35658	P35658-4 Isoform 4 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658 Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 # P35658-2 Isoform 2 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658-3 Isoform 3 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658-5 Isoform 5 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 #
VVMALGDYMGASCHAC*IGG TNVR	C134	0.996174619	P60842	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
SVTYTLAQLPC*ASMALQILW EAAR	C137	0.996170109	O14684	O14684 Prostaglandin E synthase OS=Homo sapiens GN=PTGES PE=1 SV=2 #
IVEDDASISSC*NK	C160;C245;C20 3	0.99496876	Q7Z5K2 Q7Z5K2 Q7Z5K2	Q7Z5K2 Wings apart-like protein homolog OS=Homo sapiens GN=WAPL PE=1 SV=1 # Q7Z5K2-3 Isoform 3 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL # Q7Z5K2-2 Isoform 2 of Wings apart-like protein homolog OS=Homo sapiens GN=WAPL #
NQSFC*PTVNLDKLWTLVSE QTR	C70;C70	0.993740852	P46776 E9PLL6	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 # E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 #
EAVFPFQPGSVAEVC*ITFDQ ANLTVK	C89	0.993302671	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 #
IQFNDLQSLLC*ATLQNVLR	C585	0.991879242	Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 #
LPIIGVVENMSGFIC*PK	C224;C235	0.991584259	P53384 P53384	P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 # P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 #
TFC*GTPEYLAPEVLEDNDYGR	C310;C311;C24 8;C307;C307;C2 49	0.991321861	P31749 P31751 P31749 Q9Y243 Q9Y243 M0R0P9	P31749 RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2 # P31751 RAC-beta serine/threonine- protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 # P31749-2 Isoform 2 of RAC- alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 # Q9Y243-2 Isoform 2 of RAC-gamma serine/threonine- protein kinase OS=Homo sapiens GN=AKT3 # Q9Y243 RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 PE=1 SV=1 # M0R0P9 RAC-beta serine/threonine- protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=1 #

RVDDFEAGAAAGAAPGEEDL C*AAFNVICDNVVK	C98	0.990752616	Q13158	Q13158 FAS-associated death domain protein OS=Homo sapiens GN=FADD PE=1 SV=1 # P13929 Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 # P13929-2 Isoform 2 of Beta-enolase OS=Homo sapiens GN=ENO3 # P06733-2 Isoform MBP-1 of Alpha-enolase OS=Homo sapiens GN=ENO1 # P13929-3 Isoform 3 of Beta-enolase OS=Homo sapiens GN=ENO3 # P06733 Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 #
SGTETDTFIADLVVGLC*TGQI K	C389;C361;C29 6;C346;C389	0.990405516	P13929 P13929 P06733 P13929 P06733	
GC*IVDANLSVLNLVIVK	C100	0.989533039	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 # C9JXQ7 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 # Q9Y6I9 Testis- expressed sequence 264 protein OS=Homo sapiens GN=TEX264 PE=1 SV=1 # C9JHH5 Testis-expressed sequence 264 protein (Fragment) OS=Homo sapiens GN=TEX264 PE=1 SV=7 # G3V1Q4 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # A0A0U1RRE1 Septin-7 (Fragment) OS=Homo sapiens GN=SEPT7 PE=1 SV=1 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # A0A0U1RRH9 Septin-7 (Fragment) OS=Homo sapiens GN=SEPT7 PE=1 SV=1 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 # P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 # Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C # P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 # A0A087X0R7 Protein SENP3-EIF4A1 (Fragment) OS=Homo sapiens GN=SENP3- EIF4A1 PE=4 SV=1 # Q9H4L4 Sentrin- specific protease 3 OS=Homo sapiens GN=SENP3 PE=1 SV=2 # P48059-3 Isoform 3 of LIM and senescent cell antigen-like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 # P48059-2 Isoform 2 of LIM and senescent cell antigen- like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 # P48059 LIM and senescent cell antigen-like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 PE=1 SV=4 # P48059-5 Isoform 5 of LIM and senescent cell antigen-like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 # A0A0J9YXC7 LIM and senescent cell antigen- like-containing domain protein 3 OS=Homo sapiens GN=LIMS4 PE=1 SV=1 # P48059-4 Isoform 4 of LIM and senescent cell antigen- like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 #
C*AVGSILSEGEESPSPELIDL YQK	C94;C94;C94	0.988905417	C9JXQ7 Q9Y6I9 C9JHH5	
EGGVQLLLTIVDTPGFGDAVD NSNC*WQPVIDYIDSK	C90;C73;C125;C 126;C126;C73;C 106	0.987997545	G3V1Q4 A0A0U1R RE1 Q16181 Q16181 E7EPK1 A0A0U1R RH9 E7ES33	
YDC*GEEILITVLSAMTEEA AVAIK	C159	0.986897715	P63241 P63241	
C*DLISIPK	C426;C420;C47 3	0.98605	Q9ULV4 Q9ULV4 Q9ULV4	
EDIGVGSYSVC*K	C436	0.984780826	P51812	
SLAPPDASILISNVC*SIGDHV AQELFQGSDLGMAEEAERP GK	C204;C274	0.983415	A0A087X0 R7 Q9H4L4	
CDLC*QEVVLADIGFVK	C162;C112;C10 0;C137;C162;C1 04	0.982919143	P48059 P48059 P48059 P48059 A0A0J9YX C7 P48059	

VC*ISILHAPGDDPMGYESSA ER	C61;C89	0.982008381	P60604 P60604	P60604-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 # P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 #
DTQTSITDSC*AVYR	C100	0.981387628	Q9Y5M8	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 #
QSELEPVVSLVDVLEEDDEELE NEAC*AVLGGSDSEK	C35	0.980540094	Q8N806	Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 #
KPWFLTNEVEEC*ENYFSK	C117;C99	0.980153682	Q9BQG2 E7EM93	Q9BQG2 Peroxisomal NADH pyrophosphatase NUDT12 OS=Homo sapiens GN=NUDT12 PE=1 SV=1 # E7EM93 Peroxisomal NADH pyrophosphatase NUDT12 OS=Homo sapiens GN=NUDT12 PE=1 SV=1 #
ECISIHVGQAGVQIGNACWEL YC*LEHGIQPDGQMPSDK	C25;C95;C25	0.972593344	Q9BQE3 F5H5D3 Q71U36	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 #
ADIIHAC*DIVEDAAIAYGYNNI QMTLPK	C362	0.9721475	Q9NSD9	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 #
VYQPVSC*PLSDLSENVESVV NEEK	C566;C506;C25 1;C374	0.971993397	Q99590 A0A0A0M TP7 Q99590 F8VXG7	Q99590 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 # A0A0A0MTP7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 # Q99590-2 Isoform 2 of Protein SCAF11 OS=Homo sapiens GN=SCAF11 # F8VXG7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 #
VTEDENDEPIEPSDDGTVL LSTVTAQFPGAC*GLR	C39;C39;C39;C3 9;C39	0.971557233	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
FMTPVIQDNPSGWGPC*AVP EQFR	C19 C19;M5	0.971255659	O15371 O15371 O15371	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D #
TTC*SSGSALGPGAGAAQPS ASPLEGLLDLSYPR	C12;C12;C12	0.971069057	Q96FZ5 F8WDZ3 Q96FZ5	Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=2 SV=1 # F8WDZ3 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 # Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 #
IC*DPYAWLEDPDSEQTK	C25	0.969545651	P48147	P48147 Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 #
SGTIC*SSELPGAFEAAAGFHL NEHLYNMIIR	C190	0.969081196	A0A0C4D GQ5 P04632	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #

V SVC* A E T Y N P D E E E E D T D P R	C101;C101	0.968620616	P13861 P13861	P13861 cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2 # P13861-2 Isoform 2 of cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A #
NEC*DPALALLSDYVLHNSNT MR	C459;C329	0.967888	Q13200 Q13200	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 # Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 #
AEVLISTVGPEDC*VVPFLTRP K	C38;C38	0.967841011	P56192 P56192	P56192 Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 # P56192-2 Isoform 2 of Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS #
FTLDC*THPVEDGIMDAANFE QFLQER	C25	0.967190473	P35268	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 #
TTPVDLC*LLEESVGSLEGSR	C1499	0.963908287	Q9UKK3	Q9UKK3 Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3 #
HPLTQELKEC*EGIVPVPLAE K	C105	0.963115262	P82932	P82932 28S ribosomal protein S6# mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 #
TIQFVDWC*PTGFK	C347;C281;C37 1;C347;C347	0.962033918	Q9BQE3 Q9NY65 C9J2C0 Q71U36 Q9NY65	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
NWYIQATC*ATSGDGLYEG DWLSNQLR	C159	0.961809278	P84077	P84077 ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2 #
DILKEMFPYEASTPTGISASC* R	C323;C363;C25 4	0.96085421	G5E972 P42167 P42167	G5E972 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 # P42167 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 # P42167-2 Isoform Gamma of Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO #
LNDDWAYGNLDLDPWDFQ AEEC*ALR	C674;C769	0.960851921	Q5VSL9 Q5VSL9	Q5VSL9-2 Isoform 2 of Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 # Q5VSL9 Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 PE=1 SV=1 #
DLC*FSPGLMEASHVVNDVN EAVQLVFR	C392;C362	0.960475894	Q9BXW7 Q9BXW7	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 # Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 #
SGEEDFESLASQFSDC*SSAK	C40;C113	0.960021519	K7EN45 Q13526	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 # Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 #
SAC*SLESNLEGLAGVLEADL PNYK	C44	0.959400542	Q09161	Q09161 Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 #
C*CSGAIIVLTK	C423	0.958737746	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
NAFAC*FDEEATGTIQEDYLR	C108;C114;C10 9	0.956811667	P19105 J3QRS3 O14950	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 # J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 # O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 #

SC*LSPKPPQGQEQGQEDE VVLVEGPTLPETPR	C232	0.955745367	Q8NCF5	Q8NCF5 NFATC2-interacting protein OS=Homo sapiens GN=NFATC2IP PE=1 SV=1 #
SC*TDESELLHPPELLSQEFLLL TLEQK	C10;C10;C48	0.955680313	C9J4K0 Q9BVC5 Q9BVC5	C9J4K0 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 # Q9BVC5 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 # Q9BVC5-2 Isoform 2 of Ashwin OS=Homo sapiens GN=C2orf49 #
ELELMFGC*QVEGDAAETPP RPR	C277;C251	0.955269836	Q02750 Q02750	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 #
YEAAFPFLSPC*GR	C143;C98	0.953142599	H0YF29 Q6P1X6	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 # Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 #
EC*LPLIIFLR	C41	0.952795712	P62701	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 # P55036-2 Isoform Rpn10E of 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 # Q5VWC4 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 #
SNPENNVGLITLANDC*EVLTLTPDTR	C58;C58;C43;C5 8	0.95136042	P55036 Q5VWC4 A6PVX3 P55036	A6PVX3 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=1 SV=1 # P55036 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 #
AATGEEVSAEDLGGADLHCR	C42;C229;C267	0.95064857	D6RD67 Q9HCC0 Q9HCC0	D6RD67 Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial (Fragment) OS=Homo sapiens GN=MCCC2 PE=1 SV=2 # Q9HCC0-2 Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial OS=Homo sapiens GN=MCCC2 # Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 #
VAC*ITEQVLTLVNKR	C477	0.950415525	P04843	P04843 Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 #
SLHDALC*VLAQTVK	C395;C348	0.950367455	P78371 P78371	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 # P78371-2 Isoform 2 of T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 #
VGSFGSSPPGLSSTYTGGPL GNEIASGNNGAAAGDDEDG QNLWSC*ILSEVSTR	C51	0.949629872	Q9Y6G9	Q9Y6G9 Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3 #
LC*SLLDSEDYNTCEGAFGAL QK	C142;C134	0.949059725	Q92973 Q92973	Q92973 Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 # Q92973-2 Isoform 2 of Transportin-1 OS=Homo sapiens GN=TNPO1 #
PGHLQEGFGC*VVTNRFDQL FDDESDPFVFLK	C11;C11;C11;C1 1	0.948440951	Q8NC51 Q8NC51 Q8NC51 Q8NC51	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 # Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 #



TGC*TFPEKPDFH	C318;C353;C336;C296	0.947436701	P55263 P55263 P55263 P55263	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK # P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 # P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK # P55263-3 Isoform 3 of Adenosine kinase OS=Homo sapiens GN=ADK # C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 # P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 #
VELC*SFSGYK	C6;C6;C6	0.946044619	C9JNW5 C9JXB8 P83731	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 # P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 # P62195 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 # P62195-2 Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 #
KDVLIEFYAPWC*GHCK	C555;C406	0.945358655	P13667 P30101	P29590-9 Isoform PML-3 of Protein PML OS=Homo sapiens GN=PML # P29590-11 Isoform PML-11 of Protein PML OS=Homo sapiens GN=PML # P29590-10 Isoform PML-7 of Protein PML OS=Homo sapiens GN=PML # P29590-3 Isoform PML-8 of Protein PML OS=Homo sapiens GN=PML # P29590-14 Isoform PML-14 of Protein PML OS=Homo sapiens GN=PML # P29590-4 Isoform PML-6 of Protein PML OS=Homo sapiens GN=PML # P29590 Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 # P29590-5 Isoform PML-4 of Protein PML OS=Homo sapiens GN=PML # P29590-2 Isoform PML-5 of Protein PML OS=Homo sapiens GN=PML # P29590-12 Isoform PML-12 of Protein PML OS=Homo sapiens GN=PML # P29590-13 Isoform PML-13 of Protein PML OS=Homo sapiens GN=PML # H3BT57 Protein PML OS=Homo sapiens GN=PML PE=1 SV=1 # P29590-8 Isoform PML-2 of Protein PML OS=Homo sapiens GN=PML # H3BT29 Protein PML (Fragment) OS=Homo sapiens GN=PML PE=1 SV=1 # H3BUJ5 Protein PML (Fragment) OS=Homo sapiens GN=PML PE=1 SV=1 #
FVVDVDKNIDINDVTPNC*R	C112;C104	0.943596667	P62195 P62195	
C*YASDQEVLDMHGFLR	C338;C338;C338;C338;C338;C338;C338;C338;C110;C87	0.943231766	P29590 P29590 P29590 P29590 P29590 P29590 P29590 P29590 P29590 P29590 H3BT57 P29590 H3BT29 H3BUJ5	
LPADTC*LLEFAR	C330	0.941743398	Q8NF37	Q8NF37 Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2 #
GSSC*FECTHYQSFLEYR	C188;C238	0.939653715	P21964 P21964	P21964-2 Isoform Soluble of Catechol O-methyltransferase OS=Homo sapiens GN=COMT # P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 #
DINAYNC*EEPTEK	C91	0.938977515	P30041	P30041 Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 #
SFC*SQFLPEEQAEIDQLFDA LSSDKNSPNVSSK	C13	0.938002893	Q6P9B6	Q6P9B6 TLD domain-containing protein 1 OS=Homo sapiens GN=TLDC1 PE=1 SV=2 #
AAVEEGIVLGGGC*ALLR	C442	0.937553553	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
C*FLEQIDSAVNIIR	C361;C361;C361	0.937375564	P29728 P29728 A0A087X0V5	P29728 2'-5'-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2 PE=1 SV=3 # P29728-2 Isoform p69 of 2'-5'-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2 # A0A087X0V5 2'-5'-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2 PE=1 SV=1 #

IDC*FSEVPTSVFGEK	C384	0.937014656	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #
LC*DFGVSGQLIDSMANSFVGR	C114	0.936951746	G5E9C7 Q02750 Q02750 P36507	G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 #
KITAFVPNDGC*LNFIEENDEV LVAGFGR	C90	0.936528277	P62266	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 #
DLLEFLGSVNGLC*SR	C637	0.936345	O43299	O43299 AP-5 complex subunit zeta-1 OS=Homo sapiens GN=AP5Z1 PE=1 SV=2 #
GC*EVVVSGK	C134	0.934287097	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #
GVLFGVPGAFTPGC*SK	C100;C48;C100	0.93417	P30044 P30044 P30044	P30044 Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 # P30044-2 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 # P30044-3 Isoform 3 of Peroxiredoxin-5# mitochondrial OS=Homo sapiens GN=PRDX5 #
VDVFREDLC*TK	C22	0.934049582	Q06323	Q06323 Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 #
QASLADC*LNHAVGFASR	C650	0.93345931	O43592	O43592 Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2 #
AAQLC*GAGMAAVVDK	C838;C834;C822;C833	0.93306	P19367 P19367 P19367 P19367	P19367-3 Isoform 3 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367 Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 # P19367-4 Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367-2 Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1 #
AAAPAPEEEMDEC*EQALAA EPK	C316 C266;M313	0.931527611	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
FFFDVGC*NK	C238	0.930834651	Q96QR8	Q96QR8 Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3 #
ISLGLPVGAVINC*ADNTGAK	C28;C28	0.93023533	P62829 J3KT29	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 # J3KT29 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 #
FC*PTETTMLTNILLR	C337	0.930180903	Q9Y234	Q9Y234 Lipoyltransferase 1# mitochondrial OS=Homo sapiens GN=LIPT1 PE=1 SV=1 #
FQSAAGALQEASEAYLVGLF EDTNLC*AIHAK	C111;C111	0.930093534	K7EK07 P84243	K7EK07 Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1 # P84243 Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 #
EGIC*ALGGTSELSSEGTQHS YSEEEKYAFVNWINK	C104	0.929852263	P13797	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
C*LHNFLTDGVP AEGAFTEDF QGLR	C316;C268	0.929234766	G3V1A6 P57764	G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 #
TPEDPAVQSFPLVPC*DTDQP QDKPPDWFTSYLETFR	C141;C120;C141	0.929045	Q14596 B7Z5R6 Q14596	Q14596-2 Isoform 2 of Next to BRCA1 gene 1 protein OS=Homo sapiens GN=NBR1 # B7Z5R6 Next to BRCA1 gene 1 protein OS=Homo sapiens GN=NBR1 PE=1 SV=1 # Q14596 Next to BRCA1 gene 1 protein OS=Homo sapiens GN=NBR1 PE=1 SV=3 #

YSTGSDSASFHTTSPMC*LN PDLEGPPELAYTIQQGY	C217 C213;M216	0.928912249	Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q9UET6 Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens
IIVPFVTC*GDLSSYSDDR	C238;C236	0.928525069	Q9UET6 Q9UET6	GN=FSTSJ1 PE=1 SV=2 # Q9UET6-2 Isoform 2 of Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens GN=FSTSJ1 # P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
QYDADLEQILIQWITTQC*R	C38;C59;C38	0.928183704	P37802 P37802 X6RJP6	O75934 Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 # A0A0U1RR39 E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=1 # P22681 E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=2 # Q16643-2 Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643-3 Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1 # Q16643 Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 # Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # I1E4Y6 PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1 # Q6Y7W6-3 Isoform 2 of PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 # Q6Y7W6-4 Isoform 3 of PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 # Q6Y7W6 PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1 # Q6Y7W6-5 Isoform 4 of PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 # P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 # P40939 Trifunctional enzyme subunit alpha# mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 # O60443 Non-syndromic hearing impairment protein 5 OS=Homo sapiens GN=DFNA5 PE=1 SV=2 # P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 # Q13190 Syntaxin-5 OS=Homo sapiens GN=STX5 PE=1 SV=2 # Q9UJM3 ERBB receptor feedback inhibitor 1 OS=Homo sapiens GN=ERRFI1 PE=1 SV=1 # O00194 Ras-related protein Rab-27B OS=Homo sapiens GN=RAB27B PE=1 SV=4 #
IENLELMSQHGC*NAWK	C132	0.927845354	O75934	
KAGSC*QQGSGPAASAATAS PQLSSEIENLMSQGYSYQDIQ K	C796;C840	0.927845	A0A0U1R R39 P22681	
EGTQASEGYFSQSQEEEFQAQ SEELC*AK	C615;C659;C61 3	0.927830434	Q16643 Q16643 Q16643	
YAYLNVVGMVGSIDNDFC*GT DMTIGTDSALHR	C179	0.927739837	Q01813	
LPSSTWGWQSNNTTAC*QSQ ATLSLAEIQK	C960;C959;C93 2;C938;C932	0.925877196	I1E4Y6 Q6Y7W6 Q6Y7W6 Q6Y7W6 Q6Y7W6	
ELDLSNNC*LGDAGILQLVES VR	C409	0.925237172	P13489	
TGIEQGS DAGYLC*ESQK	C322	0.92407535	P40939	
QQQDLVAFQLVGC SLQGGC *PGPEDAGSK	C371	0.923707161	O60443	
YGAVDPLLALLAVPDMSSLAC *GYLR	C223	0.92359136	P52292	
TQVLSPATAGSSSDIAPLPP PVTLPVPPPD T MSC*R	C57	0.922930583	Q13190	
SSLPPLLIPSEN LGPHEEDQ VVC*GFK	C113	0.922661574	Q9UJM3	
NWMSQLQANAYC*ENPDIVLI GNK	C123	0.922342997	O00194	

VC*ENIPIVLCGNK	C112;C130;C129;C108	0.920864292	P62826 J3KQE5 B5MDF5 F5H018	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 # J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 # B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 # F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 #
AVC*MLSNTTAVAEAWAR	C376	0.920817377	Q9BQE3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
QLFALSC*TAEEQGVLPDDL GVIR	C96;C60;C112;C75;C112;C96	0.920347509	P04899 P04899 P04899 P04899 P04899	Q92989-2 Isoform 2 of Polyribonucleotide 5'-hydroxyl-kinase Clp1 OS=Homo sapiens GN=CLP1 # Q92989 Polyribonucleotide 5'-hydroxyl-kinase Clp1 OS=Homo sapiens GN=CLP1 PE=1 SV=1 # E9PL17 Polyribonucleotide 5'-hydroxyl-kinase Clp1 OS=Homo sapiens GN=CLP1 PE=1 SV=1 # P55072 Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 #
VGAPTIPDSC*LPLGMSQEDN QLK	C274	0.917714016	Q92989 Q92989 E9PL17	P55072
QAAPC*VLFFDELDSIAK	C572	0.917435392	P55072	Q96KP1 Exocyst complex component 2 OS=Homo sapiens GN=EXOC2 PE=1 SV=1 # P49757 Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=2 # G3V3Z8 Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=1 # P49757-3 Isoform 3 of Protein numb homolog OS=Homo sapiens GN=NUMB # P49757-5 Isoform 5 of Protein numb homolog OS=Homo sapiens GN=NUMB # P49757-4 Isoform 4 of Protein numb homolog OS=Homo sapiens GN=NUMB # P49757-8 Isoform 8 of Protein numb homolog OS=Homo sapiens GN=NUMB # P49757-9 Isoform 9 of Protein numb homolog OS=Homo sapiens GN=NUMB # P49757-7 Isoform 7 of Protein numb homolog OS=Homo sapiens GN=NUMB # P49757-6 Isoform 6 of Protein numb homolog OS=Homo sapiens GN=NUMB # P49757-2 Isoform 2 of Protein numb homolog OS=Homo sapiens GN=NUMB # P55884 Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 # P55884-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B #
LAEKEDWIVDNEGLTSLPCQF EQCIVC*SLQSLK	C627	0.917301056	Q96KP1	
HTEVPTGTC*PVDPFEAQWA ALENK	C611;C467;C600;C465;C552;C405;C309;C416;C454;C563	0.91699227	P49757 G3V3Z8 P49757 P49757 P49757 P49757 P49757 P49757	
FSHQGVQLIDFSPC*ER	C384;C384	0.916097006	P55884 P55884	
TC*DISFSDPDDLNFK	C47	0.91536605	P61081	P61081 NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1 # A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #
ADHQPLTEASYVNLPTIALC* NTDSPLR	C153;C148;C148	0.914851505	A0A0C4D G17 C9J9K3 P08865	

AGKPVIC*ATQMLESNIK	C326	0.914485641	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
GYDFC*QVLQWFAER	C175	0.914037827	Q9H223	Q9H223 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 #
WVDPNSPVLEDPVLC*ALAK	C242	0.913411537	A0A0A0M SD5	A0A0A0MSD5 Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=1 #
EC*SNPSNLELYTQAILDMT YFEENKLVDEDFPEDSSSQK	C57	0.912843769	A6NDU8 A0A0C4D GW6	A6NDU8 UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 # A0A0C4DGW6 UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 #
AVGYSC*MPSNKDEDEGLVVL VFNK	C132;C180	0.912535	Q7Z3B4 Q7Z3B4	Q7Z3B4-3 Isoform 3 of Nucleoporin p54 OS=Homo sapiens GN=NUP54 # Q7Z3B4 Nucleoporin p54 OS=Homo sapiens GN=NUP54 PE=1 SV=2 #
SSC*LFCLPSFK	C29	0.910929799	Q9UNA3	Q9UNA3 Alpha-1#4-N-acetylglucosaminyltransferase OS=Homo sapiens GN=A4GNT PE=2 SV=1 #
C*WDPSQAYFTLPR	C32;C354;C348	0.910572769	I3L0Z8 O14641 I3L2N2	I3L0Z8 Segment polarity protein dishevelled homolog DVL-2 (Fragment) OS=Homo sapiens GN=DVL2 PE=1 SV=1 # O14641 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 # I3L2N2 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 #
HGFC*GIPITDTGR	C140	0.910222314	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
TVDSQGPTPVC*TPTFLER	C237	0.9093277	Q9BYG3	Q9BYG3 MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 #
DIDFLKEEEHDC*FLEEIMTK	C173	0.908990264	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #
CSSC*EPFPDGATNLSR	C122	0.908864112	O95999	O95999 B-cell lymphoma/leukemia 10 OS=Homo sapiens GN=BCL10 PE=1 SV=1 #
SSGGFVWAC*K	C308;C256	0.908489198	P48735 P48735	P48735 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 # P48735-2 Isoform 2 of Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 #
LSDFGLC*TGLK	C234	0.908105	Q15208	Q15208 Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1 #
LECVEPNC*R	C77;C77;C113;C77;C77	0.907872	P83881 Q969Q0 J3KQN4 H7BZ11 H0Y5B4	P83881 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 # Q969Q0 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 # J3KQN4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=1 # H7BZ11 Protein RPL36A-HNRNPH2 OS=Homo sapiens GN=RPL36A-HNRNPH2 PE=3 SV=2 # H0Y5B4 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=2 #
C*AAVDVEPPSK	C670;C634;C688	0.905862812	Q15020 Q15020 F8VV04	Q15020 Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1 # Q15020-4 Isoform 4 of Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 # F8VV04 Squamous cell carcinoma antigen recognized by T-cells 3 (Fragment) OS=Homo sapiens GN=SART3 PE=1 SV=1 #

				Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EUU4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # A0A0A0MR52 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q9NTX5 Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 PE=1 SV=2 # F2Z2D6 Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 PE=1 SV=1 # Q9NTX5-3 Isoform 3 of Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 # Q9NTX5-2 Isoform 2 of Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 # H0Y525 Ethylmalonyl-CoA decarboxylase (Fragment) OS=Homo sapiens GN=ECHDC1 PE=1 SV=1 # E9PJS8 Ethylmalonyl-CoA decarboxylase (Fragment) OS=Homo sapiens GN=ECHDC1 PE=1 SV=1 # A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q15185-3 Isoform 3 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # H0YL61 DTW domain-containing protein 1 (Fragment) OS=Homo sapiens GN=DTWD1 PE=1 SV=1 # Q8N5C7-3 Isoform 3 of DTW domain-containing protein 1 OS=Homo sapiens GN=DTWD1 # H0YK73 DTW domain-containing protein 1 (Fragment) OS=Homo sapiens GN=DTWD1 PE=1 SV=1 # Q8N5C7 DTW domain-containing protein 1 OS=Homo sapiens GN=DTWD1 PE=1 SV=1 # H0YML0 DTW domain-containing protein 1 (Fragment) OS=Homo sapiens GN=DTWD1 PE=1 SV=1 # H0YMP4 DTW domain-containing protein 1 OS=Homo sapiens GN=DTWD1 PE=1 SV=1 # Q96EY5-2 Isoform 2 of Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A # Q96EY5 Multivesicular body subunit 12A OS=Homo sapiens GN=MVB12A PE=1 SV=1 #
LQGINC*GPDFTPSFANLGR	C662;C622;C575;C662;C575;C466;C622;C498;C669;C498;C466;C466	0.905319572	Q04637 Q04637 E9PGM1 Q04637 Q04637 Q04637 E7EUU4 Q04637 Q04637 E7EX73 A0A0A0MR52 R52 Q04637	
SLGTPEDGMAVC*MFMQNTL TR	C133;C127;C52;C127;C52;C127	0.90525	Q9NTX5 F2Z2D6 Q9NTX5 Q9NTX5 H0Y525 E9PJS8	
HLNEIDL FHC*IDPNDSK	C62;C58;C58;C58	0.905218007	A0A087WYT3 Y3 Q15185 Q15185 Q15185	
QSQTTSIASEDPLQNLC*LAS QEV LQK	C40;C40;C40;C40;C40;C40	0.904795	H0YL61 Q8N5C7 H0YK73 Q8N5C7 H0YML0 H0YMP4	
SPLPLGFSPVC*DPMSDK	C90	0.903190437	Q96EY5 Q96EY5	

LANLAATIC*SWEDDVNHSFA K	C210;C210	0.903131205	Q9NQW6 Q9NQW6	Q9NQW6-2 Isoform 2 of Actin-binding protein anillin OS=Homo sapiens GN=ANLN # Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 #
NC*FASVFEK	C120	0.902980809	O15144	O15144 Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 #
LELASLQC*LNETLTSCTK	C394	0.902228195	Q99543	Q99543 DnaJ homolog subfamily C member 2 OS=Homo sapiens GN=DNAJC2 PE=1 SV=4 #
YQAEINDLENLGEMSGTIC* GQVWK	C174;C131;C131; 1;C147	0.901528654	O14733 O14733 O14733 O14733	O14733-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 7 OS=Homo sapiens GN=MAP2K7 # O14733 Dual specificity mitogen-activated protein kinase kinase 7 OS=Homo sapiens GN=MAP2K7 PE=1 SV=2 # O14733-4 Isoform 4 of Dual specificity mitogen-activated protein kinase kinase 7 OS=Homo sapiens GN=MAP2K7 # O14733-3 Isoform 3 of Dual specificity mitogen-activated protein kinase kinase 7 OS=Homo sapiens GN=MAP2K7 #
VYEVVNEDPETAFC*TLANR	C617;C618;C603; 3;C308	0.90108	Q9Y5T5 Q9Y5T5 Q9Y5T5 Q9Y5T5	Q9Y5T5-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 16 OS=Homo sapiens GN=USP16 # Q9Y5T5 Ubiquitin carboxyl-terminal hydrolase 16 OS=Homo sapiens GN=USP16 PE=1 SV=1 # Q9Y5T5-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 16 OS=Homo sapiens GN=USP16 # Q9Y5T5-4 Isoform 4 of Ubiquitin carboxyl-terminal hydrolase 16 OS=Homo sapiens GN=USP16 #
SELEC*VTNITLANVIR	C27;C27	0.900451801	Q9Y6W5 Q9Y6W5	Q9Y6W5-2 Isoform 2 of Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 # Q9Y6W5 Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3 #
GVWGTPGQVYDVVEVDVKD PNYDDQENC*VYETVVLPL DER	C139;C150	0.90033274	Q53EL6 Q53EL6	Q53EL6-2 Isoform 2 of Programmed cell death protein 4 OS=Homo sapiens GN=PDCD4 # Q53EL6 Programmed cell death protein 4 OS=Homo sapiens GN=PDCD4 PE=1 SV=2 #
FSLC*SDNLEGISEGPSNR	C568;C568;C568; 8;C568;C568;C568; 68;C568;C431	0.90008463	Q14C86 B4DGD8 Q14C86 Q14C86 Q14C86 Q14C86 C9IZ08 H0Y719	Q14C86-2 Isoform 2 of GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 # B4DGD8 GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=1 # Q14C86-5 Isoform 5 of GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 # Q14C86-3 Isoform 3 of GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 # Q14C86 GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2 # Q14C86-6 Isoform 6 of GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 # C9IZ08 GTPase-activating protein and VPS9 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=GAPVD1 PE=1 SV=1 # H0Y719 GTPase-activating protein and VPS9 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=GAPVD1 PE=1 SV=1 #
QVLMGPYPNPTDC*PEVGGFFD VLGNDR	C129	0.899982327	Q9H3P7	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 #

LDNWLNELEYC*TR	C139;C110;C223;C86;C65	0.899897176	Q9NP72 Q9NP72 H0Y6T8 A0A087X163 Q5W0J0	Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # H0Y6T8 Ras-related protein Rab-18 (Fragment) OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # Q5W0J0 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 #
YSLADQTSQDQSPLPPCTPT PPC*AEMR	C569	0.89934	Q06124 Q06124	Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
DSSTC*PGDYVLSVSENSR ALANVNIGSLIC*NVGAGGPA PAAGAAPAGGPAPSTAAAPA EEK	C44 C36	0.898994331 0.897281437	P46109 P05386	P46109 Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1 # P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 #
SIVC*LEDLQIGTVLTGK	C537;C912	0.896235	Q8N5C6 Q8N5C6	Q8N5C6-2 Isoform 2 of S1 RNA-binding domain-containing protein 1 OS=Homo sapiens GN=SRBD1 # Q8N5C6 S1 RNA-binding domain-containing protein 1 OS=Homo sapiens GN=SRBD1 PE=1 SV=2 # H0YND7 Diphthine--ammonia ligase (Fragment) OS=Homo sapiens GN=DPH6 PE=1 SV=1 # Q7L8W6-2 Isoform 2 of
C*EGDEVEDLYELLK	C40;C88;C88	0.895956141	H0YND7 Q7L8W6 Q7L8W6	Diphthine--ammonia ligase OS=Homo sapiens GN=DPH6 # Q7L8W6 Diphthine--ammonia ligase OS=Homo sapiens GN=DPH6 PE=1 SV=3 #
C*DQDAQNPLSAGLQGACLM ETVELLQAK	C240;C242;C124;C245;C240	0.895779942	Q13561 Q13561 H0Y198 Q13561 F8W116	Q13561 Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4 # Q13561-3 Isoform 3 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 # H0Y198 Dynactin subunit 2 (Fragment) OS=Homo sapiens GN=DCTN2 PE=1 SV=1 # Q13561-2 Isoform 2 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 # F8W116 Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=1 # Q9Y2D5-5 Isoform 3 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 # Q9Y2D5 A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 PE=1 SV=3 # Q9Y2D5-7 Isoform 5 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 # Q9Y2D5-6 Isoform 4 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 # C9JYV5 A-kinase anchor protein 2 (Fragment) OS=Homo sapiens GN=AKAP2 PE=1 SV=1 # Q9Y2D5-4 Isoform 2 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 #
AQQEQLLLQKQLQQQQQP PSQLC*TAPASSHER	C385;C296;C385;C527;C345;C527	0.894711838	Q9Y2D5 Q9Y2D5 Q9Y2D5 Q9Y2D5 C9JYV5 Q9Y2D5	R4GND3 Pleckstrin homology-like domain family A member 1 OS=Homo sapiens GN=PHLDA1 PE=1 SV=1 # Q8WV24 Pleckstrin homology-like domain family A member 1 OS=Homo sapiens GN=PHLDA1 PE=1 SV=4 #
C*CILTEEGLLIPPK	C30;C171	0.894498265	R4GND3 Q8WV24	Q96A49 Synapse-associated protein 1 OS=Homo sapiens GN=SYAP1 PE=1 SV=1 #
TQEDEEEISTSPGVSEFVSDA FDAC*NLNQEDLRK	C283	0.894351946	Q96A49	



QADSC*PYGTMYLSPADTS WR	C131	0.894057596	Q6UUUV9 M0QXN6 M0QX46 Q6UUUV9 Q6UUUV9	Q6UUUV9 CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 PE=1 SV=2 # M0QXN6 CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 PE=1 SV=1 # M0QX46 CREB- regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 PE=1 SV=1 # Q6UUUV9-3 Isoform 3 of CREB-regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 # Q6UUUV9-2 Isoform 2 of CREB- regulated transcription coactivator 1 OS=Homo sapiens GN=CRTC1 # Q16576-2 Isoform 2 of Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 # Q16576 Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 # Q5JP01 Histone-binding protein RBBP7 (Fragment) OS=Homo sapiens GN=RBBP7 PE=1 SV=1 # O94901 SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=3 # O94901-5 Isoform 5 of SUN domain- containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-8 Isoform 8 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-6 Isoform 6 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # O94901-9 Isoform 9 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 # E9PHI4 SUN domain- containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=1 #
VHIPNDDAQFDASHC*DSDK GEFGGFGSVTGK	C141;C97;C17	0.891433067	Q16576 Q16576 Q5JP01	Q14137 Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # E9PEX6 Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=1 SV=1 # P09622 Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 # P09622-2 Isoform 2 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD # P09622-3 Isoform 3 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD # P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 # P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C # A0A024R4E5 High density lipoprotein binding protein (Vigilin)# isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1 # A0A087WXU3 Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8 Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8-2 Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 # H7BXI1 Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 # A0FGR8-6 Isoform 6 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 #
LATTAC*TLGDGEAVGADSGT SSAVSLK	C63;C13;C63;C6 3;C63;C63	0.888497045	O94901 O94901 O94901 O94901 E9PHI4	
DLQPFPTC*QALVYR	C404	0.888372459	Q14137	
VMTIPYQMPASSPVIC*AGG QDR	C194	0.887971807	Q15365	
VLGAHILGPGAGEMVNEAAL ALEYGASC*EDIAR	C454;C477;C37 8;C429	0.887557757	E9PEX6 P09622 P09622 P09622	
TAFQEALDAAGDKLVVDFDS ATWC*GPKC	C32	0.887256794	P10599	
DSNNLC*LHFNPR	C43	0.887067616	P09382	
IC*DQWDALGSLTHSR	C499	0.885764617	O43707	
NDQC*YDDIR	C29;C23;C76	0.885730695	Q9ULV4 Q9ULV4 Q9ULV4	
AAC*LESAQEPAGAWGNK	C53	0.884974317	A0A024R4 E5	
AC*DLPAAVHFPDTER	C181;C181;C15 3;C123;C181	0.884832652	A0A087W XU3 A0FGR8 A0FGR8 H7BXI1 A0FGR8	

NAEFLTC*NIPTSNASNMVTEK	C97;C435;C392	0.884816053	P55265 P55265 P55265	P55265-5 Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265-4 Isoform 4 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265 Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 #
EADQKEQFSQGSPSNC*LETSLAEIFPLGK	C161;C102	0.884557902	Q9NQ88 A0A0U1RQD1	Q9NQ88 Fructose-2#6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 # A0A0U1RQD1 Chromosome 12 open reading frame 5# isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 #
VFFVESVC*DDPDVIAANILEVK	C158;C158	0.884519241	O60825 O60825	O60825-2 Isoform 2 of 6-phosphofructo-2-kinase/fructose-2#6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 # O60825 6-phosphofructo-2-kinase/fructose-2#6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 PE=1 SV=2 #
AEIPC*EDEQEHEHNGPLDNK	C626;C8;C626;C471;C455;C439	0.884038665	Q5R363 H0Y932 Q96SB4 H3BLV9 Q96SB4 Q96SB4	Q5R363 SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 # H0Y932 SRSF protein kinase 1 (Fragment) OS=Homo sapiens GN=SRPK1 PE=1 SV=1 # Q96SB4-3 Isoform 1 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 # H3BLV9 SRSF protein kinase 1 (Fragment) OS=Homo sapiens GN=SRPK1 PE=1 SV=1 # Q96SB4 SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 # Q96SB4-4 Isoform 3 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 #
YTIVVSATASDAAPLQYLAPYSGC*SMGEYFR	C294;C272;C244	0.881587175	P25705 P25705 P25705	P25705 ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 # P25705-3 Isoform 3 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 # P25705-2 Isoform 2 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 #
IETSC*SLLEQTQPATPSLWK	C487;C405	0.881299937	O60934 A0A0C4DG07	O60934 Nibrin OS=Homo sapiens GN=NBN PE=1 SV=1 # A0A0C4DG07 Nibrin OS=Homo sapiens GN=NBN PE=1 SV=1 #
GNFTLPEVAEC*FDEITYVELQKEEAQK	C648;C629	0.88080876	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
LNNLIC*DESDVK	C362;C361;C361;C361	0.880186272	Q96EB1 Q96EB1 Q96EB1 G5E9D4	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1-2 Isoform 2 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 # Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 #
SLDDSQC*GITYK	C282	0.880041318	Q9NVG8	G5E9D4 Elongation protein 4 homolog (S. cerevisiae)# isoform CRA_b OS=Homo sapiens GN=ELP4 PE=1 SV=1 # Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
EGYTSFWNDC*ISSGLR	C84;C70	0.879998148	Q9H4A6 Q9H4A5	Q9H4A6 Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 # Q9H4A5 Golgi phosphoprotein 3-like OS=Homo sapiens GN=GOLPH3L PE=1 SV=1 #

GC*QDFGWDPFCQPDGYEQ TYAEMPK	C105;C146;C129	0.879142439	Q9BY32 Q9BY32 Q9BY32	Q9BY32-3 Isoform 3 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA # Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 # Q9BY32-2 Isoform 2 of Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA # Q15459-2 Isoform 2 of Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 # Q15459 Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 # Q5XKP0 MICOS complex subunit MIC13 OS=Homo sapiens GN=MIC13 PE=1 SV=1 # A0A140TA86 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 #
EVLQDQVC*YR	C179;C244	0.878808359	Q15459 Q15459	Q15459-2 Isoform 2 of Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 # Q15459 Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 # Q5XKP0 MICOS complex subunit MIC13 OS=Homo sapiens GN=MIC13 PE=1 SV=1 # A0A140TA86 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 #
AGEVVPAMYQFSQYVC*QQ TGLQIPQLPAPPK	C60;C82	0.878486525	Q5XKP0 A0A140TA86	Q5XKP0 MICOS complex subunit MIC13 OS=Homo sapiens GN=MIC13 PE=1 SV=1 # A0A140TA86 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 #
ASVGFGGSC*FQK	C276;C209;C179	0.878433307	O60701 O60701 O60701	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # O60701-2 Isoform 2 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH # O60701-3 Isoform 3 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH #
NTVLC*NVVEQFLQADLAR	C70	0.878076051	Q14258	Q14258 E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 #
ASFENNCEIGC*FAK	C15	0.877686094	P56537	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 # Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # H0Y852 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial (Fragment) OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
SC*NGPVLVGSPQGGVDIEE VAASNPELIFK	C162;C162;C54;C162	0.876548459	Q96I99 E9PDQ8 H0Y852 Q96I99	Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # H0Y852 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial (Fragment) OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
LIDFLEC*GK	C20;C234;C72;C234;C155	0.876100744	J3QSF1 P17844 J3KRZ1 J3KTA4 P17844	J3QSF1 Probable ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens GN=DDX5 PE=1 SV=1 # P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # J3KRZ1 Probable ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens GN=DDX5 PE=1 SV=1 # J3KTA4 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # P17844-2 Isoform 2 of Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 #
CPEALFQPSFLGMESC*GIHE TTFNSIMK	C272;C272	0.876013535	P63261 P60709	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #
AIFSQPLQITDTQQGC*IAPV ELR	C716	0.875821843	Q8NBF2	Q8NBF2 NHL repeat-containing protein 2 OS=Homo sapiens GN=NHLRC2 PE=1 SV=1 #
AFVNPFPDYAAAAGALLASG AAEETGC*VRPPATTDEPGLP FHQDGK	C49	0.875794917	Q9NS86	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 #
VSLDPELEEALTSASDELTC* DLAAILGMHNLITNTK	C132	0.875434394	Q9NYL9	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 #
IIPGFMC*QGGDFTR	C62	0.874157904	P62937	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #

IQCTLQDVGSALATPC*SSAR	C132;C80;C132	0.873577486	Q96EY8 S4R3P5 F5H4Z7	Q96EY8 Cob(I)yrinic acid a#-c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # S4R3P5 Cob(I)yrinic acid a#-c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # F5H4Z7 Cob(I)yrinic acid a#-c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 #
RPYEDQQLGETTPLTIIC*QP MQPLR	C367	0.872787678	Q8TF42	Q8TF42 Ubiquitin-associated and SH3 domain-containing protein B OS=Homo sapiens GN=UBASH3B PE=1 SV=2 #
MVYSTC*SLNPIEDEAVIASLL EK	C321	0.870494274	Q08J23	Q08J23 tRNA (cytosine(34)-C(5))- methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 #
VWLQYQC*LWDMQAENIYNR	C1059	0.870437398	Q14204	Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 #
ILDILGETC*K	C225;C224;C22 5;C225;C156	0.868511791	Q15424 Q14151 Q15424 Q15424 Q15424	Q15424 Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4 # Q14151 Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1 # Q15424-4 Isoform 4 of Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB # Q15424-3 Isoform 3 of Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB # Q15424-2 Isoform 2 of Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB # E9PB90 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=1 # P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 # P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 #
FLSQIESDC*LALLQVR	C766;C794	0.867897177	E9PB90 P52789	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 # Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 # Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 # Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
QNSDFLC*QMDLLQEFYETTL EALKDAK	C130	0.867829085	P61201	A0A0A0MR02 Voltage-dependent anion- selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
DC*GATWVVLGHSER	C87;C124	0.867403185	P60174 P60174	P52657 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 # A0A0B4J1Z5 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 # Q16555-2 Isoform 2 of Dihydropyrimidinase- related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase- related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
NVTQIEPFC*LETDRR	C630;C594	0.867352582	Q9ULW0 Q9ULW0	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 # Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 #
EVFSSC*SSEVVLSGDDEEY QR	C108	0.867063726	Q09666	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 #
YKWC*EYGLTFTEK	C76;C76	0.866995805	A0A0A0M R02 P45880	
FC*DNVWTFVLNDVEFR	C68;C33	0.865475229	P52657 A0A0B4J1 Z5	
GLYDGPVC*EVSVTPK	C468;C504	0.865128328	Q16555 Q16555	
SDVC*TPGGTTIYGLHALEQG GLR	C247;C235	0.864749982	A0A0A0M QS1 Q53H96	
AKC*ELSSSVQTDINLPYLTM DSSGPK	C317	0.86443529	P38646	

FSFC*CSPEPEAEAEAAAGP GPCER	C26;C26	0.864302714	E7EMC7 Q13501	E7EMC7 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # Q13501 Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 # I3L0M9 Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # Q15370
ADDTFEALC*IEPFSSPELPD VMKPQDSGSSANEQAVQ	C111;C89;C84	0.86408	I3L0M9 Q15370 B8ZZU8	I3L0M9 Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1 # B8ZZU8 Transcription elongation factor B (SIII)# polypeptide 2 (18kDa# elongin B)# isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 #
STVLSLDWHPNNVLLAAGSC* DFK	C162	0.863328128	O15143	O15143 Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 # Q9H6R4 Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2 # Q9H6R4-4 Isoform 4 of Nucleolar protein 6 OS=Homo sapiens GN=NOL6 #
QAVDSPAASFC*R	C1034;C1031	0.863227665	Q9H6R4 Q9H6R4	Q9H6R4 Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2 # Q9H6R4-4 Isoform 4 of Nucleolar protein 6 OS=Homo sapiens GN=NOL6 # X5CMH5 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # Q03519 Antigen peptide transporter 2
VLILDEATSALDVQC*EQALQ DWNSRGDR	C641;C641;C64 1;C641	0.863188399	X5CMH5 Q03519 A0A0G2JL V0 A0A087W YD6	X5CMH5 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # Q03519 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # A0A0G2JLV0 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # A0A087WYD6 Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1 # P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
TIAEC*LADELINAAK	C172;C193;C17 2	0.86277241	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
LTESPC*ALVASQYGWSGNM ER	C645	0.862568822	P14625	P14625 Endoplasmic reticulum protein GN=HSP90B1 PE=1 SV=1 # Q9P0J1 [Pyruvate dehydrogenase [acetyl- transferring]]-phosphatase 1# mitochondrial OS=Homo sapiens GN=PDP1 PE=1 SV=3 # Q9P0J1-2 Isoform 2 of [Pyruvate dehydrogenase [acetyl-transferring]]- phosphatase 1# mitochondrial OS=Homo sapiens GN=PDP1 # E5RIV4 [Pyruvate dehydrogenase [acetyl-transferring]]- phosphatase 1# mitochondrial (Fragment) OS=Homo sapiens GN=PDP1 PE=1 SV=1 #
GMLLGVFDGHAGC*ACSQAV SER	C149 C149;M163 C174;M138	0.861688751	Q9P0J1 Q9P0J1 E5RIV4	Q9P0J1 [Pyruvate dehydrogenase [acetyl- transferring]]-phosphatase 1# mitochondrial OS=Homo sapiens GN=PDP1 # E5RIV4 [Pyruvate dehydrogenase [acetyl-transferring]]- phosphatase 1# mitochondrial (Fragment) OS=Homo sapiens GN=PDP1 PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
EC*EHCDCLQGFQLTHSLGG GTGSGMGTLLISK	C124	0.861233567	Q9BUF5	Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # Q96ME7-3 Isoform 3 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # Q96ME7 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=2 # Q96ME7-2 Isoform 2 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # G3XAG1 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=1 #
SEHGPIFFPESGQPEC*LK	C295;C324;C24 7;C323	0.860333253	Q96ME7 Q96ME7 Q96ME7 G3XAG1	Q96ME7-3 Isoform 3 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # Q96ME7 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=2 # Q96ME7-2 Isoform 2 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 # G3XAG1 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=1 # Q5T0N5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=1 # Q5T0N5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=3 # Q5T0N5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L #
FTSC*VAFFNILNELNDYAGQ R	C69;C69;C69;C6 9;C69;C69	0.859677737	Q5T0N5 S4R347 Q5T0N5 Q5T0N5 Q5T0N5	Q5T0N5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=1 # Q5T0N5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5 Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L PE=1 SV=3 # Q5T0N5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L # Q5T0N5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FBNP1L #

GLNDLQPWPNQMAIAC*GSR	C164 C194;M160	0.859275	Q9Y673 Q9Y673	Q9Y673 Dolichyl-phosphate beta-glucosyltransferase OS=Homo sapiens GN=ALG5 PE=1 SV=1 # Q9Y673-2 Isoform 2 of Dolichyl-phosphate beta-glucosyltransferase OS=Homo sapiens GN=ALG5 #
AYHEQLTVAEITNAC*FEPAN QMVK	C295	0.858446397	Q9BQE3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #
NTGIIC*TIGPASR	C49	0.857670982	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
C*EEETPSLLWGLDPVFLAFA K	C8	0.857347059	Q9H668	Q9H668 CST complex subunit STN1 OS=Homo sapiens GN=OBFC1 PE=1 SV=2 #
NIC*FTVWDVGGQDR	C62	0.85663222	P18085	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 #
YC*VRPNSGIIDPGSTVTVSV MLQPFDYDNEK	C60	0.85638862	Q9P0L0 Q9P0L0	Q9P0L0 Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 # Q9P0L0-2 Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA #
C*EFQDAYVLLSEKK	C237	0.855546222	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
AHVVPC*FDASK	C1157;C1130;C1157	0.854185499	P21333 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
TIC*AILENYQTEK	C460;C438	0.852777998	Q5T5C7 P49591	Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 #
LSSC*DSFTSTINELNHCLSLR	C92	0.852504869	P07814	P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 #
LAQAKEENVGLHQTLDQTLN ELNC*I	C283;C109;C247	0.85174337	P67936 K7EPB9 P67936	P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 #
LTVVDTPGYGDAINC*R	C146;C111;C121	0.851378522	Q15019 Q15019 Q15019	Q15019-2 Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2 # Q15019 Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 # Q15019-3 Isoform 3 of Septin-2 OS=Homo sapiens GN=SEPT2 #
ITNQVIYLNPPIEEC*R	C978	0.848513572	Q14204	Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 #
SWVFDYSYSLTGPSVC*ELVR	C118;C154;C92;C78;C154	0.847059519	Q8NB37 Q8NB37 H0YF25 H0YE25 Q8NB37	Q8NB37-3 Isoform 3 of Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 # Q8NB37 Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # H0YF25 Parkinson disease 7 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # H0YE25 Parkinson disease 7 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=PDDC1 PE=1 SV=1 # Q8NB37-2 Isoform 2 of Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 #
LLAPDC*EIIQEVGKLYPLEIVF GMNGR	C215	0.846199113	Q9NQ5	Q9NQ5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 #

LC*PQFLQLASANTAR	C264;C264;C264	0.845751532	O95630 O95630 C9JK83	O95630 STAM-binding protein OS=Homo sapiens GN=STAMBP PE=1 SV=1 # O95630-2 Isoform 2 of STAM-binding protein OS=Homo sapiens GN=STAMBP # C9JK83 STAM-binding protein (Fragment) OS=Homo sapiens GN=STAMBP PE=1 SV=1 #
C*LEELVFGDVENDEDEALLRR	C90	0.845734026	Q9Y5J1	Q9Y5J1 U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 #
EGGQYGLVAAC*AAGGQGH AMIVEAYPK	C458;C436	0.845582445	P55084 P55084	P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 # P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB #
EVC*PVLQFLCHVAK	C22;C22;C22;C22;C22	0.845092577	F8WCA1 Q9NY27 C9IZ04 Q9NY27 C9IZF4	F8WCA1 Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens GN=PPP4R2 PE=1 SV=1 # Q9NY27-2 Isoform 2 of Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens GN=PPP4R2 # C9IZ04 Serine/threonine-protein phosphatase 4 regulatory subunit 2 (Fragment) OS=Homo sapiens GN=PPP4R2 PE=1 SV=1 # Q9NY27 Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens GN=PPP4R2 PE=1 SV=3 # C9IZF4 HCG14948# isoform CRA_a OS=Homo sapiens GN=PPP4R2 PE=1 SV=1 #
GEPLWAQNVVPEAEGEDDP AGEAQAGRLPLLPC*AR	C139;C139	0.844954408	G3V2I3 A6NED2	G3V2I3 RCC1 domain-containing protein 1 OS=Homo sapiens GN=RCCD1 PE=1 SV=1 # A6NED2 RCC1 domain-containing protein 1 OS=Homo sapiens GN=RCCD1 PE=1 SV=1 #
C*QSPWTEALWVR	C228;C228	0.84450791	Q6PJG6 Q6PJG6	Q6PJG6 BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 # Q6PJG6-2 Isoform 2 of BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 #
LDGSLETTNEILDSASHDC*PL VTQTYGAAAGK	C393;C375	0.844363768	Q9Y4P8 Q9Y4P8	Q9Y4P8 WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 PE=1 SV=1 # Q9Y4P8-4 Isoform 4 of WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP1 #
GGDC*DFSTFDVPIFTEEFL DQNK	C75;C177;C177;C153;C194	0.844141017	Q9P0W2 C9J8X5 Q9P0W2 Q9P0W2 B5MDG7	Q9P0W2-2 Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B # C9J8X5 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related (Fragment) OS=Homo sapiens GN=HMG20B PE=1 SV=1 # Q9P0W2 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B PE=1 SV=1 # Q9P0W2-3 Isoform 3 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B # B5MDG7 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related (Fragment) OS=Homo sapiens GN=HMG20B PE=1 SV=2 #
LGTDESC*FNMILATR	C363;C341	0.843849647	P20073 P20073	P20073 Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 # P20073-2 Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7 #

SYIEGYVPSQADVAVFEAVSS PPPADLC*HALR	C50;C50;C50	0.843629279	P24534 F2Z2G2 C9JZW3	P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 # F2Z2G2 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 # C9JZW3 Elongation factor 1-beta (Fragment) OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 #
DQVAQLDDIVDISDEISPSVD DLALSIYPPMC*HLTVR	C172 C172;M299 C300;M171	0.842472369	O95273 O95273 O95273 O95273	O95273 Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 PE=1 SV=2 # O95273-3 Isoform 3 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 # O95273-2 Isoform 2 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 # O95273-4 Isoform 4 of Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 #
LICC*DILDVLDKHLIPAANTGE SK	C98;C76	0.841106263	P62258 P62258	P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 # P62258-2 Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE #
VAHALAEGLGVIAC*IGEK	C127;C164	0.840568167	P60174 P60174	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TP11 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3 #
TGQATVASGIPAGWMGLDC* GPSSKK	C288;C316	0.838527185	P00558 P00558	P00558-2 Isoform 2 of Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 # P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
NTPLC*DSFVFR	C429	0.837615949	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 #
SEGGFIWAC*K	C269	0.837355285	O75874	O75874 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 #
VFIMDNC*EELIPEYLNfir	C496;M371 C374	0.83690594	P07900 P07900	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
IC*ALDDNVCMFAGLTADAR	C63	0.836073333	O14818	O14818 Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1 #
DIAEPHIPC*LMPEYFEPQIK	C139	0.835624182	Q96EY7	Q96EY7 Pentatricopeptide repeat domain-containing protein 3# mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3 #
SGYNYFFSGGADDAWADVE DVTEEDC*ALR	C182;C182;C18 2;C182	0.835607641	Q8NCE2 A0A087W TZ0 Q8NCE2 Q8NCE2	Q8NCE2-3 Isoform 3 of Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 # A0A087WTZ0 Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 PE=1 SV=1 # Q8NCE2 Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 PE=1 SV=2 # Q8NCE2-2 Isoform 2 of Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 # P50579 Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VY03 Methionine aminopeptidase 2 (Fragment) OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VRR3 Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 # P50579-2 Isoform 2 of Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 # G3V1U3 Methionine aminopeptidase OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VZX9 Methionine aminopeptidase 2 (Fragment) OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VQZ7 Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VSC4 Methionine aminopeptidase 2 (Fragment) OS=Homo sapiens GN=METAP2 PE=1 SV=1 #
VQTDPPSPVIC*DLYPNGVFP K	C121;C97;C85;C 98;C121;C23;C1 20;C149	0.834216855	P50579 F8VY03 F8VRR3 P50579 G3V1U3 F8VZX9 F8VQZ7 F8VSC4	



GEASEDLC*EMALDPELLLLR DDGEEEFAGAK	C336;C644;C319; C644	0.834078305	H0YB24 Q8N163 G3V119 Q8N163	H0YB24 Cell cycle and apoptosis regulator protein 2 (Fragment) OS=Homo sapiens GN=CCAR2 PE=1 SV=1 # Q8N163 Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2 # G3V119 Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=1 # Q8N163-2 Isoform 2 of Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 # Q99961-3 Isoform 3 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 # Q99961 Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 # Q99961-2 Isoform 2 of Endophilin-A2 OS=Homo sapiens GN=SH3GL1 # Q96IJ6 Mannose-1-phosphate
EPFDLGEPEQSNGGFPC*TT APK	C213;C277;C229	0.833454666	Q99961 Q99961 Q99961	guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 # Q96IJ6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA # O76031 ATP-dependent Clp protease ATP-binding subunit clpX-like# mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2 # Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 #
LLPAITILGC*R	C389;C442	0.832824749	Q96IJ6 Q96IJ6	Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN # Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 # Q14247-2 Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN # P55210-4 Isoform 4 of Caspase-7 OS=Homo sapiens GN=CASP7 # P55210-3 Isoform Alpha' of Caspase-7 OS=Homo sapiens GN=CASP7 # P55210 Caspase-7 OS=Homo sapiens GN=CASP7 PE=1 SV=1 # A0A0A0MRL7 Caspase-7 OS=Homo sapiens GN=CASP7 PE=1 SV=1 # Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 # P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 # Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 # Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 # P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 # P31150 Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 # F5H6Q1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 # J3KR44 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 # Q96FW1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 #
NAVIPQYQALFMSDKC*ELNV TEDALK	C538	0.832583333	O76031	
DAANC*WTSLLESEYAADPW VQDQMQR	C99	0.832513864	Q8WVJ2	
C*ALGWDHQEK	C246;C246;C246 6	0.83164938	Q14247 Q14247 Q14247	
LFFIQAC*R	C161;C219;C186; C271	0.831217893	P55210 P55210 P55210 A0A0A0MRL7	
AENGLLMTPC*YTANFVAPEV LKR	C579;M480 C483;M572 C584;M556 C575 C564;M576 C559;M561	0.830377358	Q15418 Q15418 E9PGT3 P51812 Q15418 Q15418	
NTNDANSC*QIIPQNVNR	C317;C317	0.829652662	P50395 P31150	
QEPLGSDSEGVNC*LAYDEAI MAQQDR	C23;C23;C23	0.829478444	F5H6Q1 J3KR44 Q96FW1	

				Q8N6T3-2 Isoform 2 of ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 # E5RHT6 ADP-ribosylation factor GTPase-activating protein 1 (Fragment) OS=Homo sapiens GN=ARFGAP1 PE=1 SV=2 # F8W1U7 ADP-ribosylation factor GTPase-activating protein 1 (Fragment) OS=Homo sapiens GN=ARFGAP1 PE=1 SV=1 # E5RGL6 ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=1 SV=1 #
FREFLESQEDYDPC*WSLQEK	C96;C22;C22;C96;C96;C22;C96;C96;C96;C43	0.82930118	Q8N6T3 E5RHT6 F8W1U7 E5RGL6 Q8N6T3 F8VWH9 F8VWB3 E5RHC5 Q8N6T3 Q8N6T3	Q8N6T3-3 Isoform 3 of ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 # F8VWH9 ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=1 SV=1 # F8VWB3 ADP-ribosylation factor GTPase-activating protein 1 (Fragment) OS=Homo sapiens GN=ARFGAP1 PE=1 SV=1 # E5RHC5 ADP-ribosylation factor GTPase-activating protein 1 (Fragment) OS=Homo sapiens GN=ARFGAP1 PE=1 SV=2 # Q8N6T3 ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=1 SV=2 #
AINC*ATSGVVGLVNCLR	C1448	0.828909362	P49327	Q8N6T3-5 Isoform 5 of ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 # P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
DCIGGC*SDLVSLQQSGELLTR	C83	0.828832544	P35754	P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
GLIAAIC*AGPTALLAH	C106;C86;C67	0.828367326	Q99497 K7ELW0 K7EN27	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 # K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 # K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 #
DC*LIPMGITSENVAER	C136	0.82738335	C9JDE9	C9JDE9 3-ketoacyl-CoA thiolase# peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=1 #
DGSDYEGWC*WPGSAGYPDFTNPTMR	C502;C524	0.824776766	Q14697 Q14697	Q14697 Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 # Q14697-2 Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB #
ALNALC*DGLIDELNQALK	C62	0.824179139	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
SC*SGVEFSTSGHAYTDTGK	C36	0.823244749	Q9Y277	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #
NADMSEEMQQDSVEC*ATQALEK	C24 C24;M17	0.823241107	P63167 F8VXI7 F8VRV5 F8VXL2	P63167 Dynein light chain 1# cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 # F8VXI7 Dynein light chain 1# cytoplasmic (Fragment) OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 # F8VRV5 Dynein light chain 1# cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 # F8VXL2 Dynein light chain 1# cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 #

TGLC*YLPEELALQK	C46;C46;C15;C46;C15;C35	0.823142495	Q13045 J3KS54 K7EP27 Q13045 K7EP37 Q13045	Q13045-2 Isoform 2 of Protein flightless-1 homolog OS=Homo sapiens GN=FLII # J3KS54 Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=1 # K7EP27 Protein flightless-1 homolog (Fragment) OS=Homo sapiens GN=FLII PE=1 SV=1 # Q13045 Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2 # K7EP37 Protein flightless-1 homolog (Fragment) OS=Homo sapiens GN=FLII PE=1 SV=1 # Q13045-3 Isoform 3 of Protein flightless-1 homolog OS=Homo sapiens GN=FLII #
GQNGDDSSAGGDFPPPAEV EPTPEAELLAQPC*HDSEASK	C122	0.822746607	O94992	O94992 Protein HEXIM1 OS=Homo sapiens GN=HEXIM1 PE=1 SV=1 # Q8N5K1 CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 #
VVNEINIEDLC*LTK	C92	0.820951556	Q8N5K1	P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 #
EKLC*YVALDFEQEMATAASS SSLEK	C217;C917	0.820330765	P60709 Q6S8J3	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 # A0A087X239 Round spermatid basic protein 1-like protein OS=Homo sapiens GN=RSBN1L PE=1 SV=1 #
INALTAASEAAC*LIVSVDETIK NPR	C511	0.819613053	Q99832	Q6PCB5-2 Isoform 2 of Round spermatid basic protein 1-like protein OS=Homo sapiens GN=RSBN1L # Q6PCB5 Round spermatid basic protein 1-like protein OS=Homo sapiens GN=RSBN1L PE=1 SV=2 #
SIQTIC*SGLLTDVEDQAAK	C280;C10;C280	0.81932396	A0A087X239 Q6PCB5 Q6PCB5	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 # O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 # B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 #
GDLENAFLNLVQC*IQNKPLY FADR	C280;C262	0.817714435	P07355 P07355	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 # H3BPR2 Nucleoside diphosphate kinase OS=Homo sapiens GN=NME3 PE=1 SV=1 # Q13232 Nucleoside diphosphate kinase 3 OS=Homo sapiens GN=NME3 PE=1 SV=2 #
AGEGTYALDSESC*MEK	C272	0.817256293	O00541 O00541 B5MCF9	Q8TDD1 ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 # Q8TDD1-2 Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 #
LVAFC*PFASSQVALENANAV SEGVVHEDLR	C52	0.815303974	O00567	Q96KB5 Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 # Q96KB5-2 Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK #
ADELLC*WEDSAGHWLYE	C74;C158	0.814698787	H3BPR2 Q13232	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9U110 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
LGPGRPLPTFPTSEC*TSDVE PDTR	C73;C73	0.814296368	Q8TDD1 Q8TDD1	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
AFTEANDGSLC*LAMEYGGE K	C112;C112	0.813348216	Q96KB5 Q96KB5	
GAEPETGSAVSAAQC*QVGP TR	C90;C69	0.813243257	E7ERK9 Q9U110	
GPFVEAEVDPVDLEC*PDAK	C1833	0.811282033	Q09666	

EQANTAVVEDGSDC*LAAVLR	C378;C242;C242	0.811257023	A0A0A6Y YJ5 O94854 O94854	A0A0A6YYJ5 Microtubule-actin cross-linking factor 1# isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=1 # O94854-2 Isoform 2 of Uncharacterized protein KIAA0754 OS=Homo sapiens GN=KIAA0754 # O94854 Uncharacterized protein KIAA0754 OS=Homo sapiens GN=KIAA0754 PE=2 SV=4 # P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 # P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 # P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 # P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 # J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 # Q9NTK5-3 Isoform 3 of Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 # P40925 Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 # C9JRL4 Malate dehydrogenase# cytoplasmic (Fragment) OS=Homo sapiens GN=MDH1 PE=1 SV=7 # C9JF79 Malate dehydrogenase (Fragment) OS=Homo sapiens GN=MDH1 PE=1 SV=1 # P40925-3 Isoform 3 of Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 # Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 # Q9BQ39 ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1 # Q06124-2 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 # O43175 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 # Q5SZU1 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # E9PKN8 Tudor and KH domain-containing protein (Fragment) OS=Homo sapiens GN=TDRKH PE=1 SV=1 # F6TB26 Tudor and KH domain-containing protein OS=Homo sapiens GN=TDRKH PE=1 SV=1 # Q9Y2W6 Tudor and KH domain-containing protein OS=Homo sapiens GN=TDRKH PE=1 SV=2 # Q5SZR4 Tudor and KH domain containing# isoform CRA_a OS=Homo sapiens GN=TDRKH PE=1 SV=1 #
LQDAFSSIGQSC*HLDLPQIAV VGGQSAGK	C27;C27;C27;C27; C27	0.811071171	P50570 P50570 P50570 P50570 P50570	
NC*DKGQSFFIDAPDSPATLA YR	C266;C277	0.810569259	P53384 P53384	
ISDTGSAGLMLVEFFAPWC*G HCK	C57	0.810453333	P30101	
STFFNVLTSQASAEFPFC* TIDPNESRVPVDER	C75;C55;C55	0.809851518	J3KQ32 Q9NTK5 Q9NTK5	
VIVVGNPANTNC*LTASK	C137;C92;C155; C155	0.808876006	P40925 C9JRL4 C9JF79 P40925	
NHLLPDIIVTC*VQSSR	C184	0.808491113	Q9BSD7	
SLITSDKGFVMTLESLEEIQD VSC*AWK	C603	0.808210335	Q9BQ39	
YSLADQTSQDQSPLPPC*TPT PPCAEMR	C563	0.807522696	Q06124 Q06124	
NAGNC*LSPAVIVGLLK	C369;C335	0.804936855	O43175 Q5SZU1	
GMYGIENEVFLSLPC*ILNAR	C294	0.804228754	P07195	
VLLISGFVPVQC*K	C109;C109;C109; C105	0.80379	E9PKN8 F6TB26 Q9Y2W6 Q5SZR4	

SLLETNEIPSLILWGPPGC*GK	C272;C52;C272	0.803449459	Q96S55 Q96S55 Q96S55	Q96S55 ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 PE=1 SV=2 # Q96S55-3 Isoform 3 of ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 # Q96S55-2 Isoform 2 of ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 #
VLNEEC*DQNWYK	C32;C32;C32;C3 2	0.802974948	P62993 J3KT38 P62993 J3QRL5	P62993 Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1 # J3KT38 Growth factor receptor-bound protein 2 (Fragment) OS=Homo sapiens GN=GRB2 PE=1 SV=7 # P62993-2 Isoform 2 of Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 # J3QRL5 Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1 #
GYWASLDASTQTTHELTIPNN LIGC*IIGR	C293	0.802388831	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # E9PJD7 Cysteine and histidine-rich protein 1 OS=Homo sapiens GN=CYHR1 PE=1 SV=1 # Q6ZMK1 Cysteine and histidine-rich protein 1 OS=Homo sapiens GN=CYHR1 PE=1 SV=2 # Q6ZMK1-2 Isoform 2 of Cysteine and histidine-rich protein 1 OS=Homo sapiens GN=CYHR1 #
ISPVYHFVFTNESNETDYVPL PIIDSV*EK	C384;C342;C25 4	0.801760089	E9PJD7 Q6ZMK1 Q6ZMK1	Q9BQ67 Glutamate-rich WD repeat-containing protein 1 OS=Homo sapiens GN=GRWD1 PE=1 SV=1 # Q9BSH4 Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1 #
TC*ETGEPMEAESGDTSSSEG PAQVYLPGR	C11	0.800799313	Q9BQ67	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
LDSLGLCSVSC*ALEFIPNSK	C256	0.800753896	Q9BSH4	Q15646-2 Isoform p30 of 2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL # H0YGP3 2'-5'-oligoadenylate synthase-like protein (Fragment) OS=Homo sapiens GN=OASL PE=1 SV=1 # Q15646 2'- 5'-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL PE=1 SV=2 # Q15646-3 Isoform 3 of 2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL #
STLTDSLVC*K	C41	0.799809718	P13639	
IWC*FGPDGTGPNILTDITK	C651	0.799625009	P13639	
ACGGPGNFC*PSFSELQR	C188;C86;C188; C188	0.799549426	Q15646 H0YGP3 Q15646 Q15646	

				Q04206-4 Isoform 4 of Transcription factor p65 OS=Homo sapiens GN=RELA # A0A087WVP0 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=1 # A0A087X0W8 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=1 # E9PI38 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # Q2TAM5 RELA protein OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=2 # Q04206-3 Isoform 3 of Transcription factor p65 OS=Homo sapiens GN=RELA # E9PNV4 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=1 # E9PJR1 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=7 # E9PRX2 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # Q04206-2 Isoform 2 of Transcription factor p65 OS=Homo sapiens GN=RELA # E9PKH5 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # E9PQS6 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # E9PMD5 Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=1 SV=1 # E9PKV4 Transcription factor p65 OS=Homo sapiens GN=RELA PE=1 SV=1 # Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 # Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-3 Isoform APCR-3 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-2 Isoform APCR-1 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ #
DGFYEAEELC*PDR	C105;C105;C105;C74;C105;C105;C74;C92;C116;C96;C105;C105	0.799113675	Q04206 A0A087WVP0 VPO A0A087X0W8 E9PI38 Q2TAM5 Q04206 Q04206 E9PNV4 E9PJR1 E9PRX2 Q04206 E9PKH5 E9PQS6 E9PMD5 E9PKV4	
IIQFQATPC*PK	C300;C313;C298;C224;C299;C278;C238	0.798854441	Q06330 Q06330 Q06330 Q06330 Q06330 Q06330 Q06330	

					H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
LC*EPEVLNSLEETYSPPFR	C177;C261;C261;C106;C224;C261;C261;C227;C261;C261;C242	0.798747637		H0YJA2 Q6PJT7 Q6PJT7 G3V5I6 Q6PJT7 G3V256 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7	OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #
VQAQYPGVC*INNEVPEPSAE QIAK	C82	0.798498239	P50135	P50135 Histamine N-methyltransferase OS=Homo sapiens GN=HNMT PE=1 SV=1 #	
GSENEDLWAESEGTVAC*LG AEDR	C220	0.79768	Q92968	Q92968 Peroxisomal membrane protein PEX13 OS=Homo sapiens GN=PEX13 PE=1 SV=2 #	
VIEINPYLLGTMAGGAADC*S FWER	C111;C111;C60	0.797148008	P28074 P28074 H0YJM8	P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 # P28074-2 Isoform 2 of Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 # H0YJM8 Proteasome subunit beta type-5 (Fragment) OS=Homo sapiens GN=PSMB5 PE=1 SV=1 #	
HDDSSDNFC*EADDIQSPEAE YVDLLLNP	C166	0.796671825	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #	
PMC*IPPSYADLGK	C13;C13	0.795024829	A0A0A0MR02 P45880	Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 # A0A0A0MSX9 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # P41252 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 # J3KR24 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 #	
C*SGVMEFSTSGHAYTDTGK	C36	0.794915592	Q9Y277	Q99714-2 Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 # Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 #	
VMPFSTAC*NTPLSNFESHQ NYK	C185;C185;C75	0.7942	A0A0A0MSX9 P41252 J3KR24	P05141 ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 # Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #	
VC*NFLASQVPPFSR	C205;C214	0.794059494	Q99714 Q99714		
YFAGNLASGGAAGATSLC*FV YPLDFAR	C129	0.79390028	P05141		
VC*NYGLTFTQK	C65	0.793299223	Q9Y277		

DMEYFFGENWEEQVQC*PK	C127;M84 C181;M113 C98	0.793153119	A0A087W T44 P30519 P30519	A0A087WT44 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=1 # P30519 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2 # P30519-2 Isoform 2 of Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 #
VMQPQILEVNFNPDC*ER	C612	0.790906459	Q14166	Q14166 Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2 #
LVATDGAFSMDGDIAPLQEIC C*LASR	C245;C219	0.790553333	O75600 O75600	O75600-2 Isoform 2 of 2-amino-3-ketobutyrate coenzyme A ligase# mitochondrial OS=Homo sapiens GN=GCAT # O75600 2-amino-3-ketobutyrate coenzyme A ligase# mitochondrial OS=Homo sapiens GN=GCAT PE=1 SV=1 #
MAYQEYPNSQNWPEDTNFC* FQPEQVVDPIQTDPFK	C126;C126;C14 3;C126	0.790281442	P27816 P27816 E7EVA0 P27816	P27816-2 Isoform 2 of Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 # P27816-6 Isoform 6 of Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 # E7EVA0 Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1 # P27816 Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 # Q9Y2R4 Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3 #
SVANVIQQAGC*PVPEYIK	C536	0.78882041	Q9Y2R4	A0A087X028 Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=1 # A0A0A0MRN5 Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=1 # Q9NZT2 Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3 # Q9NZT2-2 Isoform 2 of Opioid growth factor receptor OS=Homo sapiens GN=OGFR #
DC*NGDTPNLSFYR	C87;C35;C87;C8 7	0.788075663	A0A087X0 28 A0A0A0M RN5 Q9NZT2 Q9NZT2	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 # Q9BSJ8-2 Isoform 2 of Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 # Q9BSJ8 Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 # Q5QPM7 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 # Q92530 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 # Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 #
GSEDLFSTC*VTNGPFIMSSN SASAANGNDSKK	C23	0.787520239	P26599	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 #
ILYLDSSSEICFPTVPGC*PGA WDVDSENPQR	C621;C611	0.78742367	Q9BSJ8 Q9BSJ8	P31946-2 Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB # P31946 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 #
QPPWC*DPLGPFVVGGEDLD PFGPR	C185;C185	0.787177773	Q5QPM7 Q92530	P84090 Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1 # P84090 Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1 # E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
VQEAPIDEHWIIEC*NDGVFQ R	C91	0.786954181	Q14353	Q5VSL9-2 Isoform 2 of Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 # Q5VSL9 Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 PE=1 SV=1 #
LNLPINIIGLAPLC*ENMPGSK	C335;C304	0.7869	P28838 P28838	
EKIEAELQDIC*NDVLELLDK	C94;C96	0.786284607	P31946 P31946	
TYADYESVNEC*MEGVCK	C28	0.78609	P84090	
TYADYESVNECMEGVC*K	C33	0.78609	P84090	
AC*GNFGIPCELR	C288;C288	0.78574	E9PBS1 P22234	
AHSNPDFLPVDNC*LQSVLG QR	C703;C798	0.785261054	Q5VSL9 Q5VSL9	



QALVEFEDVLGAC*NAVNYAA DNQIYIAGHPAFVNYSTSQK	C92;C151	0.785053571	M0QXS5 P14866	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
DHQPC*IIFMDEIDAIGGRR	C242;C228	0.784307789	A0A087X2 I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
SC*LDYQTQETK	C110;C110	0.783927351	E7EMD6 O43572	E7EMD6 A-kinase anchor protein 10# mitochondrial OS=Homo sapiens GN=AKAP10 PE=1 SV=3 # O43572 A-kinase anchor protein 10# mitochondrial OS=Homo sapiens GN=AKAP10 PE=1 SV=2 #
IDPENAEFLTALC*ELR	C476;C428	0.783826359	Q13325 Q13325	Q13325 Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 PE=1 SV=1 # Q13325-2 Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 #
LDINLLDNVNC*LYHGEGAQ QR	C34	0.78343482	O14980	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 #
ATDYPC*LLILDQNEFETLR	C145	0.782922308	Q9NVG8	Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
PMC*VESFSDYPLGR	C411;C411;C39 0	0.782841838	Q5VTE0 P68104 P68104	Q5VTE0 Putative elongation factor 1-alpha- like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 # P68104 Elongation factor 1- alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
ENFDEVVNDADIILVEFYAPW C*GHCKK	C206	0.782628506	P13667	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 #
AGAVVAVPTDTLYGLACAAS C*SAALR	C99	0.781885594	Q86U90	Q86U90 YrdC domain-containing protein# mitochondrial OS=Homo sapiens GN=YRDC PE=1 SV=1 #
LQEALDAEMLEDEAGGGGA GPGGAC*K	C57;C57	0.781730813	H3BQZ7 Q1KMD3	H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #
NNAFPC*QVNIK	C675;C712	0.781442349	Q9NQW6 Q9NQW6	Q9NQW6-2 Isoform 2 of Actin-binding protein anillin OS=Homo sapiens GN=ANLN # Q9NQW6 Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2 # P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB #
QMEKDETVSDC*SPHIANIGR	C206;C206;C23 5;C194;C232	0.780278375	P47756 P47756 B1AK88 B1AK87 B1AK85	B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
AFQYVETHGEVC*PANWTPD SPTIKPSAASK	C229;C211	0.779883118	P30048 P30048	P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 # P30048-2 Isoform 2 of Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 #

SEFYANEAC*K	C339;C339;C381;C401	0.778145273	Q86TX2 A0A087X0W7 A0A087WT95 P49753	Q86TX2 Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 # A0A087X0W7 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # A0A087WT95 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # P49753 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 # Q06124 Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 # Q06124 Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2 #
QGFWEFETLQQQEC*K	C259;C259	0.778074181	Q06124 Q06124	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B # Q12982-2 Isoform 2 of BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 # Q12982 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # H7C096 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 (Fragment) OS=Homo sapiens GN=BNIP2 PE=1 SV=1 # J3KN59 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 #
SLC*NLEESITSAGRDDLESF QLEISGFLK	C63;C63	0.777592066	Q52LJ0 Q52LJ0	H3BVG0 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=1 # Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 # Q8N1F7-2 Isoform 2 of Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 #
YVFNLAELAEVPMYVGIPE C*IK	C416 C295;M165 C357;M287 C173;M408	0.777468761	Q12982 Q12982 H7C096 J3KN59	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # O75821 Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2 # P01130-2 Isoform 2 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130 Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR PE=1 SV=1 # J3KMZ9 Low-density lipoprotein receptor (Fragment) OS=Homo sapiens GN=LDLR PE=1 SV=1 # P01130-6 Isoform 6 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130-5 Isoform 5 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130-4 Isoform 4 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130-3 Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR #
LNQVC*FDDDGTSPPQDRLT LSQFQK	C422;C422;C299	0.775502798	H3BVG0 Q8N1F7 Q8N1F7	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
ISSINSISALC*EATGADVEEV ATAIGMDQR	C241	0.774327145	O60701	
EDLNC*QEEEDPMNK	C139	0.774250048	O75821	
IGYEC*LCPDGFQLVAQR	C211;C338;C423;C217;C338;C297;C170	0.773940744	P01130 J3KMZ9 P01130 P01130 P01130	
LVPASQC*GSLIGK	C109;C109;C109;C109	0.773935	Q15366 Q15366 Q15366 Q15366	

NC*LTNFHGM DLTR	C59;C59;C96;C7 6	0.773797954	D6RB09 D6RAT0 P61247 D6RG13	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 # P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 #
IPDIVLWPTC*HDDVVK	C214	0.772996874	O00116	O00116 Alkyldihydroxyacetonephosphate synthase# peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1 #
ICPVETLVEEAIQC*AEK	C225	0.772644158	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 # Q9H4L5-3 Isoform 1c of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 # Q9H4L5 Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1 #
TCLPAPC*PSSSNISLWNILR	C484;C520	0.772085	Q9H4L5 Q9H4L5	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 # Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP #
VNDILELYGILSVDPVLSILNN DERDASALLDPMEC*TDTAEE QR	C287 C287;M285	0.771713457	Q9BTE3 Q9BTE3	Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1- phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 #
LC*SGPGIVGNVLDPSAR	C245;C245	0.770676052	Q9Y5P6 Q9Y5P6	Q9Y4R8 Telomere length regulation protein TEL2 homolog OS=Homo sapiens GN=TELO2 PE=1 SV=2 #
MDILDVLTAAQELSRPGC*L GR	C628	0.770454949	Q9Y4R8	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
AFAFVTFADDQIAQSLC*GED LIIK	C244;C244;C24 4;C244;C244	0.770444454	A0A087X2 60 A0A087W YY0 B1AKP7 Q13148 G3V162	Q86Y37 CDK2-associated and cullin domain- containing protein 1 OS=Homo sapiens GN=CACUL1 PE=1 SV=1 #
AGDELAYNSSSAC*ASSR	C362	0.769677676	Q86Y37	Q2TAA2 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 #
VILITPTPLC*ETAWEEQCIIQG CK	C137	0.768816977	Q2TAA2	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
VDLNSNGFIC*DYELHELFK	C33	0.768444602	P13797	

					P01892 HLA class I histocompatibility antigen# A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # A0A0G2JH50 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P10314 HLA class I histocompatibility antigen# A-32 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=2 # A0A140T913 HLA class I histocompatibility antigen# A-3 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # P30505 HLA class I histocompatibility antigen# Cw-8 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # A0A140T9J9 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q29963 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # P30459 HLA class I histocompatibility antigen# A-74 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # Q9GJ45 HLA class I histocompatibility antigen# A-3 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # A0A140T912 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q07000 HLA class I histocompatibility antigen# Cw-15 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P30508 HLA class I histocompatibility antigen# Cw-12 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # Q29960 HLA class I histocompatibility antigen# Cw-16 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # A0A140T9I0 HLA class I histocompatibility antigen# A-3 alpha chain (Fragment) OS=Homo sapiens GN=HLA-A PE=1 SV=1 # Q29960-2 Isoform 2 of HLA class I histocompatibility antigen# Cw-16 alpha chain OS=Homo sapiens GN=HLA-C # A0A140T975 HLA class I histocompatibility antigen# A-3 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 # Q9TNN7 HLA class I histocompatibility antigen# Cw-5 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # A0A140T9X5 HLA class I histocompatibility antigen# A-3 alpha chain (Fragment) OS=Homo sapiens GN=HLA-A PE=1 SV=1 # F1T0I1 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 # J3KNL6 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 # Q9UJU6-5 Isoform 5 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6-3 Isoform 3 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6-2 Isoform 2 of Drebrin-like protein OS=Homo sapiens GN=DBNL # Q9UJU6 Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 # Q9UJU6-4 Isoform 4 of Drebrin-like protein OS=Homo sapiens GN=DBNL # H0Y5J4 Drebrin-like protein (Fragment) OS=Homo sapiens GN=DBNL PE=1 SV=1 # B4DDD6 Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 # P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
AYLEGTG*VEWLR	C188;C188;C188;C188;C188;C188;C188;C188;C188;C188	0.767813241		P01892 A0A0G2JH50 P10314 A0A140T913 P30505 A0A140T9J9 Q29963 P30459 Q9GJ45 A0A140T912 Q07000 P30508 Q29960 A0A140T9I0 Q29960 A0A140T975 Q9TNN7 A0A140T9X5	
DSSQGPC*EPLPGPLTQPR	C107;C107	0.765845		F1T0I1 J3KNL6	
AEEEDVEPEC*IMEK	C24	0.764856016		Q9UJU6 Q9UJU6 Q9UJU6 Q9UJU6 H0Y5J4 B4DDD6	
THEAEIVEGENHTYC*IR	C2191;C2172;C2199	0.764532076		P21333 Q60FE5 P21333	

LC*WFLDEAAAR	C237	0.763927395	O95336	O95336 6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2 #
TDIQCLIPC*AIDQDPYFR	C309;C268	0.763450906	P23381 P23381	P23381 Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 # P23381-2 Isoform 2 of Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS #
LAFEIIDQYFSGDDIDEDPC*LI PEATQGGTYNFDPTANLQTK DC*IGGCSDLVSLQQSGELLT R	C495 C79	0.763158854 0.760967849	O00505 P35754	O00505 Importin subunit alpha-4 OS=Homo sapiens GN=KPNA3 PE=1 SV=2 # P35754 Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2 #
GTWEELCNSC*EMENEVLK	C652	0.75901487	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 # Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 # Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 #
TVEIC*PFSFDSR	C572;C536	0.758534069	Q9ULW0 Q9ULW0	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 # Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP # Q9Y3F4 Serine- threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 #
LGGSLIVAFEGC*PV	C146;C163	0.758275967	P60981 P60981	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # Q9H078-2 Isoform 2 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # H0YGM0 Caseinolytic peptidase B protein homolog (Fragment) OS=Homo sapiens GN=CLPB PE=1 SV=1 # P61077-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # H9KV45 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 # D6RAH7 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # A0A0A0MQU3 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # D6RFM0 Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=3 SV=1 # A0A087WY85 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # H0YAG8 Alcohol dehydrogenase class-3 (Fragment) OS=Homo sapiens GN=ADH5 PE=1 SV=1 # P11766 Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 # Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
IGFPETEEEELEEIASENSDC*I FPSAPDVK	C353;C340	0.758172366	Q9Y3F4 Q9Y3F4	
GIFPVLK*KDPVQEAWAEDVD LR	C474	0.75624494	P14618	
INEIVYFLPFC*HSELIQLVNK	C542;C577	0.754521615	Q9H078 H0YGM0	
VLLSICSLLC*DPNPDDPLVPE IAR	C113;C111;C111 1;C105;C82;C82 ;C111;C82;C112 ;C111	0.753435453	P61077 P61077 P61077 H9KV45 P62837 D6RAH7 A0A0A0M QU3 D6RFM0 A0A087W Y85 P62837	
VCLLGC*GISTGYGAAVNTAK	C161;C174	0.752186699	H0YAG8 P11766	
LEGDLTGPSVDVEVPDVELE C*PDAK	C2162	0.751811173	Q09666	

LESLQSMEMAHSGSLRDEL C*LDFPCDSPEK	C259;C386;C388; C389;C183;C321; C394;C270	0.751605222	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	B7Z4D2 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-4 Isoform 4 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95-3 Isoform 3 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=2 # B3KRD1 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-2 Isoform 2 of Syntabulin OS=Homo sapiens GN=SYBU # A0A0C4DG86 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-5 Isoform 5 of Syntabulin OS=Homo sapiens GN=SYBU #
ADC*TITMADSDFLALMTGK	C495	0.751602114	P22307	P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 # P49915 GMP synthase [glutamine- hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 # P49915-2 Isoform 2 of GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS #
VICAEOPYIC*K	C456;C357	0.751287168	P49915 P49915	Q9NVG8-2 Isoform 2 of TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 # Q9NVG8 TBC1 domain family member 13 OS=Homo sapiens GN=TBC1D13 PE=1 SV=3 #
LLQDYPITDVC*QILQK	C262;C387	0.750679566	Q9NVG8 Q9NVG8	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
GLYGIKDDVFLSVPC*ILGQN GISDLVK	C322;C293	0.750446121	P00338 P00338	Q92974-3 Isoform 3 of Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 # Q92974-2 Isoform 2 of Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 # Q92974 Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=4 # V9GYM8 Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=1 #
TGMLEELHLEPGVVQGLFPC* VDELSDIHTR	C254;C281;C282; C327	0.749595	Q92974 Q92974 Q92974 V9GYM8	H9KVA9 Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=2 # P46736 Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=2 # P46736-3 Isoform 3 of Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 # P46736-2 Isoform 1 of Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 # P46736-5 Isoform 5 of Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 # P46736-4 Isoform 4 of Lys-63- specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 # A0A0D9SF50 Lys-63- specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=1 # A0A087WZR3 Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=1 #
NLC*SQMSAVSGPLLQWLED R	C274;C273;C249; C248;C204;C159; C274;C250	0.74832	H9KVA9 P46736 P46736 P46736 P46736 A0A0D9S F50 A0A087W ZR3	

SLLINEVEASC*IR	C261;C231;C262;C262;C289;C232;C262	0.747834458	A0A087WZR9 ZR9 E2QRB3 P32322 P32322 P32322 J3QKT4 Q96C36	A0A087WZR9 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCR2 PE=1 SV=1 # E2QRB3 Pyrroline-5-carboxylate reductase 1# isoform CRA_c OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322 Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # J3QKT4 Pyrroline-5-carboxylate reductase (Fragment) OS=Homo sapiens GN=PYCR1 PE=1 SV=1 # Q96C36 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 # P46934-4 Isoform 4 of E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 # P46934 E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 PE=1 SV=4 # H0Y8X6 E3 ubiquitin-protein ligase NEDD4 (Fragment) OS=Homo sapiens GN=NEDD4 PE=1 SV=1 #
VDEFPLC*GHMVSDEYEQLS SEALEAAR	C49	0.745624482	P27635	P46934-4 Isoform 4 of E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 # P46934 E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 PE=1 SV=4 # H0Y8X6 E3 ubiquitin-protein ligase NEDD4 (Fragment) OS=Homo sapiens GN=NEDD4 PE=1 SV=1 #
TSGSEDDNAEQAELEPGW VVLDQPDAAC*HLQQQQEPL PLPPGWEER	C182;C601;C192	0.745542472	P46934 P46934 H0Y8X6	P46934-4 Isoform 4 of E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 # P46934 E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 PE=1 SV=4 # H0Y8X6 E3 ubiquitin-protein ligase NEDD4 (Fragment) OS=Homo sapiens GN=NEDD4 PE=1 SV=1 #
DTC*SYVNVEDVSGAISHLSL GEIPAMAQPFVSSEER	C271	0.744905	P46976	P46976-2 Isoform GN-1 of Glycogenin-1 OS=Homo sapiens GN=GYG1 #
WLLLC*NPGLADTIVEK	C496	0.743562478	P11216	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 #
VC*EDLDTSVNLAWTSGTNC TR	C210;C210	0.74250656	A0A0A0MR02 R02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
GLC*ESVVEADLVEALEK	C84;C79;C79;C84;C84;C84	0.741850891	Q8WVV9 Q8WVV9 C9IYN3 D6W592 Q8WVV9 B7WPG3	Q8WVV9-5 Isoform 5 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # Q8WVV9-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL # C9IYN3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=2 # D6W592 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # Q8WVV9 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 # B7WPG3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 #

				A0A0G2JH50 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P30505 HLA class I histocompatibility antigen# Cw-8 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q95604 HLA class I histocompatibility antigen# Cw-17 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # A0A140T9J9 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q29963 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # A0A140T912 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P30508 HLA class I histocompatibility antigen# Cw-12 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # Q07000 HLA class I histocompatibility antigen# Cw-15 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q29960 HLA class I histocompatibility antigen# Cw-16 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # Q29865 HLA class I histocompatibility antigen# Cw-18 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P04222 HLA class I histocompatibility antigen# Cw-3 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # Q29960-2 Isoform 2 of HLA class I histocompatibility antigen# Cw-16 alpha chain OS=Homo sapiens GN=HLA-C # A0A140T9M0 HLA class I histocompatibility antigen# Cw-6 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P30510 HLA class I histocompatibility antigen# Cw-14 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 # Q9TNN7 HLA class I histocompatibility antigen# Cw-5 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # P30504 HLA class I histocompatibility antigen# Cw-4 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 # C9J8E1 MAP kinase-activated protein kinase 3 (Fragment) OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 # Q16644 MAP kinase-activated protein kinase 3 OS=Homo sapiens GN=MAPKAPK3 PE=1 SV=1 # P11586 C-1-tetrahydrofolate synthase# cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 # F5H2F4 C-1-tetrahydrofolate synthase# cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=1 # X6RA14 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=1 # P10768 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 # E9PJE4 COMM domain-containing protein 5 (Fragment) OS=Homo sapiens GN=COMMMD5 PE=1 SV=1 # H0YEQ6 COMM domain-containing protein 5 (Fragment) OS=Homo sapiens GN=COMMMD5 PE=1 SV=1 # Q9GZQ3 COMM domain-containing protein 5 OS=Homo sapiens GN=COMMMD5 PE=1 SV=1 #
GGSC*SQAASSNSAQGSDES LIACKA	C351;C345;C351; C345;C345;C345; C305;C351;C345; C345	0.741619648	A0A0G2JH50 H50 P30505 Q95604 A0A140T9J9 Q29963 A0A140T912 P30508 Q07000 Q29960 Q29865 P04222 Q29960 A0A140T9M0 P30510 Q9TNN7 P30504	
KETTQNALQTPC*YTPYYVAP EVLGPEK	C203;C203	0.740829711	C9J8E1 Q16644	
GDLNDCFIPC*TPK	C147;C203	0.739707498	P11586 F5H2F4	
CPALYWLSGLTC*TEQNFISK	C27;C56	0.738657082	X6RA14 P10768	
DQLQELC*IPQDLVGLASVV FGSQRPLLDVAQQGAWL PHVADFR	C117;C63;C117	0.73771	E9PJE4 H0YEQ6 Q9GZQ3	



QQYLC*QPLLDVLANIR	C507;C578;C618;C552	0.736672103	Q96RN5 Q96RN5 Q96RN5 G3V1P5	Q96RN5-3 Isoform 3 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 # Q96RN5-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 # Q96RN5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=2 # G3V1P5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=1 #
THC*LALQEALGPGPGPTGD DDYSR	C323;C287;C347	0.736075926	Q8N490 Q8N490 Q8N490	Q8N490-3 Isoform 3 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490-4 Isoform 4 of Probable hydrolase PNKD OS=Homo sapiens GN=PNKD # Q8N490 Probable hydrolase PNKD OS=Homo sapiens GN=PNKD PE=1 SV=2 #
IGTSGGIGLEPGTVVITEQAV DTC*FK	C162	0.735967022	Q16831	Q16831 Uridine phosphorylase 1 OS=Homo sapiens GN=UPP1 PE=1 SV=1 #
GPQLFHMDPSGTFVQC*DAR	C165;C107	0.735535	P28066 P28066	P28066 Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 # P28066-2 Isoform 2 of Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 #
C*FIVGADNVGSK	C27;C27;C27;C13;C27;C27;C27;C27	0.73525	F8VWS0 P05388 F8VU65 F8VPE8 G3V210 F8VRK7 P05388 F8VQY6	F8VWS0 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # F8VU65 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # F8VPE8 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # G3V210 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # F8VRK7 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 # P05388-2 Isoform 2 of 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 # F8VQY6 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #
GSLQLFPC*AKYQMVQDGAA AELLVR	C4021	0.732294687	Q5VST9 Q5VST9 H3BPX2 Q5VST9 Q5VST9 A6NGQ3	Q5VST9-2 Isoform 2 of Obscurin OS=Homo sapiens GN=OBSCN # Q5VST9-3 Isoform 3 of Obscurin OS=Homo sapiens GN=OBSCN # H3BPX2 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=2 # Q5VST9 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3 # Q5VST9-6 Isoform 5 of Obscurin OS=Homo sapiens GN=OBSCN # A6NGQ3 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=4 #
DQELYFFHELSPGSC*FFLPK	C343;C376	0.731866108	P26639 P26639	P26639 Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 # P26639-2 Isoform 2 of Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS #
SGGLQTPEC*LSR	C439	0.731414997	P85037	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 #
VDDEILGFISEATPLGGIQAAS TESC*NQQLDLALCR	C561	0.731171379	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
AHEILPNLVC*CSAK	C148	0.730219441	P50990	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
ERESLNASIVDAINQAADC*W GIR	C121;C167	0.729870188	A0A087WYB4 YB4 Q9UJZ1	A0A087WYB4 Stomatatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 # Q9UJZ1 Stomatatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 #

YGDLDSSLISFGPC*QTPTLG FCVER	C217;C217;C217; 7;C217	0.729115	O95985 O95985 O95985 C9JEI7	O95985-3 Isoform 3 of DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B # O95985 DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B PE=1 SV=1 # O95985-2 Isoform 2 of DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B # C9JEI7 DNA topoisomerase (Fragment) OS=Homo sapiens GN=TOP3B PE=1 SV=1 # E9PBC6 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E7EMZ9 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3 # O95359-3 Isoform 3 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 #
MSEPTPC*SGSSFEETEALV NTAAK	C2577;C2528;C 2573;C2573	0.728484113	E9PBC6 E7EMZ9 O95359 O95359	Q96JB2-2 Isoform 2 of Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 # Q96JB2 Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3 # Q86W42 THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1 # Q86W42-2 Isoform 2 of THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 # O00743 Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1 # O00743-3 Isoform 3 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C # O00743-2 Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C # Q15084-2 Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-4 Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-5 Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 # Q15084-3 Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 #
AAAENLPVPAELPIEDLC*SLT SQSLPIELTSVVPSTEDILLK	C65;C65	0.727812516	Q96JB2 Q96JB2	
AQVPGSSPGLLSLSLNQPPA APEC*K	C314;C290	0.727084259	Q86W42 Q86W42	
GAFC*DLVWSDPEDVDTWAI SPR	C192;C229;C17 0	0.726768974	O00743 O00743 O00743	
IELTPSNFNREVIQSDSLWLV EFYAPWC*GHCQR	C107;C60;C103; C55;C52	0.725946316	Q15084 Q15084 Q15084 Q15084 Q15084	
EAESC*DCLQGFQLTH	C127;C127;C10 9	0.725886745	P68371 P04350 Q5JP53	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
VFIMDSC*DELIPEYLNFR	C366	0.725451294	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
LLQC*DPSSASQF	C185	0.725293323	P37235	P37235 Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3 # Q7Z2W4-2 Isoform 2 of Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 # C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
MALDALLQEIALSEPQLC*EVL QVAGPDR	C38;M21 C38	0.72354648	Q7Z2W4 C9J6P4 Q7Z2W4	
NMIENSMFEEEPDVVDLAKE PC*LHPLEPDEVEYEPR	C35	0.723526667	Q9UIQ6	Q9UIQ6 Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP PE=1 SV=3 #

GYDAPLC*NLLLFK	C420;C379	0.72243993	O60488 O60488	O60488 Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2 # O60488-2 Isoform Short of Long-chain-fatty- acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 #
DSGLFC*VPLTALLEQDQR	C278;C323	0.721925577	Q8N392 Q8N392	Q8N392-2 Isoform 2 of Rho GTPase- activating protein 18 OS=Homo sapiens GN=ARHGAP18 # Q8N392 Rho GTPase- activating protein 18 OS=Homo sapiens GN=ARHGAP18 PE=1 SV=3 #
FALNHPELVEGLVLINVDPC*A K	C166;C71;C77;C 154;C166	0.720967608	Q5TH30 F8WBF9 Q9UGV2 Q9UGV2 Q9UGV2	Q5TH30 NDRG family member 3# isoform CRA_c OS=Homo sapiens GN=NDRG3 PE=1 SV=1 # F8WBF9 Protein NDRG3 OS=Homo sapiens GN=NDRG3 PE=1 SV=1 # Q9UGV2- 3 Isoform 3 of Protein NDRG3 OS=Homo sapiens GN=NDRG3 # Q9UGV2-2 Isoform 2 of Protein NDRG3 OS=Homo sapiens GN=NDRG3 # Q9UGV2 Protein NDRG3 OS=Homo sapiens GN=NDRG3 PE=1 SV=2 #
INDALSC*EYECR	C216;C216	0.720779756	Q52LJ0 Q52LJ0	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #
WTQTLSELDAVPC*VNFR	C188	0.719887786	Q9Y266	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 #
RPLNPLASGQGTSEENTFY S WLEGLC*VEK	C241	0.719193314	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 #
SIQFVDWC*PTGFK	C347;C347	0.718932078	P68363 P68366	P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
DEFTNTC*PSDKEVEIAYSDV AK	C234	0.71875462	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
VSC*LGVTDDGMAVATGSWD SFLK	C317;C317	0.7185525	P62879 P62873	P62879 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 # P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 #
SLPSAVYC*IEDK	C674	0.717694446	O43290	O43290 U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 #
LCSLLDSEDYNTC*EGAFGAL QK	C153;C145	0.717391221	Q92973 Q92973	Q92973 Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 # Q92973-2 Isoform 2 of Transportin-1 OS=Homo sapiens GN=TNPO1 #
FLENTPSSLNIEDLFLSLAQ YYC*SK	C283;C146;C28 3	0.716014376	Q9NUY8 E9PGE5 Q9NUY8	Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 # E9PGE5 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=1 # Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 #
VLFPGCTPPAC*LLDGLVR	C414;C440	0.715757987	Q66K74 Q66K74	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 # E9PKU4 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 #
AQLNIGNVLPVGTMPGIVC *CLEEKPGDR	C114;M107 C114	0.715080992	E9PKU4 E9PKZ0 G3V1A1 P62917	E9PKZ0 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 # G3V1A1 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=1 # P62917 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 #
LISP NLGVVFFNAC*EAASR	C316;C342	0.714549978	Q66K74 Q66K74	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 #

FGVIC*LEDLIEHIAFP GK	C184	0.712016656	Q6DKI1	Q6DKI1 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 #
VPAFEGDDGFC*VFESNAIAY YVSNEELR	C68;C118	0.711870911	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
EFC*SYLQYLEYLSQNRPPPN AYELFAK	C278	0.711653655	O14744	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 #
NENC*TLQFEAAWALTNIASG TSQQT K	C139	0.711421792	O60684	O60684 Importin subunit alpha-7 OS=Homo sapiens GN=KPNA6 PE=1 SV=1 #
LIC*CDILDVLDKHLIPAANTGE SK	C97	0.711312461	P62258	P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 #
EKFTTPIEETGGEGC*PAVALI Q	C87;C122;C73	0.71047	Q9NP84 Q9NP84 I3L1J9	Q9NP84-2 Isoform 2 of Tumor necrosis factor receptor superfamily member 12A OS=Homo sapiens GN=TNFRSF12A # Q9NP84 Tumor necrosis factor receptor superfamily member 12A OS=Homo sapiens GN=TNFRSF12A PE=1 SV=1 # I3L1J9 Tumor necrosis factor receptor superfamily member 12A OS=Homo sapiens GN=TNFRSF12A PE=1 SV=1 #
VVMALGDYMGASC*HACIGG TNVR	C131	0.710145	P60842	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
LC*PGGQLPFLLYGTEVHTDT NK	C59	0.70951964	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
DSGYGDIWC*PER	C137;C213;C17 6;C228;C228;C2 28;C228;C176	0.708967227	E9PMS6 J3KP06 F8WD26 Q8WWI1 Q8WWI1 Q8WWI1 Q8WWI1 E9PMP7	E9PMS6 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=1 # J3KP06 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 # F8WD26 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 # Q8WWI1-4 Isoform 4 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # Q8WWI1 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 # Q8WWI1-3 Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # Q8WWI1-2 Isoform 2 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # E9PMP7 LIM domain only protein 7 (Fragment) OS=Homo sapiens GN=LMO7 PE=1 SV=7 #
AAPAQSPAAPDPEASPLAEP PQEQLAPWSPQTPAPPC*S R	C100	0.70887324	P83111	P83111 Serine beta-lactamase-like protein LACTB# mitochondrial OS=Homo sapiens GN=LACTB PE=1 SV=2 #
DLGPTLLVHGVTPTVC*TDL	C911	0.708287304	Q9BXP2	Q9BXP2 Solute carrier family 12 member 9 OS=Homo sapiens GN=SLC12A9 PE=1 SV=1 #
WNTDNTLGTEIAIEDQIC*QGL K	C103;C103	0.708098058	A0A0A0M R02 P45880	A0A0A0MR02 Voltage-dependent anion- selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #
NDAPEEAGEGC*VAAILGETE VQQFLR	C57;C57	0.707162885	Q96DC7 Q96DC7	Q96DC7 Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 PE=1 SV=2 # Q96DC7-2 Isoform 2 of Transmembrane and coiled-coil domain-containing protein 6 OS=Homo sapiens GN=TMCO6 #
NESC*SENYTTDFIYQLYSEE GK	C641	0.705913293	Q01813	Q01813 ATP-dependent 6- phosphofruktokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 #

MSDSADKPIDNDAEGVWSPD IEQSFQEALAIYPPC*GR	C144;C53;C53;C 38;C53	0.70579873	H0YJCZ6 H0YEJ9 P28347 P28347 H0YE88	H0YJCZ6 Transcriptional enhancer factor TEF-1 (Fragment) OS=Homo sapiens GN=TEAD1 PE=1 SV=2 # H0YEJ9 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=1 # P28347 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=2 # P28347-2 Isoform 2 of Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 # H0YE88 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=1 #
ICELLPEAAINDVYLAPLLQC* LIEGLSAEPR	C455	0.705770069	Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 #
KLDTNSDGLDFSEFLNLIGG LAMAC*HDSFLK	C91	0.703309091	P31949	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 #
ENPDLAC*LQSIIFDEERSPEE QAK	C63	0.703073926	O95801	O95801 Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 #
SVVC*QESDLPDELLYGR	C187	0.702711447	Q9NS86	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 #
C*SEGSFLLTTFPRPVTVEPM DQLDDEEGLPEK	C208	0.70241495	Q15233	Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 #
FFACAPNYSYAALCEC*LR	C513;C484	0.702124215	Q96RS6 Q96RS6	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 # Q96RS6-2 Isoform 2 of NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 #
HEEFCVPMVMVPATVSNNVP GSDFSIGADTALNTITDTC*DR	C563	0.702024669	Q01813	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFBK PE=1 SV=2 #
VVETSALLC*TAQHLLAAVQSS GAPATASGPQVDNTGGPEA WDSPLRR	C150	0.701342177	Q9H6W3	Q9H6W3 Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 OS=Homo sapiens GN=NO66 PE=1 SV=2 #
NLSFFLTPPC*AR	C492;C492;C49 4	0.701263808	P42224 P42224 J3KPM9	P42224 Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 # P42224 Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 # J3KPM9 Signal transducer and activator of transcription OS=Homo sapiens GN=STAT1 PE=1 SV=1 #
FQSSAVMALQEASEAYLVGL FEDTNLC*A	C111	0.701247701	Q71DI3	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 #
ELEAVC*QDVLSLLDNYLIK	C97	0.701243846	P61981	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 #
METYC*SSGSTDTSPVIDAVT HALTATTPYTR	C201 C288;M197	0.701241928	Q02338 E9PCG9	Q02338 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 # E9PCG9 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=1 #
VTEPSAPC*QALVSIGDLQAT FHGIR	C795	0.701233751	Q9UPN7	Q9UPN7 Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5 #
DAVFDGSSC*ISPTIVQQFGY QR	C27;C27	0.701044161	P04049 P04049	P04049-2 Isoform 2 of RAF proto-oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 # P04049 RAF proto-oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 PE=1 SV=1 #
QLC*EDWEVPEPVAR	C45;C45;C45	0.701015876	D6RCP9 P27707 D6RFG8	D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #
DIC*NDVLSLLEK	C94	0.700270963	P63104	P63104 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 #

YSESLLC*SNLESATYSNR	C222	0.699183625	Q15785	Q15785 Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2 #
NDQELISDPLQQC*FK	C86;C86;C86	0.698967719	H0YL91 H0YLN7 Q15650	H0YL91 Activating signal cointegrator 1 OS=Homo sapiens GN=TRIP4 PE=1 SV=1 # H0YLN7 Activating signal cointegrator 1 OS=Homo sapiens GN=TRIP4 PE=1 SV=1 # Q15650 Activating signal cointegrator 1 OS=Homo sapiens GN=TRIP4 PE=1 SV=4 #
SIAEQAHDELAYDPNYMSPFA QFAC*DNGLNVR	C278	0.698864	Q8NI37	Q8NI37 Protein phosphatase PTC7 homolog OS=Homo sapiens GN=PPTC7 PE=2 SV=1 #
EGGGGISCVLQDGC*VFEK	C198	0.698325	P36551	P36551 Oxygen-dependent coproporphyrinogen-III oxidase# mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 #
GDFYVIEYAAC*DATYNEIVTL ER	C109	0.697789663	P51116	P51116 Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 #
C*DENILWLDYK	C152	0.697747453	P14618	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
GPAVGIDLGTYSYC*VGVFQHGK	C17;C17;C17	0.697271715	P11142 P11142 E9PKE3	P11142 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 # P11142-2 Isoform 2 of Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 # E9PKE3 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 #
TDGEGEDPEC*LGEKG	C340	0.697122253	Q8WZA9	Q8WZA9 Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1 #
DFNEEC*PR	C178;C239;C270	0.697097488	Q13418 Q13418 A0A0A0MTH3	Q13418-2 Isoform 2 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK # Q13418 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 # A0A0A0MTH3 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1 #
ESAQCVGDEFLNC*K	C200	0.696912759	Q9Y5X2	Q9Y5X2 Sorting nexin-8 OS=Homo sapiens GN=SNX8 PE=1 SV=1 #
IGEGLDQALPC*LTELILTNN LVELGDLPLASLK	C89;C89	0.696302857	P09661 H0YKK0	P09661 U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 # H0YKK0 Small nuclear ribonucleoprotein polypeptide A' isoform CRA_a OS=Homo sapiens GN=SNRPA1 PE=1 SV=1 #
TYDPSGDSTLPTC*SK	C439	0.695753781	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #
GSQMGTVQPIPC*LLSMPTR	C531 C559;M523	0.693570494	Q9NZB2 Q9NZB2	Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A # Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 #
EEC*PVFTPPGGETLDQVK	C114;C55	0.69286245	Q9NQ88 A0A0U1RQD1	Q9NQ88 Fructose-2#6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 # A0A0U1RQD1 Chromosome 12 open reading frame 5# isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 #
TDPSEQVEGNC*EIVNELIAAS TQK	C612	0.692235839	Q8NEM2	Q8NEM2 SHC SH2 domain-binding protein 1 OS=Homo sapiens GN=SHCBP1 PE=1 SV=3 #
DVPLADPGLDNDVGVVEVGG GGC*LEER	C62	0.691108288	Q9NPA3	Q9NPA3 Mid1-interacting protein 1 OS=Homo sapiens GN=MID1IP1 PE=1 SV=1 #
GFTDADNTWEPEENLDC*PE LIEAFLNSQK	C69	0.689726682	Q13185	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 #

C*IPYAVLLEALALR	C110;C110;C110; C110;C110	0.688685	F5H248 Q9UBW8 F5H4U8 F5GYF7 F5H7C6	F5H248 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # Q9UBW8 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5H4U8 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5GYF7 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=7 # F5H7C6 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 # Q8IWZ3-6 Isoform 6 of Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 #
LTSSVSC*ALDEAAAALTR	C181	0.688617447	Q8IWZ3	Q8IWZ3-6 Isoform 6 of Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 #
KIDQSEFEGFEYINPLLSAE EC*V	C595	0.687857268	P41743	P41743 Protein kinase C iota type OS=Homo sapiens GN=PRKCI PE=1 SV=2 #
IEEDVVVTDSGIELLTC*VPR	C403;C467	0.687373182	P12955 P12955	P12955-3 Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
STAPVMDLLGLDAPVAC*SIA NSK	C116;C166;C191; C196	0.686613333	Q8WU79 Q8WU79 A0A087WV97 Q8WU79	Q8WU79-3 Isoform 3 of Stromal membrane-associated protein 2 OS=Homo sapiens GN=SMAP2 # Q8WU79-2 Isoform 2 of Stromal membrane-associated protein 2 OS=Homo sapiens GN=SMAP2 # A0A087WV97 Stromal membrane-associated protein 2 OS=Homo sapiens GN=SMAP2 PE=1 SV=1 # Q8WU79 Stromal membrane-associated protein 2 OS=Homo sapiens GN=SMAP2 PE=1 SV=1 #
QASLFPDEKEDNLLGTTCC*LIA TAVITLTFNEPSAEDSK	C651;C651	0.686605	Q01780 Q01780	Q01780-2 Isoform 2 of Exosome component 10 OS=Homo sapiens GN=EXOSC10 # Q01780 Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 #
VADSSPFALELLISDDCFVLD NGLC*GK	C275;C290	0.686107605	P40121 P40121	P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 #
C*PQDQGWNAEITLQMVQYK	C125	0.685897808	R4GND3 Q8WV24	R4GND3 Pleckstrin homology-like domain family A member 1 OS=Homo sapiens GN=PHLDA1 PE=1 SV=4 #
EITSLDTENIDEILNNADVALV NFYADWC*R	C58	0.685332003	Q9BS26	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 #
CDVTQSQPLGAVPLPPADC* VLSTLCLDAACPDLPTYCR	C159	0.685264426	P40261	P40261 Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 #
YASIC*QQNGIVPIVEPEILPD GDHDLKR	C178;C178;C232; C178	0.683557351	P04075 H3BQN4 P04075 P09972	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # H3BQN4 Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=1 SV=1 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA # P09972 Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 #

YMAC*CLLYR	C385;M313 C315 C315;M320 C282;M383 C322;M313 C315;M280	0.68333	Q9BQE3 A6NHL2 F5H5D3 Q71U36 A6NHL2 P68366	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
EDPTVSALLTSEKDWQGFL LYLQNSPEAC*DYGL	C209;C237	0.682816882	P78417 P78417	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q9UI30-2 Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # P23381 Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 # P23381-2 Isoform 2 of Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS #
IC*PVEFNPNFVAR	C33;C33;C33	0.682219583	Q9UI30 Q9UI30 F5GX77	A6NHK2 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P62304 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 # P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
YVEPIEDVPC*GNIVGLVGVD QFLVK	C466	0.680938359	P13639	O43264 Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 # O43264-2 Isoform 2 of Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 # Q7Z2W4-2 Isoform 2 of Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 # C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
AAAGEDYKADC*PPGNPAPT SNHGPDATEAEEDFVDPWTV QTSSAK	C62;C21	0.680742118	P23381 P23381	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 #
IEGC*IIGFDEYMNLVLDAAEEI HSK	C6	0.680648583	A6NHK2 P62304	
RPTEIC*ADPQFIIGGATR	C82	0.678059662	P17655	
DGTVLC*ELINALYPEGQAPV KK	C63;C84;C63	0.677590657	P37802 P37802 X6RJP6	
LAPILC*DGTATFVLDLVPGFR	C568;C568	0.676995269	O43264 O43264	
NSNVDSYLESYQSC*PR	C645;C767;C64 5	0.676846689	Q7Z2W4 C9J6P4 Q7Z2W4	
LEKPNEGYLEFFVDC*SASAT PEFEGR	C85	0.675988344	Q15024	



				E9PLU1 Mitochondrial fission regulator 1-like (Fragment) OS=Homo sapiens GN=MTFR1L PE=1 SV=1 # Q9H019-3 Isoform 3 of Mitochondrial fission regulator 1-like OS=Homo sapiens GN=MTFR1L # Q9H019-2 Isoform 2 of Mitochondrial fission regulator 1-like OS=Homo sapiens GN=MTFR1L # E9PLU1 Q9H019 Q9H019 E9PSD6 Q9H019 C9JF50 E9PRK5 E9PRW1
ASFETLPNISDLC*LR	C52;C52;C52;C52;C52	0.675854969		E9PSD6 Q9H019 C9JF50 E9PRK5 E9PRW1
GVPGAIVNSSQC*SQR	C138;C137;C136	0.67328	Q7Z4W1 J3QS36 J3KS22	Q7Z4W1 L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 # J3QS36 L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=1 SV=1 # J3KS22 L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=1 SV=7 #
APPGGC*EERELALALQEAL PAVR	C117	0.672316667	Q5RKV6	Q5RKV6 Exosome complex component MTR3 OS=Homo sapiens GN=EXOSC6 PE=1 SV=1 #
TDVLVLSCL*DLITDVALHEVVD LFR	C106;C106;C106	0.672159584	Q9NR50 Q9NR50 Q9NR50	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 #
GLGTDEDSLIEIIC*SR	C151;C133	0.672156772	P07355 P07355	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 #
ALANSLAC*QGK	C339;C393	0.672121516	P04075 P04075	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA #
HGLEVIYMIPIDEYCV*VQQLK	C651;C529	0.67151	P07900 P07900	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
ITSC*IFQLLQEAGIK	C63;C63	0.67063398	E9PBS1 P22234	E9PBS1 Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1 # P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
IAVYSC*PFDGMITETK	C225;C244	0.670631829	P50990 P50990	P50990-2 Isoform 2 of T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 # P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
QIPAITC*IQSQWR	C781	0.670329547	P46940	P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 #
EALAEASAWC*YLYGTGSVA GVYLPGSR	C3821	0.668720019	Q15149	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 #
DTC*YSPKPSVYLSTPSSASK	C540	0.667245417	Q9Y5K6	Q9Y5K6 CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 #
ETVYC*LNDDDETEVLKEDIQ GFR	C296	0.666917316	P13010	P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 #

DDFAYCLNCF*DLyak	C330;C324;C214	0.666873391	A0A0A0MSG2 SG2 J3KNW4 Q14192	A0A0A0MSG2 Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=1 # J3KNW4 Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=1 # Q14192 Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3 #
DVIELTDDSFDKNVLDSEdV WMVEFYAPWC*GHCK	C238;M182 C187 C242;M187 C195;M230 C190;M179	0.666330822	Q15084 Q15084 Q15084 Q15084	Q15084-2 Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-4 Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-5 Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 # Q15084-3 Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 #
EIGLWFHPEELVDYTSC*AQN WIYE	C145;C170	0.666313996	P15531 P15531	P15531 Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 # P15531-2 Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 #
AAIGC*GIVESILNWVK	C441;C431;C405;C486	0.666154776	P11388 P11388 P11388 P11388	P11388-3 Isoform 3 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A # P11388-2 Isoform 2 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A # P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 # P11388-4 Isoform 4 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A #
APPSLTDc*IGTVDSR	C20;C20	0.665957208	Q9NZZ3 Q9NZZ3	Q9NZZ3 Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1 # Q9NZZ3-2 Isoform 2 of Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 #
NLSLDIDLVPsLc*EDLLSSVD QPLK	C36;C36;C65;C24;C62	0.662834349	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
VTEAPC*YPGAPSTEASGQT GPQEPTSAR	C523	0.66071675	P40222	P40222 Alpha-taxilin OS=Homo sapiens GN=TXLNA PE=1 SV=3 #
SPGVVISDDEPGYDLDFC*IP NHYAEDLER	C23	0.65976	P00492	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
TDVNKIEEFLEEVLC*PPK	C100	0.658016733	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
C*AVSDVEMQEHYDEFFEEV FTEMEEK	C67;C67	0.654367783	Q01081 PODN76	Q01081 Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3 # PODN76 Splicing factor U2AF 35 kDa subunit-like protein OS=Homo sapiens GN=U2AF1L5 PE=3 SV=1 #
VNSDC*DSVLPsNFLGGNIF DPLNLNLLDDEEVSr	C177	0.653598556	Q7L2J0	Q7L2J0 7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1 #
LEGDLTGPSVGVVDPDVELE C*PDAK	C1900	0.651254582	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
LSEAAC*EDEDSASEGLGELF LDGLSTENPHGAR	C238	0.648731848	O95801	O95801 Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 #

VVLPV*SVQEYQVGLYSVA EASK	C13;C15;C13;C1 3	0.648355204	P48739 P48739 P48739 A0A0A0M SW4	P48739 Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2 # P48739-3 Isoform 3 of Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB # P48739-2 Isoform 2 of Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB # A0A0A0MSW4 Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=1 #
NSLIELPDDYSC*LLNQASHF R	C1603	0.647496667	Q8IWW7	Q8IWW7 E3 ubiquitin-protein ligase UBR1 OS=Homo sapiens GN=UBR1 PE=1 SV=1 # E9PKU4 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 # E9PKZ0 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 # G3V1A1 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=1 # P62917 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 #
AQLNIGNVLPVGTMPGIVC C*LEEKPGDR	C115;C115;C11 5;C115	0.646737098	E9PKU4 E9PKZ0 G3V1A1 P62917	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 # A0A087WZU8 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-8 Isoform 8 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # E7ESS1 Cellular tumor antigen p53 (Fragment) OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-7 Isoform 7 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-9 Isoform 9 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # Q969U7-2 Isoform 2 of Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 # V9GZ55 Proteasome assembly chaperone 2 (Fragment) OS=Homo sapiens GN=PSMG2 PE=1 SV=1 # K7ENR6 Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 PE=1 SV=1 # Q969U7 Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 PE=1 SV=1 # Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 #
VGMGSGSIC*ITQEVLAGR QATAVYK	C331	0.645902166	P12268	
C*SDSDGLAPPQHLIR	C171;C182;C18 2;C50;C143;C18 2;C182;C50;C14 3;C50;C143;C14 3;C50	0.645293541	A0A087W ZU8 J3KP33 P04637 P04637 P04637 P04637 P04637 E7ESS1 P04637 P04637 A0A0U1R QC9 P04637 P04637	
C*IPEIDDSEFCIR	C137;C176;C16 8;C168	0.6439	Q969U7 V9GZ55 K7ENR6 Q969U7	
SQEATEAAPSC*VGDMADTP R	C84	0.642497674	Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8 Q9UHD8	

DSVNPQVMVLLGC*GALSST CGQLASYPLALVR	C372;C391	0.64192	Q6NUK1 Q6NUK1	Q6NUK1-2 Isoform 2 of Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 # Q6NUK1 Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2 # O60828-2 Isoform 2 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828 Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # H7C053 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # O60828-3 Isoform 3 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # C9JQA1 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 # O60828-7 Isoform 7 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828-6 Isoform 6 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # O60828-4 Isoform 4 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 # Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 # Q5VUC6 Glycylpeptide N-tetradecanoyltransferase OS=Homo sapiens GN=NMT2 PE=1 SV=1 # O60551 Glycylpeptide N-tetradecanoyltransferase 2 OS=Homo sapiens GN=NMT2 PE=1 SV=1 # Q53T59 HCLS1-binding protein 3 OS=Homo sapiens GN=HS1BP3 PE=1 SV=1 # H7BZ19 HCLS1-binding protein 3 (Fragment) OS=Homo sapiens GN=HS1BP3 PE=1 SV=1 # F8WDN8 HCLS1-binding protein 3 (Fragment) OS=Homo sapiens GN=HS1BP3 PE=1 SV=2 # H7C0Y9 HCLS1-binding protein 3 (Fragment) OS=Homo sapiens GN=HS1BP3 PE=1 SV=1 # H7BZZ1 HCLS1-binding protein 3 (Fragment) OS=Homo sapiens GN=HS1BP3 PE=1 SV=1 #
VFDPSC*GLPYWADTDLV SWLSPHDPNSVVTK	C60;C60;C49;C60; C60;C60;C60; C60	0.640337136	O60828 O60828 H7C053 O60828 C9JQA1 O60828 O60828 O60828	
TEVMALVPPADC*R	C220	0.63929	Q14353	
AMELLSAC*QGPAR	C104 C91;M98	0.637805	Q5VUC6 O60551	
LFDDPDLGGAIPLGDSLLLPA AC*ESGGPTPSLSHR	C287;C40;C81;C 80;C106	0.6372983	Q53T59 H7BZ19 F8WDN8 H7C0Y9 H7BZZ1	
GPVLAEDFLDIMGQPINPQC *R	C162	0.637054858	P21281	P21281 V-type proton ATPase subunit B# brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 #
TC*FETFPDKVAIQLNDTHPAL SIPELMR	C326	0.63543066	P11216	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 # A0A0A0MT55 Sarcosine dehydrogenase# mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 # Q9UL12 Sarcosine dehydrogenase# mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 # Q5SYV2 Sarcosine dehydrogenase# mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 # Q9UL12-2 Isoform 2 of Sarcosine dehydrogenase# mitochondrial OS=Homo sapiens GN=SARDH #
SQC*QLIDSSDLGMISIQGPA SR	C391;C671;C99; C503	0.635395	A0A0A0M T55 Q9UL12 Q5SYV2 Q9UL12	
DLPTSPVDLVINCLDC*PENV FLR	C413	0.634973529	Q96F86	Q96F86 Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1 #



LALDCSGQQVAVDLFLLSGQ YSDLASLGC*ISR	C704	0.627328977	O95486	O95486 Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2 # Q15084-2 Isoform 2 of Protein disulfide- isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-4 Isoform 4 of Protein disulfide- isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-5 Isoform 5 of Protein disulfide- isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 # Q15084-3 Isoform 3 of Protein disulfide- isomerase A6 OS=Homo sapiens GN=PDIA6 # G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # Q6P2E9 Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1 # H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YLC2 Proteasome subunit alpha type OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 # HOYMA1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YKT8 Proteasome subunit beta type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 # P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G # E9PK47 Alpha-1#4 glucan phosphorylase OS=Homo sapiens GN=PYGL PE=1 SV=1 # P06737 Glycogen phosphorylase# liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 # P01130-2 Isoform 2 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130 Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR PE=1 SV=1 # J3KMZ9 Low-density lipoprotein receptor (Fragment) OS=Homo sapiens GN=LDLR PE=1 SV=1 # P01130-6 Isoform 6 of Low- density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130-5 Isoform 5 of Low- density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130-4 Isoform 4 of Low- density lipoprotein receptor OS=Homo sapiens GN=LDLR # P01130-3 Isoform 3 of Low- density lipoprotein receptor OS=Homo sapiens GN=LDLR # Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 # P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 # P17858 ATP-dependent 6- phosphofructokinase# liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 #
DVIELTDDSFDKNVLDSEDV WMVEFYAPWCGHC*K	C241;M182 C190 C193;M179 C245;M187 C198;M230	0.625355573	Q15084 Q15084 Q15084 Q15084 Q15084	
SEVEEVDFAGWLC*K	C287;C384	0.625260702	G5E9C7 P36507	
ETC*STLAESPR	C838	0.624328299	Q6P2E9	
YLLQYQEPIPC*EQLVTALCDI K	C107;C76;C107; C107;C107;C10 7;C83	0.620575506	H0YL69 H0YN18 P25789 H0YLC2 H0YMZ1 H0YMA1 H0YKT8	
FPEELTQTFMSC*NLITGMFQ R	C389 C339;M387	0.619788426	P26641 P26641	
TLQNTMINLGLQNAC*DEAIY QLGLDIEELEEEIEDAGLNG GLGR	C109;C109	0.619081346	E9PK47 P06737	
IGYECLC*PDGFQLVAQR	C213;C340;C42 5;C219;C340;C2 99;C172	0.618200805	P01130 P01130 J3KMZ9 P01130 P01130 P01130	
SDITKLEVDIAVNAANSSLLG GGGVDGC*IHR	C186	0.617873069	Q9BQ69	
IC*PVETLVEEAIQCAEK	C213	0.615780897	P30084	
TYSHLNIAGLVGSIDNDFC*GT DMTIGTDSALHR	C170	0.615571805	P17858	

AILQQLGLNSTC*DDSILVK	C817;C813;C801;C812	0.61483704	P19367 P19367 P19367 P19367	P19367-3 Isoform 3 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367 Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 # P19367-4 Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367-2 Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1 # A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB #
NSFYMGTC*QDEPEQLDDWNR	C1891;C1893;C1907;C771	0.613667291	A0A087WY61 Q14980 Q14980 Q14980	Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 # M0R0X3 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # M0QZ22 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # A0A087WUK6 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # A0A087WZT0 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # Q5PRF9 Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # M0QY61 Protein Smaug homolog 2 (Fragment) OS=Homo sapiens GN=SAMD4B PE=1 SV=1 # P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 #
IECSDNGDGTC*SVSYLPTKPGEYFVNILFEEVHIPGSPFKVLTC*TDLEQGNFFLDFENAQPTSESEKEIYNQVNVVLK	C1095 C10	0.612685 0.6123494	O75369 Q9NUQ9	
GWNEC*EQTVALLSLLK	C20;C20;C20;C20;C20;C20	0.61179967	M0R0X3 M0QZ22 A0A087WUK6 A0A087WZT0 Q5PRF9 M0QY61	
SSSVTTSETQPC*TPSSSDYSDLQR	C334	0.611490791	P50552	
SSTETC*YSAIPK	C2477	0.611315157	O75369	
C*GETAFIAPQCEMPIEWVVC R	C81	0.609796293	E9PBS1 P22234	
EGLLLWC*QR	C154;C154;C173;C154;C154	0.607757954	P12814 P12814 O43707 P12814 P12814	
TTSSANNPNLMYQDEC*DR	C507;C586;C507;C584;C505	0.606219877	Q92841 H3BLZ8 Q92841 Q92841 Q92841	
LHDAIVEVWTC*LLR	C470	0.605961052	O00429	
ALVLDC*HYPEDEVGQEDEAESDIFSIR	C186	0.605437463	Q07021	

ADASSTPSFQQAFASSC*TIS SNGPGQR	C928	0.60321156	Q68CZ2	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 # Q96IZ6-2 Isoform 2 of Methyltransferase-like protein 2A OS=Homo sapiens GN=METTL2A # A0A087WW35 Methyltransferase-like protein 2A OS=Homo sapiens GN=METTL2A PE=1 SV=1 # Q6P1Q9 Methyltransferase-like protein 2B OS=Homo sapiens GN=METTL2B PE=1 SV=3 # Q6P1Q9-2 Isoform 2 of Methyltransferase-like protein 2B OS=Homo sapiens GN=METTL2B # Q96IZ6 Methyltransferase-like protein 2A OS=Homo sapiens GN=METTL2A PE=1 SV=5 # Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 # A0A0C4DG31 RNA exonuclease 4 (Fragment) OS=Homo sapiens GN=REXO4 PE=1 SV=1 # Q9GZR2 RNA exonuclease 4 OS=Homo sapiens GN=REXO4 PE=1 SV=2 # Q9GZR2-2 Isoform 2 of RNA exonuclease 4 OS=Homo sapiens GN=REXO4 # P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 # Q6UN15-4 Isoform 4 of Pre-mRNA 3'-end- processing factor FIP1 OS=Homo sapiens GN=FIP1L1 # Q6UN15-5 Isoform 5 of Pre- mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 # Q6UN15 Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 PE=1 SV=1 # A0A0B4J203 Uncharacterized protein OS=Homo sapiens PE=3 SV=1 # O75934 Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 # O76003 Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 # P52788 Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 # P52788-2 Isoform 2 of Spermine synthase OS=Homo sapiens GN=SMS # A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 # Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 # Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 # Q5BIX2 Chromosome 18 open reading frame 25# isoform CRA_a OS=Homo sapiens GN=ARKL1 PE=1 SV=1 # Q96B23-2 Isoform 2 of Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 # A0A087WVF1 Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=1 # K7EQH1 Uncharacterized protein C18orf25 (Fragment) OS=Homo sapiens GN=C18orf25 PE=1 SV=1 # Q96B23 Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=2 #
ISDLEIC*ADEFPGSSATYR	C35;C106;C171; C106;C171	0.602482733	Q96IZ6 A0A087W W35 Q6P1Q9 Q6P1Q9 Q96IZ6	
VEQNSEPC*AGSSSESDLQT VFK	C260	0.602225254	Q8N806	
ILGLVQQAIEHC*SIQDAQAA MR	C210;C382;C21 0	0.59875854	A0A0C4D G31 Q9GZR2 Q9GZR2	
TDICQGALGDC*WLLAAIASLT LNEEILAR	C105	0.596960349	P17655	
AC*ANPAAGSVILLENLR	C108	0.593748956	P00558	
ITAEDC*TMEVTPGAEIQDGR	C201;C201;C21 6;C216	0.59302	Q6UN15 Q6UN15 Q6UN15 A0A0B4J2 03	
NDITAWQEC*VNNSMAQLEH QAVR	C106	0.588040934	O75934	
ELEASEELDTIC*PK	C229	0.585636851	O76003	
YFTQGNC*VNLTEALSLYEEQ LGR	C318;C265	0.58557932	P52788 P52788	
TC*YPLESRPSLSLGTITDEE MK	C1921	0.58553	A0A087W Y61 Q14980 Q14980 Q14980	
DGVADSTVISSMPC*LLMELR	C57;C57;C57;C5 7;C57	0.580856942	Q5BIX2 Q96B23 A0A087W VF1 K7EQH1 Q96B23	



				J3KRX5 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621-2 Isoform 2 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 # J3QLC8 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=1 # A0A087WXM6 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # A0A0A0MRF8 Protein RPL17-C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 # A0A0A6YYL6 Protein RPL17-C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 # P18621 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 # J3QQT2 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621-3 Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 #
INPYMSSPC*HIEMILTEK	C144 C144;M102 C144;M140 C134;M140 C106;M140 C106;M130	0.578760364	J3KRX5 P18621 J3QLC8 A0A087WXM6 A0A0A0MRF8 A0A0A6YYL6 P18621 J3QQT2 P18621	
LMGLLSDPELGPAAADGFSL MSDC*TDVLTR	C869;C848	0.577196679	Q96T76 Q96T76	Q96T76-8 Isoform 5 of MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 # Q96T76 MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 # O14929 Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1 #
VDEFDC*VEADVEGK	C101	0.575112889	O14929	P35658-4 Isoform 4 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658 Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 # P35658-2 Isoform 2 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658-3 Isoform 3 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 # P35658-5 Isoform 5 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 #
VC*ATLPSTVAVTVCWSPK	C186;C186;C186; 6;C186;C186	0.57501167	P35658 P35658 P35658 P35658	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
HLTYLDGGDIINALC*FSPNR	C240	0.573407904	P63244	Q32MZ4-3 Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 # Q32MZ4 Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2 # C9JTC6 Leucine-rich repeat flightless-interacting protein 1 (Fragment) OS=Homo sapiens GN=LRRFIP1 PE=1 SV=1 #
EIDC*LSPEAQK	C14;C14;C14;C14	0.571562604	Q32MZ4 Q32MZ4 C9JTC6 Q32MZ4	Q32MZ4-2 Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 #
IVSC*GNAIIELLR	C21	0.571205	Q12768	Q12768 WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=1 SV=1 #
VAAAFQSEDPADPC*ALLQR	C402	0.569508941	Q8N8A6	Q8N8A6 ATP-dependent RNA helicase DDX51 OS=Homo sapiens GN=DDX51 PE=1 SV=3 #
TDDYLDQPC*LETVNR	C202	0.569421462	P31150	P31150 Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 #
VETELQGVC*DTVLGLLDShLI K	C96	0.56919664	P31947	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 #
NFPAIGGTGPTSDTGWGC*M LR	C74	0.569055	Q9Y4P1	Q9Y4P1 Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B PE=1 SV=2 #

VLSSC*PQAGEATLLAPSTEA GGGLTCASAPQGTLR	C88;C86	0.566065	O15446 O15446	O15446-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP # O15446 DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP PE=1 SV=1 #
GTLTLC*PYHSDR	C779;C649	0.565552275	Q13200 Q13200	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 # Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 #
SKDAAFQNVLTHVC*LD	C359	0.565490866	Q8NBU5	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 #
SQTIYEIIDNSQGFYVC*PVEP QNR	C291	0.564447116	Q9Y617	Q9Y617 Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 #
EEFASTC*PDDEEIELAYEQV AK	C223	0.563545743	O00299	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
ISGPNPLSC*LK	C207	0.55956	Q9BRU9	Q9BRU9 rRNA-processing protein UTP23 homolog OS=Homo sapiens GN=UTP23 PE=1 SV=2 #
VVTAGAIIPFLAPGQSLPDSL MQFGGATPWTPLSAC*GEPS GTR	C403;M354 C368 C403;M389	0.558349183	Q9BUK6 Q9BUK6 Q9BUK6 Q9BUK6	Q9BUK6 Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 PE=1 SV=1 # Q9BUK6-2 Isoform 2 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 # Q9BUK6-3 Isoform 3 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 # Q9BUK6-7 Isoform 7 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 #
LIC*DFPFDGLLEER	C670;C681	0.557815395	Q96JC1 Q96JC1	Q96JC1-2 Isoform 2 of Vam6/Vps39-like protein OS=Homo sapiens GN=VPS39 # Q96JC1 Vam6/Vps39-like protein OS=Homo sapiens GN=VPS39 PE=1 SV=2 #
NLQTCMEVLEALYDGS LGDC *KEAAEIYR	C817;C816	0.557606667	Q9BXJ9 A0A0B4J1 W3	Q9BXJ9 N-alpha-acetyltransferase 15# NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 # A0A0B4J1W3 N-alpha-acetyltransferase 15# NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
NC*NDFQYESK	C112	0.557443104	Q04917	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 #
LLFSQGC*NWIQQYSFGPEK	C177	0.556872697	Q9NUU6	Q9NUU6 Inactive ubiquitin thioesterase FAM105A OS=Homo sapiens GN=FAM105A PE=2 SV=1 #
EGIAISDTTTF*GTPEYLAP EVIR	C322	0.556535517	Q96BR1	Q96BR1 Serine/threonine-protein kinase Sgk3 OS=Homo sapiens GN=SGK3 PE=1 SV=1 #
IEC*SDNGDGTCSVSYLPTKP GEYFVNILFEVHHPGSPFK	C1087;C1087;C1087;C1087;C1087	0.555167028	O75369 O75369 O75369 O75369 O75369	O75369 Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 # O75369-9 Isoform 9 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-3 Isoform 3 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-8 Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB #
YAC*GLWGLSPASR	C26;C457;C175	0.55474553	H7C0N4 Q15637 H7C561	H7C0N4 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 # Q15637-6 Isoform 6 of Splicing factor 1 OS=Homo sapiens GN=SF1 # H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 #
FSTQGMGTFNPADYSDSTST DVC*GTK	C208	0.5532425	Q5T6F2	Q5T6F2 Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBAP2 PE=1 SV=1 #
YIPDEADFLLGMATVNNC*VS YR	C468;C409	0.552169077	Q14790 Q14790	Q14790-9 Isoform 9 of Caspase-8 OS=Homo sapiens GN=CASP8 # Q14790 Caspase-8 OS=Homo sapiens GN=CASP8 PE=1 SV=1 #
MLPTYVC*ATPDGTEKGDFLA LDLGGTNFR	C517	0.551642169	P52789	P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #

AAQGPPAPAVPPNTDVMAC* TQTALLQK	C146;C152;C11 5	0.55055	H0YEB6 O60232 G3V1B8	H0YEB6 Sjogren syndrome/scleroderma autoantigen 1 (Fragment) OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # O60232 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 # G3V1B8 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 #
EMSC*IAEDVIIVTSSLTK	C97	0.548748162	Q9Y678	Q9Y678 Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 # Q9NYL2-3 Isoform 3 of Mitogen-activated protein kinase kinase kinase MLT OS=Homo sapiens GN=ZAK # Q9NYL2-2 Isoform 2 of Mitogen-activated protein kinase kinase MLT OS=Homo sapiens GN=ZAK # D4Q8H0 Mitogen-activated protein kinase kinase MLT OS=Homo sapiens GN=pk PE=1 SV=1 # Q9NYL2 Mitogen-activated protein kinase kinase kinase MLT OS=Homo sapiens GN=ZAK PE=1 SV=3 #
FDDLQFFENC*GGGSFGSVY R	C22;C22;C22;C2 2	0.547289553	Q9NYL2 Q9NYL2 D4Q8H0 Q9NYL2	Q9BTX1-2 Isoform 2 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 # Q9BTX1 Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 PE=1 SV=2 # Q9BTX1-4 Isoform 4 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 # Q9BTX1-5 Isoform 5 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 # Q9BTX1-6 Isoform 6 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 #
MAGIFDVNTC*YGSPQSPQLI R	C467;C468;C46 8;C428;C353	0.54340567	Q9BTX1 Q9BTX1 Q9BTX1 Q9BTX1 Q9BTX1	P11586 C-1-tetrahydrofolate synthase# cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 # A0A087WVM4 Monofunctional C-1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # Q6UB35 Monofunctional C-1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # F5H2F4 C-1-tetrahydrofolate synthase# cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=1 # B7ZM99 MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 #
QGFGNLPIC*MAK	C863;C841;C90 6;C919;C907	0.541986859	P11586 A0A087W VM4 Q6UB35 F5H2F4 B7ZM99	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YN18 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
LNEDMAC*SVAGITSDANVLT NELR	C74;C43;C74;C7 4	0.541119823	H0YL69 H0YN18 P25789 H0YMZ1	Q9UL15-2 Isoform 2 of BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 # Q9UL15 BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 PE=1 SV=1 #
TELQGLIGQLDEVSLEKNPC*1 R	C368;C327	0.540685	Q9UL15 Q9UL15	E9PBC6 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # E7EMZ9 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=1 # O95359 Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3 # O95359-3 Isoform 3 of Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 #
LPQQSYNFDPTDC*DESVPD FK	C2378;C2329;C 2374;C2374	0.53504	E9PBC6 E7EMZ9 O95359 O95359	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
SNELGDVGVHC*VLQGLQTP SCK	C75	0.535019916	P13489	

C*EQPFFWNIK	C290	0.534573106	Q8IWB7	Q8IWB7 WD repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=WDFY1 PE=1 SV=1 #
NPFGVLPVLENSQGQLIYESA ITC*EYLDEAYPGKK	C62;C90	0.533635403	P78417 P78417	P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
STMSLPPGLLGNSWGEGAPA WVLLDECGLGLEDTPHVC* WEPQAQGR	C505;M421 C457	0.532946206	G3V1A6 P57764	G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 #
ENKPSIIFIDEIDSLC*GSR	C240	0.530285	O75351	O75351 Vacuolar protein sorting-associated protein 4B OS=Homo sapiens GN=VPS4B PE=1 SV=2 #
IYFGSNIPNMFVDSSC*ALK	C310	0.52756	O75477	O75477 Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 #
PC*GEDWLSHPLGIVQGFFA QNGVNPDWEK	C3;C3	0.523087596	Q9BTE3 Q9BTE3	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 # Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP #
VDVEC*PDVNIIEGPEGK	C2806	0.518212582	Q09666	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
GLPWSC*SADEVQR	C22;C22;C22	0.515561898	P31943 G8JLB6 E9PCY7	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # E9PCY7 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 #
TMPIGPDVSLLENLAAETC*FF SGADLR	C685	0.513514418	Q9BVQ7	Q9BVQ7 Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2 #
GIFGFTDSDC*IGK	C274;C233	0.51012647	P23381 P23381	P23381 Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 # P23381-2 Isoform 2 of Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS #
ILYSQC*GDVMR	C33;C32	0.507055559	G8JLA2 P60660	G8JLA2 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660-2 Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 #
FSNPYSIEYSELDC*EEGWTQ LK	C140	0.506746066	O14879	O14879 Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 #
TDDYLDQPC*YETINR	C202	0.505324691	P50395	P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 #
C*PEALFQPSFLGMESCGIHE TTFNSIMK	C257	0.5052875	P63261 P60709	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #
VMAEANHFIDLSQIPC*NGK	C620	0.503816667	O15294	O15294 UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3 #
FIQENIFGIC*PHMTEDNKDLI QGK	C244	0.501902992	P30101	P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 #
QEC*GEPALPSASEEQVAQD TEEVFR	C14;C14;C14	0.499988168	A0A0A0M RG8 Q16611 Q16611	A0A0A0MRG8 Bcl-2 homologous antagonist/killer OS=Homo sapiens GN=BAK1 PE=1 SV=1 # Q16611-2 Isoform 2 of Bcl-2 homologous antagonist/killer OS=Homo sapiens GN=BAK1 # Q16611 Bcl-2 homologous antagonist/killer OS=Homo sapiens GN=BAK1 PE=1 SV=1 #

EFGRIDLINC*AAGNFLCPAG ALSFNFAFK	C113;C101;C12 2	0.49927	Q9NUI1 Q4VXZ8 A0A0J9YY 83	Q9NUI1 Peroxisomal 2#4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 # Q4VXZ8 Peroxisomal 2#4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 # A0A0J9YY83 Peroxisomal 2#4-dienoyl-CoA reductase (Fragment) OS=Homo sapiens GN=DECR2 PE=1 SV=1 #
QC*TGLQGFLVFHSGGGTG SGFTSLLMER	C129;C199;C12 9;C129	0.49763288	Q9BQE3 F5H5D3 Q71U36 P68366	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
SVDGSPTTAFTVLEC*EGSR	C525;C550	0.493168361	M0R2P6 Q8TBC3	M0R2P6 SH3KBP1 binding protein 1# isoform CRA_c OS=Homo sapiens GN=SHKBP1 PE=1 SV=1 # Q8TBC3 SH3KBP1-binding protein 1 OS=Homo sapiens GN=SHKBP1 PE=1 SV=2 #
SDLYSSC*DR	C338	0.492979847	Q96E39	Q96E39 RNA binding motif protein# X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 #
ETGANLAIC*QWGFDEANH LLLQNNLPAVR	C281;C264;C30 2	0.491525954	E9PCA1 B7ZAR1 P48643	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 #
GVGLLIAGYDDMGPHIFQTC* PSANYFDCR	C123 C148;M115 C154;M140	0.486576667	P25786 P25786 F5GX11	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 # P25786 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 # F5GX11 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 #
YMACC*LLYR	C316;M280 C316;M320 C316 C323;M313 C283;M383 C386;M313	0.48118	Q9BQE3 A6NHL2 F5H5D3 Q71U36 A6NHL2 P68366	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
IPC*DSPQSDPVDTPSTK	C1250;C1251	0.4807994	A0A087W V66 P46013	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 # P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 #
C*IPALDSLTPANEDQK	C447	0.477722892	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
C*SNDSFSVIADYFGR	C346;C880;C89 0;C890	0.477124594	A0A0G2J S92 B7Z879 Q9H270 A0A087W XL6	A0A0G2JS92 Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens GN=VPS11 PE=1 SV=1 # B7Z879 Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens GN=VPS11 PE=1 SV=1 # Q9H270 Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens GN=VPS11 PE=1 SV=1 # A0A087WXL6 Vacuolar protein sorting 11 (Yeast)# isoform CRA_a OS=Homo sapiens GN=VPS11 PE=1 SV=1 #



WGLVC*AGLADMARPAEK	C54;C54	0.423645	Q5R3B4 O95563	Q5R3B4 Mitochondrial pyruvate carrier 2 (Fragment) OS=Homo sapiens GN=MPC2 PE=1 SV=1 # O95563 Mitochondrial pyruvate carrier 2 OS=Homo sapiens GN=MPC2 PE=1 SV=1 #
IHESAGLPFFEIVDAPLNIC*E SR	C155;C155	0.419301141	O95340 O95340	O95340 Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2 # O95340-2 Isoform B of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 #
TDGFGIDTC*R	C144;C144	0.407042977	A0A0C4D GQ5 P04632	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #
ATPPQIVNGDQYC*GDYELFV EAVEQNTLQEFLK	C204;C71	0.401664664	A0A087W V23 Q9H299	A0A087WV23 SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGR3 PE=1 SV=1 # Q9H299 SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGR3 PE=1 SV=1 #
LFNC*SASLDWPR	C456;C439	0.40090831	Q9Y4W2 Q9Y4W2	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 # Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L #
VPFLVLEC*PNLK	C14	0.398742299	Q9NRP0	Q9NRP0 Oligosaccharyltransferase complex subunit OSTC OS=Homo sapiens GN=OSTC PE=1 SV=1 #
AITIAGIPQSIIEC*VK	C158;C158;C158; C158;C158;C158; C158	0.394643961	Q15366 Q15366 Q15366 Q15366 Q15366 Q15366	Q15366-8 Isoform 8 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-7 Isoform 7 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
KNPFGLVPVLENSQGGQLIYES AITC*EYLDEAYP	C62;C90;C90	0.39234545	P78417 P78417 P78417	P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 # P78417-2 Isoform 2 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 #
LTPTYGDLNHLVSATMSGV TTC*LRFPQQLNA	C239;C239;C239; C239;C221	0.385871685	Q13885 P68371 Q9BVA1 P04350 Q5JP53	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
LVFLAC*CVAPTNR	C301	0.385435303	Q14566	Q14566 DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 #
GGTLFGGEVC*K	C684	0.384493891	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #
IVPFYGGNC*VTDEFEEIGI DIILR	C159;C118	0.38267136	Q9UL15 Q9UL15	Q9UL15-2 Isoform 2 of BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 # Q9UL15 BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 PE=1 SV=1 #

SLSDC*VNYIVQDSK	C406	0.381042707	O15111	O15111 Inhibitor of nuclear factor kappa-B kinase subunit alpha OS=Homo sapiens GN=CHUK PE=1 SV=2 #
LLYEALVDC*K	C175	0.373412677	Q7L2H7	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #
DPC*HGVTCPQETC*K	C1645 C1656 C1656;C1645	0.368277369	Q9Y6R7 A0A087W XI2	Q9Y6R7 IgGfC-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3 # A0A087WXI2 IgGfC-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=1 # C9JRY4 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=1 # Q96IW7 Vesicle-trafficking protein SEC22a OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JNJ8 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JNZ0 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=8 #
TNTAVRPYC*FIEFDNFIQR	C111;C111;C111 1;C111	0.368207103	C9JRY4 Q96IW7 C9JNJ8 C9JNZ0	Q96IW7 Vesicle-trafficking protein SEC22a OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JNJ8 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=1 # C9JNZ0 Vesicle-trafficking protein SEC22a (Fragment) OS=Homo sapiens GN=SEC22A PE=1 SV=8 #
STC*SLTPALAAHFSENLIK	C553;C450;C50 8;C401	0.366775788	Q9BTA9 Q9BTA9 Q9BTA9 A0A0A0M RT2	Q9BTA9 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=3 # Q9BTA9-5 Isoform 4 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC # Q9BTA9-2 Isoform 2 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC # A0A0A0MRT2 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=1 #
EVIFLGPAPAC*PEAWGSPEP GPAESSADMDGSGR	C1196	0.360210822	O15061	O15061 Synemin OS=Homo sapiens GN=SYNM PE=1 SV=2 # Q9Y679-2 Isoform Short of Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 # Q9Y679-3 Isoform 3 of Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 # Q9Y679 Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 PE=1 SV=1 #
TGC*VDLTITNLEGAFAVMP EDITK	C325;C325;C39 1	0.357028367	Q9Y679 Q9Y679 Q9Y679	K7EM18 Eukaryotic translation initiation factor 1 OS=Homo sapiens GN=EIF1 PE=1 SV=1 # P41567 Eukaryotic translation initiation factor 1 OS=Homo sapiens GN=EIF1 PE=1 SV=1 # O60739 Eukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2 # K7EQP2 Eukaryotic translation initiation factor 1 (Fragment) OS=Homo sapiens GN=EIF1 PE=1 SV=1 #
FAC*NGTVIEHPEYGEVIQLQ GDQR	C69;C69;C69;C1 7	0.353039065	K7EM18 P41567 O60739 K7EQP2	Q8TC07-3 Isoform 3 of TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 # Q8TC07-2 Isoform 2 of TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 # Q8TC07 TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 PE=1 SV=2 #
NDSPTQIPVSSDVC*R	C677;C669;C68 6	0.351592224	Q8TC07 Q8TC07 Q8TC07	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
KFLDGNEMTLADC*N	C189	0.349155	Q9Y696	Q9BQA1 Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1 #
DPC*AAPNEGFCASAGVQTEA GVADLTWVGER	C65	0.341683465	Q9BQA1	Q99986 Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 #
VGLPIGQGGFGC*IYLADMNS SESVGSDAPCVVK	C50	0.3390875	Q99986	P35568 Insulin receptor substrate 1 OS=Homo sapiens GN=IRS1 PE=1 SV=1 #
SSASVSGSPSDGGFISSDEY GSSPC*DFR	C436	0.333489475	P35568	P21796 Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 #
YQIDPDAC*FSAK	C232	0.33166857	P21796	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
FLDGNELTLADC*NLLPK	C178	0.331096073	O00299	



IDILINCAAGNFLC*PAGALSFN NAFK	C120;C108;C12 9	0.328394166	Q9NUI1 Q4VXZ8 A0A0J9YY 83	Q9NUI1 Peroxisomal 2#4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 # Q4VXZ8 Peroxisomal 2#4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 # A0A0J9YY83 Peroxisomal 2#4-dienoyl-CoA reductase (Fragment) OS=Homo sapiens GN=DECR2 PE=1 SV=1 #
GAC*YGDDACFVAR	C57	0.328392712	Q8NI37	Q8NI37 Protein phosphatase PTC7 homolog OS=Homo sapiens GN=PPTC7 PE=2 SV=1 #
NAEDC*LYELPENIR	C70;C145	0.32046992	A0A087X2 F5 Q9NZ63	A0A087X2F5 Uncharacterized protein C9orf78 OS=Homo sapiens GN=C9orf78 PE=1 SV=1 # Q9NZ63 Uncharacterized protein C9orf78 OS=Homo sapiens GN=C9orf78 PE=1 SV=1 #
AITIAGVPQSVTEC*VK	C158	0.313183919	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # P51114-2 Isoform 2 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # B4DXZ6 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # E9PFF5 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # E7EU85 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=1 # P51114-3 Isoform 3 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # P51114 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3 #
GEFYVIEYAAC*DATYNEIVTF ER	C99;C86;C50;C1 4;C14;C99	0.302365514	P51114 B4DXZ6 E9PFF5 E7EU85 P51114 P51114	P51114-2 Isoform 2 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # P51114-3 Isoform 3 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 # P51114 Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3 #
IGLAVC*YDMR	C188	0.2893445	Q86X76 Q86X76 Q86X76 Q86X76	Q86X76-4 Isoform 5 of Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 # Q86X76-3 Isoform 4 of Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 # Q86X76-2 Isoform 1 of Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 # Q86X76 Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 PE=1 SV=2 #
SGDAAIVEMVPGKPMC*VES FSQYPPLGR	C411	0.28822285	Q05639	Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 #
YAEYFLRPMLQYVC*DNSPE VR	C917;C933;C85 5;C915	0.269891811	H0Y8C6 O00410 O00410 O00410	H0Y8C6 Importin-5 (Fragment) OS=Homo sapiens GN=IPO5 PE=1 SV=1 # O00410-3 Isoform 3 of Importin-5 OS=Homo sapiens GN=IPO5 # O00410-2 Isoform 2 of Importin-5 OS=Homo sapiens GN=IPO5 # O00410 Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 #
LDQEDALLGSYPVDDGC*R	C83;C66;C83	0.26305	K7EK42 K7EL99 Q99426	K7EK42 Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=1 # K7EL99 Tubulin-folding cofactor B (Fragment) OS=Homo sapiens GN=TBCB PE=1 SV=2 # Q99426 Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2 #
ETYQSVYNWQYVHCLFLWC* R	C416	0.254285	Q9Y3T9	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 #
ESGC*VLGLRPGAQESPVS WPEGSK	C369;C437;C22 7	0.251666527	Q6ZUT6 Q6ZUT6 Q6ZUT6	Q6ZUT6-4 Isoform 4 of Uncharacterized protein C15orf52 OS=Homo sapiens GN=C15orf52 # Q6ZUT6 Uncharacterized protein C15orf52 OS=Homo sapiens GN=C15orf52 PE=1 SV=1 # Q6ZUT6-2 Isoform 2 of Uncharacterized protein C15orf52 OS=Homo sapiens GN=C15orf52 #

AVLFC*LSEDKK	C77;C22;C39;C39	0.24578691	E9PK25 G3V1A4 P23528 E9PP50	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 # O43252 Bifunctional 3'-phosphoadenosine 5'- phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2 #
TDSCDVNDC*VQVVELLQER	C212	0.239425062	O43252	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q12802-4 Isoform 3 of A-kinase anchor protein 13 OS=Homo sapiens GN=AKAP13 # Q12802-2 Isoform 2 of A-kinase anchor protein 13 OS=Homo sapiens GN=AKAP13 # Q12802 A-kinase anchor protein 13 OS=Homo sapiens GN=AKAP13 PE=1 SV=2 #
NC*DCLQGFLTHSLGGGTG SGMGTLISK	C474	0.234386859	A0A0B4J269	
ESESEPADPGDVEEEMDSI TEVPANC*SVLR	C1548;C1548;C1548	0.234263333	Q12802 Q12802 Q12802	
LVLANNC*PALR	C52;C52	0.230042424	P62888 E5R199	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5R199 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 # A0A087WZU8 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-8 Isoform 8 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 # E7ESS1 Cellular tumor antigen p53 (Fragment) OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-7 Isoform 7 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 # P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 # P04637-9 Isoform 9 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 #
TC*PVQLWVDSTPPPGTR	C130;C141;C141; C9;C102;C141; C141;C9;C102; C9;C102;C102;C9	0.22523	A0A087WZU8 J3KP33 P04637 P04637 P04637 P04637 E7ESS1 P04637 P04637 A0A0U1RQC9 QC9 P04637 P04637	
C*GVPDVAQFVLTEGNPR	C92	0.224862862	P03956	P03956 Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3 # Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 #
HTGCC*GDNDPIDVCEIGSK	C114	0.220119697	Q15181	
AC*LISLGYDVENDRQGEAEF NR	C793	0.218705	O43707	
AFDTAGNGYC*R	C223	0.195775821	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 # P47974 Zinc finger protein 36# C3H1 type-like 2 OS=Homo sapiens GN=ZFP36L2 PE=1 SV=3 # A0A087WUU9 Zinc finger protein 36# C3H1 type-like 2 OS=Homo sapiens GN=ZFP36L2 PE=1 SV=1 #
FPGAANGSSC*GSAAAGGPT SYGTLKEPSGGGGTALLNK	C87;C87	0.195338561	P47974 A0A087WUU9	
SSLQYSSPAPDGC*GDQTLG DLLLTPTR	C646	0.191788209	P22102	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 #
ECENCDC*LQGFQLTHSLGG GTGSGMGTLLISK	C476	0.1800975	A0A0B4J269	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 #
KEC*ENCDC*LQGFQLTHSLG GGTSGMGTLLISK	C471	0.174086023	A0A0B4J269	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 #

GNEFEDYC*LK	C102	0.168297144	P26196	P26196 Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 #
KITIADC*GQLE	C161	0.158145999	P62937	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #
ITNSLTVLC*SEK	C86;C153;C158;C66;C207	0.157790471	H0YGJ7 O75822 H0YLP3 O75822	H0YGJ7 Eukaryotic translation initiation factor 3 subunit J (Fragment) OS=Homo sapiens GN=EIF3J PE=1 SV=1 # O75822-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J # O75822-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J # H0YLP3 Eukaryotic translation initiation factor 3 subunit J (Fragment) OS=Homo sapiens GN=EIF3J PE=1 SV=1 # O75822 Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2 #
NVGTGLVGAPAC*GDVMK	C69	0.101405	Q9H1K1 Q9H1K1	Q9H1K1 Iron-sulfur cluster assembly enzyme ISCU# mitochondrial OS=Homo sapiens GN=ISCU PE=1 SV=2 # Q9H1K1-2 Isoform 2 of Iron-sulfur cluster assembly enzyme ISCU# mitochondrial OS=Homo sapiens GN=ISCU # O60313 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3 # E5KLJ9 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # O60313-2 Isoform 2 of Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 # E5KLJ6 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # E5KLK1 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # E5KLJ5 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 #
EGC*TVSPETISLNVK	C375;C394;C412;C393;C376;C430	0.09905	O60313 E5KLJ9 O60313 E5KLJ6 E5KLK1 E5KLJ5	O60313 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 # E5KLJ6 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # E5KLK1 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 # E5KLJ5 Dynamin-like 120 kDa protein# mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=1 #
MAC*GLVASNLNLKPGECLR	C3	0.098967595	P09382	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 # Q9UPQ0-10 Isoform 10 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0-2 Isoform 2 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 # Q9UPQ0 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=1 # D6RD46 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=1 # Q9UPQ0-4 Isoform 4 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 #
C*SPTVAFVEFPSSPQLK	C669;C669;C669;C669;C657	0.063742817	Q9UPQ0 Q9UPQ0 Q9UPQ0 D6RD46 Q9UPQ0	Q9UPQ0 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=4 # D6RD46 LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=1 # Q9UPQ0-4 Isoform 4 of LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 #
ATENC*AKEAISDAALEATEN EPLNK	C879;C879;C879	0.053342332	Q14966 Q14966 Q14966	Q14966-3 Isoform 3 of Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 # Q14966-4 Isoform 4 of Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 # Q14966 Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 PE=1 SV=2 #

				Q9HCF6-6 Isoform 6 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-5 Isoform 5 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-2 Isoform 2 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-11 Isoform 11 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q9HCF6-3 Isoform 3 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # E9PBI7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # A2A3F3 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=2 SV=4 # Q9HCF6-7 Isoform 7 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F4 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # G5E9G1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # H7BYP1 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=2 # Q9HCF6-4 Isoform 4 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # A2A3F7 Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1 # Q9HCF6-8 Isoform 8 of Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 # Q5XKE5 Keratin# type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 # A0A0A0MRJ6 Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=1 # H7BY58 Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=1 # C9J0F2 Protein-L-isoaspartate(D-aspartate) O-methyltransferase (Fragment) OS=Homo sapiens GN=PCMT1 PE=1 SV=1 # P22061-2 Isoform 2 of Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 # P22061 Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 # O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
AAFPGGGLGDKVEDLTCC*HP ER	C1594;C1584;C1582;C1609;C1594;C1454;C1441;C1607;C1597;C1444;C1441;C1431;C1572;C1586;C1554	0.029165562	Q9HCF6 Q9HCF6 Q9HCF6 Q9HCF6 E9PBI7 A2A3F3 Q9HCF6 Q9HCF6 A2A3F4 G5E9G1 H7BYP1 Q9HCF6 A2A3F7 Q9HCF6	
KQC*QQLQTAIAEAQR	C383	0.029052357	Q5XKE5	
ALDVGSGSGILTAC*FAR	C153;C153;C64;C95;C95	0.026799627	A0A0A0MRJ6 H7BY58 C9J0F2 P22061 P22061	
KFLDGNELTLADC*N	C178	0.015606705	O00299	

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				H3BU60 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # H3BUH3 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # B7ZAR9 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=1 # Q8NCN5-2 Isoform 2 of Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR # H3BV59 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # A8MT40 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # Q8NCN5 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 #
FFAFWGQDINNLTPLEC*GR ESR	C93;C118;C93;C 80;C93;C635;C7 35	0.00174069	H3BU60 H3BUH3 B7ZAR9 Q8NCN5 H3BV59 A8MT40 Q8NCN5	

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**Table A3.7**

IsoTOP-ABPP analysis of JNS 1-40 in vivo in 231MFP proteomes (tumor xenograft).

Peptide	Modified residue	Average area ratio	Uniprot ID	Protein
DNTIEHLLPLFLAQLKDEC*PE VR	C377	5.74732667	P30153	P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
NMMAAC*DPR	C303;C303;C231;C303;C650;C231;C303;C266;C285;C303	3.16807	Q13509 P07437 Q5ST81 P68371 A0A0B4J269 69 Q13509 P04350 K7ESM5 Q5JP53 Q9BUF5	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # Q5ST81 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q13509-2 Isoform 2 of Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #
C*PEALFQPSFLGMESCGIHE TTFNSIMK	C257;C257	2.98053933	P63261 P60709	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #
DANDVPIQC*EISPLISYAGEG LESYVADK	C481;C464;C480	2.921965	Q16222 Q16222 Q16222	Q16222 UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3 # Q16222-2 Isoform AGX1 of UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 # Q16222-3 Isoform 3 of UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 #
ESTLEAIGYIC*QDIDPEQLQD K	C158;C13	2.850132	Q14974 Q14974	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
TLQNTMVNLALENAC*DEATY QLGLDMEELEEIEEDAGLGN GGLGR	C109	2.795376	P11217	P11217 Glycogen phosphorylase# muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 #
DYVLNC*SILNPLLLTK	C208	2.79139	O60684	O60684 Importin subunit alpha-7 OS=Homo sapiens GN=KPNA6 PE=1 SV=1 #
AVC*MLSNTTAIAEAWAR	C361;C310;C400;C376;C376;C376	2.76036	P68366 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
VFSANSTAAC*TELAQ	C48;C19	2.71604	Q14558 Q14558	Q14558-2 Isoform 2 of Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 # Q14558 Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=2 #

FYPWTIDNKYYASADINLC*VV PNK	C61	2.702445	Q6PD74	Q6PD74 Alpha- and gamma-adaptin-binding protein p34 OS=Homo sapiens GN=AAAGAB PE=1 SV=1 # P12955-2 Isoform 2 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD # P12955 Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3 #
IEEDVVVTDSGIELLTC*VPR	C426;C467	2.70144786	P12955 P12955	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 #
IIQENLNLALNSASAIGC*HV NIGAEDLR	C209	2.68859786	P13797	Q9H8X2 Inositol-pentakisphosphate 2-kinase OS=Homo sapiens GN=IPPK PE=1 SV=1 # Q14865 AT-rich interactive domain-containing protein 5B OS=Homo sapiens GN=ARID5B PE=1 SV=3 # Q14865-3 Isoform 3 of AT-rich interactive domain-containing protein 5B OS=Homo sapiens GN=ARID5B #
PFFFPSNGLASGPHC*TRAVI R	C253	2.67774	Q9H8X2	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 # Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 #
DTFDHPTLIENESIC*DEFAPN LK	C241;C241	2.66609	Q14865 Q14865	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #
FLDALELSQSPMLLELMTEVL C*R	C1767	2.65298667	P78527	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 # J3KTF8 Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDI PE=1 SV=7 # P52565 Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI PE=1 SV=3 # P52565-2 Isoform 2 of Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI # J3QX2 Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI PE=1 SV=1 # J3KRY1 Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDI PE=1 SV=1 #
FFACAPNYSYAALCEC*LR	C513	2.63402	Q96RS6	I3L3Q4 Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=1 SV=1 # Q9HC38-2 Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 # Q9HC38 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 # F6TLX2 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 #
LVVPASQC*GSLIGK	C109;C109;C109; 9;C109	2.5939	Q15366 Q15366 Q15366 Q15366	Q9UGI8 Testin OS=Homo sapiens GN=TES PE=1 SV=1 # Q9UGI8-2 Isoform 2 of Testin OS=Homo sapiens GN=TES # A0A087WYS6 Proteasome (Prosome# macropain) subunit# alpha type# 8# isoform CRA_b OS=Homo sapiens GN=PSMA8 PE=1 SV=1 # Q8TAA3-5 Isoform 3 of Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 #
FFYDQAFAYGGVSGLYDFG PVGC*ALK	C155	2.557185	P41250	
VAVSADPNVNVVVVGLTLV C*SSAPGPLELDLTGDLESFK	C79;C79;C79;C79; 9;C79	2.48144091	J3KTF8 P52565 P52565 J3QX2 J3KRY1	
ALLGYADNQC*K	C182;C182;C197; C386	2.47681333	I3L3Q4 Q9HC38 Q9HC38 F6TLX2	
C*GQEEHDVLLSNEEDRK	C46;C37	2.46336	Q9UGI8 Q9UGI8	
ICALDDHVC*MAFAGLTADAR	C46;C72	2.42041	A0A087WYS6 Q8TAA3	

GAFC*DLVWSDPEDVDTWAI SPR	C192;C229;C17 0	2.41109	O00743 O00743 O00743	O00743 Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1 # O00743-3 Isoform 3 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C # O00743-2 Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C #
TLQSLAC*GK	C774;C787;C59 1;C769	2.395805	K4DI93 Q13620 Q13620 Q13620	K4DI93 Cullin 4B# isoform CRA_e OS=Homo sapiens GN=CUL4B PE=1 SV=1 # Q13620 Cullin-4B OS=Homo sapiens GN=CUL4B PE=1 SV=4 # Q13620-3 Isoform 3 of Cullin-4B OS=Homo sapiens GN=CUL4B # Q13620-1 Isoform 2 of Cullin-4B OS=Homo sapiens GN=CUL4B #
LQLEYC*SLSAASCEPLASVL R	C152	2.346955	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 # H0YMV8 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=1 SV=1 # Q71UM5 40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3 # P42677 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 #
LTEGC*SFR	C93;C77;C77	2.337585	H0YMV8 Q71UM5 P42677	P49588-2 Isoform 2 of Alanine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=AARS # P49588 Alanine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 # F8W8D4 NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=1 # Q8TBC4-2 Isoform 2 of NEDD8- activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 # Q8TBC4 NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=2 # P55265-2 Isoform 2 of Double-stranded RNA- specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265-5 Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR #
AEVAAEFLNDRVPC*NVVP HFNK	C98;C125;C139	2.26032333	F8W8D4 Q8TBC4 Q8TBC4	H0YCK3 Double-stranded RNA-specific adenosine deaminase (Fragment) OS=Homo sapiens GN=ADAR PE=1 SV=1 # P55265-4 Isoform 4 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR # P55265 Double-stranded RNA- specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 # P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # P46777 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 # Q5T7N0 60S ribosomal protein L5 (Fragment) OS=Homo sapiens GN=RPL5 PE=1 SV=2 # P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 # P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 # P55060 Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 # P35241-5 Isoform 5 of Radixin OS=Homo sapiens GN=RDX # P35241 Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 #
RNAEFLTC*NIPTSNASNNMV TTEK	C392;C97;C387; C435;C392	2.233535	P55265 P55265 H0YCK3 P55265 P55265	
LEIC*NLTPDTLTSDTYKK	C341	2.19761333	P17655	
KITIADC*GQLE	C161	2.1612	P62937	
C*ELLYEGPPDDEAAMGIK	C369	2.13468	P13639	
IEGDMIVC*AAYAHLPK	C76;M23 C26	2.1176125	P46777 Q5T7N0	
LGEWVGLC*K	C92	2.0869	P25398	
AFTKPEEAC*SFILSADFPALV VK	C134	2.050646	P22102	
SQIC*DAAALYAQK	C272	2.00269	P55060	
EAILNDEIYC*PPETAVLLASY AVQAK	C117;C117	1.96172667	P35241 P35241	



YGIIC*MEDLIHEIYTVGK	C186	1.95996421	P18124 A8MUD9	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 # A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 #
DLTTAGAVTQC*YR	C80;C109;C80;C109	1.93125333	M0R3D6 M0R117 M0R1A7 Q02543	M0R3D6 60S ribosomal protein L18a (Fragment) OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R117 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R1A7 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 #
C*NWILDGDLYHK	C104;C65;C117	1.910895	O43237 B4E2E0 Q9Y6G9	O43237 Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1 # B4E2E0 Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1 # Q9Y6G9 Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3 #
LQVEPAVDTSQVQC*YGPGE EGQGVFR	C1260;C1233;C1260	1.87598	P21333 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
NMNC*IEMGGNPLENSGFEP GAFDGLK	C187;C204	1.8720875	P21810 C9JKG1	P21810 Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 # C9JKG1 Biglycan (Fragment) OS=Homo sapiens GN=BGN PE=1 SV=1 #
FVLSGANIMC*PGLTSPGAK	C113;M113 C114 C101;M112	1.8692375	Q9ULC4 Q9ULC4 Q9ULC4	Q9ULC4-2 Isoform 2 of Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 # Q9ULC4 Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1 # Q9ULC4-3 Isoform 3 of Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 #
GC*STVLSPEGSAQFAAQIFG LSNHLVWSK	C374	1.8347	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
TLIQNC*GASTIR	C417;C410;C455	1.82635	P49368 B4DUR8 P49368	P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 # B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 # P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 #
STPYEC*GFDPMSPAR	C39	1.812155	P03897	P03897 NADH-ubiquinone oxidoreductase chain 3 OS=Homo sapiens GN=MT-ND3 PE=1 SV=1 #
NC*IVLIDSTPYR	C100;C80	1.80461	P62241 Q5JR95	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 # Q5JR95 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=1 #
DLQPFTC*QALVYR	C292;C404	1.77545	Q14137 Q14137	Q14137-2 Isoform 2 of Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 # Q14137 Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 #
TIEEYAVC*PDLK	C160	1.73690667	P36871	P36871 Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 #
LQAFSAAIESC*NK	C342	1.70974	Q02790	Q02790 Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 #
LQDEELDPEFVQQVADFC*S YIFSNSK	C270	1.69742	P32455	P32455 Guanylate-binding protein 1 OS=Homo sapiens GN=GBP1 PE=1 SV=2 #
C*AMTALSSK	C158	1.69565	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
AC*LIFDFEIDAIGGAR	C270	1.65441	P35998	P35998 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 #

SSGEIVYC*GQVFEK	C35;C64;C35;C6 4	1.6354675	M0R3D6 M0R117 M0R1A7 Q02543	M0R3D6 60S ribosomal protein L18a (Fragment) OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R117 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # M0R1A7 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 # Q9BY44-4 Isoform 4 of Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A # Q9BY44 Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=1 SV=3 #
C*DPVDFDGTGPR	C245;C306	1.6353	Q9BY44 Q9BY44	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 # Q13162 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 # Q13867 Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1 # Q8WUM4-2 Isoform 2 of Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCC6IP # Q8WUM4 Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCC6IP PE=1 SV=1 #
INALTAASEAAC*LIVSVDETIK NPR	C511	1.61987333	Q99832	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
HGEVC*PAGWKPGSETIIPDP AGK	C245	1.616425	Q13162	Q13162 Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 #
LNSDPQFVLAQNVGTTDLL DIC*LK	C40	1.5658075	Q13867	Q13867 Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1 #
SCVLFNC*AALASQIAAEQNL DNDEGLK	C127;C127	1.54969	Q8WUM4 Q8WUM4	Q8WUM4-2 Isoform 2 of Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCC6IP # Q8WUM4 Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCC6IP PE=1 SV=1 #
TVPFC*STFAAFFTR	C394;C386	1.50066625	P29401 P29401	P29401-2 Isoform 2 of Transketolase OS=Homo sapiens GN=TKT # P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 #
MSVIEEGDC*KR	C437	1.4768575	P11216	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 #
LNISFPATGC*QK	C12	1.476848	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #
TDC*SPIQFESAWALTNIASG TSEQTK	C133	1.47376333	P52292	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
VSC*LGVTDDGMAVATGSW DSFLK	C317;C273;C31 7	1.470435	P62879 E7EP32 P62873	P62879 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 # E7EP32 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=1 # P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 #
KPVVDCVSVPC*FYTDAER	C146	1.445085	P34932	P34932 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 #
AC*LISLGYDIGNDPQGEAEF AR	C774	1.439285	P12814	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 #
ATC*IGNNSAAAVSMLK	C163;C163;C16 3	1.425115	H0YL69 P25789 H0YMZ1	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
LTESPC*ALVASQYGWSGNM ER	C645	1.415894	P14625	P14625 Endoplasmic reticulum chaperone protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 # E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
AVLFC*LSEDKK	C77;C22;C39;C3 9	1.415312	E9PK25 G3V1A4 P23528 E9PP50	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
QAFTDVATGSLGQGLGAAC* GMAYTGK	C133	1.40718833	P29401	P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 #

FVTTEFEPC*FDAADFIR	C220;C252;C252	1.403075	P50440 P50440 P50440	P50440-2 Isoform 2 of Glycine amidinotransferase# mitochondrial OS=Homo sapiens GN=GATM # P50440 Glycine amidinotransferase# mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 # P50440-3 Isoform 3 of Glycine amidinotransferase# mitochondrial OS=Homo sapiens GN=GATM #
LC*PQFLQLASANTAR	C264;C264;C264	1.384435	O95630 O95630 C9JK83	O95630-2 Isoform 2 of STAM-binding protein OS=Homo sapiens GN=STAMBP PE=1 SV=1 # O95630-2 Isoform 2 of STAM-binding protein OS=Homo sapiens GN=STAMBP # C9JK83 STAM-binding protein (Fragment) OS=Homo sapiens GN=STAMBP PE=1 SV=1 #
VLEALKDLINEAC*WDISSSG VNLQSMDSHVSLVQLTLR	C27	1.381515	P12004	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 # O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 #
ASVGFGGSC*FQK	C276;C209;C179	1.37357667	O60701 O60701 O60701	O60701-2 Isoform 2 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH # O60701-3 Isoform 3 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH #
TSGLMTRHC*TANGTWTGTA PDCTIISCGDPGLANGIQFG TDFTFNK	C2881;M3015 C3020 C3019;M3016 C2437;M2877 C3020;M3016	1.371425	H7BXU2 F5GZ18 A0A0U1R QY1 Q96PZ7 E5RIG2	H7BXU2 CUB and sushi domain-containing protein 1 (Fragment) OS=Homo sapiens GN=CSMD1 PE=1 SV=1 # F5GZ18 CUB and sushi domain-containing protein 1 OS=Homo sapiens GN=CSMD1 PE=1 SV=2 # A0A0U1RQY1 CUB and sushi domain-containing protein 1 OS=Homo sapiens GN=CSMD1 PE=1 SV=1 # Q96PZ7 CUB and sushi domain-containing protein 1 OS=Homo sapiens GN=CSMD1 PE=1 SV=2 # E5RIG2 CUB and sushi domain-containing protein 1 OS=Homo sapiens GN=CSMD1 PE=1 SV=1 #
LVDFPMDGHAC*PLKFGSYA YPK	C186	1.35979	P48169	P48169 Gamma-aminobutyric acid receptor subunit alpha-4 OS=Homo sapiens GN=GABRA4 PE=2 SV=2 # Q9BTT0 Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1 # Q9BTT0-3 Isoform 3 of Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E #
C*PNLTYLNLSGNK	C87;C39	1.3589525	Q9BTT0 Q9BTT0	P30041 Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 # P23526-2 Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHCY # P23526 Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 # Q9UKK9 ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1 #
DFTPVC*TTELGR	C47	1.35044	P30041	A6NFX8 ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1 # A6NJU6 ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=2 #
FDNLYGC*R	C167;C195	1.34275	P23526 P23526	P62424 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 # B0YJC4 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=1 # P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 #
TLHYEC*IVLVK	C76;C89;C76	1.320285	Q9UKK9 A6NFX8 A6NJU6	Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 #
TC*TTVAFTQVNSDKGALAK	C199	1.31715	P62424	
QVQSLTC*EVDALK	C328;C328	1.31708333	B0YJC4 P08670	
DLLSETADPPFFVLNSDVIC*DF PFQAMVQFHR	C113	1.29298	Q9Y5P6 Q9Y5P6	

FSGYQQDC*QELLAFLLDG LHEDLNR	C352;C356;C38 1	1.27860667	Q9Y4E8 Q9Y4E8 Q9Y4E8	Q9Y4E8-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 # Q9Y4E8-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 # Q9Y4E8 Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 PE=1 SV=3 #
MLPTYVC*ATPDGTEKGDFL ALDLGGTNFR	C517 C489;M511	1.27009	E9PB90 P52789	E9PB90 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=1 # P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 #
GC*TATLGNFAK	C229	1.26475571	P15880	P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 #
LNEDMAC*SVAGITSDANVLT NELR	C74;C74;C74	1.26350545	H0YL69 P25789 H0YMZ1	H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
EKLC*YVALDFENEMATAASS SSLEK	C219	1.25399438	P68133 P68032 P62736	P68133 Actin# alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 # P68032 Actin# alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 # P62736 Actin# aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 #
TNHIGHTGYLNTVTVSPDGSL C*ASGGK	C207	1.23907333	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
VFNVFC*LYGNVEK	C345;C404	1.22830667	M0QXS5 P14866	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
TLQNTMVNLGLQNAC*DEAIY QLGLDLEEEIEEDAGLNG GLGR	C109	1.22594091	P11216	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 #
VC*TLAIIDPGDSDIIR	C92;C92	1.21123526	P62888 E5RI99	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #
LLLC*GGAPLSATTQR	C450	1.20914	O95573	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 #
LGDESC*FNMILATR	C363	1.19875	P20073 P20073	P20073 Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 # P20073-2 Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7 #
HLEEPLSLQELDTSSGVLLPF FDPDTNIVYLC*GK	C285	1.1785575	P31146	P31146 Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 #
LEYC*EALAMLR	C349	1.16447	P14868	P14868 Aspartate--tRNA ligase# cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 #
QYPWGVAEVENGEHC*DFTI LR	C279;C280;C280; C260	1.16143	Q16181 Q16181 E7EPK1 E7ES33	Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 #
MVYSTC*SLNPIEDEAVIASLL EK	C85;M316 C321;M281 C286	1.14901	Q08J23 Q08J23 Q08J23	Q08J23-3 Isoform 3 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 # Q08J23 tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 # Q08J23-2 Isoform 2 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 #
ILLLC*VGEAGDTVQFAEYIQK	C46	1.14147	P49721	P49721 Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 #

				F8VZ49 Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens GN=HNRNPA1 PE=1 SV=1 # P09651 Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 # F8W617 Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=2 # Q32P51 Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2 # P09651-2 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 # F8W646 Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens GN=HNRNPA1 PE=1 SV=1 # P09651-3 Isoform 2 of Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 # A0A0B4J2A4 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # P42765 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 #
SHFEQWGTLTDC*VVMR	C62	1.11721333	F8VZ49 P09651 F8W617 Q32P51 P09651 F8W646 P09651	
LC*GSGFQSIIVNGCQEICVK	C89;C92	1.090655	A0A0B4J2 A4 P42765	
INGC*YEALSGGATTEGFEDF TGGIAEWYELK	C191	1.088478	P17655	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # O14579 Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3 # A0A087X0I4 Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=1 # M0QXB4 Coatomer protein complex# subunit epsilon# isoform CRA_g OS=Homo sapiens GN=COPE PE=1 SV=1 #
NAFYIGSYQQC*INEAQR	C34;C33;C34	1.088475	O14579 A0A087X0 I4 M0QXB4	
ITVPFLEQC*PIR	C57	1.08372667	P48147	P48147 Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 #
GYDFC*QVLQWFAER	C175;C175	1.0791825	Q9H223 A0A087W UA5	Q9H223 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 # A0A087WUA5 EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 #
DMGSC*EIYPQTIQHNPNGR	C351;M319 C322	1.06561	P35606 P35606	P35606 Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2 # P35606-2 Isoform 2 of Coatomer subunit beta' OS=Homo sapiens GN=COPB2 #
GPC*IINYEDNGIIK	C208	1.05176	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #
FSHQGVQLIDFSPC*ER	C384;C384	1.04428143	P55884 P55884	P55884 Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3 # P55884-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B #
ESFEGQMTEDNIEVGIC*NEA GFR	C213;M203 C213	1.01647	A0A024R A52 P25787	A0A024RA52 Proteasome subunit alpha type OS=Homo sapiens GN=PSMA2 PE=1 SV=1 # P25787 Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 #
IGAFGYMEC*SAK	C159	0.989185	P61586	P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 #
ELQEGTYVMVAGPSFETVAE C*R	C206	0.988755	P00491	P00491 Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 #
LTDC*VVMRDPASK	C50	0.983978	P22626 P22626 A0A087W UI2	P22626 Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 # P22626-2 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 # A0A087WUI2 Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=1 #
YIYDQC*PAVAGYGPQLPD YNR	C453	0.983295	P31930	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 #

TASLC*LERTDVC*HEAEPVR	C202 C209 C209;C202	0.971935	Q8NAP3 D6RBC4	Q8NAP3 Zinc finger and BTB domain-containing protein 38 OS=Homo sapiens GN=ZBTB38 PE=1 SV=2 # D6RBC4 Zinc finger and BTB domain-containing protein 38 (Fragment) OS=Homo sapiens GN=ZBTB38 PE=1 SV=1 #
QNVAYEYLC*HLEEAQR	C45	0.97002667	P46940	P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 #
VCENIPIVLC*GNK	C120;C138;C137;C116	0.96845667	P62826 J3KQE5 B5MDF5 F5H018	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 # J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 # B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 # F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 #
VLDALFPCVQGGTTAIPGAF GC*GK	C221;C254	0.96716	P38606 P38606	P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A # P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 #
YLEC*SALTQR	C113;C157;C157;C113;C176;C150;C113	0.93443333	J3QLK0 P60763 P15153 B1AH78 P63000 B1AH77 P63000 B1AH80 J3KSC4	J3QLK0 Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens GN=RAC3 PE=1 SV=1 # P60763 Ras-related C3 botulinum toxin substrate 3 OS=Homo sapiens GN=RAC3 PE=1 SV=1 # P15153 Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 # B1AH78 Ras-related C3 botulinum toxin substrate 2 (Fragment) OS=Homo sapiens GN=RAC2 PE=1 SV=1 # P63000 Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1 # B1AH77 Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 # P63000-2 Isoform B of Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 # B1AH80 Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 # J3KSC4 Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens GN=RAC3 PE=1 SV=1 #
INISEGNC*PER	C54;C54;C54;C54;C54;C54;C35;C54;C54;C46;C54	0.92594111	Q15366 Q15366 Q15366 Q15366 Q15366 F8VZX2 H3BRU6 Q15366 Q15366 F8VXH9 Q15365	Q15366-8 Isoform 8 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-5 Isoform 5 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-7 Isoform 7 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # F8VZX2 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # H3BRU6 Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # Q15366-4 Isoform 4 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # F8VXH9 Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #
ISTILFGAAYTC*LEAATGR	C369	0.9234925	Q9H4A4	Q9H4A4 Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 #

FMC*AQLPNPVLDSISIIDTPGI LSGEK	C152;M137 C138;M151 C152	0.91795667	A0A024R5 71 Q9H4M9 C9JC03	A0A024R571 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=1 # Q9H4M9 EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 # C9JC03 EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=1 SV=1 # P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 # G3V4W5 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # P34897-3 Isoform 3 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # P34897-2 Isoform 2 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 #	
YYGGAEEVVDIEILLC*QR	C119;C119;C98; C119	0.915715	P34897 G3V4W5 P34897 P34897	P49589-2 Isoform 2 of Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS # B4DKY1 Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=1 # P49589 Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=3 # P49589-3 Isoform 3 of Cysteine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=CARS # P02042 Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 # Q92747 Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2 # Q92747-2 Isoform 2 of Actin- related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A # O15143 Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 # E9PF58 Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=1 #	
DLLSDWLDSTLGC*DVTDNSI FSK	C204;C217;C20 4;C287	0.91487	P49589 B4DKY1 P49589 P49589	Q92747 Q92747 O15143 E9PF58	Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C # P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 # P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # E9PCY7 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 # Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 #
TFSQSELHC*DKLHVDPENF R	C94	0.89822625	P02042		
STVLSLDWHPNNVLLAAGSC *DFK	C162;C115;C16 2;C162	0.88778125	Q92747 Q92747 O15143 E9PF58		
NMQEPIALHEMDTSNGVLLP FYDPDTSIIYLC*GK	C283;M315 C336 C289;M262	0.883	Q9ULV4 Q9ULV4 Q9ULV4		
HGFC*GIPITDTGR	C140	0.881915	P12268		
GLPWSC*SADEVQR	C22;C22;C22	0.880845	P31943 G8JLB6 E9PCY7		
TDVLVLSCLDLITDVALHEVVD LFR	C106;C106;C10 6	0.87918	Q9NR50 Q9NR50 Q9NR50		

VEDMAELTC*LNEASVLHNLK	C95;M86 C91;M90 C95 C95;M90	0.87547	P35580 P35579 P35580 P35580 P35580 P35580	P35580-4 Isoform 4 of Myosin-10 OS=Homo sapiens GN=MYH10 # P35579 Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 # P35580 Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 # P35580-3 Isoform 3 of Myosin-10 OS=Homo sapiens GN=MYH10 # P35580-2 Isoform 2 of Myosin-10 OS=Homo sapiens GN=MYH10 # P35580-5 Isoform 5 of Myosin-10 OS=Homo sapiens GN=MYH10 #
TQLGAIYIDASC*LTWEGQQF Q GK	C38;C38	0.87318375	H3BRV9 P61970	H3BRV9 Nuclear transport factor 2 (Fragment) OS=Homo sapiens GN=NUTF2 PE=1 SV=1 # P61970 Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1 # Q86TX2 Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 # A0A087X0W7 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # A0A087WT95 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 # P49753 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 #
SEFYANEAC*KR	C339;C339;C38 1;C401	0.87147	Q86TX2 A0A087X0 W7 A0A087W T95 P49753	P49753 Acyl-coenzyme A thioesterase 2# mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 # P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 # G3V4W5 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # P34897-3 Isoform 3 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # P34897-2 Isoform 2 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 #
AALEALGSC*LNNK	C91;C91;C70;C9 1	0.86934667	P34897 G3V4W5 P34897 P34897	P34897 Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 # G3V4W5 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 # P34897-3 Isoform 3 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 # P34897-2 Isoform 2 of Serine hydroxymethyltransferase# mitochondrial OS=Homo sapiens GN=SHMT2 #
QPGC*LLEQLVLYDIWSEEM EDR	C427	0.86876333	P13489	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 # O00159-3 Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C # O00159 Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 # F5H6E2 Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=1 # O00159-2 Isoform 2 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C #
C*PENAFFLDHVR	C783;C802;C77 8;C767	0.864635	O00159 O00159 F5H6E2 O00159	O00159-2 Isoform 2 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C # Q9Y221 60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens GN=NIP7 PE=1 SV=1 # Q9Y221-2 Isoform 2 of 60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens GN=NIP7 # J3QLW7 60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens GN=NIP7 PE=1 SV=1 #
YIGENLQLLVDRPDGTYC*FR	C36;C36;C36	0.86098	Q9Y221 Q9Y221 J3QLW7	J3QLW7 60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens GN=NIP7 PE=1 SV=1 # P36871 Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 #
LSLC*GEESFGTGS DHIR	C374	0.85977	P36871	P36871 Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 # Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #
INDALSC*EYECR	C216;C216	0.83972	Q52LJ0 Q52LJ0	Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B # P56192 Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 # F8VPL7 Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=1 #
LFVSDGVPGC*LPVLAAGR	C12;C12	0.830835	P56192 F8VPL7	F8VPL7 Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=1 # P09661 U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 #
IGEGLDQALPC*LTELITNNS LVELGDLPLASLK	C89;C89	0.82954636	P09661 H0YKK0	H0YKK0 Small nuclear ribonucleoprotein polypeptide A' isoform CRA_a OS=Homo sapiens GN=SNRPA1 PE=1 SV=1 #



GTSQADC*AVLIVAAGVGEFE AGISK	C111;C111;C11 1;C111	0.82896	Q5VTE0 P68104 Q05639 P68104	Q5VTE0 Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 # P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 # Q7Z2W4-2 Isoform 2 of Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 # Q7Z2W4-3 Isoform 3 of Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 # C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 # Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 #
MALDALLQEIALSEPQLC*EV LQVAGPDR	C38;M21 C38	0.82892333	Q7Z2W4 Q7Z2W4 C9J6P4 Q7Z2W4	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 # P62136-2 Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA # P62136 Serine/threonine-protein phosphatase PP1- alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 # P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 # E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 # E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 #
ALVDGPC*TQVR	C42;C42	0.82711667	E7EPB3 P50914	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 # P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 # E9PP50 Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=7 #
IC*GDIHGQYYDLLR	C73;C62	0.82370667	P62136 P62136	A0A087W YC1 P34932 P34932 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=1 # P59998 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 # F8WCF6 Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4-TLL3 PE=3 SV=1 # P59998-3 Isoform 3 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 # P29401 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 #
NQSFC*PTVNLDKLWTLVSE QTR	C70;C70;C13	0.82215467	P46776 E9PLL6 E9PJD9	
HFVLDEC*DK	C197	0.81985667	O00148	
VNQAIWLLC*TGAR	C155;C176;C15 5	0.81896	P46782 M0R0R2 M0R0F0	
HELQANC*YEEVKDR	C177;C122;C13 9;C139	0.81531385	E9PK25 G3V1A4 P23528 E9PP50	
KFDEVLVNHFC*EEFGK	C245;C245	0.808795	A0A087W YC1 P34932	
ATLQAALC*LENFSSQVVER	C21;C21;C40	0.80642375	P59998 F8WCF6 P59998	
MAAISESNINLCGSHC*GVSI GEDGPSQMALEDLAMFR	C417	0.80425	P29401	

NLSDLIDLVPVSLC*EDLLSSVD QPLK	C36;C36;C65;C2 4;C62	0.80129333	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
FC*TGLTQIETLFK	C254	0.7968375	P12277	P12277 Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 # P61160-2 Isoform 2 of Actin-related protein 2 OS=Homo sapiens GN=ACTR2 # P61160 Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 #
VVVC*DNGTGFVK	C11;C11	0.7967	P61160 P61160	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 # G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # H3BRW9 Dual- specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=1 # Q02750 Dual specificity mitogen- activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 #
LGTLAPFC*CPWEQLTQDWE SR	C705	0.79661	Q99575	Q16531 DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 # F5H157 Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=1 SV=1 # Q15286 Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 # P19623 Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 # B7Z4D2 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-4 Isoform 4 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95-3 Isoform 3 of Syntabulin OS=Homo sapiens GN=SYBU # Q9NX95 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=2 # B3KRD1 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-2 Isoform 2 of Syntabulin OS=Homo sapiens GN=SYBU # A0A0C4DG86 Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=1 # Q9NX95-5 Isoform 5 of Syntabulin OS=Homo sapiens GN=SYBU # P84077 ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2 # P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 # P30566 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 # Q02809-2 Isoform 2 of Procollagen-lysine#2- oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 # Q02809 Procollagen- lysine#2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 #
LC*DFGVSGQLIDSMANSFV GTR	C114;C31;C207; C181;C211	0.79499	G5E9C7 H3BRW9 Q02750 Q02750 P36507	
IGRPSETGIIGIIDPEC*R	C128	0.79167	Q16531	
ENVNVEEMFNC*ITELVLR	C147;C163	0.79115	F5H157 Q15286	
DEFSYQEMIANLPLC*SHPNP R	C89	0.7876975	P19623	
LESLQSMEMAHSGSLRDEL C*LDFPCDSPEK	C259;C386;C38 8;C389;C183;C3 21;C394;C270	0.786375	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	
NWYIQATC*ATSGDGLYEGL DWLSNQLR	C159	0.78564455	P84077	
VVMALGDYMGASCHAC*IGG TNVR	C134	0.78305	P60842	
YASPEMC*FVFSDR	C27	0.77958	P30566	
VGVDYEGGGC*R	C727;C680	0.77000333	Q02809 Q02809	

EENVGLHQTLTDLNQLNLC*I	C283;C109;C247	0.76978333	P67936 K7EPB9 P67936	P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 # K7EPB9 Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1 # P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 # Q14697 Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 # Q14697-2 Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB #
WNYRDEADVLEVDQGFDDH NLPC*DVIWLDIEHADGK	C423;C445	0.76736	Q14697 Q14697	P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 # P09960 Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 # Q92973 Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 # Q92973-2 Isoform 2 of Transportin-1 OS=Homo sapiens GN=TNPO1 #
ALNWDSFNTGDC*FILDGQ NIFAWCGGK	C165;C165	0.76427333	P40121 P40121	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 # O75874 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 #
PEIVDTC*SLASPASVCR	C8	0.763845	P09960	Q9Y490 Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 #
SEC*LNNIGDSSPLIR	C103;C95	0.762465	Q92973 Q92973	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 #
VPANVSVVDLTC*R	C247	0.76088143	P04406	A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #
SEGFIWAC*K	C269	0.75454	O75874	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
ALC*GFTEAAAQAAYLVGVS DPNSQAGQQGLVEPTQFAR	C1434	0.74981	Q9Y490	P13807 Glycogen [starch] synthase# muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2 # P13807-2 Isoform 2 of Glycogen [starch] synthase# muscle OS=Homo sapiens GN=GYS1 #
FDPTQFQDC*IIQGLTETGTD LEAVAK	C35;C67;C39	0.74719636	Q7L1Q6 Q7L1Q6 Q7L1Q6	B4E3S0 Coronin OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C #
GQVLSVC*VEEENIIPYITNVL QNPDLALR	C332;C328;C328	0.74582778	A0A087WVQ6 VQ6 Q00610 Q00610	P61081 NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1 # P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 #
KDC*EVVMMIGLPGAGK	C497	0.74317	Q00839 Q00839	
YLC*AGAVDFYNNLENFNVD KEAGER	C214;C150	0.742005	P13807 P13807	
NGSLIC*TASK	C85;C196;C190; C243	0.736915	B4E3S0 Q9ULV4 Q9ULV4 Q9ULV4	
TC*DISFSDPDDLNFK	C47	0.73517333	P61081	
DAFEHIVTQFSSVPVSVVSDS YDIYNAC*EK	C287	0.73367923	P43490	

EGGVQLLLTIVDTPGFGDAV DNSNC*WQPVIDYIDSK	C125;C126;C126; C106	0.73336667	Q16181 Q16181 E7EPK1 E7ES33	Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 # Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # P09104 Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3 # P13929 Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 # P06733-2 Isoform MBP-1 of Alpha-enolase OS=Homo sapiens GN=ENO1 # P13929-3 Isoform 3 of Beta-enolase OS=Homo sapiens GN=ENO3 # P06733 Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 # P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 # Q15102 Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PFAH1B3 PE=1 SV=1 # MOR389 Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens GN=PFAH1B3 PE=1 SV=7 # MOR323 Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens GN=PFAH1B3 PE=1 SV=1 # MQXS6 Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens GN=PFAH1B3 PE=1 SV=1 # MQZT2 Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens GN=PFAH1B3 PE=1 SV=7 # MOR1K3 Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens GN=PFAH1B3 PE=1 SV=1 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # P08237-3 Isoform 3 of ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM # P08237 ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 # Q86SQ6-1 Isoform 1 of Adhesion G protein-coupled receptor A1 OS=Homo sapiens GN=ADGRA1 # P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 # P26639 Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 # P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 #
ISAFGYLEC*SAK	C159;C159;C159; 9	0.73013667	Q5JR08 P08134 E9PQH6	
AYHEQLSVAEITNAC*FEPAN QMVK	C280	0.72435706	P68366 P68363 Q71U36 P68366	
SGETEDTFIADLVVGLC*TGQI K	C389;C389;C296; C346;C389	0.7222188	P09104 P13929 P06733 P13929 P06733	
LSSC*DSFTSTINELNHCLSLR	C92	0.7162	P07814	
DKEPEVFIGDSLVLQMHQC* EIWR	C55;C55;C55;C55; 5;C55;C50	0.714865	Q15102 MOR389 MOR323 MQXS6 MQZT2 MOR1K3	
DLEEDHAC*IPIKK	C567	0.710925	P13639	
IC*DQWDNLGALTQK	C480	0.7080125	P12814	
SSYLNIVGLVGSIDNDFC*GT DMTIGTDSALHR	C241;C170	0.703335	P08237 P08237	
PSPGAAMLVC*EETLELGAQ GCWGSTSPR	C210	0.70319667	Q86SQ6	
SSLQYSSPAPDGC*GDQTLG DLLLTPTR	C646	0.70085	P22102	
TTPYQIAC*GISQGLADNTVIA K	C107	0.6978	P26639	
VFADYEAYMQC*QAQVDQLY R	C784	0.69736833	P11216	

LC*LNICVGESGDR	C21;C19;C20	0.697025	P62913 Q5VVC8 P62913	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 # Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 # P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 #
MSSYAFFVQTC*R	C23	0.6954325	B2RPK0	B2RPK0 Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 #
C*LHNFLTDGVPAEGAFTEDF QGLR	C316;C268	0.69506833	G3V1A6 P57764	G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 #
AVASQLDC*NFLK	C153;C207;C19 3;C193	0.69171833	H0YJS8 A0A087X2 I1 P62333 H0YJC0	H0YJS8 26S protease regulatory subunit 10B (Fragment) OS=Homo sapiens GN=PSMC6 PE=1 SV=2 # A0A087X211 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # H0YJC0 26S protease regulatory subunit 10B (Fragment) OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
TC*LLISYTTNK	C18;C18;C18	0.69133	P60953 Q5JYX0 P60953	P60953-1 Isoform 1 of Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 # Q5JYX0 Cell division control protein 42 homolog (Fragment) OS=Homo sapiens GN=CDC42 PE=1 SV=1 # P60953 Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2 #
HDDSSDNFC*EADDIQSPEA EYVDLLLNP	C166	0.68937316	Q96HE7	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 #
TNLLQVC*ER	C985;C1053	0.689325	P18206 P18206	P18206-2 Isoform 1 of Vinculin OS=Homo sapiens GN=VCL # P18206 Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 #
TIAEC*LADELINAAK	C172;C193;C17 2;C102	0.688685	P46782 M0R0R2 M0R0F0 M0QZN2	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0QZN2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 #
LC*LISTFLEDGIR	C32;C32;C32	0.68267	O15260 Q5T8U5 O15260	O15260 Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3 # Q5T8U5 Surfeit 4 OS=Homo sapiens GN=SURF4 PE=1 SV=1 # O15260-2 Isoform 2 of Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 #
ECISIHVGQAGVQIGNACWEL YC*LEHGIQPDGQMPSDK	C25	0.6764025	Q9BQE3 Q71U36	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 #
LDTNSDGQLDFSEFLNLIGGL AMAC*HDSFLK EGTSSSQGIPQLVSNISAC*Q VIAEAVR	C91 C29	0.67606038 0.67601556	P31949 Q99832	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 # Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
NAFAC*FDEEATGTIQEDYLR	C108;C114;C10 9	0.67478471	P19105 J3QRS3 O14950	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 # J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 # O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 #

MQHLNPDPLIPEQITTDITP EC*LVSPR	C520;M498 C520	0.67478	Q96AC1 Q96AC1 Q96AC1	Q96AC1-2 Isoform 2 of Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 # Q96AC1-3 Isoform 3 of Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 # Q96AC1 Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1 #
KDYEEIGPSIC*R	C408	0.67303714	P61158	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
AYHEQLTVAEITNAC*FEPAN QMVK	PTM index from ip2	0.672346	uniprot	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # K7EK42 Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=1 # K7EL99 Tubulin-folding cofactor B (Fragment) OS=Homo sapiens GN=TBCB PE=1 SV=2 # Q99426 Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2 #
LDQEDALLGSYPVDDGC*R	C377	0.66734667	P30153	
VTQNLPMKEGC*TEVSLLR	C303;C303;C23 1;C303;C650;C2 31;C303;C266;C 285;C303	0.663156	Q13509 P07437 Q5ST81 P68371 A0A0B4J2 69 Q13509 P04350 K7ESM5 Q5JP53 Q9BUF5	H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #
TVYGGGC*SEMLMAHAVTQL ANR	C257;C257	0.66228	P63261 P60709	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 # P78371-2 Isoform 2 of T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 # Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 #
SQEATEAAPSC*VGDMADTP R	C481;C464;C48 0	0.65835	Q16222 Q16222 Q16222	P25705 ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 # P25705-3 Isoform 3 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 # P25705-2 Isoform 2 of ATP synthase subunit alpha# mitochondrial OS=Homo sapiens GN=ATP5A1 #
YTIVVSATASDAAPLQYLAPY SGC*SMGEYFR	C158;C13	0.65535318	Q14974 Q14974	K7ERZ3 Perilipin-3 (Fragment) OS=Homo sapiens GN=PLIN3 PE=1 SV=1 # O60664-3 Isoform 3 of Perilipin-3 OS=Homo sapiens GN=PLIN3 # O60664 Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 # O60664-2 Isoform 2 of Perilipin-3 OS=Homo sapiens GN=PLIN3 # O60664-4 Isoform 4 of Perilipin-3 OS=Homo sapiens GN=PLIN3 # P13674-2 Isoform 2 of Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 # P13674-3 Isoform 3 of Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 # P13674 Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2 #
DIAQQLQATC*TSLGSSIQGL PTNVKDQVQQAR	C109	0.65478	P11217	
SFLTAEDC*FELGK	C208	0.65476	O60684	
WLVLC*NPGLAEVIAER	C361;C310;C40 0;C376;C376;C3 76	0.6516375	P68366 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P11217 Glycogen phosphorylase# muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 #

VHSPSGALEEC*YVTEIDQDK YAVR	C48;C19	0.65009467	Q14558 Q14558	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
ADIIIVSELLGSFADNELSPEC* LDGAQHFLK	C61	0.64330429	Q6PD74	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 # O14744-5 Isoform 5 of Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 #
EC*LPLIIFLR	C426;C467	0.638965	P12955 P12955	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 # P45974-2 Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 # P45974 Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 #
AQVPFSSC*LEAYGAPEQVD DFWSTALQAK	C209	0.635905	P13797	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #
C*FIVGADNVGSK	C253	0.63459778	Q9H8X2	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
ILATGANVILTTGGIDDMC*LK	C241;C241	0.633358	Q14865 Q14865	O00273-2 Isoform DFF35 of DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA # O00273 DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1 #
EDLSSIIILLSEEDLQMLVDAP C*SDLAQELR	C1767	0.633254	P78527	O75083 WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 #
GPVTDVAYSHDGAFLAVC*D ASK	C513	0.632293	Q96RS6	Q96NY7-2 Isoform A of Chloride intracellular channel protein 6 OS=Homo sapiens GN=CLIC6 # Q96NY7 Chloride intracellular channel protein 6 OS=Homo sapiens GN=CLIC6 PE=2 SV=3 #
AGYDGESIGNC*PFSQR	C109;C109;C109 9;C109	0.6320525	Q15366 Q15366 Q15366 Q15366	Q14697 Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 # Q14697-2 Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB #
SSEC*MKDDPITLFLVALSPQG TAQGELFLDDGHTFNQTR	C155	0.62975125	P41250	P11216 Glycogen phosphorylase# brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 # P11217 Glycogen phosphorylase# muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 # E9PK47 Alpha-1#4 glucan phosphorylase OS=Homo sapiens GN=PYGL PE=1 SV=1 # P06737 Glycogen phosphorylase# liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 #
LAAC*FLDSMATLGLAAYGYG IR	C79;C79;C79;C79 9;C79	0.62629091	J3KTF8 P52565 P52565 J3QQX2 J3KRY1	P50991-2 Isoform 2 of T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 # P50991 T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 # Q92597 Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1 #
AQDIEAGDGTTSVVIIAGSLLD SC*TK	C182;C182;C197 7;C386	0.623615	I3L3Q4 Q9HC38 Q9HC38 F6TLX2	Q16222 UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3 # Q16222-2 Isoform AGX1 of UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 # Q16222-3 Isoform 3 of UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 #
FALNNPEMVEGLVLINVNPC* AEGWMDWAASK	C46;C37	0.62184909	Q9UGI8 Q9UGI8	
TNPTEPVGVVC*R	C46;C72	0.62157	A0A087W YS6 Q8TAA3	
GTFATLSELHC*DK	C192;C229;C170	0.61753	O00743 O00743 O00743	P68871 Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 #

LGEVSVESENYVQAVEEFQS C*LNLQEQYLEAHDR	C774;C787;C59 1;C769	0.61733333	K4DI93 Q13620 Q13620 Q13620	P49321-2 Isoform 2 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321-4 Isoform 4 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # P49321-3 Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP # Q5T624 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=1 # P49321 Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 # Q07866-6 Isoform N of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-7 Isoform P of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 # Q07866-4 Isoform J of Kinesin light chain 1 OS=Homo sapiens GN=KLC1 #
YEVAVPLC*K	C152	0.61449333	P13489	P08237-2 Isoform 2 of ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM # P08237-3 Isoform 3 of ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM # P08237 ATP-dependent 6-phosphofructokinase# muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 # Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=7 # Q5JR07 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # C9JX21 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # Q5JR05 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOA PE=4 SV=1 # C9JNR4 Transforming protein RhoA (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOA PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOA PE=1 SV=1 # A0AVT1 Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1 #
C*NENYTTDFINLYSEEGK	C93;C77;C77	0.613006	H0YMV8 Q71UM5 P42677	
LVIVGDGAC*GK	C152;C152	0.61114286	P49588 P49588	
LYATVYC*IPFAEEDLSADALL NILSEVK	C98;C125;C139	0.610985	F8W8D4 Q8TBC4 Q8TBC4	
IAEDLGGPYVWGQYDLLVLP PSFPYGGMENPC*LTFVTPTL LAGDK	C392;C97;C387; C435;C392	0.61061875	P55265 P55265 H0YCK3 P55265 P55265	P09960-3 Isoform 3 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H # P09960 Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 # P09960-2 Isoform 2 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H # P09960-4 Isoform 4 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H #
TTYQALPC*LPSMYGYPNR	C341	0.61043	P17655	P53621 Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 # A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #
DHQPC*IIFMDEIDAIGGR	C161	0.60822	P62937	
ISGADINSIC*QESGMLAVR	C369	0.60678	P13639	P43686-2 Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 # P43686 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 # S4R369 39S ribosomal protein L37# mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=1 # Q9BZE1 39S ribosomal protein L37# mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2 #
NHIENQDEC*VLNVISHAR	C76;M23 C26	0.60533	P46777 Q5T7N0	



VSDTVVEPYNATLSVHQLVE NTDETYC*IDNEALYDICFR	C92	0.60519727	P25398	P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # Q5ST81 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # A0A087X054 Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 # Q9Y4L1 Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 # Q9Y4L1-2 Isoform 2 of Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 # A0A087WWI4 Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 # E9PJ21 Hypoxia up-regulated protein 1 (Fragment) OS=Homo sapiens GN=HYOU1 PE=1 SV=1 # K7EQK2 Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 # P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 # P17858 ATP-dependent 6- phosphofructokinase# liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 # Q9NP72-2 Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 # Q9NP72 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # H0Y6T8 Ras-related protein Rab-18 (Fragment) OS=Homo sapiens GN=RAB18 PE=1 SV=1 # A0A087X163 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # Q5W0J0 Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 # H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 # P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 # Q9Y617 Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 # G8JLA2 Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1 # P60660-2 Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 # P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 # P62258-2 Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE # Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #
VEFEELC*ADLFEVPGPVQ QALQSAEMSLDEIEQVILVGG ATR	C134	0.6018625	P22102	
YYTSASGDENVSLKDYC*TR	C272	0.600975	P55060	
C*HDYYTTEFLYNLYSSEGK	C117;C117	0.598795	P35241 P35241	
LDNWLNELETYC*TR	C186	0.59776667	P18124 A8MUD9	
LYQVEYAMEAIGHAGTC*LGI LANDGVLLAAER	C80;C109;C80;C 109	0.59684	M0R3D6 M0R117 M0R1A7 Q02543	
VFIMDNC*EELIPEYLNfir	C104;C65;C117	0.59312088	Q43237 B4E2E0 Q9Y6G9	
SQTIYEIIDNSQGFYVC*PVEP QNR	C1260;C1233;C 1260	0.58987	P21333 Q60FE5 P21333	
ILYSQC*GDVMR	C187;C204	0.58954667	P21810 C9JKG1	
LICC*DILDVLDK	C113;M113 C114 C101;M112	0.589365	Q9ULC4 Q9ULC4 Q9ULC4	
LEVDAIVNAANSSLLGGGGV DGC*IHR	C374	0.58867625	P22234	

MVSDINNAWGC*LEQVEKGY EEWLLNEIR	C417;C410;C45 5	0.5877475	P49368 B4DUR8 P49368	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 #  P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # P68371 Tubulin beta- 4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # Q01813 ATP-dependent 6- phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # P23381 Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2 # P23381-2 Isoform 2 of Tryptophan--tRNA ligase# cytoplasmic OS=Homo sapiens GN=WARS # P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # P27361 Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 PE=1 SV=4 # E9PQW4 Mitogen-activated protein kinase OS=Homo sapiens GN=MAPK3 PE=1 SV=1 # P28482 Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3 # E9PJF0 Mitogen-activated protein kinase OS=Homo sapiens GN=MAPK3 PE=1 SV=1 # P27361-3 Isoform 3 of Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 # P60228 Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 # P17858 ATP-dependent 6- phosphofructokinase# liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 # Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 # P61160-2 Isoform 2 of Actin-related protein 2 OS=Homo sapiens GN=ACTR2 # P61160 Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 # P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
VSDTVVEPYNATLSVHQLVE NTDETYCIDNEALYDIC*FR	C39	0.58769	P03897	
YAYLNVVGMVGSIDNDFC*G TDMTIGTDSALHR	C100;C80	0.58759294	P62241 Q5JR95	
DRTDIQCLIPC*AIDQDPYFR	C292;C404	0.58710222	Q14137 Q14137	
CPEALFQPSFLGMESC*GIHE TTFNSIMK	C160	0.58681647	P36871	
HYLDQLNHILGILGSPSQEDL NC*I	C342	0.57799333	Q02790	
VWNLANC*K	C270	0.57727	P32455	
ECESVLVNDFFLVAC*LEDFIE NAR	C158	0.57619667	Q99832	
SLHDALC*VVK	C270	0.574812	P35998	
VNIEGGAIALGHPLGASGC*R	C35;C64;C35;C6 4	0.57435	M0R3D6 M0R117 M0R1A7 Q02543 Q9BY44 Q9BY44	
VDLNSNGFIC*DYELHELFFK	C245;C306	0.57382632	Q9BY44 Q9BY44	
TYSHLNIAGLVGSIDNDFC*G TDMTIGTDSALHR	C511	0.570745	Q99832	
LLYEALVDC*KK	C245	0.5688	Q13162	
IEC*SDNGDGTCSVSYLPTKP GEYFVNILFEEVHIPGSPFK	C40	0.568015	Q13867	
VC*EEIAIPSK	C127;C127	0.565769	Q8WUM4 Q8WUM4	
LC*YVGYNIEQEQQK	C394;C386	0.56452429	P29401 P29401	
C*EFQDAYVLLSEK	C437	0.56142714	P11216	

LNIIISNLDC*VNEVIGIR	C12	0.56142333	P62753	P30154-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B # P30154-5 Isoform 5 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B # P30154 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #
INPVC*PADLVIDHSIQVDFNR	C133	0.56110125	P52292	P21399 Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 # O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 #
DVLNLVYLC*EALNLPEVAR	C317;C273;C317	0.55931333	P62879 E7EP32 P62873	O60701-2 Isoform 2 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH # O60701-3 Isoform 3 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH #
YDC*SSADINPIGGISK	C146	0.55602333	P34932	Q6IA69 Glutamine-dependent NAD(+) synthetase OS=Homo sapiens GN=NADSYN1 PE=1 SV=3 # Q6IA69-2 Isoform 2 of Glutamine-dependent NAD(+) synthetase OS=Homo sapiens GN=NADSYN1 #
EGVVEC*SFVK	C774	0.5552475	P12814	P40926 Malate dehydrogenase# mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 # P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
VIGSGC*NLDSAR	C163;C163;C163	0.55398	H0YL69 P25789 H0YMZ1	P50135 Histamine N-methyltransferase OS=Homo sapiens GN=HNMT PE=1 SV=1 #
VQAQYPGVC*INNEVVEPSA EQIAK	C645	0.55328333	P14625	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 #
NWYVQPSC*ATSGDGLYEGL TWLTSNYKS	C77;C22;C39;C39	0.55153429	E9PK25 G3V1A4 P23528 E9PP50	Q70CQ2 Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens GN=USP34 PE=1 SV=2 # Q70CQ2-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens GN=USP34 # Q70CQ2-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens GN=USP34 #
SLFGGVITNNVSLDC*EHVS QTAEFFYTVRC	C133	0.549195	P29401	P40227 T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 #
NAIDDGC*VVPGAGAVEVAM AEALIK	C220;C252;C252	0.547265	P50440 P50440 P50440	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 #
NIC*FTVWDVGGQDR	C264;C264;C264	0.54621222	O95630 O95630 C9JK83	P62304 Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 #
IEGC*IIGFDEYMNLVLDDAEE IHSK	C27	0.54523889	P12004	P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
AVSTGVQAGIPMPC*FTTALS FYDGYR	C276;C209;C179	0.54380625	O60701 O60701 O60701	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 #
LILADALC*YAHTFNPK	C2881;M3015 C3020 C3019;M3016 C2437;M2877 C3020;M3016	0.543028	H7BXU2 F5GZ18 A0A0U1R QY1 Q96PZ7 E5RIG2	

LNPPAQLPNSEGLC*EFLEYV AESLEPPSPFELLEPPPTSGGF LR	C186	0.54248	P48169	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 #
MADC*GGLPQISQPAK	C87;C39	0.54068667	Q9BTT0 Q9BTT0	Q92597 Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1 #
YNLSPSIFFC*ATPPDDGNLC R	C47	0.540545	P30041	Q00796 Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 # H0YLA4 Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=1 #
ELETVC*NDVLSLLDK	C167;C195	0.54007444	P23526 P23526	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 #
SNPENNVGLITLANDC*EVLT TLTPDTGR	C76;C89;C76	0.53902	Q9UUK9 A6NFX8 A6NJU6	P55036-2 Isoform Rpn10E of 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 # Q5VWC4 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 #
DVQIGDIVTVGEC*RPLSK	C199	0.53749556	P62424	A6PVX3 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=1 SV=1 # P55036 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 #
YDC*GEEILITVLSAMTEEA AV AIK	C328;C328	0.53358182	B0YJC4 P08670	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 # M0R1H5 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=1 #
C*LGKPADVYLIDEPSAYLDS EQR	C113	0.533455	Q9Y5P6 Q9Y5P6	P63241-2 Isoform 2 of Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A # P63241 Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 #
LC*VQNSPQEAR	C352;C356;C38 1	0.53268	Q9Y4E8 Q9Y4E8 Q9Y4E8	P61221 ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 #
AAAFVTSPPSPDPTTDFLN SLLSC*GDLQVTGSAHCTFNT AQK	C517 C489;M511	0.53267	E9PB90 P52789	P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 # P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
SLDLFNC*EITNLEDYR	C229	0.53263	P15880	E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
SLC*NLEESITSAGRDDLESF QLEISGFLK	C74;C74;C74	0.532074	H0YL69 P25789 H0YMZ1	E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
STFFNVLTNSQASAENFPFC* TIDPNESR	C219	0.53194167	P68133 P68032 P62736	A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #
				Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
				Q9BTT0 Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1 # Q9BTT0-3 Isoform 3 of Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E #
				Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #
				J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 #

TIC*SSVDKLDK	C207	0.53173333	P63244	P12081-4 Isoform 4 of Histidine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=HARS # B3KWE1 Histidine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=1 # P12081 Histidine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # P40227 T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 # Q96G03 Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4 # P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 # P15374 Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 # contaminant_UBIQUITIN10 no description#
VTDGALVVVDCVSGVC*VQT ETVLR	C345;C404	0.529326	M0QXS5 P14866	
ATVAPEDVSEVIFGHVLAAGC *GQNPVR	C109	0.52674667	P11216	
LTLACGGVALNSFDDLSPDC* LGHAGLVYEYTLGEEK	C92;C92	0.5266975	P62888 E5RI99	
YYAELC*APPGNSDPEQLKK	C450	0.52589	O95573	
YAIC*SALAASALPALVMSK	C363	0.5247675	P20073 P20073	
PVC*AVLLLLFPITEK	C285	0.524425	P31146	
DVIELTDDSFDKNVLDSEDV WMVEFYAPWC*GHCK	C349	0.524112	P14868	Q15084-2 Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-4 Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084-5 Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 # Q15084-3 Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 # P48735 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 # P48735-2 Isoform 2 of Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 #
NYDGDVQSDILAQFGSLGL MTSVLVC*PDGK	C279;C280;C280;C260	0.523445	Q16181 Q16181 E7EPK1 E7ES33	
VVMALGDYMGASC*HACIGG TNVR	C85;M316 C321;M281 C286	0.52253	Q08J23 Q08J23 Q08J23	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 #
GNIPAESYFFIDILLDIRDEI AGC*IEK	C46	0.521655	P49721	K7EJR3 26S proteasome non-ATPase regulatory subunit 8 (Fragment) OS=Homo sapiens GN=PSMD8 PE=1 SV=7 # P48556 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2 # R4GMR5 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=1 #
LC*YVALDFEQEMATVASSSS LEK	C62	0.52149333	F8VZ49 P09651 F8W6I7 Q32P51 P09651 F8W646 P09651	A5A3E0 POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 #
LEGDLTGPSVDVEVPDVELE C*PDAK	C89;C92	0.52078	A0A0B4J2 A4 P42765	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 # P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
THEAEIVEGENHTYC*IR	C191	0.52055333	P17655	Q9Y6E0-2 Isoform A of Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 # B4DR80 Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 # Q9Y6E0 Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1 #
IIDLEEAEDIEDIQQEITVLSQ C*DSPYVTK	C34;C33;C34	0.52001	O14579 A0A087X0 I4 M0QXB4	

EIYTHFTC*ATDTK	C57	0.51996	P48147	P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P08754 Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # K7ERN7 Notchless protein homolog 1 OS=Homo sapiens GN=NLE1 PE=1 SV=1 # A0A0A0MRH0 Notchless protein homolog 1 OS=Homo sapiens GN=NLE1 PE=1 SV=1 # Q9NVX2 Notchless protein homolog 1 OS=Homo sapiens GN=NLE1 PE=1 SV=4 # P55809 Succinyl-CoA:3-ketoacid coenzyme A transferase 1# mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 # P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 # Q8NCW5 NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP PE=1 SV=2 #
LQLVC*NALLAQEDPLPLAFF VHDAEIVSSLGK	C175;C175	0.51994	Q9H223 A0A087W UA5	A0A087X1H6 Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=1 # Q8IZP2 Putative protein FAM10A4 OS=Homo sapiens GN=ST13P4 PE=5 SV=1 # P50502 Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 # H7C311 Hsc70-interacting protein (Fragment) OS=Homo sapiens GN=ST13 PE=1 SV=1 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 #
DIPDGATVLVGGFGLC*GIPE NLIDALLK	C351;M319 C322	0.51753	P35606 P35606	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 # P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 #
YLAEVAC*GDDRK	C208	0.5170375	P36578	
YLSQEEAQAQVDQELFNEYQF SVDQLMELAGLSC*ATAIAK	C384;C384	0.517022	P55884 P55884	
LLGHWEAAHDLALAC*K	C213;M203 C213	0.516295	A0A024R A52 P25787	
VLC*ELADLQDKEVGDGTTT VVIIAAELLK	C159	0.51514	P61586	
DAANC*WTSLLSEYAADPW VQDQMQR	C206	0.51416	P00491	
C*IESLIAVFQK	C50	0.513448	P22626 P22626 A0A087W UI2	
VIEINPYLLGTMSGC*AADCQ YWER	C453	0.51129636	P31930	

C*DYENVPTTVFTPLEYGAC GLSEEK	C202 C209 C209;C202	0.511038	Q8NAP3 D6RBC4	E9PIR7 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 # A0A087WSY9 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=2 # Q16881 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3 # Q16881-3 Isoform 3 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-4 Isoform 4 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-6 Isoform 6 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-5 Isoform 5 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-2 Isoform 2 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # F8W809 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 # A0A087WSW9 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 #
LRPLSYPD TDVILMC*FSVDS PDSLENIPEK	C45	0.5085625	P46940	P62745 Rho-related GTP-binding protein RhoB OS=Homo sapiens GN=RHOB PE=1 SV=1 #
ITVVGVGQVGMAC*AISILGK	C120;C138;C13 7;C116	0.507977	P62826 J3KQE5 B5MDF5 F5H018	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 #
LEFSIYPAPQVSTAVVEPYNS ILTTHHTLEHSDC*AFMVDNE AIYD	C221;C254	0.506275	P38606 P38606	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
IISNASC*TTNCLAPLAK	C113;C157;C15 7;C157;C157;C1 13;C176;C150;C 113	0.50583484	J3QLK0 P60763 P15153 B1AH78 P63000 B1AH77 P63000 B1AH80 J3KSC4 Q15366 Q15366 Q15366 Q15366 Q15366 Q15366 Q15366 F8VZX2 H3BRU6 Q15366 Q15366 F8VXH9 Q15365	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
FAELVYTGFWHSPEC*EFVVR	C54;C54;C54;C5 4;C54;C54;C54; C35;C54;C54;C4 6;C54	0.50569667		P00966 Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 #

AWVWNTHADFADEC*PKPEL LAIR	C369	0.504635	Q9H4A4	C9JXG8 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=2 # P43487 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # C9JJ34 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # F6WQW2 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # C9JGV6 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=7 # P43487-2 Isoform 2 of Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #
TIQFVDWC*PTGFK	C152;M137 C138;M151 C152	0.50419	A0A024R5 71 Q9H4M9 C9JC03	P31153 S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 # P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G # P25940 Collagen alpha-3(V) chain OS=Homo sapiens GN=COL5A3 PE=1 SV=3 # P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A # P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 # P23921 Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 # P61163 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 # Q16658 Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 # P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 # Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP # Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 # O95373 Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 # Q9Y5S9-2 Isoform 2 of RNA-binding protein 8A OS=Homo sapiens GN=RBM8A # Q9Y5S9 RNA-binding protein 8A OS=Homo sapiens GN=RBM8A PE=1 SV=1 # P06737 Glycogen phosphorylase# liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 # P06737-2 Isoform 2 of Glycogen phosphorylase# liver form OS=Homo sapiens GN=PYGL #
TC*NVLVALEQQSPDIAQGVH LDR	C119;C119;C98; C119	0.50361667	P34897 G3V4W5 P34897 P34897 P49589	
KAAAPAPEEEMDEC*EQALA AEPK	C204;C217;C20 4;C287	0.50310222	B4DKY1 P49589 P49589	
ALGVQGGQAGVPEGPGFC* PQR	C94	0.50292	P02042	
YSNSDVIIYVGC*GER	C162;C115;C16 2;C162	0.50088615	Q92747 Q92747 O15143 E9PF58	
RVETNQDWSLMC*PNECPGL DEVWGEEFEK	C283;M315 C336 C289;M262	0.500335	Q9ULV4 Q9ULV4 Q9ULV4	
AC*YLSINPQKDETLETEK	C140	0.50011333	P12268	
VGKDELFALEQSC*AQVVLQ AANER	C22;C22;C22	0.49995625	P31943 G8JLB6 E9PCY7 Q9NR50	
GLC*AIAQAESLR	C106;C106;C10 6	0.498135	Q9NR50 Q9NR50	
C*VLPEEDSGELAKPK	C95;M86 C91;M90 C95 C95;M90	0.49473	P35580 P35579 P35580 P35580 P35580	
MKFDVFEDFISPTTAAQTLFF TAC*SK	C38;C38	0.49460625	H3BRV9 P61970 Q86TX2	
EAQAAMEGLNGQDLMGQPI SVDWC*FVR	C339;C339;C38 1;C401	0.49403333	A0A087X0 W7 A0A087W T95 P49753	
WLLLC*NPGLAELIAEK	C91;C91;C70;C9 1	0.494025	P34897 G3V4W5 P34897 P34897	



YWLC*AATGPSIK	C427	0.493354	P13489	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
HGLEVIYMIPIDEYCVQQLK	C783;C802;C778;C767	0.49328926	O00159 O00159 F5H6E2 O00159	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 # P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 #
LATGSDDNC*AAFFEGPPFK	C36;C36;C36	0.49156	Q9Y221 Q9Y221 J3QLW7	O75083 WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 #
FPEELTQTFMSC*NLITGMFQR	C374	0.49075313	P36871	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
GEELSC*EER	C216;C216	0.48964818	Q52LJ0 Q52LJ0	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 # H3BUZ9 Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=1 # P34949 Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=2 #
VFPLSC*AVQQYAWGK	C12;C12	0.489565	P56192 F8VPL7	H3BPP3 Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=1 # H3BMZ9 Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=1 # M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
IQHPSNVLHFFNAPLEVTEENFFEIC*DELGVK	C89;C89	0.48937	P09661 H0YKK0	A0A087WUL9 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=1 # Q9UNM6 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2 #
SSDEAVILC*K	C111;C111;C111;C111	0.489	Q5VTE0 P68104 Q05639 P68104	O00154-7 Isoform 7 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 # O00154 Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3 # O00154-6 Isoform 6 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 # O00154-5 Isoform 5 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 # O00154-4 Isoform 4 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 #
TDFLSPMC*IGEVAHVSAEITYTSK	C38;M21 C38	0.48747	Q7Z2W4 Q7Z2W4 C9J6P4 Q7Z2W4	P28066 Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 # P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #
IVEIDAHIGC*AMSGLIADAK	C42;C42	0.4841275	E7EPB3 P50914	
SYC*AEIAHNVSSK	C73;C62	0.48401	P62136 P62136	

QLFALSC*TAESEQVLPDDL GVIR	C70;C70;C13	0.482785	P46776 E9PLL6 E9PJD9	P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
C*ELSSSVQTDINLPYLTMDS SGPK	C197	0.48251875	O00148	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 # H0YBG6 Stress-70 protein# mitochondrial (Fragment) OS=Homo sapiens GN=HSPA9 PE=1 SV=1 #
FC*DNVWTFVLNDVEFR	C155;C176;C15 5	0.4820325	P46782 M0R0R2 M0R0F0	P52657 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 # A0A0B4J1Z5 Transcription initiation factor IIA subunit 2 OS=Homo sapiens GN=GTF2A2 PE=1 SV=1 #
QVLMGPYPNPTDC*PEVGFFD VLGNDR	C177;C122;C13 9;C139	0.48199	E9PK25 G3V1A4 P23528 E9PP50	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 #
DAIITC*NPEEFIVEALQLPNF QQSVQEYR	C245;C245	0.48115	A0A087W YC1 P34932	Q9BQ52 Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=ELAC2 PE=1 SV=2 # G5E9D5 ElaC homolog 2 (E. coli)# isoform CRA_a OS=Homo sapiens GN=ELAC2 PE=1 SV=1 #
DEFTNTC*PSDKEVEIAYSDV AK	C21;C21;C40	0.48071	P59998 F8WCF6 P59998	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
LVLANNC*PALR	C417	0.479935	P29401	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5R199 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #
DFLTGMC*LFLQSLR	C36;C36;C65;C2 4;C62	0.479215	P47756 P47756 B1AK88 B1AK87 B1AK85	Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB # Q9Y5P6 Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 #
ENSTLNC*ASFTAGIVEAVLT HSGFPAK	C254	0.47868333	P12277	Q8IUR0 Trafficking protein particle complex subunit 5 OS=Homo sapiens GN=TRAPPC5 PE=1 SV=1 #
LPTDLTAC*DNR	C11;C11	0.47558	P61160 P61160	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 #
EGLLLWC*QR	C705	0.47462667	Q99575	P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 #
VWAEPCLIDAAKEEYNGVIE EFLATGEK	C114;C31;C207; C181;C211	0.47461	G5E9C7 H3BRW9 Q02750 Q02750 P36507	Q9H4A4 Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 #
YFTQGNC*VNLTEALSLYEEQ LGR	C128	0.47412	Q16531	P52788 Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2 # P52788-2 Isoform 2 of Spermine synthase OS=Homo sapiens GN=SMS #

VC*NFLASQVPFPSR	C147;C163	0.47302667	F5H157 Q15286	Q99714-2 Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 # Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 # Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
GNFTLPEVAEC*FDEITYVEL QKEEAQK	C89	0.47220692	P19623	
FMPIMQWLYFDALEC*LPEDK EVLTEDK	C259;C386;C388; C389;C183;C321; C394;C270	0.470405	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	P22314 Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 # P22314-2 Isoform 2 of Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 #
LDINLLDNVNC*LYHGEGAQ QR	C159	0.46803833	P84077	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 # P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 #
DC*GATWVVLGHSER	C134	0.46771857	P60842	
WTQTLSELDAVDFC*VNFR	C27	0.46752167	P30566	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 # Q13813-2 Isoform 2 of Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 # Q13813 Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 # A0A0D9SGF6 Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=1 # Q13813-3 Isoform 3 of Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 # A0A0D9SF54 Spectrin alpha chain# non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=1 #
EC*EDVMDWINDKEAIVTSEE LGQDLEHVEVLQK	C727;C680	0.46652	Q02809 Q02809	P08574 Cytochrome c1# heme protein# mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3 # E9PBW4 Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=1 # P69891 Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2 # P69892 Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 # Q16698 2#4-dienoyl-CoA reductase# mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 # Q16698-2 Isoform 2 of 2#4-dienoyl-CoA reductase# mitochondrial OS=Homo sapiens GN=DECR1 #
HGGEDYVFSLLTYC*EPPT GVSLR	C283;C109;C247	0.465575	P67936 K7EPB9 P67936	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 # P11498 Pyruvate carboxylase# mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 # P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
GTFAQLSELHC*DK	C423;C445	0.465215	Q14697 Q14697	
LGTVEELANLAAFLC*SDYAS WINGAVIK	C165;C165	0.46337667	P40121 P40121	
LVPATQC*GSLIGK	C8	0.46317	P09960	
FLYEC*PWR	C103;C95	0.46196	Q92973 Q92973	
EGIC*ALGGTSELSSSEGTHQS YSEEEKYAFVNWINK	C247	0.46126154	P04406	
HLYTLDDGGDIINALC*FSPNR	C269	0.46048286	O75874	
IC*LAEAFLTADTILNLTQNISE GLVVYPK	C1434	0.46043889	Q9Y490	P30566 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 #
MYGISLC*QAILDETKGDYK	C35;C67;C39	0.45981	Q7L1Q6 Q7L1Q6 Q7L1Q6	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 #

VAASC*GAIQYIPTELDQVRK	C332;C328;C328	0.459694	A0A087WVQ6 Q00610 Q00610	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 #
VPAFEGDDGFC*VFESNAIAY YVSNEELR	C497	0.45926833	Q00839 Q00839	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #
IYGFYDEC*KR	C214;C150	0.45681333	P13807 P13807	P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 #
C*AVVDVPPFGGAK	C85;C196;C190;C243	0.45651	B4E3S0 Q9ULV4 Q9ULV4 Q9ULV4	P00367-3 Isoform 3 of Glutamate dehydrogenase 1# mitochondrial OS=Homo sapiens GN=GLUD1 # P00367 Glutamate dehydrogenase 1# mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2 # P00367-2 Isoform 2 of Glutamate dehydrogenase 1# mitochondrial OS=Homo sapiens GN=GLUD1 #
QPAIMPGQSYGLEDDGSC*SY KDFSESER	C47	0.45624778	P61081	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
ITDFIKFDTGNLC*MVTGGAN LGR	C287	0.455515	P43490	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 #
EDPTVSALLTSEKDWQGFLE LYLQNSPEAC*DYGL	C125;C126;C126;C106	0.45446667	Q16181 Q16181 E7EPK1 E7ES33	P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
DGTVLC*ELINALYPEGQAPV KK	C159;C159;C159	0.45375706	Q5JR08 P08134 E9PQH6	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
LTIIVSDPSHC*NVLR	C280	0.453705	P68366 P68363 Q71U36 P68366 P09104 P13929	P78346-2 Isoform 2 of Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 # P78346 Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1 #
SDIDEVALQGIEFWSNVC*DE EMDLAIEASEAAEQGRPPEH TSK	C389;C389;C296;C346;C389	0.452645	P06733 P13929 P06733	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 #
NYLPAINGIVFLVDC*ADHSR	C92	0.45253	P07814	Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 #
IC*ELLPEAAINDVYLAPLLQC LIEGLSAEPR	C55;C55;C55;C55;C50	0.45229778	Q15102 M0R389 M0R323 M0QXS6 M0QZT2 M0R1K3	J3QKQ5 Importin subunit beta-1 (Fragment) OS=Homo sapiens GN=KPNB1 PE=1 SV=1 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
HPSAVTAC*NLDLENLVTDSN R LPIGDVATQYFADRD MF C*A GR	C567 C480	0.4522 0.45107	P13639 P12814	Q9Y678 Coatamer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 # Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
MVHNGIEYGDMQLIC*EAYHL MK	C241;C170	0.44904222	P08237 P08237	P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
KAC*ADATLSQITNNIDPVGR	C210	0.4490275	Q86SQ6	P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 #

YDLLFMPPSFPPFGGMENPCL TFVTPC*LLAGDR	C646	0.44620833	P22102	Q9H4A4 Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 #
ELLNPVVEFVSHPTTC*R	C107	0.44539	P26639	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 # E9PEX6 Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=1 SV=1 # P09622 Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 # P09622-2 Isoform 2 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD # P09622-3 Isoform 3 of Dihydrolipoyl dehydrogenase# mitochondrial OS=Homo sapiens GN=DLD # K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 # K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 # Q13526 Peptidyl-prolyl cis-trans isomerase NIMA- interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 #
VLGAHILGPGAGEMVNEAAL ALEYGASC*EDIAR	C784	0.44523286	P11216	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 # P31948-2 Isoform 2 of Stress-induced- phosphoprotein 1 OS=Homo sapiens GN=STIP1 # P31948-3 Isoform 3 of Stress- induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 # F5H783 Stress-induced- phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 # P31948 Stress- induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 # F5GXD8 Stress- induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 #
IKSGEEDFESLASQFSDC*SS AK	C21;C19;C20	0.4437875	P62913 Q5VVC8 P62913	
SIQFVDWC*PTGFK	C23	0.442986	B2RPK0	
ALSVGNIDDALQC*YSEAIK	C316;C268	0.44236	G3V1A6 P57764	
AGSDGESIGNC*PFSQR	C153;C207;C19 3;C193	0.442325	H0YJS8 A0A087X2 I1 P62333 H0YJC0 P60953 Q5JYX0 P60953	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
TVTLQGNLDPC*ALYASEEEI GQLVK	C18;C18;C18	0.44207		P06132 Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2 # Q15437 Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2 # Q15436 Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 # Q9NQR4 Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 # K7EMD6 Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Fragment) OS=Homo sapiens GN=SGTA PE=1 SV=1 # O43765 Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1 # A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 # P09525 Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 #
AVLNPLC*QVDYR	C166	0.44117667	Q96HE7	
VGLGIC*YDMR	C985;C1053	0.44094	P18206 P18206	
AIELNPANAVYFC*NR	C172;C193;C17 2;C102	0.4408675	P46782 M0R0R2 M0R0F0 M0QZN2	
YVDIAIPC*NNK	C32;C32;C32	0.44056875	O15260 Q5T8U5 O15260	
FLT VLC*SR	C25	0.43909	Q9BQE3 Q71U36	

FMTPVIQDNPSGWGPC*AVP EQFR	C91	0.43753	P31949	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # P63010-2 Isoform 2 of AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 # A0A087X253 AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 # P63010 AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 # E9PJF7 Translationally-controlled tumor protein (Fragment) OS=Homo sapiens GN=TPT1 PE=1 SV=1 # Q5W0H4 Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 # J3KPG2 Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 # A0A0B4J2C3 Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 # P13693 Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 #
NNIDVFYFSC*LIPLNVLFVED GK	C29	0.43748	Q99832	
EIADGLC*LEVEGK	C108;C114;C109	0.43687	P19105 J3QRS3 O14950	
QTVADQVLVGSYC*VFSNQG GLVHPK	C520;M498 C520	0.433225	Q96AC1 Q96AC1 Q96AC1	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 #
EVWLETPQADDFWC*EGEP YGPBK	C408	0.432135	P61158	Q96SZ5 2-aminoethanethiol dioxygenase OS=Homo sapiens GN=ADO PE=1 SV=2 #
C*TGGEVGATSALAPK	PTM index from ip2	0.430995	uniprot	P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 #
TLPTLQELHLSDNLLGDAGLQ LLCEGLLDPQC*R	C377	0.430276	P30153 Q13509 P07437 Q5ST81 P68371	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
QLALWDPENLEEPMALQELD SSNGALLPFYDPDTSVVYVC* GK	C303;C303;C231; C303;C650;C231; C303;C266;C285; C303	0.42916	A0A0B4J269 Q13509 P04350 K7ESM5 Q5JP53 Q9BUF5	Q9BR76 Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 #
IEKELEAVC*QDVLSLLDNYLI K	C257;C257	0.4291437	P63261 P60709 Q16222	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 #
SAGVQC*FGPTAEAAQLESS KR	C481;C464;C480	0.42909333	Q16222 Q16222	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 #
ICELLPEAAINDVYLAPLLQC* LIEGLSAEPR	C158;C13	0.428735	Q14974 Q14974	J3QKQ5 Importin subunit beta-1 (Fragment) OS=Homo sapiens GN=KPNB1 PE=1 SV=1 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
LQEVEC*EEQR	C109	0.42788333	P11217	Q13596 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3 # Q13596-3 Isoform 3 of Sorting nexin-1 OS=Homo sapiens GN=SNX1 # H0YK42 Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=1 # Q13596-2 Isoform 1A of Sorting nexin-1 OS=Homo sapiens GN=SNX1 #
YSYVC*PDLVK	C208	0.42787714	O60684	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #

IWC*FGPDGTGPNILTDITK	C361;C310;C400;C376;C376;C376	0.426905	P68366 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
LFNTAVC*ESK	C48;C19	0.42592333	Q14558 Q14558	Q9BXJ9 N-alpha-acetyltransferase 15# NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
HFADLLPGFLQAVNDSC*YQ NDDSVLK	C61	0.4255	Q6PD74	O00410-3 Isoform 3 of Importin-5 OS=Homo sapiens GN=IPO5 # O00410 Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 #
NLVLVDELDSLSPILFC*QIAD LANEDTPQLYVACGR	C426;C467	0.42537	P12955 P12955	Q15393 Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 #
TDIC*QGALGDCWLLAAIASL TLNDTLLHR	C209	0.42487333	P13797	P07384 Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 #
DVAWAPSIGLPTSTIASC*SQ DGR	C253	0.42412	Q9H8X2	P55735-3 Isoform 3 of Protein SEC13 homolog OS=Homo sapiens GN=SEC13 # A8MXL6 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=1 # P55735-2 Isoform 2 of Protein SEC13 homolog OS=Homo sapiens GN=SEC13 # A0A0C4DFR6 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=1 # P55735 Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3 #
IISNASC*TTNC*LAP	C241;C241	0.42381	Q14865 Q14865	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
IADSIGC*STNNILFLTDVTR	C1767	0.42294667	P78527	Q9UHY7 Enolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1 #
ALNALC*DGLIDELNQALK	C513	0.42247333	Q96RS6	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #
TWYVQATC*ATQGTGLYEGL DWLSNELSK	C109;C109;C109;C109	0.422245	Q15366 Q15366 Q15366 Q15366	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 #
IISNASCTTNC*LAPLAK	C155	0.42107333	P41250	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #
HGGLSSDAQESLEVAIQC*LE TAFGVTVEDSDLALPQTLPEI FEAAATGK	C79;C79;C79;C79;C79	0.4208075	J3KTF8 P52565 P52565 J3QQX2 J3KRY1	K7EMD6 Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Fragment) OS=Homo sapiens GN=SGTA PE=1 SV=1 # O43765 Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1 #
VC*ENIPIVLCGNK	C182;C182;C197;C386	0.42044692	I3L3Q4 Q9HC38 Q9HC38 F6TLX2	F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 #
LISPNLGVFFNAC*EAASR	C46;C37	0.419695	Q9UGI8 Q9UGI8	Q66K74-2 Isoform 2 of Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S # Q66K74 Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 #
FC*DNSSAIQGK	C46;C72	0.41958	A0A087W YS6 Q8TAA3	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #
C*RDVFEPAR	C192;C229;C170	0.41885	O00743 O00743 O00743	Q9NX46 Poly(ADP-ribose) glycohydrolase ARH3 OS=Homo sapiens GN=ADPRHL2 PE=1 SV=1 #
LEGDLTGPSVGVEVPDVELE C*PDAK	C774;C787;C591;C769	0.41879833	K4DI93 Q13620 Q13620 Q13620	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 #
TIIP LISQC*TPK	C152	0.41876167	P13489	P40926 Malate dehydrogenase# mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 #

VIEINPYLLGTMSGCAADC*Q YWER	C93;C77;C77	0.418345	H0YMV8 Q71UM5 P42677	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 # X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 # P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 # P63151-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A # P63151 Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1 # O43414-3 Isoform 3 of ERI1 exoribonuclease 3 OS=Homo sapiens GN=ERI3 # H0Y4B0 ERI1 exoribonuclease 3 (Fragment) OS=Homo sapiens GN=ERI3 PE=1 SV=1 # O43414-2 Isoform 2 of ERI1 exoribonuclease 3 OS=Homo sapiens GN=ERI3 # F6QUN3 ERI1 exoribonuclease 3 (Fragment) OS=Homo sapiens GN=ERI3 PE=1 SV=1 # O43414 ERI1 exoribonuclease 3 OS=Homo sapiens GN=ERI3 PE=1 SV=2 #
SFNIVDIKAPANMEELTEVITAA EFHPNSC*NTFVYSSSK	C152;C152	0.41808286	P49588 P49588	O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 #
VMLPGQC*QYLGLPVADYFK	C98;C125;C139	0.4174	F8W8D4 Q8TBC4 Q8TBC4	P26038 Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 # P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 # P30048-2 Isoform 2 of Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 # A0A087WYC1 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=1 # P34932 Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 # P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 # D6RD47 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=1 # O15144 Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 # Q2NL82 Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 # Q9P2T1 GMP reductase 2 OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # H0YNJ6 GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1 # Q9P2T1-2 Isoform 2 of GMP reductase 2 OS=Homo sapiens GN=GMPR2 # P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 # P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC # P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 # I3L0K2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # I3L3M7 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 # Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 #
AC*LISLGYDVENDRQGEAEF NR	C392;C97;C387; C435;C392	0.41697	P55265 P55265 H0YCK3 P55265 P55265	
EGILNDDIYC*PPETAVLLASY AVQSK	C341	0.416329	P17655	
AFQYVETHGEVC*PANWTPD SPTIKPSAASK	C161	0.41612	P62937	
LMSANASDLPLSIEC*FMNDV DVSGMTNR	C369	0.415905	P13639	
ITAFVPNDGC*LNFIENDEVL VAGFGR	C76;M23 C26	0.41544364	P46777 Q5T7N0	
NC*FASVFEK	C92	0.41537333	P25398	
DTGTVHLNELGNTQNFMLLC *PR	C134	0.41502375	P22102	
VGIGPGSVC*TTR	C272	0.41405667	P55060	
LPITVLNGAPGFINLC*DALNA WQLVK	C117;C117	0.41387	P35241 P35241	
LSLDGQNIYNAC*CTLR	C186	0.4134525	P18124 A8MUD9	
SWC*PDCVQAEPVVR	C80;C109;C80;C 109	0.413192	MOR3D6 MOR117 MOR1A7 Q02543	



ASC*LYGQLPK	C104;C65;C117	0.41281	O43237 B4E2E0 Q9Y6G9	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 #  Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC #
EALEAESAWC*YLYGTGSVA GVYLPGSR	C1260;C1233;C1260	0.41230167	P21333 Q60FE5 P21333	Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
SCYDLSC*HAR	C187;C204	0.41145	P21810 C9JKG1	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 #
IYC*ALSGSAADAQAVADMAA YQLELHGIELEEPPLVLAAN VVR	C113;M113 C114 C101;M112	0.41099	Q9ULC4 Q9ULC4 Q9ULC4	A0A0G2JJA7 Proteasome subunit beta type OS=Homo sapiens GN=PSMB9 PE=1 SV=1 #
YTC*GEAPDYDR	C374	0.41088	P22234	P21266 Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3 # Q5VTE0 Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 # P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 #
SGDAAIVDMVPGKPMC*VES FSDYPLGR	C417;C410;C45 5	0.41044444	P49368 B4DUR8 P49368	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 # P53396-2 Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY #
KPASFMTSIC*DER	C39	0.40997714	P03897	Q9NZA1 Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3 # Q9NZA1-3 Isoform 3 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 # Q9NZA1-2 Isoform 1 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 #
AGIDGESIGNC*PFSQR	C100;C80	0.40988	P62241 Q5JR95	P52907 F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
TIDGQQTIAC*IESHQFQPK	C292;C404	0.40825167	Q14137 Q14137	P07437 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 # Q5ST81 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #
LVSSPC*CIVTSTYGWTANME R	C160	0.40776875	P36871	P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 # A0A0A0MSR2 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-5 Isoform 5 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 # E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 # E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 # P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 # P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 #
LTPTYGDLNHLVSATMSGV TTC*LR	C342	0.40773417	Q02790	
VSMILQSPAFC*EELESMIQE QFKK	C270	0.40615	P32455	

IIPLEEGLQLPSPTATSQLPL ESDAVEC*LNYQHYK	C158	0.40537857	Q99832	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK #
FQSSAVMALQEASEAYLVGL FEDTNLC*AIHAK	C270	0.4040675	P35998	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 # P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK # P55263
TGC*TFPEKPDFH	C35;C64;C35;C6 4	0.40113	M0R3D6 M0R117 M0R1A7 Q02543	Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 # P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK # A0A087WX29 TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #
VTEDENDEPIEPSDDGTVL LSTVTAQFPGAC*GLR	C245;C306	0.400387	Q9BY44 Q9BY44	O43776 Asparagine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 # O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-2 Isoform 4 of Dynamin- 1-like protein OS=Homo sapiens GN=DNM1L # O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 # O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 # O00429-7 Isoform 7 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L # P07737 Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 #
LMTDTINEPILLC*R	C511	0.40037	Q99832	P15259 Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3 # A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #
LHDAIVEVVC*LLR	C245	0.4001	Q13162	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 # Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 # Q00796 Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 # H0YLA4 Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=1 #
AGWNAYIDNLMADGTC*QDA AIVGYKDSVWAAVPGK	C40	0.3995525	Q13867	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
FC*GWFDAELSEK	C127;C127	0.39912556	Q8WUM4 Q8WUM4	
ECFGACLFTC*YDLLRPDVVL ETAWR	C394;C386	0.398285	P29401 P29401	
ASFENNCEIGC*FAK	C437	0.397955	P11216	
WKGFTDADNTWEPEENLDC* PELIEAFLNSQK	C12	0.39785333	P62753	
LPDNVTFEEGALIEPLSVGIH AC*R	C133	0.396485	P52292	
AC*QSIYPLHDFVFR	C317;C273;C31 7	0.39643462	P62879 E7EP32 P62873	
ITVVGVGAVGMAC*AISILMK	C146	0.395836	P34932	

SLHDALC*VLAQTVK	C774	0.39559	P12814	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 # F8VQ14 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=1 # F5GWF6 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=2 # P78371-2 Isoform 2 of T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 # Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 # P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 # P49419-4 Isoform 4 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # F8VS02 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=1 # A0A140T9V3 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=1 #
YAGLSTC*FR	C163;C163;C163	0.39494	H0YL69 P25789 H0YMZ1	
GSDC*GIVNVNIPTSGAEIGG AFGGEK	C645	0.394488	P14625	
GEHGFIGC*R	C77;C22;C39;C39	0.39441333	E9PK25 G3V1A4 P23528 E9PP50	Q16658 Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 #
C*PNPEEGESVLELSLR	C133	0.39426778	P29401	Q6PCE3 Glucose 1#6-bisphosphate synthase OS=Homo sapiens GN=PGM2L1 PE=1 SV=3 #
EGALC*EENMR	C220;C252;C252	0.3930625	P50440 P50440 P50440	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
KC*GETAFIAPQCEMPIEWV CR	C264;C264;C264	0.392298	O95630 O95630 C9JK83	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
EITSLDTENIDEILNNADVALV NFYADWC*R	C27	0.39176714	P12004	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 # O95571 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 # M0QXB5 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 # M0QY80 Persulfide dioxygenase ETHE1# mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=1 # H0YE58 Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1 # P29692-3 Isoform 3 of Elongation factor 1-delta OS=Homo sapiens GN=EEF1D # E9PRY8 Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1 # A0A087X1X7 Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1 # E9PQZ1 Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1 # P29692-4 Isoform 4 of Elongation factor 1-delta OS=Homo sapiens GN=EEF1D # H0YE72 Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1 # P29692 Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5 # P29692-2 Isoform 2 of Elongation factor 1-delta OS=Homo sapiens GN=EEF1D # E9PK01 Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1 #
QMFEPVSC*TFTYLLGDR	C276;C209;C179	0.39121833	O60701 O60701 O60701	
SSILLDVKPWDDETDMQLE AC*VR	C2881;M3015 C3020 C3019;M3016 C2437;M2877 C3020;M3016	0.39071333	H7BXU2 F5GZ18 A0A0U1R QY1 Q96PZ7 E5RIG2	

VPLASQGLGPGSTVLLVVDK C*DEPLSILVR	C186	0.39036667	P48169	P05161 Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5 # A0A096LNZ9 Ubiquitin-like protein ISG15 (Fragment) OS=Homo sapiens GN=ISG15 PE=1 SV=5 # A0A096LPJ4 Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=1 #
FQYEC*GNYSGAAEYLYFFR	C87;C39	0.388528	Q9BTT0 Q9BTT0	P60228 Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 #
ELDLSNNC*LG DAGILQLVES VR	C47	0.38809429	P30041	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
ENFDEVVNDADII LVEFYAPW C*GHCK	C167;C195	0.387632	P23526 P23526	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 #
SNGLGPMMSGNTAYPVISC* PPLTPDWGVQDVWSSLR	C76;C89;C76	0.38634125	Q9UKK9 A6NFX8 A6NJU6	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
YASIC*QQNGIVPIVEPEILPD GDHDLKR	C199	0.38576895	P62424	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA # Q05BK6 Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=1 # C9JUE0 Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=1 SV=1 # Q92734 Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2 # Q92734-3 Isoform 3 of Protein TFG OS=Homo sapiens GN=TFG # C9JJP5 Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=1 SV=1 # Q92734-2 Isoform 2 of Protein TFG OS=Homo sapiens GN=TFG # Q92734-4 Isoform 4 of Protein TFG OS=Homo sapiens GN=TFG # C9JTY3 Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=1 SV=1 # Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 #
YKDEEDGLITIFDSSDLSFAIQ C*SR	C328;C328	0.38523	B0YJC4 P08670	
LTALDYHNPAGFNC*KDETEF R	C113	0.3850025	Q9Y5P6 Q9Y5P6	
AAGIIHLGATSC*YVGDNTDLII LR	C352;C356;C381	0.38443571	Q9Y4E8 Q9Y4E8 Q9Y4E8	P30566 Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 #
C*LQILAAGFLP GSVGITDPC ESGNFR	C517 C489;M511	0.38423667	E9PB90 P52789	B4DY09 Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=1 # Q12905 Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
YINENLIVNTDELGRDC*LINA AK	C229	0.38409333	P15880	
IPQSHIQQIC*ETILTSGENLA R	C74;C74;C74	0.383675	H0YL69 P25789 H0YMZ1	O43813 LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1 #
AEVLIS TVGPEDC*VVPFLTR PK	C219	0.382945	P68133 P68032 P62736	P56192 Methionine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 #
MGVEAVIALLEATPDTPAC*V VSLNGN	C207	0.38179	P63244	Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFBP PE=1 SV=2 # O95373 Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 #
GIDQC*IPLFVEAALER	C345;C404	0.381765	M0QXS5 P14866	P26639 Threonine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 # Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 # A0A0A0MT01 Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1 # P06396 Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1 # A0A0A0MS51 Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1 # P06396-3 Isoform 3 of Gelsolin OS=Homo sapiens GN=GSN # P06396-2 Isoform 2 of Gelsolin OS=Homo sapiens GN=GSN # P06396-4 Isoform 4 of Gelsolin OS=Homo sapiens GN=GSN #
DQELYFFHELSPGSC*FFLPK SSVNC*PFSSQDMKYSPFF VFGEK	C109 C92;C92	0.38120667 0.37996	P11216 P62888 E5RI99	
ATEVPVSWESFNNGDC*FILD LGNNIHQWCGSNSNR	C450	0.37889	O95573	

DVGLPLC*QALVEAEDGNPD RVLELLLPIR	C363	0.377255	P20073 P20073	Q5R314 Tetratricopeptide repeat protein 38 OS=Homo sapiens GN=TTC38 PE=1 SV=1 # P12814 Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 # O43707 Alpha- actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # Q15056 Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5 # Q15056-2 Isoform Short of Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H #
C*QLEINFNTLQTK	C285	0.37720222	P31146	
GFC*YVEFDEVDLSKEALTYD GALLGDR	C349	0.376303	P14868	
AC*ANPAAGSVILLENLR	C279;C280;C28 0;C260	0.37611789	Q16181 Q16181 E7EPK1 E7ES33	P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
TNC*NVAVINVGAPAAGMNA AVR	C85;M316 C321;M281 C286	0.373395	Q08J23 Q08J23 Q08J23	Q01813 ATP-dependent 6- phosphofructokinase# platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 # P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #
AHVVPC*FDASK	C46	0.37279	P49721	
LSLEPLPC*YQLELDAVAEV K	C62	0.371862	F8VZ49 P09651 F8W6I7 Q32P51 P09651 F8W646 P09651	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2 #
TIC*AILENYQTEK	C89;C92	0.37149333	A0A0B4J2 A4 P42765	Q5T5C7 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 # P49591 Serine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 # P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
LWNTLGVK*K	C191	0.371302	P17655	
C*TPSVISFGSK	C34;C33;C34	0.3712375	O14579 A0A087X0 I4 M0QXB4	Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 # O14818 Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1 #
ICALDDNVC*MAFAGLTADAR	C57	0.36952	P48147	
NWYIQATC*ATSGDGLYEGL DWLANQLK	C175;C175	0.368085	Q9H223 A0A087W UA5	P61204 ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 #
NIELIC*QENEGENDPVLQR	C351;M319 C322	0.3677075	P35606 P35606	Q15691 Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3 #
GNYLSFGC*PEYGQLGHNSD GK	C208	0.36765333	P36578	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 # O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D #
TQGNVFATDAILATLMSK*TR	C384;C384	0.36747	P55884 P55884	
MNPNSPSITYDISQLFDFIDDL ADLSC*LVIYR	C213;M203 C213	0.3669925	A0A024R A52 P25787	P84090 Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1 # P15170 Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1 # P15170-2 Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 # P15170-3 Isoform 3 of Eukaryotic peptide chain release factor GTP- binding subunit ERF3A OS=Homo sapiens GN=GSPT1 #
EQSDFC*PWYIGLPIFYLDN LPNFR	C159	0.366493	P61586	

IIQFQATPC*PK	C206	0.36641333	P00491	Q06330-7 Isoform 7 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330 Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3 # Q06330-4 Isoform 4 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # D6R927 Recombining-binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=1 # Q06330-5 Isoform 5 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ # Q06330-6 Isoform 6 of Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ #
GTLTLC*PYHSDR	C50	0.366195	P22626 P22626 A0A087W UI2	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 #
IQFNDLQSLLC*ATLQNVLR	C453	0.366194	P31930	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
IVSNASC*TTNCLAPLAK	C202 C209 C209;C202	0.36524333	Q8NAP3 D6RBC4	O14556 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 # P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 # P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 # X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 #
QYDADLEQILIQWITTQC*R	C45	0.36506933	P46940	
IEEFLEAVLC*PPRYPK	C120;C138;C137; C116	0.36493167	P62826 J3KQE5 B5MDF5 F5H018	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
C*SEGSFLLTFFPRPVTVEPM DQLDDEEGLPEK	C221;C254	0.36351167	P38606 P38606	Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 #
AILPC*QDTPSVK	C113;C157;C157; C113;C176;C150;C113	0.3633175	J3QLK0 P60763 P15153 B1AH78 P63000 B1AH77 P63000 B1AH80 J3KSC4 Q15366 Q15366 Q15366 Q15366 Q15366 Q15366 F8VZX2 H3BRU6 Q15366 Q15366 F8VXH9 Q15365	P09960-3 Isoform 3 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H # P09960 Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 # P09960-2 Isoform 2 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H # P09960-4 Isoform 4 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H #
IAVYSC*PFDGMITETK	C54;C54;C54;C54; C54;C54;C54;C54; C35;C54;C54;C46; C54	0.36218167	F8VZX2 H3BRU6 Q15366 Q15366 F8VXH9 Q15365	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #
DIC*NDVLSLLEK	C369	0.36098385	Q9H4A4	B0AZS6 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 # P63104 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 #
LDYFLLSHSLLPALC*DSK	C152;M137 C138;M151 C152	0.36004	A0A024R5 71 Q9H4M9 C9JC03	P27695 DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2 #

EAVQC*VQELASPSLLFIVR	C119;C119;C98; C119	0.35979	P34897 G3V4W5 P34897 P34897	Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EUU4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
GLYDGPVC*EVSVTPK	C204;C217;C204; C287	0.35973833	P49589 B4DKY1 P49589 P49589	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
RPTEIC*ADPQFIIGGATR	C94	0.35871333	P02042	O14556 Glyceraldehyde-3-phosphate dehydrogenase# testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 #
VPTPDVSVVDLTC*R	C162;C115;C162; C162	0.358402	Q92747 Q92747 O15143 E9PF58 Q9ULV4 Q9ULV4 Q9ULV4	Q6ZVN8 Hemojuvelin OS=Homo sapiens GN=HFE2 PE=1 SV=1 #
GD LAFHSAVHGIEDLMIQHN C*SRQGPTAPPPPR	C283;M315 C336 C289;M262	0.35619	Q9ULV4 Q9ULV4 Q9ULV4	Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 #
VLTC*TDLEQGNFFLDFENA QPTESEK	C140	0.356188	P12268	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 #
ASFENNC*EIGCFAK	C22;C22;C22	0.355545	P31943 G8JLB6 E9PCY7	P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
AEGSDVANAVLDGADC*IMLS GETAK	C106;C106;C106; 6	0.355482	Q9NR50 Q9NR50 Q9NR50	Q13347 Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1 #
ITSAVWGPLGEC*IIAGHESG ELNQYSAK	C95;M86 C91;M90 C95 C95;M90	0.354	P35580 P35579 P35580 P35580 P35580 P35580	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 #
LMDLDVEQLGIPEQEYSC*VV K	C38;C38	0.35369333	H3BRV9 P61970 Q86TX2	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 #
IAVAAQNC*YK	C339;C339;C38 1;C401	0.3529275	A0A087X0 W7 A0A087W T95 P49753 P34897	O75083 WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 #
C*FSIDNPGYEPEVVAVHPG GDTVAIGGVDGNVR	C91;C91;C70;C91; 1	0.35270214	G3V4W5 P34897 P34897	

IVGYFVSGC*DPSIMGIGPVP AISGALK	C427	0.35251	P13489	A0A0B4J2A4 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # P42765 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 # P25325 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3 # B1AH49 Sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=1 # P25325-2 Isoform 2 of 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST #
HIPGAAFFDIDQC*SDR	C783;C802;C77 8;C767	0.35251	O00159 O00159 F5H6E2 O00159	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 # P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 #
GDLENAFLNLVQC*IQNKPLY FADR	C36;C36;C36	0.35236714	Q9Y221 Q9Y221 J3QLW7	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 # P62263 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 # E5RH77 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=1 # Q9H6Q4-3 Isoform 3 of Cytosolic Fe-S cluster assembly factor NARFL OS=Homo sapiens GN=NARFL # Q9H6Q4 Cytosolic Fe-S cluster assembly factor NARFL OS=Homo sapiens GN=NARFL PE=1 SV=1 #
NC*LTNFHGMDLTR	C374	0.351235	P36871	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 # Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 # Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 # Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 #
FTLDC*THPVEDGIMDAANFE QFLQER	C216;C216	0.35103429	Q52LJ0 Q52LJ0	Q14315 Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3 # Q14315-2 Isoform 2 of Filamin-C OS=Homo sapiens GN=FLNC #
EEQVISLGPQVAEGENVFGV C*HIFASFNDTFVHVTDLSGK	C12;C12	0.35013	P56192 F8VPL7	
LLEEEGVSLPDLEPAPLDSLC *SGASAEPTSHR	C89;C89	0.34986333	P09661 H0YKK0	
DGSC*GVAYVQEPGDYEVS VK	C111;C111;C11 1;C111	0.34827	Q5VTE0 P68104 Q05639 P68104	
WG TIEVENTHC*EFAYLR	C38;M21 C38	0.34811	Q7Z2W4 Q7Z2W4 C9J6P4 Q7Z2W4	
IEC*QDNGDGSCAVSYLPTPEP GEYTINILFAEAHIPGSPFK	C42;C42	0.34784333	E7EPB3 P50914	



VLLSICSLLC*DPNPDDPLVPE IAR	C73;C62	0.347362	P62136 P62136	P61077-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 # H9KV45 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 # D6RAH7 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # A0A0A0MQU3 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 # D6RFM0 Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=3 SV=1 # A0A087WY85 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 # P62837 Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1 #
TVFAEHISDEC*K	C70;C70;C13	0.346546	P46776 E9PLL6 E9PJD9	P39023 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 #
AQILVLTYPILIGNYGIPPEMD EFLGC*K	C197	0.34647	O00148	F8VPD4 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 # P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 #
NIC*FTVWDVGGQDK	C155;C176;C155	0.34609	P46782 M0R0R2 M0R0F0 E9PK25	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 #
IEAELQDIC*NDVLELLDK	C177;C122;C139;C139	0.34590089	G3V1A4 P23528 E9PP50 A0A087W	P31946-2 Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB # P31946 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 #
LVSSPCC*IVTSTYGW TANMER	C245;C245	0.34566	YC1 P34932	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90A1 PE=1 SV=4 #
KNPFGLVPVLENSQGGQLIYES AITC*EYLDEAYPGK	C21;C21;C40	0.34525	P59998 F8WCF6 P59998	P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
VADSSPFALELLISDDC*FVLD NGLCGK	C417	0.3448	P29401	P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 #
C*AEGYALYAQALTDQQQFG K	C36;C36;C65;C24;C62	0.34476333	P47756 P47756 B1AK88 B1AK87 B1AK85	O94826 Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70 PE=1 SV=1 #
VLTMPETC*R	C254	0.34437	P12277	Q99460-2 Isoform 2 of 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 # Q99460 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 # Q01970 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 PE=1 SV=2 #
NEANQPLC*LPALLIYTEASD YIPDDHQDYAEALINPIK	C11;C11	0.34423333	P61160 P61160	Q01970-2 Isoform 2 of 1-phosphatidylinositol 4#5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 #
LEKPNEGYLEFFVDC*SASAT PEFEGR	C705	0.34352333	Q99575	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 #

FLGPEIFFHPEFANPDFTQPI SEVVDEVIQNC*PIDVR	C114;C31;C207; C181;C211	0.343499	G5E9C7 H3BRW9 Q02750 Q02750 P36507	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
TDGFGIDTC*R	C128	0.34329571	Q16531	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # K7ELJ7 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # K7EKD8 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #
LGYAGNTEPQFIIPSC*IAIK	C147;C163	0.343204	F5H157 Q15286	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 # X6RA14 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=1 # P10768 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 #
C*PALYWLSGLTCTEQNFISK	C89	0.34293	P19623	
NEC*DPALALLSDYVLHNSNT MR	C259;C386;C388; C389;C183;C321; C394;C270	0.342525	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 # Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 #
QALVEFEDVLGAC*NAVNYA ADNQIYIAGHPAFVNYSTSQK	C159	0.34247667	P84077	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #
LSALGNVTTC*NDYVALVHPD LDRETEEILADV LK	C134	0.34228167	P60842	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 # P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
GIFPVLK*K	C27	0.34157727	P30566	Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
GQLC*ELSCSTDYR	C727;C680	0.34133667	Q02809 Q02809	P35606 Coatamer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2 # P35606-2 Isoform 2 of Coatamer subunit beta' OS=Homo sapiens GN=COPB2 #
YGAVDPLLALLAVPDMSSLA C*GYLR	C423;C445	0.34117667	Q14697 Q14697	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 #
YNFFTGC*PK	C165;C165	0.341155	P40121 P40121	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 #
LPACVVDC*GTGYTK	C8	0.341068	P09960	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 # P30613 Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR PE=1 SV=2 # P30613-2 Isoform L-type of Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR #
AETSDVANAVLDGADC*IMLS GETAK	C103;C95	0.34082	Q92973 Q92973	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
MC*LFAGFQR	C247	0.34075	P04406	
NEC*LEAGTLFQDPSFPAIPS ALGFK	C269	0.34043	O75874	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
AFFPC*FDTPAVK	C1434	0.34029	Q9Y490	Q9H4A4 Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 #

VIGIEC*SSISDYAVK	C35;C67;C39	0.34012815	Q7L1Q6 Q7L1Q6 Q7L1Q6	E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # H7C211 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 # Q99873-2 Isoform 2 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
KHPNEIC*VPMSVEFEELLK	C332;C328;C328	0.33998	A0A087WVQ6 Q00610 Q00610	Q12874 Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1 #
NTGIIC*TIGPASR	C497	0.33976167	Q00839 Q00839	P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 #
C*SVLPLSQNQEFMPFVK	C214;C150	0.33871	P13807 P13807	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 #
ECSIYLIGGSIPEEDAGKLYNT C*AVFGPDGTLAK	C85;C196;C190; C243	0.33816	B4E3S0 Q9ULV4 Q9ULV4 Q9ULV4	Q9NQR4 Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 # H7C579 Omega-amidase NIT2 (Fragment) OS=Homo sapiens GN=NIT2 PE=1 SV=7 #
IIATAVC*HTDAYTLGADPEG CFPVILGHEGAGIVESVGEGV TK	C47	0.33614	P61081	P11766 Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 #
LVIGQNGILSTPAVSC*IIR	C287	0.33488	P43490	P36871 Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3 #
GFEVVMTEPIDEYC*VQQLK	C125;C126;C126; C106	0.33377364	Q16181 Q16181 E7EPK1 E7ES33	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
YDGSTIVPGEQGAEQHFQI QC*TDDVR	C159;C159;C159 9	0.333028	Q5JR08 P08134 E9PQH6 P68366	Q14019 Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3 #
LTVVDTPGYGDAINC*R	C280	0.33250556	P68363 Q71U36 P68366	C9JQJ4 Septin-2 (Fragment) OS=Homo sapiens GN=SEPT2 PE=1 SV=1 #
QMEKDETVSDC*SPHIANIGR	C389;C389;C296; C346;C389	0.3303775	P09104 P13929 P06733 P13929 P06733	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
HFIMQVVCEATQC*PDTR	C92	0.33	P07814	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
YMACC*LLYR	C55;C55;C55;C55; 5;C55;C50	0.3294275	Q15102 M0R389 M0R323 M0QXS6 M0QZT2 M0R1K3	

HTGC*CGDNDPIDVCEIGSK	C567	0.329105	P13639	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 # H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
YLLQYQEPIPC*EQLVTALCDIK	C480	0.32742	P12814	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 # Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 #
SNTGGQAFPPQC*VFDHWQILPGDPFDNSSRPSQVVAETR	C241;C170	0.3267	P08237 P08237	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
ESC*LEAYTGIVQGLK	C210	0.32666667	Q86SQ6	P50238 Cysteine-rich protein 1 OS=Homo sapiens GN=CRIP1 PE=1 SV=3 # H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 #
AEPPQC*TSLAWSADGQTLFAGYTDNLVR	C646	0.325979	P22102	P11142 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 # E9PKE3 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 # P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #
C*NKEVYFAER	C107	0.32515	P26639	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 # P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 #
LQEALDAEMLEDEAGGGGA GPGGAC*K	C784	0.32504667	P11216	P07741 Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 #
GPAVGIDLGTYSYC*VGVFQHGK	C21;C19;C20	0.32479429	P62913 Q5VVC8 P62913	P39687 Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1 # Q92688-2 Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B # Q92688 Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 # H0YN26 Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1 # P07737 Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 #
VFIMDSC*DELIPEYLNfir	C23	0.32476176	B2RPK0	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB #
C*CSGAIIVLTK	C316;C268	0.324102	G3V1A6 P57764 H0YJS8	B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #
LNLPIINIIGLAPLC*ENMPSGK	C153;C207;C193;C193	0.323895	A0A087X2 I1 P62333 H0YJC0 P60953	P28074 Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 #
VVVVDDLLATGGTMNAAC*ELLGR	C18;C18;C18	0.32306	Q5JYX0 P60953	
SLDLFNC*EVTNLNDYR	C166	0.321575	Q96HE7	
C*YEMASHLR	C985;C1053	0.31996571	P18206 P18206	
DYLLC*DYNR	C172;C193;C172;C102	0.31969	P46782 M0R0R2 M0R0F0 M0QZN2	
VIEINPYLLGTMAGGAADC*SFWER	C32;C32;C32	0.31933042	O15260 Q5T8U5 O15260	

ALANSLAC*QGK	C25	0.319058	Q9BQE3 Q71U36	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA #
AAQDFSTC*R	C91	0.31849	P31949	P06132 Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2 # P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 # E7EQ61 Ubiquitin-like modifier-activating enzyme 5 OS=Homo sapiens GN=UBA5 PE=1 SV=1 # C9JRV9 Ubiquitin-like modifier- activating enzyme 5 (Fragment) OS=Homo sapiens GN=UBA5 PE=1 SV=7 # Q9GZZ9 Ubiquitin-like modifier-activating enzyme 5 OS=Homo sapiens GN=UBA5 PE=1 SV=1 # Q9GZZ9-2 Isoform 2 of Ubiquitin-like modifier- activating enzyme 5 OS=Homo sapiens GN=UBA5 # E7EWE1 Ubiquitin-like modifier- activating enzyme 5 OS=Homo sapiens GN=UBA5 PE=1 SV=1 #
LC*YVALDFEQEMATAASSSS LEK	C29	0.31824083	Q99832	
ISNGGLEEGKPVDLVLS*VD NFEAR	C108;C114;C10 9	0.31812	P19105 J3QRS3 O14950	
NALVSHLDGTTTPVC*EDIGR	C520;M498 C520	0.31756667	Q96AC1 Q96AC1 Q96AC1	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 # P60484-2 Isoform alpha of Phosphatidylinositol 3#4#5-trisphosphate 3-phosphatase and dual- specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN # P60484-3 Isoform 3 of Phosphatidylinositol 3#4#5- trisphosphate 3-phosphatase and dual- specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN # P60484 Phosphatidylinositol 3#4#5-trisphosphate 3- phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # A0A0U1RR63 Phosphatidylinositol 3#4#5-trisphosphate 3- phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 # A0A087WT17 Phosphatidylinositol 3#4#5-trisphosphate 3- phosphatase and dual-specificity protein phosphatase PTEN OS=Homo sapiens GN=PTEN PE=1 SV=1 #
PFC*EDLDQWLSEDDNHVAA IHC*KAGK	C408	0.31727	P61158	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 # P04843 Dolichyl-diphosphooligosaccharide- protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 #
LMWLFGC*PLLLDDVAR	PTM index from ip2	0.31668	uniprot	
VAC*ITEQVLTLVNKR	C377	0.31617667	P30153	
FIC*EQDQHQNFLR	C303;C303;C23 1;C303;C650;C2 31;C303;C266;C 285;C303	0.31495	Q13509 P07437 Q5ST81 P68371 A0A0B4J2 69 Q13509 P04350 K7ESM5 Q5JP53 Q9BUF5	Q92598 Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 # Q92598-2 Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 #
YSNSALGHVNC*TIK	C257;C257	0.31487667	P63261 P60709	Q9NQC3-2 Isoform 2 of Reticulon-4 OS=Homo sapiens GN=RTN4 # F8W914 Reticulon OS=Homo sapiens GN=RTN4 PE=1 SV=1 #

ADPDGPEAQAEAC*SGER	C481;C464;C480	0.31474667	Q16222 Q16222 Q16222	D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # D6RC52 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 # Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 # J3QSY4 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 # P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 # Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 # K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 # P54578-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 # A6NJA2 Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=2 # P54578-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 # P54578 Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3 #
VGMGSGSIC*ITQEVLAGGRP QATAVYK	C158;C13	0.31472	Q14974 Q14974	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #
VTVAGLAGKDPVQC*SR	C109	0.31462	P11217	O43707 Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 # P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 # P14625 Endoplasmic reticulum chaperone ERK9 OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 # E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9UI10-3 Isoform 3 of Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 # Q9UI10-2 Isoform 2 of Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 # A0A087WTA5 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 # Q9UI10 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 #
YEPFSFADDIGSNNC*GYIDL QAVLTHQGR	C208	0.3137	O60684	P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 # P10768 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 # Q01813 ATP-dependent 6-phosphofructokinase# platelet type OS=Homo sapiens GN=PFBK PE=1 SV=2 # P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 #
DDVFLSVPK*ILGQNGISDLV K	C361;C310;C400;C376;C376;C376	0.31337628	P68366 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
IC*DQWDALGSLTHSR	C48;C19	0.31322818	Q14558 Q14558	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #
SIC*TTVLELLDKYLIANATNP ESK GYEVIYLTPEVDEYC*IQALPE FDGKR	C61 C426;C467	0.31274455 0.31242214	Q6PD74 P12955 P12955	
LLNLVYDVTPELVDLITELG MIPC*SSVPVLR	C209	0.31178	P13797	
TGQATVASGIPAGWMGLDC* GPESKK	C253	0.31014333	Q9H8X2	
VFEHDSVELNC*K	C241;C241	0.309955	Q14865 Q14865	
NESC*SENYTTDFIYQLYSEE GK	C1767	0.30929	P78527	
C*ATSKPAFFAEK	C513	0.30786	Q96RS6	
TFC*QLILDPIFK	C109;C109;C109;C109	0.306702	Q15366 Q15366 Q15366 Q15366	
TDVNKIEEFLEEVLC*PPK	C155	0.30649867	P41250	

VSLLEIYSGC*TK	C79;C79;C79;C79;C79	0.306385	J3KTF8 P52565 P52565 J3QQX2 J3KRY1	P25685-2 Isoform 2 of DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 # M0R080 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # M0QZD0 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # M0R1D6 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # Q9UDY4 DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1 # M0QXK0 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 # P25685 DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 # M0QYT3 DnaJ homolog subfamily B member 1 (Fragment) OS=Homo sapiens GN=DNAJB1 PE=1 SV=1 #
AGAIAPC*EVTVPAQNTGLGP EK	C182;C182;C197;C386	0.305784	I3L3Q4 Q9HC38 Q9HC38 F6TLX2	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #
C*DENILWLDYK	C46;C37	0.30574063	Q9UGI8 Q9UGI8	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM #
VDEFPLC*GHMVSDEYEQLS SEALEAAR	C46;C72	0.30570636	A0A087WYS6 Q8TAA3	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 #
NFEATLGWLQEHAC*SR	C192;C229;C170	0.30562	O00743 O00743 O00743	Q9P2J5-2 Isoform 2 of Leucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=LARS # Q9P2J5 Leucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 #
DAGYEFDIC*FTSVQK	C774;C787;C591;C769	0.305102	K4DI93 Q13620 Q13620 Q13620	P18669 Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 #
ETVYC*LNDDDETEVLKEDIIGFR	C152	0.30496273	P13489	P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 #
DVC*TELLPLIKPQGR	C93;C77;C77	0.30425333	H0YMV8 Q71UM5 P42677	P16152 Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 #
AINC*ATSGVVGLVNCLR	C152;C152	0.30392	P49588 P49588	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
DFNPNWMSAVEILDNDNFLG AENAFNLFVC*QK	C98;C125;C139	0.30350429	F8W8D4 Q8TBC4 Q8TBC4	Q16531 DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 #
VQTDPPSPVIC*DLYPNGVFPK	C392;C97;C387;C435;C392	0.30291	P55265 P55265 H0YCK3 P55265 P55265	P50579 Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VY03 Methionine aminopeptidase 2 (Fragment) OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VRR3 Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 # P50579-2 Isoform 2 of Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 # G3V1U3 Methionine aminopeptidase OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VZX9 Methionine aminopeptidase 2 (Fragment) OS=Homo sapiens GN=METAP2 PE=1 SV=1 # F8VQZ7 Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 #
LLC*GLLAER	C341	0.30288	P17655	P14174 Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 #

GC*GTVLLSGPR	C161	0.30220333	P62937	J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 # Q07020 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 # Q07020-2 Isoform 2 of 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 # H0YHA7 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 # P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 # P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P17655-2 Isoform 2 of Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 # P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 # P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 # P55072 Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 # P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 # P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 # P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 #
AGKPVIC*ATQMLESNIK	C369	0.3016119	P13639	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #
WNDNC*PSWNTIDPEER	C76;M23 C26	0.30020667	P46777 Q5T7N0	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
TLPTLQELHLSNLLGDAGLQ LLC*EGLLDPQCR	C92	0.299735	P25398	Q9BR76 Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 #
SC*GSSTPDEFPTDIPGTK	C134	0.29924167	P22102	O60568 Procollagen-lysine#2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 #
LGDVISIQPC*PDVK	C272	0.29918	P55060	O60674 Tyrosine-protein kinase JAK2 OS=Homo sapiens GN=JAK2 PE=1 SV=2 # P78417-3 Isoform 3 of Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 # P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 #
ALANVNIGSLIC*NVGAGGPA PAAGAAPAGGPAPSTAAAPA EEK	C117;C117	0.29850714	P35241 P35241	P31150 Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 #
VADSSPFALELLISDDCFVLD NGLC*GK	C186	0.29805667	P18124 A8MUD9	A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #
FSPNSSNPIIVSC*GWDK	C80;C109;C80;C109	0.29789333	M0R3D6 M0R117 M0R1A7 Q02543 O43237 B4E2E0 Q9Y6G9	P46777 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 # Q5T7N0 60S ribosomal protein L5 (Fragment) OS=Homo sapiens GN=RPL5 PE=1 SV=2 # P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 #
LC*PGGQLPFLLYGTEVHTDT NK	C104;C65;C117	0.297604	P21333 Q60FE5 P21333	
NVLLSAGC*DNVLIWNVGTA EELYR	C1260;C1233;C1260	0.2966575	P21810 C9JKG1	
DVFSGSDTDPDMAFC*K	C187;C204	0.29658	P21810 C9JKG1	
MGMAC*LTMTEMEGTSTSSI YQNGDISGNANSMK	C113;M113 C114 C101;M112	0.29594667	Q9ULC4 Q9ULC4 Q9ULC4	
NPFGLVPVLENSQGQLIYESA ITC*EYLDEAYPGKK	C374	0.29451	P22234	
TDDYLDQPC*LETVNR	C417;C410;C455	0.294166	P49368 B4DUR8 P49368	
AHIAQLC*EK	C39	0.29407667	P03897	
VGLTNYAAAYC*TGLLLAR	C100;C80	0.294025	P62241 Q5JR95	
GMYGIENEVFLSLPC*ILNAR	C292;C404	0.2938081	Q14137 Q14137	



AILQQLGLNSTC*DDSILVK	C160	0.293595	P36871	P19367-3 Isoform 3 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367 Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 # P19367-4 Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1 # P19367-2 Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1 #
AMFESQSEDELTPFDMSIQC*IQSVYISK	C342	0.29338	Q02790	P12956 X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 #
LSC*FAQTVSPA EK	C270	0.29297	P32455	Q16658 Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3 #
YLLQYQEPIPCQLVTALC*DIK	C158	0.29280571	Q99832	P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P10809 60 kDa heat shock protein#
AAVEEGIVLGGGC*ALLR	C270	0.29254667	P35998	mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #
DSAQC*AAIAER	C35;C64;C35;C64	0.29187	M0R3D6 M0R117 M0R1A7 Q02543	Q96RS6 NudC domain-containing protein 1 OS=Homo sapiens GN=NUDC1 PE=1 SV=2 #
IGSC*TQQDVELHVQK	C245;C306	0.2911025	Q9BY44 Q9BY44	P14868 Aspartate--tRNA ligase# cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 #
HVIPMNPNTNDLFLNAVGDGIVLC*K	C511	0.2910375	Q99832	P13796 Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 #
AWSTGDC*DNGGDEWEQEIR	C245	0.29079	Q13162	Q9BRF8 Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3 #
C*LDAISSLLYLPPEQQTDDLLR	C40	0.2896	Q13867	Q16401-2 Isoform 2 of 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 # Q16401 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3 #
EDEEESLNEVGYDDIGGC*R	C127;C127	0.28852444	Q8WUM4 Q8WUM4	P55072 Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 #
NIHGSDSVESAEKEIGLWFHPEELVDYTSC*AQNWIYE	C394;C386	0.28823167	P29401 P29401	P15531 Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 # P15531-2 Isoform 2 of Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 # A0A087WV23 SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 # Q9H299 SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1 #
ATPPQIVNGDQYC*GDYELFV EAVEQNTLQEFLK	C437	0.28560222	P11216	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 #
NC*NDFQYESK	C12	0.28494667	P62753	Q14697 Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 #
TRDGS DYEGWC*WPGSAGY PFTNPTMR	C133	0.28443	P52292	Q14697-2 Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB #
AGLPCQDLEFVQFHPTGIYAGCLITEGC*R	C317;C273;C317	0.28385	P62879 E7EP32 P62873	P31040-2 Isoform 2 of Succinate dehydrogenase [ubiquinone] flavoprotein subunit# mitochondrial OS=Homo sapiens GN=SDHA # P31040 Succinate dehydrogenase [ubiquinone] flavoprotein subunit# mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 # D6RFM5 Succinate dehydrogenase [ubiquinone] flavoprotein subunit# mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=1 #
GPQLFHMDPSGTFVQC*DAR	C146	0.282775	P34932	P28066 Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3 # P28066-2 Isoform 2 of Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 #
DLIMDNC*EELIPEYLN FIR	C774	0.2827	P12814	Q58FG1 Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1 #

LRPLSYPTDVLIMC*FSIDSP DSLENIPEK	C163;C163;C16 3	0.28220375	H0YL69 P25789 H0YMZ1	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 # P61586 Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 # P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 # E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 # P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 # Q8IU8 Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 PE=1 SV=2 # Q8IU8-2 Isoform 2 of Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 # Q12906-3 Isoform 3 of Interleukin enhancer- binding factor 3 OS=Homo sapiens GN=ILF3 # Q12906-2 Isoform 2 of Interleukin enhancer- binding factor 3 OS=Homo sapiens GN=ILF3 # Q12906-5 Isoform 5 of Interleukin enhancer- binding factor 3 OS=Homo sapiens GN=ILF3 # Q12906 Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 # Q12906-4 Isoform 4 of Interleukin enhancer- binding factor 3 OS=Homo sapiens GN=ILF3 # K7EKJ9 Interleukin enhancer-binding factor 3 (Fragment) OS=Homo sapiens GN=ILF3 PE=1 SV=1 # Q12906-7 Isoform 7 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 # Q12906-6 Isoform 6 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 # P52209 6-phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 # P52209-2 Isoform 2 of 6- phosphogluconate dehydrogenase# decarboxylating OS=Homo sapiens GN=PGD #
LIC*CDILDVLDK	C645	0.28161692	P14625 E9PK25 G3V1A4 P23528 E9PP50	
ASHIQLDSLPEVPLLVDVPC*L SAQLDSDSILNIVK	C77;C22;C39;C3 9	0.28005		
GDLDELVLCC*K	C133	0.28001	P29401	
VGTGEPC*CDWVGDEGAGH FVK	C220;C252;C25 2	0.279955	P50440 P50440 P50440	
TDDYLDQPC*YETINR	C264;C264;C26 4	0.279947	O95630 O95630 C9JK83	P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 #
EGILSDEIYC*PPETAULLGSY AVQAK	C27	0.27906533	P12004	P15311 Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 # E7EQR4 Ezrin OS=Homo sapiens GN=EZR PE=1 SV=3 # P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #
QC*TGLQGFLVFHSGGGTG SGFTSLLMER	C276;C209;C17 9	0.27890333	O60701 O60701 O60701	
TDICQGALGDC*WLLAAIASL TLNEEILAR	C2881;M3015 C3020 C3019;M3016 C2437;M2877 C3020;M3016	0.278022	H7BXU2 F5GZ18 A0A0U1R QY1 Q96PZ7 E5RIG2	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 #
YFAGNLASGGAAGATSLC*F VYPLDFAR	C186	0.27796	P48169	P12236 ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 # P12235 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 # P05141 ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 # V9GYG0 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=1 #

EFC*SYLQYLEYLSQNRPPN AYELFAK	C87;C39	0.27783	Q9BTT0 Q9BTT0	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 # O14744-5 Isoform 5 of Protein arginine N- methyltransferase 5 OS=Homo sapiens GN=PRMT5 # X6RA14 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=1 # P10768 S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 # P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # Q01518 Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 # Q01518-2 Isoform 2 of Adenylyl cyclase- associated protein 1 OS=Homo sapiens GN=CAP1 # P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TP11 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3 # P23526-2 Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHCY # P23526 Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 # A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q15185-3 Isoform 3 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 # P31150 Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 # O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 # P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB # M0QY67 Electron transfer flavoprotein subunit beta (Fragment) OS=Homo sapiens GN=ETFB PE=1 SV=1 # P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 # E9PCY7 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # P55072 Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 # A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 # P07741 Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2 #
SVSAFAPICNPVLC*PWGK	C47	0.277575	P30041	
IC*GDIHGQYTDLLR	C167;C195	0.27671	P23526 P23526	
ALLVTASQC*QQPAENK	C76;C89;C76	0.27663333	Q9UUK9 A6NFX8 A6NJU6	
VPADTEVVC*APPTAYIDFAR	C199	0.27621077	P62424	
GETDEEYLWC*IEQTLYFK	C328;C328	0.2757625	B0YJC4 P08670	
HLNEIDLFC*IDPNDSK	C113	0.275634	Q9Y5P6 Q9Y5P6	
NTNDANSC*QIIPQNVNR	C352;C356;C38 1	0.27554333	Q9Y4E8 Q9Y4E8 Q9Y4E8	
EEFASTC*PDDEEIELAYEQV AK	C517 C489;M511	0.27473478	E9PB90 P52789	
HSMNFC*EIAVEEAVR	C229	0.27387	P15880	
DLNYC*FSGMSDHR	C74;C74;C74	0.27321833	H0YL69 P25789 H0YMZ1	
AIANEC*QANFISIK	C219	0.27263571	P68133 P68032 P62736	
LPVIGGLLDVDC*SESVIK	C207	0.272065	P63244	
GFLFGPSLAQELGLGC*VLIR	C345;C404	0.27125	M0QXS5 P14866	

HAC*VPVDFEEVHVSSNADE EDIR	C109	0.26946333	P11216	G5E9Q7 Isocitrate dehydrogenase [NAD] subunit# mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 # E9PF84 Isocitrate dehydrogenase [NAD] subunit# mitochondrial (Fragment) OS=Homo sapiens GN=IDH3G PE=1 SV=1 # P51553 Isocitrate dehydrogenase [NAD] subunit gamma# mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 # E7EQB8 Isocitrate dehydrogenase [NAD] subunit# mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 # P51553-2 Isoform 2 of Isocitrate dehydrogenase [NAD] subunit gamma# mitochondrial OS=Homo sapiens GN=IDH3G # Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EUU4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # E9PIR7 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 # A0A087WSY9 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=2 # Q16881 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3 # Q16881-3 Isoform 3 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-4 Isoform 4 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-6 Isoform 6 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-5 Isoform 5 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # Q16881-2 Isoform 2 of Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 # F8W809 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 # A0A087WSW9 Thioredoxin reductase 1# cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1 #
AASLLLEILGLLC*K	C92;C92	0.26922	P62888 E5RI99	
YVEPIEDVPC*GNIVGLVGVD QFLVK	C450	0.26897786	O95573	
YLGIPGDKEYCISDDDLFSLP YC*PGK	C363	0.26895667	P20073 P20073	

NALANPLYC*PDYR	C285	0.26828	P31146	H3BRG4 Cytochrome b-c1 complex subunit 2# mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=1 # H3BSJ9 Cytochrome b-c1 complex subunit 2# mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=1 # P22695 Cytochrome b-c1 complex subunit 2# mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 # H3BP04 Cytochrome b-c1 complex subunit 2# mitochondrial (Fragment) OS=Homo sapiens GN=UQCRC2 PE=1 SV=1 # O43390-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR # O60506 Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 # O43390-3 Isoform 3 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR # O60506-3 Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP # O43390 Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 #
GFC*FLEYEDHK	C349	0.26826429	P14868	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 # O14744-5 Isoform 5 of Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 #
DLNC*VPEIADTLGAVAK	C279;C280;C280;C260	0.2675	Q16181 Q16181 E7EPK1 E7ES33	P07355-2 Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2 # P07355 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 # O75131 Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 #
GLGTDEDSLIEIIC*SR	C85;M316 C321;M281 C286	0.26744964	Q08J23 Q08J23 Q08J23	P22314 Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 # P22314-2 Isoform 2 of Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 #
NC*LNPQFSK	C46	0.26727667	P49721	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
DNPGVVTC*LDEAR	C62	0.26718333	F8VZ49 P09651 F8W6I7 Q32P51 P09651 F8W646 P09651	P12081-4 Isoform 4 of Histidine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=HARS # B3KWE1 Histidine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=1 # P12081 Histidine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2 #
SNELGDVGVHC*VLQGLQTP SCK	C89;C92	0.2668875	A0A0B4J2 A4 P42765	
LLNQLQYC*EEAGIPLVAIIGE QELK	C191	0.26642545	P17655	

AVFPEGPC*EEPLQLR	C34;C33;C34	0.266395	O14579 A0A087X0 I4 M0QXB4	Q96P48 Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=3 # Q96P48-3 Isoform 3 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # E7EU13 Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=1 # Q96P48-7 Isoform 7 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # Q96P48-2 Isoform 2 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # Q96P48-1 Isoform 1 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # Q96P48-4 Isoform 4 of Arf-GAP with Rho-GAP domain# ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 # P45880-1 Isoform 1 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 # P45880-2 Isoform 2 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 # A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 # P07814 Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 # P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 # P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 # P55072 Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 # P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 # A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 # P60900 Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 # P60900-2 Isoform 2 of Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 # P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 # P30050-2 Isoform 2 of 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 # Q9BXJ9 N-alpha-acetyltransferase 15# NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
WC*EYGLTFTEK	C57	0.26470667	P48147	
YNVYPTYDFAC*PIVDSIEGVT HALR	C175;C175	0.26393667	Q9H223 A0A087W UA5	
ICPVETLVVEEAIQC*AEK	C351;M319 C322	0.26285	P35606 P35606	
DSNNLC*LHFNPR	C208	0.262315	P36578	
LADDVDLEQVANETHGHVGA DLAALC*SEAALQAIR	C384;C384	0.26208	P55884 P55884	
LMEPIYLVEIQC*PEQVVGGIY GVLNR	C213;M203 C213	0.261988	A0A024R A52 P25787	
HSSLAGC*QIINYR	C159	0.261808	P61586	
IADISQVYTQNAEMRPLGCC* MILIGIDEEQGPQVYK	C206	0.26158	P00491	
HPHDIIDDINSGAVEC*PAS	C50	0.26119667	P22626 P22626 A0A087W UI2	
HFIEITDDQDFDHTYC*MR	C453	0.261015	P31930	

PGHLQEGFGC*VVTNRFDQL FDDESDPFEVLK	C202 C209 C209;C202	0.26061	Q8NAP3 D6RBC4	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 # Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA- binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 #
TADDRVNPC*IGGVILFHETLY QK	C45	0.26037	P46940	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 # P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA #
AAVLVQQWVSYADTELIPAA C*GATLPALGLR	C120;C138;C13 7;C116	0.25994714	P62826 J3KQE5 B5MDF5 F5H018	P26640 Valine--tRNA ligase OS=Homo sapiens GN=VAR5 PE=1 SV=4 #
FGANAILGVSLAVC*K	C221;C254	0.25951222	P38606 P38606	P09104 Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3 # P13929 Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 # P06733-2 Isoform MBP-1 of Alpha-enolase OS=Homo sapiens GN=ENO1 # P13929-3 Isoform 3 of Beta-enolase OS=Homo sapiens GN=ENO3 # P06733 Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 #
IYEGQVEVTGDEYNVESIDG QPGAFTC*YLDAGLAR	C113;C157;C15 7;C157;C157;C1 13;C176;C150;C 113	0.25902625	J3QLK0 P60763 P15153 B1AH78 P63000 B1AH77 P63000 B1AH80 J3KSC4 Q15366 Q15366 Q15366 Q15366 Q15366 Q15366 F8VZX2 H3BRU6 Q15366 Q15366 F8VXH9 Q15365	P46777 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 # Q5T7N0 60S ribosomal protein L5 (Fragment) OS=Homo sapiens GN=RPL5 PE=1 SV=2 #
AHEILPNLVCC*SAK	C54;C54;C54;C5 4;C54;C54;C54; C35;C54;C54;C4 6;C54	0.25855	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #	
C*LYASVLTQPR	C369	0.25841	Q9H4A4	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
TALKEDGVLCC*QGECQWLH LDLIK	C152;M137 C138;M151 C152	0.25623	A0A024R5 71 Q9H4M9 C9JC03 P34897 G3V4W5 P34897 P34897	P19623 Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 #
ALQSNIIFPC*DEVMQLLLENL GNENVHR	C119;C119;C98; C119	0.25615	P49589 B4DKY1 P49589 P49589	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 #
VC*ISILHAPGDDPMGYESSA ER	C204;C217;C20 4;C287	0.254605	P60604-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 # P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 # Q9H7B4-3 Isoform 3 of Histone-lysine N- methyltransferase SMYD3 OS=Homo sapiens GN=SMYD3 # Q9H7B4 Histone-lysine N- methyltransferase SMYD3 OS=Homo sapiens GN=SMYD3 PE=1 SV=4 # Q9H7B4-2 Isoform 2 of Histone-lysine N-methyltransferase SMYD3 OS=Homo sapiens GN=SMYD3 #	
EHSLIEDLILLEEC*DANIR	C94	0.25457	P02042	

LPADVSPINYSLC*LKPDLLDF TFEGK	C162;C115;C16 2;C162	0.25386	Q92747 Q92747 O15143 E9PF58	P55786 Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 # E9PLK3 Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=1 # P55786-2 Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS #
ELC*QGLGQPGSVLR	C283;M315 C336 C289;M262	0.253472	Q9ULV4 Q9ULV4 Q9ULV4	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
LTLVC*ESAPGPITMDLTGDL EALKK	C140	0.25311	P12268	P52566 Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=3 #
TAFQEALDAAGDKLVVDFD ATWC*GPKK	C22;C22;C22	0.25182	P31943 G8JLB6 E9PCY7	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 #
ELEQVC*NPIISGLYQGAGGP GPGGFGAQQPK	C106;C106;C10 6	0.25118	Q9NR50 Q9NR50 Q9NR50	A0A0G2JIW1 Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1 # P0DMV8 Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1 # P0DMV9 Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1 #
TEDSGLQTVIAAATQC*ALS TSQLVACTK	C95;M86 C91;M90 C95 C95;M90	0.25115	P35580 P35579 P35580 P35580 P35580 P35580	Q9Y490 Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 #
C*IPYAVLLEALALR	C38;C38	0.25087	H3BRV9 P61970	F5H248 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # Q9UBW8 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5H4U8 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 # F5GYF7 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=7 # F5H7C6 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 #
GC*DVVVIPAGVPR	C339;C339;C38 1;C401	0.25021	Q86TX2 A0A087X0 W7 A0A087W T95 P49753	P40926 Malate dehydrogenase# mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 #
TTANAIYC*PPK	C91;C91;C70;C9 1	0.24995	P34897 G3V4W5 P34897 P34897	O00231 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 # O00231-2 Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 # P40121-2 Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG # P40121 Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 # A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #
ALNWDSFNTGDCFILDLGQNI FAWC*GK	C427	0.249222	P13489	P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # J3KTA4 Probable ATP- dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 #
ADHQPLTEASYVNLPTIALC* NTDSPLR	C783;C802;C77 8;C767	0.2484075	O00159 O00159 F5H6E2 O00159	
LIDFLEC*GK	C36;C36;C36	0.247055	Q9Y221 Q9Y221 J3QLW7	



NVVTIFSAPNYC*YR	C374	0.245375	P36871	P67775 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 # P62714 Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 #
LHIVQVVC*K	C216;C216	0.243824	Q52LJ0 Q52LJ0	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
DIVDSIKGELSGHFEDLLLAIV NC*VR	C12;C12	0.24370222	P56192 F8VPL7	P12429 Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 # D6RA82 Annexin OS=Homo sapiens GN=ANXA3 PE=1 SV=1 # P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
IIHEDGYSEEEC*R	C89;C89	0.24323	P09661 H0YKK0	B4DW73 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 # Q16822 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 # H0YML5 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 #
QC*PIMDPAWEAPEGVPIDAII FGGR	C111;C111;C111 1;C111	0.24228	Q5VTE0 P68104 Q05639 P68104	Q7Z6Z7 E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 # Q7Z6Z7-2 Isoform 2 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 # Q7Z6Z7-3 Isoform 3 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 #
FVESILSNNTTDDHC*QEFVN QK	C38;M21 C38	0.241785	Q7Z2W4 Q7Z2W4 C9J6P4 Q7Z2W4	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 # O75369 Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 # O75369-9 Isoform 9 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-3 Isoform 3 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-8 Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB #
C*AGNEDIITLR	C42;C42	0.24070143	E7EPB3 P50914	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
AHIANPSGASTEC*FVTDNAD GTYQVEYTPFEK	C73;C62	0.24025667	P46776 E9PLL6 E9PJD9	Q96FX7 tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens GN=TRMT61A PE=1 SV=1 #
ETVSEESNVLC*LSK	C70;C70;C13	0.23987	P46782 MOR0R2 MOR0F0	P43490 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 #
FCSFSPC*IEQVQR	C197	0.2387325	O00148	P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 # F2Z2G2 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 # C9JZW3 Elongation factor 1-beta (Fragment) OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 #
VYSYFEC*R	C155;C176;C155 5	0.23706	E9PK25 G3V1A4 P23528 E9PP50	
SYIEGYVPSQADVAVFEAVS SPPPADLC*HALR	C177;C122;C139 9;C139	0.23674786		

C*DISLQFFLPFSLGK	C245;C245	0.23616	A0A087W YC1 P34932 P59998	P13010 X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 #
IVLTNPVC*TEVGEK	C21;C21;C40	0.23615333	F8WCF6 P59998	P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 #
IIPGFMC*QGGDFTR	C417	0.23433063	P29401	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #
LGDVGMAELC*PGLLHPSSR	C36;C36;C65;C24;C62	0.233465	P47756 P47756 B1AK88 B1AK87 B1AK85	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 #
EDQSILC*TGESGAGK	C254	0.23321333	P12277	P35579 Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 # B1PS43 Myosin heavy chain 11 smooth muscle isoform OS=Homo sapiens GN=MYH11 PE=1 SV=1 # P35580 Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 # P35749 Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3 # M0QY43 Myosin-14 (Fragment) OS=Homo sapiens GN=MYH14 PE=1 SV=7 # Q7Z406 Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 # Q7Z406-5 Isoform 5 of Myosin-14 OS=Homo sapiens GN=MYH14 # Q7Z406-2 Isoform 2 of Myosin-14 OS=Homo sapiens GN=MYH14 # P35580-2 Isoform 2 of Myosin-10 OS=Homo sapiens GN=MYH10 # P35580-3 Isoform 3 of Myosin-10 OS=Homo sapiens GN=MYH10 # P35749-4 Isoform 4 of Myosin-11 OS=Homo sapiens GN=MYH11 # Q7Z406-4 Isoform 4 of Myosin-14 OS=Homo sapiens GN=MYH14 # P35580-5 Isoform 5 of Myosin-10 OS=Homo sapiens GN=MYH10 # P35580-4 Isoform 4 of Myosin-10 OS=Homo sapiens GN=MYH10 # Q7Z406-6 Isoform 6 of Myosin-14 OS=Homo sapiens GN=MYH14 # P35749-3 Isoform 3 of Myosin-11 OS=Homo sapiens GN=MYH11 # P35749-2 Isoform 2 of Myosin-11 OS=Homo sapiens GN=MYH11 # J3KQ18 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=1 # P30046-2 Isoform 2 of D-dopachrome decarboxylase OS=Homo sapiens GN=DDT # P30046 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 # B5MC82 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=4 SV=2 # A6NHG4 D-dopachrome decarboxylase-like protein OS=Homo sapiens GN=DDTL PE=2 SV=1 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 # A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q15185-3 Isoform 3 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 #
VNVTVRPGLAMALSGSTEP *AQLSISSIGVVGTAEDNR	C11;C11	0.23253333	P61160 P61160	P61160 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 # B5MC82 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=4 SV=2 # A6NHG4 D-dopachrome decarboxylase-like protein OS=Homo sapiens GN=DDTL PE=2 SV=1 # Q16181-2 Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7 # Q16181 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7EPK1 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 # E7ES33 Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=3 # A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 # Q15185-3 Isoform 3 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 #
ADTLTPEEC*QQFK	C705	0.2308575	Q99575	P63279 SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1 #
LTFSC*LGGSDFNK	C114;C31;C207;C181;C211	0.230208	G5E9C7 H3BRW9 Q02750 Q02750 P36507	
QILLGIQELLNEPNIQDPAQAE AYTIYC*QNR	C128	0.22873571	Q16531	

AC*PRPEGLNFQDLK	C147;C163	0.227232	F5H157 Q15286	P15927-3 Isoform 3 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 # P15927-2 Isoform 2 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 # P15927 Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1 # B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #
KLLDLVQQSC*NYK	C89	0.22680333	P19623	
ITSC*IFQLLQEAGIK	C259;C386;C388;C389;C183;C321;C394;C270	0.225894	B7Z4D2 Q9NX95 Q9NX95 Q9NX95 B3KRD1 Q9NX95 A0A0C4D G86 Q9NX95	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #
C*LAAALIVLTESGR	C159	0.22497667	P84077	P14618-2 Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM # Q04446 1#4-alpha-glucan-branching enzyme OS=Homo sapiens GN=GBE1 PE=1 SV=3 # E9PGM4 1#4-alpha-glucan-branching enzyme OS=Homo sapiens GN=GBE1 PE=1 SV=1 # P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 # P04899-2 Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-6 Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-3 Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 # P04899-5 Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 #
NSADGLNMFDTGTDSC*YFHS GPR	C134	0.22468	P60842	
LEEEDEDEEDGESGC*TFLV GLIQK	C27	0.223848	P30566	
ITHSPLTIC*FPEYTGANKYDE AASYIQSK	C727;C680	0.22255	Q02809 Q02809	
TYDATTHFETTC*DDIK	C283;C109;C247	0.22084	P67936 K7EPB9 P67936	P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 # P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TP11 # P60174 Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3 # Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 # Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C # Q92597 Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1 # Q02790 Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 # Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 # Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 #
VAHALAEGLGVIAC*IGEK	C423;C445	0.22053857	Q14697 Q14697	
VTWDSSFC*AVNPR	C165;C165	0.21974	P40121 P40121	
DLEIERPMPGHTVTLQCPAL LVVGDSSPAVDAVVEC*NSK	C8	0.2180125	P09960	
TQLAVC*QQR	C103;C95	0.217435	Q92973 Q92973	
FQLTDC*QIYEVLSVIR	C247	0.216905	P04406	

VEDLTFTSPFC*LQVK	C269	0.2163675	O75874	E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # H7C211 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 # Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 # Q99873-2 Isoform 2 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 # Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #
SSWVMTC*AYAPSGNYVAC GGLDNICSIYNLK	C1434	0.215385	Q9Y490	Q9HAV0 Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3 # P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 # H3BUH3 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # B7ZAR9 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=1 # Q8NCN5-2 Isoform 2 of Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR # H3BV59 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # A8MT40 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # Q8NCN5 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 #
FFAFWGQDINNLTPLEC*GR ESR	C35;C67;C39	0.21518333	Q7L1Q6 Q7L1Q6 Q7L1Q6	Q9HAV0 Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3 # P62873 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3 # H3BUH3 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # B7ZAR9 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=1 # Q8NCN5-2 Isoform 2 of Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR # H3BV59 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial (Fragment) OS=Homo sapiens GN=PDPR PE=1 SV=1 # A8MT40 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 # Q8NCN5 Pyruvate dehydrogenase phosphatase regulatory subunit# mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 #
VETELQGVC*DTVLGLLDL SHLIK	C332;C328;C328	0.21406917	A0A087W VQ6 Q00610 Q00610	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 #
EAVFPFQPGSVAEVC*ITFDQ ANLTVK	C497	0.214	Q00839 Q00839	P09382 Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 # O75369 Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 # O75369-9 Isoform 9 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-3 Isoform 3 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-8 Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB #
VVPC*LVTPVTGR	C214;C150	0.21302	P13807 P13807	O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-3 Isoform 3 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-8 Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB #
GC*ITIIGGGDTATCCA K	C85;C196;C190; C243	0.211908	B4E3S0 Q9ULV4 Q9ULV4 Q9ULV4	P00558 Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 #
STLTDSLVC*K	C47	0.2099	P61081	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #
AC*GNFGIPCELR	C287	0.20979571	P43490	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #

GFGFVC*FSSPEEATK	C125;C126;C126;C106	0.20978909	Q16181 Q16181 E7EPK1 E7ES33	B1ANR0 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC4 PE=1 SV=1 # Q13310 Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1 # Q13310-2 Isoform 2 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 # P11940 Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 # A0A087WTT1 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 # Q13310-3 Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 # P11940-2 Isoform 2 of Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 # E7EQV3 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 #
SLSTTNVFAC*SDRPTVIYSS NHK	C159;C159;C159	0.20914	Q5JR08 P08134 E9PQH6	Q16531 DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 # A0A0A0MSX9 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # P41252 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 # J3KR24 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 #
ISEVFDC*WFESGSMFYAQV HYPFENKR	C280	0.20887	P68366 P68363 Q71U36 P68366	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
SPGVVISDDEPGYDLDFC*I PNHYAEDLER	C389;C389;C296;C346;C389	0.20885083	P09104 P13929 P06733 P13929 P06733	E7ERF2 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 # P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 #
GANDFMC*DEMER	C92	0.20813667	P07814	P60981-2 Isoform 2 of Dextrin OS=Homo sapiens GN=DSTN # P60981 Dextrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #
LGGSLIVAFEGC*PV	C55;C55;C55;C55;C50	0.20578	Q15102 M0R389 M0R323 M0QXS6 M0QZT2 M0R1K3	P40925 Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 # P40925-3 Isoform 3 of Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 # P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 # Q9NQR4 Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 # H7C579 Omega-amidase NIT2 (Fragment) OS=Homo sapiens GN=NIT2 PE=1 SV=7 # A0A087WVQ6 Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1 # Q00610-2 Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC # Q00610 Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 #
VIVVGNPANTNC*LTASK	C567	0.20499889	P13639	P19623 Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 # Q9UMS4 Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1 # Q9BXJ9 N-alpha-acetyltransferase 15# NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 #
HTGPGILSMANAGPNTNGSQ FFIC*TAK	C480	0.200355	P12814	
TLSPGDSFSTFDTPYC*R	C241;C170	0.19972	P08237 P08237	
VIQC*FAETGQVQK	C210	0.199566	Q86SQ6	
TALKEDGVLCCQGEC*QWLH LDLIK	C646	0.19767	P22102	
IWSVPNASC*VQVVR	C107	0.19183	P26639	
EALEHLC*TYEK	C784	0.189715	P11216	

GC*WDSIHVVEVQEK	C21;C19;C20	0.189535	P62913 Q5VVC8 P62913	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 # D6RAF8 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=1 # Q14103-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD # Q14103-3 Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD # H0Y8G5 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=7 # D6RD83 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=1 # D6RF44 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=7 # H0YA96 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=1 # D6RBQ9 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=1 # Q14103 Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 # Q14103-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD # J3KQ18 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=1 # P30046-2 Isoform 2 of D-dopachrome decarboxylase OS=Homo sapiens GN=DDT # P30046 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 # B5MC82 D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=4 SV=2 # A6NHG4 D-dopachrome decarboxylase-like protein OS=Homo sapiens GN=DDTL PE=2 SV=1 #
FGEVVDC*TLKLDPITGR	C23	0.188005	B2RPK0	Q14376 UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2 #
LC*AAAASILGKPADR	C316;C268	0.18253833	G3V1A6 P57764	P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 # P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 # P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 # E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 #
EGDVAAC*YANPSLAQEELG WTAALGLDR	C153;C207;C19 3;C193	0.17615	H0YJS8 A0A087X2 I1 P62333 H0YJC0	
LQDAFSSIGQSC*HLDLPQIA VVGQSAGK	C18;C18;C18	0.17409333	P60953 Q5JYX0 P60953	
ETGANLAIC*QWGFDDDEANH LLLQNNLPAVR	C166	0.1734525	Q96HE7	

NHDEESLEC*LCR	C985;C1053	0.172705	P18206 P18206	O43432-3 Isoform 3 of Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 # A0A0A0MSA7 Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=1 # Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # O43432-4 Isoform 4 of Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 # A0A0U1RQK7 Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=1 # Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 # Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # E7E0U4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 # Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 # O43432 Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=2 # Q9BWD1 Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 # Q9BWD1-2 Isoform 2 of Acetyl-CoA acetyltransferase# cytosolic OS=Homo sapiens GN=ACAT2 # A0A0A0MSX9 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # P41252 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 # J3KR24 Isoleucine--tRNA ligase# cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1 # P50991-2 Isoform 2 of T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 # P50991 T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 # H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 # Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 # O75369 Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 # O75369-9 Isoform 9 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-2 Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-3 Isoform 3 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-8 Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB # O75369-6 Isoform 6 of Filamin-B OS=Homo sapiens GN=FLNB #
QASVGAGIPYSVPAWSCQMI C*GSGLK	C172;C193;C17 2;C102	0.170755	P46782 M0R0R2 M0R0F0 M0QZN2	
NNDLC*YWVPELVR	C32;C32;C32	0.16839	O15260 Q5T8U5 O15260	
DIEREDIEFIC*K	C25	0.16466	Q9BQE3 Q71U36	
C*DYMDEVTYGELEKEEAQPI VTK	C91	0.16084	P31949	
VGEAGLLSVDC*SEAGPGAL GLEAVSDSGTK	C29	0.158805	Q99832	

C*SEGVFLLTTTPRPVIVEPLE QLDDEDGLPEK	C108;C114;C109	0.155624	P19105 J3QRS3 O14950	P23246-2 Isoform Short of Splicing factor# proline- and glutamine-rich OS=Homo sapiens GN=SFPQ # P23246 Splicing factor# proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 # P48739 Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2 # B3KYB7 Phosphatidylinositol transfer protein beta isoform (Fragment) OS=Homo sapiens GN=PITPNB PE=1 SV=7 # P48739-3 Isoform 3 of Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB # P48739-2 Isoform 2 of Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB # A0A0A0MSW4 Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=1 # Q96C19 EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1 #
VVLPC*SVQEYQVGLYSVA EASK	C520;M498 C520	0.15508	Q96AC1 Q96AC1 Q96AC1	P18669 Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 # Q92841-3 Isoform 4 of Probable ATP- dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # H3BLZ8 Probable ATP- dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 # P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # Q92841-2 Isoform 3 of Probable ATP- dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # Q92841 Probable ATP- dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 # J3KTA4 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # Q92841-1 Isoform 2 of Probable ATP- dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 #
AAAGELQEDSGLC*VLAR	C408	0.151464	P61158	
YADLTEDQLPSC*ESLK	PTM index from ip2	0.14691	uniprot	
GDGPIC*LVLAPTR	C377	0.1463	P30153	
LIAQAC*VSIFPDSGHFNVDNI R	C303;C303;C23 1;C303;C650;C2 31;C303;C266;C 285;C303	0.14593	Q13509 P07437 Q5ST81 P68371 A0A0B4J2 69 Q13509 P04350 K7ESM5 Q5JP53 Q9BUF5	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 #  F8W0J6 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # P55209-2 Isoform 2 of Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 # F8W543 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # H0YIV4 Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # P55209 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F8VV59 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # F5H4R6 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 # B7Z9C2 Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 #
SEPDDSDPFSFDGPEIMGC* TGCQIDWK	C257;C257	0.14329	P63261 P60709	



FLDGNELTLADC*NULLPK	C481;C464;C480	0.14302111	Q16222 Q16222 Q16222 Q14974 Q14974	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 #
LVEALC*AEHQINLIK	C158;C13	0.140885		P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 # Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #
TCNC*ETEDYGEKFDENDVIT CFANFESDEVELSYAK	C109	0.14075	P11217	Q9Y262 Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 # B0QY90 Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 # B0QY89 Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 #
GDPQVYEELFSYSC*PK	C208	0.13716667	O60684	
DLNHVC*VISETGK	C361;C310;C400;C376;C376;C376	0.134615	P68366 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #
IC*PVEFNPNFVAR	C48;C19	0.132554	Q14558 Q14558	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # Q9UI30-2 Isoform 2 of Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # I3L470 H(+)/Cl(-) exchange transporter 7 (Fragment) OS=Homo sapiens GN=CLCN7 PE=1 SV=1 # P51798-2 Isoform 2 of H(+)/Cl(-) exchange transporter 7 OS=Homo sapiens GN=CLCN7 # H0Y2M6 Chloride channel 7# isoform CRA_c OS=Homo sapiens GN=CLCN7 PE=1 SV=1 # P51798 H(+)/Cl(-) exchange transporter 7 OS=Homo sapiens GN=CLCN7 PE=1 SV=2 #
RWVIC*ALIGILTGLVACFIDIV VENLAGLK	C61	0.13252	Q6PD74	P29144 Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 # Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 # H0YL69 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # P25789 Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 # H0YMZ1 Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=7 #
YEDLAPC*ITLK	C426;C467	0.123765	P12955 P12955	
KLLAPDC*EIIQEVGK	C209	0.11843714	P13797	
YLLQYQEPIPC*EQLVTALC*DIK	C253	0.11688667	Q9H8X2	
IDTHNIIVNQLVFPDPEKPC*K	C241;C241	0.11670333	Q14865 Q14865	O43681 ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2 # A0A087WXS7 ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=1 # P49419-2 Isoform 2 of Alpha-amino adipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha-amino adipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 #
GEVITTYC*PANNEPIAR	C1767	0.11666	P78527	
C*IPALDSLTPANEDQK	C513	0.11306667	Q96RS6	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #

EYGSC*SHHYQQLLSLEQG AQEESR	C109;C109;C109; C109	0.11041	Q15366 Q15366 Q15366 Q15366	Q15149-7 Isoform 7 of Plectin OS=Homo sapiens GN=PLEC # Q15149-9 Isoform 9 of Plectin OS=Homo sapiens GN=PLEC # Q15149-8 Isoform 8 of Plectin OS=Homo sapiens GN=PLEC # Q15149 Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 # Q15149-5 Isoform 5 of Plectin OS=Homo sapiens GN=PLEC # Q15149-3 Isoform 3 of Plectin OS=Homo sapiens GN=PLEC # Q15149-2 Isoform 2 of Plectin OS=Homo sapiens GN=PLEC # Q15149-6 Isoform 6 of Plectin OS=Homo sapiens GN=PLEC # Q15149-4 Isoform 4 of Plectin OS=Homo sapiens GN=PLEC #
SC*NGPVLVGSPQGGVDIEE VAASNPELIFK	C155	0.10338	P41250	Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 # E9PDQ8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=1 # Q96I99-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Homo sapiens GN=SUCLG2 #
TPC*NAGTFSQPEK	C79;C79;C79;C79; C79	0.10051	J3KTF8 P52565 P52565 J3QQX2 J3KRY1	O43684 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 # J3QT28 Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=1 SV=1 # O43684-2 Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 # J3QSX4 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 #
KPFPINHGSETDELLEDAIE VC*K	C182;C182;C197; C386	0.09996	I3L3Q4 Q9HC38 Q9HC38 F6TLX2	P15374 Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCLH3 PE=1 SV=1 # contaminant_UBIQUITIN10 no description#
VVETDPSPYC*IVAPDVIHCE GEPKR	C46;C37	0.09767333	Q9UGI8 Q9UGI8	P55072 Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 #
TLTGTVIDSGDGVTHVIPVAE GYVIGSC*IK	C46;C72	0.0946175	A0A087W YS6 Q8TAA3 O00743 O00743 O00743 K4DI93	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 #
LSQERPGVLLNQFPC*ENLLT VK	C192;C229;C170	0.0845	O00743 O00743 O00743 K4DI93	Q14166 Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2 #
QLIC*DPSYVKDR	C774;C787;C591; C769	0.07615	Q13620 Q13620 Q13620	P50395 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2 #
ELEVLLMC*NK	C152	0.0748525	P13489	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 # A0A087WUD3 Oligosaccharyltransferase complex subunit OSTC OS=Homo sapiens GN=OSTC PE=1 SV=1 # Q9NRPO Oligosaccharyltransferase complex subunit OSTC OS=Homo sapiens GN=OSTC PE=1 SV=1 # Q9NRPO-2 Isoform 2 of Oligosaccharyltransferase complex subunit OSTC OS=Homo sapiens GN=OSTC #
VPFLVLEC*PNLK	C93;C77;C77	0.06994	H0YMV8 Q71UM5 P42677	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #
C*TVFHGAQVEDAFR	C152;C152	0.066415	P49588 P49588	P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 #
QLSSSVTGLTNIEENC*QR	C98;C125;C139	0.0386	F8W8D4 Q8TBC4 Q8TBC4	

LLAQDTCLPCDCFPHGSHSR TC*DMATGQCAC*K	C392;C97;C387; C435;C392	0.0364	P55265 P55265 H0YCK3 P55265 P55265	Q9NYQ6 Cadherin EGF LAG seven-pass G- type receptor 1 OS=Homo sapiens GN=CELSR1 PE=1 SV=1 #
IPGGIIEDSC*VLR	C341	0.02497333	P17655	P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 # B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 # P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 #
PSHAVIPADQDC*SSRSR	C161	0.021595	P62937	F5GX32 DNA repair protein RAD52 homolog OS=Homo sapiens GN=RAD52 PE=1 SV=1 # A0A087WT08 Zinc finger protein 221 OS=Homo sapiens GN=ZNF221 PE=4 SV=1 #
SALNVHC*K	C369	0.00851333	P13639	Q9UK13 Zinc finger protein 221 OS=Homo sapiens GN=ZNF221 PE=2 SV=3 # Q9NYT6 Zinc finger protein 226 OS=Homo sapiens GN=ZNF226 PE=2 SV=2 # P78345 Ribonuclease P protein subunit p38 OS=Homo sapiens GN=RPP38 PE=1 SV=2 # Q5VUC3 Ribonuclease P protein subunit p38 (Fragment) OS=Homo sapiens GN=RPP38 PE=1 SV=7 #
RELLLVLC*K	C76;M23 C26	0.006977	P46777 Q5T7N0	Q93100-3 Isoform 3 of Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB # Q93100-2 Isoform 2 of Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB # Q93100 Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB PE=1 SV=3 # Q93100-4 Isoform 4 of Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB #
NRQTLC*SLLPR	C92	0.00147667	P25398	P40925 Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4 # P40925-3 Isoform 3 of Malate dehydrogenase# cytoplasmic OS=Homo sapiens GN=MDH1 #
ENFSC*LTR	C134	0.00123	P22102	