Determining the effects of DOT1L interacting proteins on cellular reprogramming

by

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Determining the effects of DOT1L interacting proteins on cellular reprogramming

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ABSTRACT

Fully differentiated cells can be reprogrammed into induced pluripotent stem cells (iPSCs) by ectopic expression of transcription factors. However, the mechanism behind this cell fate change is not fully elucidated. Epigenetic regulators have important roles during embryonic development as well as somatic cell reprogramming. Previously, it has been shown that inhibition of DOT1L, the histone H3 lysine 79 methyltransferase, increases the efficiency of reprogramming via regulation of lineage specific genes. DOT1L is recruited to chromatin and act in concert with a number of additional chromatin regulators. However, the role of such DOT1L-interacting proteins in reprogramming remains unknown.

In the first part of this thesis, novel DOT1L interactors were identified using the BioID method in which a promiscuous BirA ligase (BirA*) was employed to biotinylate DOT1L-proximal proteins, *in vivo*. Biotinylated proteins were pulleddown by Streptavidin and identity of the proteins was determined by LC-MS/MS. The resulting novel interaction candidates were investigated for their effects on reprogramming. Candidate genes were knocked-down in human fibroblasts via shRNAs followed by reprogramming. Our results indicated that knock-down of AF10 (*MLLT10*), significantly increased the iPSC generation efficiency, suggesting that it acts as a barrier to reprogramming similar to DOT1L. This finding was verified by CRISPR/Cas9 mediated knockout of AF10. Combining DOT1L inhibition or knockout with AF10 suppression did not result in an additive enhancement of reprogramming, suggesting that these two chromatin factors act in the same pathway.

In the second part of this thesis, known direct and functional interactors of DOT1L were curated from the literature and their effects on reprogramming was investigated through loss of function experiments. Suppression of *Mixed Lineage Leukemia 1 (MLL1)* expression via RNA interference or CRISPR/Cas9 significantly increased reprogramming efficiency. To determine how MLL1 prevents reprogramming, RNA-sequencing was performed. MLL1 suppression resulted in downregulation of fibroblast-specific genes and accelerated the activation of pluripotency-related genes.

Taken together, this study uncovered two important chromatin factors that act as barriers to reprogramming and contributed to our understanding of epigenetic mechanisms that maintain cell identity.

Key words: Reprogramming, DOT1L, BioID, AF10, MLL1

ÖZETÇE

Tamamen farkhlaşmış hücreler ektopik transkripsiyon faktörleri ile uyarılmış plüripotent kök hücrelere (uPKH) yeniden programlanabilmektedir. Fakat bu hücre kaderi değişiminin arkasında yatan mekanizma hala tam olarak açıklanamamıştır. Embriyonik gelişim sürecinde olduğu gibi somatik hücre yeniden programlanmasında da epigenetik düzenleyicilerin büyük rolü bulunmaktadır. Bundan önce, Histon H3 lizin 79 metiltransferazı olan DOT1L'in susturulması durumunun, soya özgü genleri düzenleyerek yeniden programlama verimini arttırdığı gösterilmiştir. DOT1L, kromatine çağırılarak bir dizi diğer kromatin düzenleyiciler ile uyum halinde hareket etmektedir. Fakat bu tip DOT1L-etkileşimli proteinlerin yeniden programlama üzerindeki rolü halen bilinmemektedir.

Bu tezin ilk kısmında, DOT1L-yakınsal proteinleri biyotinlemekle görevli, seçici olmayan BirA ligazı (BirA*) içeren BioID metodu kullanılarak; özgün DOT1L-etkileşimli proteinler in vivo olarak belirlenmiştir. Biyotinlenen proteinler Streptavidin ile çöktürülüp LC-MS/MS ile tanılanmıştır. Elde edilen özgün DOT1L-etkileşimli protein adaylarının yeniden programlama üzerindeki etkileri incelenmiştir. İnsan fibroblast hücrelerinde shRNA'lar ile aday genlerin ifadeleri baskılanıp bu hücreler yeniden programlanmıştır. Elde ettiğimiz sonuçlar, AF10'un (*MLLT10*) baskılanmasının uPKH oluşum verimini arttırdığını ve yeniden programlama üzerinde DOT1L'e benzer şekilde bariyer görevi olduğunu göstermektedir. Bu bulgu, CRISPR/Cas9aracılığıyla AF10'un susturulması ile de doğrulanmıştır. DOT1L-baskılanması ve AF10-susturulması durumlarının bir arada uygulanmasıyla, ek bir artışın görülmemesi, bu iki kromatin faktörünün aynı yolakta etkili olduğunu akla getirmektedir.

Bu tezin ikinci kısmında, bilinen DOT1L'e doğrudan ve işlevsel bağlanan proteinler literatürden belirlenerek, bu genlerin yeniden programlama üzerindeki etkileri işlevsel kayıp deneyleri ile incelenmiştir. RNA interferans veya CRISPR/Cas9 ile Mixed Lineage Leukemia (*MLL1*) ifadesinin baskılanması yeniden programlama verimini arttırmıştır. MLL1'in yeniden programlamayı nasıl engellediğini belirlemek için, RNA-dizileme analizi yapılmıştır. MLL1'in baskılanması fibroblastlara-özgü genlerin baskılanması ve plüripotentlere-özgü genlerin etkinleşme hızında ivmelenme ile sonuçlanmıştır.

Bir arada ele alındığında, bu çalışma iki önemli kromatin belirleyicisinin yeniden programlama üzerinde bariyer olarak davrandığını ortaya çıkarmış ve hücre kimliğinin devamlılığını sağlayan epigenetik mekanizmaları anlamamıza katkı sağlamıştır.

Anahtar kelimeler: Yeniden programlama, DOT1L, BioID, AF10, MLL1

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ABBREVIATIONS

AML	acute myeloid leukemia
AP	Antarctic Phosphatase
APEX	ascorbate peroxidase
BD	bromodomain
BioID	Proximity dependent biotin identification
BirA*	promiscuous BirA ligase
BSA	bovine serum albumin
cDNA	complementary DNA
ChIP	chromatin immunoprecipitation
ChIP-seq	chromatin immunoprecipitation followed by sequencing
CHIR	CHIR99021
co-IP	co-immunoprecipitation
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
CTD	C-terminal domain
DAB	3,3 diaminobenzidine
DMEM	Dulbecco's Modified Eagle Medium
DMSO	Dimethyl sulfoxide
DNA	deoxyribonucleic acid
DNMTs	DNA methyltransferases
Dot	<u>d</u> isruptors <u>of</u> <u>t</u> elomeric silencing
DOT1L	Dot1-like
DotCom	DOT1L complex
DOX	doxycycline
DSB	double strand brake
DTT	Dithiothreitol
EAPs	ENL-associated proteins
ECT spe.	ectodermal specifiers
EDTA	Ethylenediaminetetraacetic acid
EpiSCs	Epiblast Stem Cells
EPZ	EPZ004777 (DOT1L inhibitor)
ESCs	embryonic stem cells
FDR	false discovery rate
Frskln	Forskolin

FYR	phenylalanine-tyrosine rich
GFP	Green Fluorescent Protein
GSEA	gene set enrichment analysis
HDAC	histone deacetylase
HEK293T	human embryonic kidney 293T cells
HMG	high-mobility group
HRP	horseradish peroxidase
IPL	in vivo proximal labeling
IR	ionizing radiation
iDOT1L	inhibitor of DOT1L
iPSCs	induced pluripotent stem cells
KD	knock-down
kDa	kilo Dalton
KO	knock-out
KOSR	knock-out serum replacement
LBD	LEDGF binding domain
LC-MS/MS	Liquid chromatography-tandem mass spectrometry
LTR	Long terminal repeat
MBM	MENIN binding motif
ME spe.	Mesendodermal specifiers
MEF	mouse embryonic fibroblasts
MET	mesenchymal to epithelial transition
MLL1	Mixed Lineage Leukemia 1
mut	mutant
nd	not detected
neaa	Non-essential amino acids
NEB	new viingland biolabs
NES	normalized enrichment score
n.s.	not significant
NT	non-targeting
OE	overexpression
OM-LZ	Octamer motif-leucine zipper
OSKM	Oct4, Sox2, Klf4 and c-Myc
PB	PiggyBac
PBS	Phosphate-buffered saline
PFA	paraformaldehyde
PHD	plant homeodomain
PPIs	protein-protein interactions
\mathbf{PSM}	peptide spectrum matches

PZP domain	PHD1-Zn-Knuckle-PHD2 domain
qPCR	quantitative real-time PCR
RNA	ribonucleic acid
RNAPII	RNA Polymerase II
\mathbf{RT}	room temperature
s.d.	standard deviation
SAM	S-adenosyl-L-methionine
SCNT	somatic cell nuclear transfer
SEC	superelongation complex
SET domain	\underline{S} uvar3-9, \underline{E} nhancer of Zeste, \underline{T} rithorax
$\rm sgRNA/gRNA$	single guide RNA/guide RNA
shRNA	short hairpin RNA
Sir	silent information regulator
TAD	transactivation domain
Tran.	Tranylcypromine
UV	ultraviolet radiation
Vit. C	vitamin C
VPA	valproic acid
Win	WDR5 interaction motif
wt	wild-type
XEN-like cells	extraembryonic endoderm-like cells

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Chapter 1- Introduction

1.1 Somatic cells can be reprogrammed to pluripotent stem cells

Cellular reprogramming can be defined as changing the fate of a differentiated cell into a pluripotent state. There have been three main advances that led to the discovery of somatic cell reprogramming. The first of these advances was the development of somatic cell nuclear transfer (SCNT) method as it proved that somatic cell nuclei have the same genetic material as their progenitor embryonic counterparts¹. The second advance was the ability to culture and maintain pluripotent cells under in vitro conditions, beginning first with the isolation of teratocarcinoma cells² and then followed by the isolation and successful propagation of embryonic stem cells (ESCs) from early embryos³. Lastly, the appreciation of the importance of transcription factors during lineage commitment has led to the possibility of changing cell fates by ectopic expression of these factors⁴. All these advances culminated in the question of whether certain transcription factors can change the fate of fully differentiated cells into pluripotent state.

In 2006, Takahashi and Yamanaka demonstrated that expression of four specific transcription factors (Oct4, Sox2, Klf4 and c-Myc; OSKM in short) triggers reprogramming of mouse somatic cells into embryonic stem cell-like cells, which are called induced pluripotent stem cells (iPSCs)⁵. Following iPSC generation from mouse somatic cells, the same group also demonstrated

that human somatic cells can be successfully reprogrammed into pluripotent state with the same four factors which are now called Yamanaka factors⁶.

1.1.1 Induced pluripotent stem cells vs. embryonic stem cells

ESCs are isolated from the inner cell mass of blastocysts. They are capable of differentiating into cells derived from all three germ layers; therefore ESCs are called as "pluripotent" cells. Inner cell mass cells are naturally existing pluripotent cells whereas iPSCs are generated *in vitro* from differentiated cells with ectopic expression of Yamanaka factors (OSKM).

In mice, pluripotent stem cells can be isolated from 2 different stages of embryonic development: ESCs are isolated from preimplantation inner cell mass whereas Epiblast Stem Cells (EpiSCs) are isolated from epiblast of post implantation embryo. Even though these cells are both called as pluripotent cells, they have slightly different capacities in terms of their potency. While ESCs are called as "naïve", EpiSCs are called as "primed" because they are more committed cells than ESCs. Morphologically, EpiSCs are more flattened in contrast to dome shaped mouse ESCs. Developmentally, EpiSCs are inefficient in generating chimeras while ESCs can contribute to 3 germ-layers by forming a chimera when injected into a mouse blastocyst. Epigenetically, female ESCs have both active X chromosomes (XaXa) while EpiSCs show X chromosome inactivation (XaXi)⁷.

Conventional mouse iPSCs resemble EpiSCs but they can be easily converted to naïve state with certain growth conditions, however, it is harder to have human iPSCs in the naïve state⁸. In addition, human ESCs resemble mouse EpiSCs even though human ESCs are also isolated from preimplanted embryos⁹. Still, with specific conditions, naïve state human ESCs can be isolated¹⁰. There are attempts of making naïve human iPSCs ^{11,12} but protocols remain experimentally challenging.

In definition, iPSCs are pluripotent similar to ESCs, however there are diverse studies that investigate whether iPSCs are indeed similar to ESCs. First reports demonstrated that iPSCs are different from ESCs in terms of their DNA methylation and gene expression pattern even though both cell lines have similar pluripotency properties^{13–15}. However, these differences were abrogated as iPSCs maintained in the culture for longer period of time since fully reprogrammed iPSCs will survive while intermediate stage cells will eliminated^{15,16}. Moreover, human iPSCs resulted in heterogeneous status for X chromosome re-activation, whereas ESCs have both active X chromosomes. One study reported that using SNL feeder cells and iPSC derivation with retroviruses promote the re-activation of some of the X-linked genes¹⁷. This shows that iPSC derivation and their culture conditions have a role in epigenetic memory erasure as much as passaging period of iPSCs. In contrast to these comparison studies, there is lack of consensus in the ESCs epigenetic pattern. For example, two studies^{18,19} that were published at the same time, demonstrated different DNA methylation pattern for ESCs and blastocysts²⁰. Hence, even ESCs that were grown in vitro do not exhibit the same DNA methylation status as embryos that were in their natural environment. Despite differential epigenetic features of iPSCs, mouse iPSCs can generate normal mice in tetraploid complementation assay which shows that fully reprogrammed iPSCs are *bona fide* $pluripotent^{21-23}$. However, this kind of assays is not ethically suitable for human iPSCs; therefore less stringent assays (such as in vitro differentiation or teratoma formation) are performed to show pluripotency of human iPSCs.

1.1.2 Derivation of iPSCs

Following mouse and human iPSC derivation, somatic cells of different species were reprogrammed; such as monkey²⁴, rat²⁵, pig²⁶, cattle, horse, sheep, goat, and rabbit²⁷. Somatic cells from all these different animals were successfully reprogramed with OSKM induction which shows the evolutionary conservation of pluripotency. In addition, reprogramming can be achieved from different source cell types such as fibroblasts, mature B cells, hepatocytes and keratinocytes²⁸. These findings show that OSKM transcription factors are broadly effective to achieve pluripotency from various starting somatic cells.

However, OSKM is not the only route to generate iPSCs (Figure 1). There are several different approaches that can also result in reprogramming of somatic cells. For example, c-Myc can be replaced with L-Myc or N-Myc²⁹ or with other transcription factors such as Tbx3³⁰ or Glis1³¹. Besides, somatic cell reprogramming can be achieved without c-Myc albeit at much reduced efficiency^{5,32}. Knock down of *let-7* can promote human somatic cell reprogramming as much as c-Myc³³. Other replacements can be made, too: Sox1, Sox3 and Rcor2³⁴ can replace Sox2; or Klf2 and Klf5 can replace Klf4³². Moreover, orphan nuclear receptor Esrrb can replace both Klf4 and c-Myc³⁵. Similarly, silencing Dot1L, the H3K79 methyltransferase, can also replace

Klf4 and c-Myc³⁶. Furthermore, Lin28 and Nanog is used as an alternative to Klf4 and c-Myc for reprogramming and this cocktail is called as OSLN³⁷. Histone variants TH2A and TH2B can replace Sox2 and c-Myc for mouse fibroblast reprogramming but they also require phosphorylated NPM (P-NPM) which is a histone chaperone³⁸.

In addition to these alternatives, another approach to reprogramming was postulated in 2013: reprogramming with lineage specifiers. In this method, mouse cells were reprogrammed by counteracting lineage specifiers that are non-pluripotency related genes and this phenomenon was defined as "seesaw model"³⁹. A few months later, Belmonte group replicated the similar kind of reprogramming with human cells⁴⁰. They both showed that Oct4 can be replaced by mesendodermal specifiers and Sox2 can be replaced by ectodermal specifiers.

In mouse reprogramming, Oct4 can be replaced with other factors such as $Nr5a2^{41}$, $Sall4^{42}$, E-cadherin⁴³ or Tet1⁴⁴. In human cells, Oct4 can be replaced with lineage specifiers as explained above. Recently, it was demonstrated that Oct4 can be replaced with another transcription factor Nkx3-1 in both mouse and human reprogramming⁴⁵. Also, human and mouse cells can be reprogrammed with miRNA clusters without any need of exogenous expression of Yamanaka factors. For example, direct transfection of miR-200c/302s/369s mature miRNAs can reprogram both mouse and human somatic cells⁴⁶. Moreover, miR-302/367 can also reprogram human fibroblasts however, it requires HDAC2 degrading valproic acid (VPA) to reprogram MEFs⁴⁷.



Figure 1. Different combinations of transgenes and chemicals for reprogramming

Alternative reprogramming methods were curated in the image below and referred in the text. Yamanaka factors are filled with blue, chemicals are colored as green. Images on left side depict the cell type origin of given combination. (ME spe., mesendodermal specifiers; ECT spe., ectodermal specifiers; VPA, valproic acid; Vit. C, vitamin C; EPZ, EPZ004777; CHIR, CHIR99021; Tran., Tranylcypromine; Frskln, Forskolin) Adapted from Theunissen and Jaenisch, 2014⁴⁸.

There are number of different ways to increase the reprogramming efficiency. Other than changing the reprogramming factors, additions can be made to enhance the efficiency. For instance, using vitamin C can boost the iPSC generation and it can also replace c-Myc⁴⁹. Inhibition of a histone methyltransferase, DOT1L with small molecule EPZ004777 was identified to enhance reprogramming as well as replace Klf4 and c-Myc³⁶. In addition, silencing of p53 significantly increases reprogramming and can replace Klf4 and c-Myc in OSKM reprogramming⁵⁰. Inhibition of p53 pathway can increase the survival of cells; however, it is counter argued that reprogramming without p53 may resulted in transformed iPSCs⁵¹. This shows the complexity of production of pluripotent cells and the increase in the efficiency may decrease the quality of iPSCs. There are still many aspects to be resolved in the molecular mechanisms of reprogramming.

Another trend in reprogramming is replacing transcription factor induction with chemical treatments so that the usage of viral induction can be bypassed. For this goal, Hou *et. al.* proposed a chemical cocktail that can generate iPSCs from mice⁵². In their first report, they used <u>VPA</u>, <u>CHIR99021</u>, <u>616452</u> and <u>Tranylcypromine</u> (VC6T) chemical cocktail to reprogram MEFs with Oct4 induction⁵³. Then, they identified <u>F</u>orskolin as a substitution of expression of Oct4 and included D<u>Z</u>Nep to the cocktail (VC6TFZ)⁵². Same group also established that there is an intermediate state of extraembryonic endoderm (XEN)-like cells in the process of chemical reprogramming⁵⁴. In that study, they also demonstrated that two different DOT1L inhibitors (EPZ004777 and SGC0946) promote the chemical reprogramming of MEFs⁵⁴. EPZ004777 was previously revealed to enhance reprogramming of OSKM-induced human fibroblasts⁵⁵. This shows that DOT1L is a barrier to reprogramming and its inhibition promotes both transcription factor induced reprogramming of human fibroblasts and chemical reprogramming of MEFs. However, chemical reprogramming has not yet been successfully achieved with human somatic cells. So far, it was shown that 3 Yamanaka factors were replaced with small molecules (TGF β i, PDK1a, HDACi, MEKi) but the process still requires Oct4 induction⁵⁶. Further investigations are continuing in this field since chemical reprogramming can be very useful for therapeutic usage of iPSCs.

There are different methods to deliver genes into cells for reprogramming (Table 1). The first experiment of reprogramming was done with retroviruses⁵. However later, lentiviral delivery was favored since its infection efficiency is higher therefore reprogramming efficiency is higher³⁷. To use iPSCs for therapeutical purposes, integration of OSKM plasmids would be disadvantageous, because these genes may reactivate even after differentiation; or these integrations may disrupt a functional gene in the genome. Therefore, non-integrating methods was employed for iPSC generation such as a denoviruses 5^{57} or Sendai viruses 5^{58} . Also non-integrating OSKM DNAs can be transfected to the cells without using any viruses. Episomal plasmids are a commonly used delivery system of this kind⁵⁹. Using OSKM RNA molecules⁶⁰ or their recombinant proteins⁶¹ can also reprogram somatic cells but with recombinant proteins, the efficiency of reprogramming drops dramatically. In summary, there are many different delivery methods for OSKM factor for reprogramming. According to goal of a reprogramming experiment, one those methods can be picked. In this study, I preferred O-S and K-M containing two lentiviral plasmids since their reprogramming

efficiency is very high when compared with other methods and preparation of lentiviruses is cost-effective as well as easy.

Table 1. Diverse delivery methods for iPSC generation

Main viral and non-viral delivery of reprogramming factors was summarized in the table with their advantages and disadvantages. These methods can be used with different cocktails that were explained in the text. DOX, doxycycline; PB, *PiggyBac*; LTR, Long terminal repeat. (Adapted from⁶² Gonzales et. al. 2011)

Delivery Methods				Advantages	Disadvantages	
	Retrovi	rus		-very efficient and stable	-genomic integration -only dividing cells	
Viral		Co pr	onstitutive omoter	-very efficient and stable	-genomic integration -residual expression of transgenes	
	Lenti- virus	In	ducible promoter	-very efficient and stable	-genomic integration -transgenes in genome but silenced in the absence of DOX	
		Ex (w	ccisable lentivirus ith LoxP sites)	-transgene free -little scar on genome	-possible LTR integration close to oncogene	
	Adenov	irus		-transgene free -no genomic integration	-slow and inefficient	
	Sendai v	virus		-transgene free -no genomic integration	-takes too much time for viruses to completely lost in the iPSCs	
Non-viral		rative	PB transposase	-transgene free -average efficiency	-genomic integration -negative selection strongly advised	
	DNA	Integ	DNA with LoxP sites	-transgene free -average efficiency	-genomic integration	
	based	egrative	Non-replicative vectors	-transgene free -no genomic integration	-slow and inefficient -need to check numerous lines to find integration-free ones	
		Non-int	Episomal vectors	-transgene free -no genomic integration	-need to check numerous lines to find integration-free ones -Labour-intensive	
	RNA ba	ased		-no transgene or genomic integration -no need to screen colonies	-Multiple transfections required	
	Protein	base	d	-no transgene or genomic integration -no need to screen colonies	-slow and inefficient	

1.1.3 Stages of iPSC generation

Reprogramming has multiple steps including morphological, epigenetic and metabolic changes. The order of these events may vary or their time latency may differ but at the end of a successful reprogramming, all these changes need to be fulfilled. There are 3 main phases of events which can be listed as initiation, maturation and maintenance (or stabilization). In the first, initiation stage, molecular signatures of the starting cell type gradually disappear. Starting cell generally changes its morphology by a mesenchymal to epithelial transition (MET)⁶³. Also, proliferation capacity of starting cell adapts to ESC-like state, becoming more resistant to apoptosis and senescence⁶⁴. Also during the initial stage, metabolism of cells shifts from oxidative phosphorylation towards glycolysis. It was shown that in the hypoxic conditions, reprogramming is more efficient than under normoxic conditions⁶⁵. In the maturation phase, second wave of transcriptional changes take place which includes the upregulation of endogenous pluripotency markers such as Fbox15, Sall4, Oct4, Nanog and Esrrb⁶⁴. This step is a bottleneck for reprogramming because the proportion of cells that can pass through this step is quite \log^{66} . At the end of this intermediate step, transgenes are silenced which requires nascent pluripotent cells to self-renew independent of ectopic transcription factors. The main event of maintenance stage is the independence of transgenes and endogenous pluripotency genes take over the control for reprogramming to finalize⁶⁴. Since cells are pluripotent at this point, epigenetic changes such as DNA methylations regulate epigenetic memory erasure which fine-tunes the detailed epigenetic signature of new cell fate. For example in mice, cells undergo telomere elongation and in female cells X chromosome reactivates at this stage⁶⁷.

1.1.4 Transcriptional changes and chromatin reorganization during reprogramming

Transcription is tightly regulated process because cell identity is directly correlated with the gene expression profile of a cell. Expression of a gene can start a cascade of intracellular events; therefore transcription is regulated in multiple steps to ensure the controlled regulation. For example, initiation of a transcription requires the transcription factor binding and these bindings recruits many other accessory proteins to transcription start site. After transcription starts, expressed genes are controlled by post-transcriptional regulations and mRNAs can be degraded by miRNAs or lncRNAs to regulate genes that are going to be silenced. All transcriptional regulation events work in harmony to fine tune gene expression so that cell state can be determined. In the case of reprogramming, the cell fate is turned back to the ESC stage by changing global gene expression profile. This includes the activation of pluripotency related genes while at the same time, erasure of lineage specific gene expression signatures.

After discovery of direct reprogramming, many researchers showed that gene expression is drastically changed when a somatic cell is reprogrammed into $iPSCs^{68-70}$. Gene expression analysis shows that iPSCs have similar gene expression profile with ESCs, and they are very different from the starting cell's gene expression profile⁷⁰. To activate the pluripotency genes, a positive

feedback loops play a role between endogenous OSK and induced OSK. Towards the end of reprogramming, iPSCs are independent from transgenic OSK since endogenous OSK becomes active. Since gene expression profile illustrates the characteristics of a cell, there are bioinformatics tools to depict the resemblance of an iPS colony to ESC. For instance, CellNET⁷¹ is a powerful tool to understand whether an iPS colony is *bona fide* iPSC, or still carrying its starting cell traces. Benefiting from such bioinformatics tools can accelerate the molecular knowledge about reprogramming so that we can find an easier and more precise way to achieve *bona fide* iPSCs.

Another key regulator of gene expression is epigenetic status of the cell. Hence, cell fate is determined with epigenetic factors due to their effect on dynamic chromatin state. Chromatin state can be defined as methylation status of DNA and histone code (post-translational modifications on histone tails in nucleosome). All heritable changes in gene expression that does not change the DNA sequence are referred as epigenetics. Epigenetics contributes to differential gene expression in every cell type. Since life starts with a single cell, zygote and whole organisms form from cells that are divided from zygote and all different cell types have same genetic code; epigenetic regulations are responsible from this diversity. Formation of somatic cells from pluripotent cells during development requires many epigenetic changes and conversely somatic cell reprogramming also requires extensive epigenetic changes⁶⁸. DNA methylation and histone modifications control the gene expression together and these modifications have different outcomes as they can activate or inactivate gene expression. Histone acetylation and methylation are the most studied modifications on histories, but there are many other marks on histones such as phosphorylation, ubiquitination, sumoylation, crotonylation, etc.

DNA methylation: One of the most important events in initiation of reprogramming is demethylation of promoters of endogenous OSK since pluripotency genes are silenced in somatic cells. DNA hypomethylation can be achieved actively via Tet enzymes or passively with cell division in the absence of DNA methyltransferases $(DNMTs)^{72}$.

Histone acetylation: Acetylation of lysines on histones neutralizes the positive charge, therefore negatively charged DNA binds loosely to the histones. Acetylation of histones correlates with active transcription as it promotes DNA accessibility to transcription factors. For example, treating cells with valproic acid (VPA), an histone deacetylase (HDAC) inhibitor, yields more iPSC colonies⁷³. Open chromatin structure might favor the activation of pluripotency-related genes activation. As a result, OSKM can easily activate pluripotency circuit.

Histone methylation: There are multiple Lysine (K) residues on histone tails that can be mono-, di-, tri-methylated. Different from acetylation of histones, methylation of each residue has distinct effect on gene expression regulation. In general, H3K4, H3K36 and H3K79 methylations are correlated with active genes while H3K9 and H3K27 methylations are related with silenced genes. There are also bivalent histones that have both active mark H3K4me3 and repressive mark H3K27me3 at the same time⁷⁴. Bivalency has an essential role during development since erasure of one mark results in robust differentiation of cells.

H3K4 methylation: In ESCs, H3K4me3 mark is present on almost every promoter regardless of their activity, however the active genes have Polymerase II bound on the promoter whereas inactive genes have H3K27me3 marks, too⁷⁵. H3K4 methylation is modified with MLL complex proteins and those proteins are effective on ESC self-renewal and differentiation regulation. For example, WDR5 protein is an essential component of MLL complex and it directly interacts with OCT4⁷⁶. Also, it is known that WDR5 is required for both ESC self-renewal and iPSC generation⁷⁶. Conversely, another component of MLL complex, DPY30 is required for maintaining the neuronal differentiation of stem cells⁷⁷. Demethylation of H3K4 residue is also very important to maintain the balance of self-renewal and differentiation. KDM1a (LSD1) is a H3K4me2 demethylase and its deficiency triggers ESCs to differentiate⁷⁸. Also it was shown that H3K4me3/2 demethylase, KDM5b is essential for self-renewal of ESCs⁷⁹. Even though it is clear that H3K4 methylation is important for regulation of pluripotency, effect of other components of MLL complex need to be investigated.

H3K9 methylation: H3K9 methylation is associated with transcriptional silencing. Knock-down of Jmjd1a and Jmjd2c, H3K9 demethylases, blocks the self-renewal of $ESCs^{80}$. When H3K9 methyltransferase Suv39H1 was knocked-down, it increases the reprogramming efficiency³⁶. On the contrary, another H3K9 methyltransferase EHMT1 knock-down decreases reprogramming significantly³⁶. Therefore, it is controversial how H3K9 methylation effects reprogramming.

H3K27 methylation: H3K27 methylation is a well-known modification for gene silencing and that also generates bivalency together with H3K4me3

mark. PRC2 complex methylates H3K27 residue and the proteins in this complex (Jarid2, Mtf2 and Esprc2p48) promote reprogramming⁸¹. Conversely, knock-down of Jarid2, Mtf2 and Esprc2p48 significantly decreases the reprogramming⁸¹. Knock-down of H3K27 demethylase, Jmjd3 increases reprogramming⁸². On the contrary, H3K27 demethylase, UTX was demonstrated as an essential protein for reprogramming⁸³.

H3K36 methylation: H3K36 methylation has a role in transcriptional elongation and this mark is largely found in gene bodies of actively transcribed genes. H3K36 demethylase, Kdm2b enhances reprogramming and vitamin-C synergistically promotes reprogramming with Kdm2b⁸⁴.

H3K79 methylation: H3K79 methylation found on actively transcribed genes. When H3K79 methylation decreases, reprogramming efficiency increases due to the faster silencing of fibroblast specific genes and enhanced MET^{36} . DOT1L is the sole enzyme that methylates H3K79 residue and its knock-down or inhibition with small molecule inhibitors result in increased iPSC generation³⁶. Even though DOT1L is the sole enzyme that has the catalytic activity to H3K79 methylation, it acts with other proteins (AF9, AF10, AF17, ENL) as a complex. Other proteins' effect on self-renewal or reprogramming is not known.

Chromosome remodelers: Chromosome remodelers are also key players of epigenetic regulations hence they are important during reprogramming. For example, overexpression of BAF complex proteins increases the reprogramming efficiency via promoting Oct4 binding to its target sequences in the genome⁸⁵.
All these examples show that epigenetic regulation has a crucial role in reprogramming. According to all these information, it is not surprising to see that epigenetic researches gained a lot of attention in the stem cell field. To unravel the molecular basis of reprogramming, better understanding of transcriptional order of events and epigenetic regulations is required.

1.2 Epigenetic modifiers as barriers and enhancers of reprogramming

As discussed previously, the importance of epigenetics on reprogramming was appreciated very quickly in the stem cell field. Many of the epigenetic modifiers were tested for their effect on reprogramming in different labs. Some of the epigenetic regulatory proteins were found to be "barriers" of reprogramming since their silencing increase the iPSC generation. On the other hand, other epigenetic regulators were identified as "enhancers" of reprogramming due to their overexpression facilitates the reprogramming. Similar to enhancers, a few proteins were characterized as "essentials" of reprogramming since their silencing blocks the reprogramming event even in the presence of OSKM factors. In summary, enhancer epigenetic regulators facilitate the reprogramming while barriers obstruct the reprogramming.

As previously described, DNMT1, the maintenance DNA methyltransferase is a barrier while Tet DNA demethylases are enhancers of reprogramming. Triple knock-out of Tet1/2/3 proteins in the mice resulted in impaired reprogramming which showed that Tet proteins are essential for reprogramming⁸⁶. PRCD2 complex proteins and BAF complex are also enhancers of reprogramming while DOT1L and HDAC are barriers of reprogramming^{36,73,81,85}. In addition to these, there are many other barriers and enhancers identified. For example, H3K9 methyltransferase, Suv39H1 depletion increases reprogramming efficiency therefore it is a barrier³⁶. On the contrary, H3K9 demethylase, Kdm3/4 overexpression enhances reprogramming hence Kdm3/4 is an enhancer of reprogramming⁸⁷. Also, a histone variant can be a barrier or enhancer of reprogramming. For instance, MacroH2A is a barrier of reprogramming since its deletion increases the reprogramming⁸⁸. It has been shown that MacroH2A occupies pluripotency genes silent in fibroblasts⁸⁸ therefore its deletion favors the pluripotency.

Even though many barriers and enhancers of reprogramming were identified (**Table 2**), the crosstalk between these epigenetic regulators during reprogramming should be further investigated. The reprogramming process is complicated and many proteins need to function in synchrony. All these new findings will increase the understanding of the molecular orchestra of reprogramming so that *bona fide* iPSCs can be produced more efficiently and safely.

Table 2. Epigenetic regulators of somatic cell reprogramming and their effects

Table is adapted from previously published review⁸⁹. (OE, overexpression; KD, knock-down; KO, knock-out; +, enhancer of reprogramming; -, inhibitor of reprogramming; M, mouse; H, human)

	$\mathbf{Protein}$	Phenotype	Species
	BRG1 and BAF155	OE +	М
Chromatin	BRM and BAF170	KD +	М
	CHD1L	OE +; KD -	М
Remodelers	CHD4	KD +	М
	INO80	KD -	М
	BMI1	KD -; OE +	М, Н
	RING1	KD -	Н
	WDR5	KD -	М
	LSD1	KD +	Н
	EHMT1 and SETDB1	KD -	Н
	$\rm EHMT1/2$ and $\rm SETDB1$	KD +	М
	SUV39H1/2	KD +	М, Н
Histone	JMJD1A/1B, 2B, 2C	KD-	М, Н
	EED and SUZ12	KD -	Н
Modifiers	EZH1	KD +	Н
	EZH2	KD -; KO -; OE +	М, Н
	JMJD3	KD +; KO +; OE -	М, Н
	UTX	KD -; KO -	М, Н
	$\rm JHDM1A/1B$	KD -; OE +	М
	DOT1L	KD +	М, Н
	GCN5	KD -	М, Н
	HDAC2	KD +	М
	DNMT1	KD +	М, Н
DNA Modifiers	AID	KD -; KO -; OE +	М, Н
	TET1, 2, 3	KD -; OE +	М
	ASF1A	KD -; OE +	Н
Other	CHAF1A, B	KD +	М
Eniconotie	MacroH2A	KD +; KO +; OE -	М, Н
Epigenetic	BRD4	KD -; OE +	М, Н
Regulators	CBX3	KD +	М
	SIN3A	KD +	М

1.3 Dot1L (H3K79methyltransferase) acts as a barrier to reprogramming

Reprogramming requires global remodeling of the epigenome, therefore investigation of chromatin regulators' role in reprogramming can provide more insight. In a previous study, an shRNA screen was performed to identify chromatin modifiers that have an effect on reprogramming in human origin fibroblasts³⁶. Dot1L, along with SUV39H1 and YY1 were identified as blockers of reprogramming. It was reported that knock down of DOT1L can substitute Klf4 and c-Myc in reprogramming factors³⁶. ChIP-seq of DOT1L inhibited cells showed that the decrease in the H3K79 methylation levels in the generation of $pluripotency^{36}$. specific genes accelerated lineage Correspondingly, shRNA-mediated silencing of Dot1L in mESCs impairs the differentiation into embryoid body and DOT1L regulated genes were identified as differentiation related genes⁹⁰. These studies show that DOT1L and H3K79 methylation have crucial roles in pluripotency and yet, it is unclear how DOT1L acts in pluripotency and differentiation. Further studies are required to reveal DOT1L's mechanism of action and H3K79 methylation during reprogramming.

DOT1L is a histone lysine methyltransferase that is responsible of mono-, di-, tri-methylation of H3K79 residue. Unlike other histone modifications, H3K79 is localized in the globular domain of histone and DOT1L can catalyze methylation specifically in the nucleosome structure⁹¹. DOT1L is the sole enzyme that is capable of H3K79 methylation and the same modification is carried out in other organisms with homologs of DOT1L. Even though DOT1L was discovered as a blocker of reprogramming, its mechanism of action during reprogramming is still unclear.

1.3.1 Discovery of Dot1 protein

Dot1 gene was identified in a study that was investigating the <u>d</u>isruptors <u>of</u> <u>t</u>elomeric silencing (Dot) in *S. cerevisiae*⁹². In this genetic screen was performed to identify genes that have a role during telomeric silencing and Dot1 was the strongest candidate therefore gene was named as Dot1. The major function of Dot1 is H3K79 methylation, and DOT1L is the only H3K79 methyltransferase⁹³. When the mammalian homolog of Dot1 was identified, it was named as Dot1-like (DOT1L) protein, also referred as KMT4, and it has been revealed that DOT1L is evolutionarily conserved from yeast to human⁹⁴. When DOT1L was discovered as a H3K79 methyltransferase (KMT) due to the absence of SET domain (<u>S</u>uvar3-9, <u>E</u>nhancer of Zeste, <u>T</u>rithorax) in DOT1L⁹².

1.3.2 Structure of DOT1L protein

Crystal structure of catalytic domain of human DOT1L protein in complex with methyl donor SAM (S-adenosyl-L-methionine) was identified in 2003^{91} . This work demonstrated how SAM can bind to a pocket at the N-terminus of DOT1L⁹¹. It was also demonstrated that SAM cannot bind to GSG₁₆₃₋₁₆₅RCR mutant of DOT1L⁹⁴ and in structural analysis it was shown that indeed these amino acids were found in the backside of the SAM binding pocket⁹¹. GSG₁₆₃₋₁₆₅RCR mutation is within the DxGxGxG signature motif that was previously found in SAM binding proteins⁹⁵. This motif is found in hDOT1L as DLGSGVGQ and mutation of GSG residue blocks DOT1L binding to SAM⁹⁴. In the structural study, it was also claimed that lysine binding channel of DOT1L is separate from SAM binding pocket; therefore they claimed that multiple rounds of H3K79 methylation can be processed without releasing from the enzyme⁹¹.

In previous studies, it was shown that DOT1L methylates H3K79 in the nucleosome form rather than free histone form⁹⁴. In the structural study it was demonstrated that "*DOT1L interacts with all four histones on the same side of the nucleosome disk surface*"⁹¹ which explains the reason for DOT1L preferring the nucleosome structure to perform enzymatic activity. This finding was supporting DOT1L's binding to ubiquitinated H2B, since it was demonstrated that H2BK123 ubiquitination is required for H3K79 methylation in yeast⁹⁶. Later, it was confirmed biochemically that H2B ubiquitination is required for H3K79 methylation in human, as well⁹⁷.

1.3.3 DOT1L's diverse roles in the cell

Researchers discovered that Histone H3 is methylated at the globular residue of lysine 79 and Dot1 and its mammalian homolog of DOT1L protein was found to be the sole responsible histone methyltransferase for H3K79 methylation^{94,98–100}. Even though structural properties of DOT1L resembles arginine methyltransferases⁹³, DOT1L's arginine methyltransferase activity could not be demonstrated¹⁰⁰. However, in recent studies, DOT1L's diverse functions in cellular activities have been discovered in telomeric silencing, transcriptional regulation, cell cycle regulation, DNA damage response, development and leukemia.

1.3.3.1 Role of DOT1L in telomeric silencing

As stated previously, yeast Dot1 plays a role in telomeric silencing. Dot1's effect on heterochromatin formation was dependent on Sir (silent information regulator) proteins, since Sir3 binds H3K79 and silences genes at telomeric region¹⁰¹. Since Sir3 and Dot1 compete to bind to the same residue, the interplay between H3K79 methylation and Sir Protein binding regulates the telomeric silencing. Similar mechanism was also revealed in human. Sir2 homolog SIRT1 was demonstrated to regulate histone deacetylation-dependent silencing interplaying with DOT1L¹⁰². DOT1L blocks SIRT1's binding therefore promotes open chromatin whereas SIRT1 binding to chromatin stimulates the silencing¹⁰².

1.3.3.2 Role of DOT1L in transcriptional regulation

DOT1L plays a role in elongation of transcription. DOT1L is recruited to different transcriptional elongation complexes (**Figure 2**). For example, DOT1L was found in a complex with AF4, AF9, AF10, ENL and p-TEFb,

where p-TEFb phosphorylates the C-terminal domain (CTD) of RNA Polymerase II (RNAPII)¹⁰³. Phosphorylation of RNAPII from its CTD is a key event during transition from initiation to elongation of transcription. Also, DOT1L was found in core ENL-associated proteins (EAPs) along with AF4 and p-TEFb¹⁰⁴. Later, DOT1L complex (DotCom) was identified along with AF9, AF10, AF17, ENL and Wnt pathway proteins¹⁰⁵. On the other hand, there are other elongation complexes that do not contain DOT1L, such as superelongation complex (SEC) and AEP (AF4, ENL, p-TEFb)^{106,107}. Presence of DOT1L not being consistently found in all the elongation complexes points to two possible reasons: (1) insufficient experimental designs, (2) dynamic elongation complexes formed for transcription of subset genes at different time points of cell cycle. Although DOT1L is not found in every elongation complex, it plays a role in elongation of at least a subset of genes.



Figure 2. Interaction partners of DOT1L during transcriptional elongation

1.3.3.3 Role of DOT1L in DNA damage response

A few studies have associated DOT1L with double strand brake (DSB) repairs. In the first study that detected the DNA repair role of DOT1L, 53BP1 protein was found to bind to methylated H3K79¹⁰⁸. 53BP1 protein binds to p53, which is important in DNA damage response pathways¹⁰⁹. Later, yeast homolog of 53BP1, Rad9, was also demonstrated to bind to methylated H3K79¹¹⁰. It has been shown that DOT1L knock down increases sensitivity to ionizing radiation (IR) and ultraviolet radiation (UV) in both yeast and mammalian cells^{111,112}. For example, HLA-B-associated transcript 3 (BAT3) protein recruits DOT1L to the chromatin site, and BAT3 knockdown decreases 53BP1 foci, and sensitizes cells to IR¹¹³. Even though it is unclear how H3K79 methylation regulates DNA damage response, DOT1L performs strategic H3K79 methylation marks on the genome to protect genomic stability. It was established that H3K79 methylation is enriched around the origin of replication sites in genome and loss of DOT1L disrupts replication¹¹⁴. Taken together, DOT1L has a primary role in maintaining genomic stability via H3K79 methylation at DNA damage site and origin of replication region. However, there are still many unknowns on how DOT1L regulates DNA damage pathways.

1.3.3.4 Role of DOT1L in cell cycle regulation

Histone methylation pattern is an important regulator of cell cycle, therefore when H3K79 methylation was found, its abundance in different cell cycle phases were investigated. Interestingly, literature shows no consensus on cell cycle regulation effect of DOT1L, since different organisms displayed distinct H3K79 methylation patterns. In yeast, H3K79 methylation levels are low in the G1 and gradually increases through S, G2 and M phases¹¹⁵. On the contrary, HeLa cells have high H3K79me2 levels in G1 phase which gradually decrease through S and G2 phase and increase again during M phase⁹⁴. In mouse ESCs, DOT1L knock out did not affect proliferation, however, in vitro differentiation of DOT1L-KO ESCs displayed defects in proliferation and cells were arrested at G2/M phase⁹⁰. In erythroid lineage cells, DOT1L-KO resulted in G0/G1 accumulation¹¹⁶. Different organisms and different cell types exhibiting different patterns of H3K79 methylation shows that cell cycle regulation of DOT1L is not conserved evolutionarily. To understand the cell cycle regulation system of DOT1L, further studies are required.

1.3.3.5 Role of DOT1L in embryonic development

In fly embryogenesis, H3K79 methylation was not detected until gastrulation. After that, increasing levels of H3K79 methylation pointed out importance of *grappa*, fly ortholog of yeast Dot1, for developmental genes¹¹⁷. It was also reported that *grappa* is associated with Wnt signaling pathway because knock down of *grappa* affects Wingless target genes (*senseless, frizzled 3* and *homothorax*) that are actively transcribed¹⁰⁵. For mouse embryogenesis, H3K79me2 can be detected after blastocyst stage¹¹⁸. Dot1L knock out mouse embryo is lethal after day 10 when organogenesis of cardiovascular system starts¹¹⁹. Even though mouse oocyte has detectable methylation on H3K79, remaining methylation disappears following fertilization¹¹⁸. This observation implies the existence of an active demethylation enzyme(s), because during fertilization, H3K79 methylation loss was independent from DNA synthesis. However, to date, a histone demethylase that specifically targets H3K79 residue has not been identified. In 2017, KDM4D was proposed to be H3K79me3 demethylation regulator¹²⁰. However, it is not certain that KDM4D can demethylate H3K79me3 residue all by itself, therefore H3K79 demethylation activity needs to be further investigated.

1.3.3.6 Role of DOT1L in leukemia

In many cases of Acute Myeloid Leukemia (AML), rearrangement of the *Mixed Lineage Leukemia (MLL)* locus takes place, resulting in the production of MLL fusion proteins. Role of DOT1L during leukemia was revealed as many of the MLL fusion proteins were found to interact with it. MLL is a H3K4 methyltransferase and has a regulatory role during hematopoiesis. However, in some cases *MLL* gene translocates to other chromosomes and translocation product translates an in frame fusion protein. Some examples of leukemia associated MLL fusion proteins are MLL-AF9, MLL-AF10, MLL-ENL. Interesting aspect of the translocations is the fact that fusion partners of MLL are usually the interactors of DOT1L¹²¹. It is hypothesized that DOT1L's aberrant recruitment via fusion partner of MLL causes the leukemia phenotype. In the case of MLL-AF10 fusion protein triggering leukemia, HoxA9 gene is upregulated and this contributes to the leukemia phenotype¹²¹. Moreover, deletion of HoxA9 in MLL-AF10 fusion prevents

transformation. Similarly, upregulation of HoxA5 gene was responsible in CALM-AF10 translocated leukemia¹²². Other than AF10, there are a few protein fusions of MLL such as AF4 (AFF4), AF9 (MLLT3), AF17 (MLLT6) and ENL (MLLT1) which are all involved in elongation complex binding partners of DOT1L¹²³. Since DOT1L has an important role during leukemia, one of the approaches of treatment for leukemia was using small molecule inhibitors for DOT1L. The most efficient DOT1L inhibitors were EPZ004777, EPZ005676 and SGC0946 which were tested for their therapeutic effect on leukemia. However, using these drugs might result in side effects such as disruption in normal hematopoiesis because DOT1L has a role during normal hematopoiesis as well¹²⁴.

1.3.4 Known protein interactions of DOT1L

DOT1L has many protein-protein interactions that have been identified to date. The first interaction of DOT1L was found in 2005, with $AF10^{121}$. This interaction was very important because it associates DOT1L with leukemia. Later, it was shown that DOT1L was interacting with AF9, AF17 and ENL as well (Figure 3)^{93,104,105}. In 2010, affinity purification of DOT1L was performed, followed by mass spectrometry for identification of proteins that are directly interacting with DOT1L¹²⁵. In that study, a few new interactions of DOT1L was detected and NPM1, HNRNPM, DDX21 interactions were also validated with pull-down assays¹²⁵. In 2011, DOT1L was pulled down with STAT1¹²⁶ and AF4¹²⁷. In 2012, DOT1L was pulled down with BAT3¹¹³. All these proteins were direct interactors of DOT1L and their interactions

were validated with immunoprecipitation methods. However, there are also functional interactions of DOT1L, where the proteins do not physically interact with it but work in parallel in similar cellular activities. MLL1 is one of those functional interactors of DOT1L. Their aberrant cooperation results in leukemia which shows that MLL1 and DOT1L's co-existence in the chromatin should be tightly regulated⁹³. This makes MLL1 an important functional interactor of DOT1L. SIRT1 and CDK9 are also functional interactors of DOT1L where CDK9 and DOT1L work in parallel in transcriptional elongation. CDK9 is a subunit of p-TEFb and even-though p-TEFb does not interact directly with DOT1L, they coexist in elongation complexes^{103,128}. On the other hand, SIRT1 and DOT1L work in opposite functions. DOT1L inhibits SIRT1 binding to chromatin therefore they are working in reverse¹⁰². While DOT1L makes active mark H3K79me, SIRT1 carries out deacetylation of H3K9 which is a repressive mark¹⁰². Even though some of the DOT1L interactors were identified; DOT1L-mediated H3K79 methylation mechanism is still unclear. Therefore, different approaches on protein interaction studies are required to identify not only direct interactions but also functional interactions of DOT1L.



Figure 3. Schematic representation of the DOT1L protein

Ubiquitin-interaction motif (UIM) is located N-terminus of DOT1L, a lysinerich region is required for nucleosome binding and interacts with the ubiquitin H2B. Within the lysine-rich region, there is a nucleosome/DNAbinding motif. Adapted from Castelli *et. al.*¹²⁹.

1.4 Hypothesis

It has been established that DOT1L acts as a potent blocker of reprogramming of somatic cells. However, it is not known whether the proteins that are interacting with DOT1L have any role in reprogramming. I hypothesize that DOT1L's interactome contributes to reprogramming, and investigating the key factors in DOT1L's interactome will reveal the molecular mechanism of DOT1L's action during reprogramming.

Chapter 2- Materials and Methods

2.1 Plasmids and cloning procedures

For reprogramming experiments and OSKM transcription factor overexpression pSIN-O2S (Addgene # 21162) and pSIN-K2M (Addgene # 21164) vectors were used. For viral packaging of plasmids, pCMV_VSV-G (Addgene # 8454) envelope protein expressing plasmid was used along with viral packaging plasmids. For lentivirus production, pCMV-dR8.2 Δ VPR (Addgene # 8455) packaging plasmid was used while pUMVC (Addgene # 8449) packaging plasmid was used for retrovirus production.

Table 3. List of cloning primer sequences

Primer Name	5' to 3' Sequence
$DOT1L\text{-}BioID\text{-}Q5_top$	TGGATATCTGCAGAATTCACcATGGGGGGAGAAGCTGGAGCT
$\rm DOT1L\text{-}BioID\text{-}Q5_bottom$	AGCTCCAGCTTCTCCCCCATgGTGAATTCTGCAGATATCCA
shCloning Forward	GATGGCTGCTCGAGAAGGTATAT <u>TGCTGTTGACAGTGAGCG</u>
shCloning Reverse	GTCTAGAGGAAT <u>TCCGAGGCAGTAGGCA</u>
XhoI-AF10 cloning-Fwd	TATAACTCGAGATGGTCTCTAGCGACC
AF10 cloning-stop-XhoI-Rev	GAAAGCTGGGTCTAGATATCTCGAG

2.1.1 BirA*-DOT1L fusion protein expression plasmid cloning

BirA* cDNA was used from pcDNA3.1-mycBioID (Addgene # 35700) vector which was a gift from Nurhan Özlü (Koc University). DOT1L wildtype (wt) and mutant (GSG 163-165 RCR) cDNA plasmids were described previously³⁶. cDNA sequence of DOT1L was confirmed by sequencing the entire DOT1L in plasmids with primers in **Table 8**. To make a fusion protein, first pcDNA3.1mycBioID vector was cut with EcoRI (NEB) and KpnI (NEB) enzymes and then treated with Antarctic Phosphatase (AP, NEB). Then, DOT1L cDNAs were cut with EcoRI (NEB) and KpnI (NEB) enzymes and ligated (Quick Ligase, NEB) into pcDNA3.1-mycBioID. Ligation product was transformed into DH5α competent bacteria.

In the second step, pcDNA3.1-mycBioID vector was cut with XhoI (NEB) and then treated with AP. Then, DOT1L cDNAs that were previously cloned into pcDNA3.1-mycBioID, were cut with XhoI (NEB) enzyme and ligated (Quick Ligase, NEB) into XhoI-cut pcDNA3.1-mycBioID vector. Ligation product was transformed into DH5α competent bacteria.

In the third step, BirA*-DOT1L fusion was cloned into pENTR1A vector. NheI cut site was necessary at the end of DOT1L cDNA therefore; an NheI cut site was added into BamHI cut site at the end of DOT1L using short double-stranded oligos phosphorylated with T4 Polynucleotide kinase. The sequences of inserted oligos are listed in the **Table 3**. Then, NheI cut site added BirA*-DOT1L wt and mut fusion proteins were cut with NheI (NEB) and ligated with XbaI-cut AP-treated pENTR1A no ccDB (Addgene # 17398). Since XbaI and NheI has compatible restriction enzyme sites, BirA*-DOT1L wt and mut fusion sequence was ligated into pENTR1A vector. Ligation product was transformed into Stbl3 competent bacteria.

In fourth step, 1 nucleotide was added between the junction of BirA^{*} and DOT1L so that codon order of fusion protein will be in frame with BirA^{*} and DOT1L. For this cloning, Q5 Site-Directed Mutagenesis Kit (NEB) was used with primers that are listed in the **Table 3**. This cloning procedure was confirmed with sequencing of the base addition site with primers in **Table 8**. In the last step, in frame BirA^{*}-DOT1L wt and mut fusion sequences cloned into an expression plasmid pLEX-307 (Addgene # 41392) via LR cloning (Invitrogen). All these cloning steps are summarized in **Figure 4**.



Figure 4. Cloning steps of BirA*-DOT1L fusion protein expressing plasmid

2.1.2 shRNA cloning into pSMP vector

RNAi Codex (<u>http://cancan.cshl.edu/cgi-bin/Codex/Codex.cgi</u>) was used to design specific shRNAs to each gene of interest (**Table 4**). Synthetic 97-mer oligonucleotides (Macrogen Inc.) were cloned into pSMP plasmid. As a control shRNA, a firefly luciferase targeting shRNA plasmid, pSMP-Luc (shFF, Addgene # 36394) was used. shControl plasmid (shFF) was used as a backbone for cloning of other shRNAs (**Figure 5**).



Figure 5. Sketch of shRNA cloned pSMP plasmid

pSMP-Luc (shFF) vector was cut with EcoRI (NEB) and XhoI (NEB) enzymes and treated with AP enzyme. shRNA oligos were amplified with shCloning primers (**Table 3**) and PCR products were cut with EcoRI (NEB) and XhoI (NEB) enzymes. After enzymatic digestion, PCR products were run in a 2% agarose gel. 110bp bands were cut out and gel purified (Gel extraction kit, MN). Gel extracted oligos were ligated (Quick Ligase, NEB) into pSMP backbone. Ligation product was transformed into Stbl3 competent bacteria. All vectors were confirmed by Sanger sequencing using MSCV-fwd primer (CCCTTGAACCTCCTCGTTCGACCT).

shRNA Name	5' to 3' Sequence		
shAF10-1	TGCTGTTGACAGTGAGCGAGCCGAGAACCCGCTGGTTTATTAGTGAAGCCACAGATGTAATAAACCAGCGGGTTCTCGGCCTGCCT		
shAF10-2	TGCTGTTGACAGTGAGCGCGGTCATATGATCAAAGTTTAATAGTGAAGCCACAGATGTATTAAACTTTGATCATATGACCTTGCCTACTGCCTCGGA		
shNONO-1	TGCTGTTGACAGTGAGCGAAGGAAGGAAATGAGGAAACTATTAGTGAAGCCACAGATGTAATAGTTTCCTCATTTCTTCCTCCTGCCTACTGCCTCGGA		
shNONO-2	TGCTGTTGACAGTGAGCGAATGGAAGAGCTGCACAACCAATAGTGAAGCCACAGATGTATTGGTTGTGCAGCTCTTCCATCTGCCTACTGCCTCGGA		
shKAISO-1	TGCTGTTGACAGTGAGCGAGGCAGTTATTAGGAGTGAAATTAGTGAAGCCACAGATGTAATTTCACTCCTAATAACTGCCCTGCCTACTGCCTCGGA		
shKAISO-2	TGCTGTTGACAGTGAGCGCCTGTAGCAAGATGCTGTTTAATAGTGAAGCCACAGATGTATTAAACAGCATCTTGCTACAGATGCCTACTGCCTCGGA		
shSIN3B-1	TGCTGTTGACAGTGAGCGCGCGGGAAATTGATTATGCATTAGTGAAGCCACAGATGTAATGCATAATCAATTTCCCGGCTTGCCTACTGCCTCGGA		
shSIN3B-2	TGCTGTTGACAGTGAGCGCCCGCTGCATCGCACCGCATCTTCAATAGTGAAGCCACAGATGTATTGAAGAGTGCGATGCAGCGGATGCCTACTGCCTCGGA		
shAF17-1	TGCTGTTGACAGTGAGCGGGCATTGAAGAGGACTGATAAGTAGTGGAAGCCACAGATGTACTTATCAGTCCTCTTCAATGCCTGCC		
shAF17-2	TGCTGTTGACAGTGAGCGACAGGCTGTCTCAACAGCCTTATAGTGAAGCCACAGATGTATAAGGCTGTTGAGACAGCCTGGTGCCTACTGCCTCGGA		
shMRE11-1	TGCTGTTGACAGTGAGCGCCCTAATAGTTTGAACAGATATTAGTGAAGCCACAGATGTAATATCTGTTCAAACTATTAGGTTGCCTACTGCCTCGGA		
shMRE11-2	TGCTGTTGACAGTGAGCGAGGCCATGAACATGAGTGTAAATAGTGAAGCCACAGATGTATTTACACTCATGTTCATGGCCCTGCCTACTGCCTCGGA		
shENL-1	TGCTGTTGACAGTGAGCGACAGCAGATTGTGAATCTGATCTAGTGAAGCCACAGATGTAGATCAGATTCACAATCTGCTGCTGCCTACTGCCTCGGA		
shENL-2	TGCTGTTGACAGTGAGCGCGGATTGTTTCTTTCCTGGATTTAGTGAAGCCACAGATGTAAATCCAGGAAAGAAA		
shNUMA1-1	TGCTGTTGACAGTGAGCGAGCACTGAAGAGGGACAGCAAATAGTGAAGCCACAGATGTATTTGCTGTCCCTCTTCAGTGCCTGCC		
shNUMA1-2	TGCTGTTGACAGTGAGCGCGCCTTGAAGAGAAGAACGAAATAGTGAAGCCACAGATGTATTTCGTTCTTCTCTTCAAGGCATGCCTACTGCCTCGGA		
shTPR-1	TGCTGTTGACAGTGAGCGACCCAAGTCTGTCCAGAACAAATAGTGAAGCCACAGATGTATTTGTTCTGGACAGACTTGGGCTGCCTACTGCCTCGGA		
shTPR-2	TGCTGTTGACAGTGAGCGCGCGCCCCCCATAGACGTGTAAATAGTGAAGCCACAGATGTATTTACACGTCTATGGAGGTGCTTGCCTACTGCCTCGGA		
shDDX21-1	TGCTGTTGACAGTGAGCGCGCCATCCCTTTGATTGAGAAATAGTGAAGCCACAGATGTATTTCTCAATCAA		
shDDX21-2	TGCTGTTGACAGTGAGCGCGCTGATCAAGTGGAAGAGATTTAGTGAAGCCACAGATGTAAATCTCTTCCACTTGATCAGCATGCCTACTGCCTCGGA		
shAF4-1	TGCTGTTGACAGTGAGCGCGCGCTTACTCTGTCTACTCAGAATAGTGAAGCCACAGATGTATTCTGAGTAGACAGAGTAAGCTTGCCTACTGCCTCGGA		
shAF4-2	TGCTGTTGACAGTGAGCGACAGCTACAAGAATTAACCAAATAGTGAAGCCACAGATGTATTTGGTTAATTCTTGTAGCTGCTGCCTACTGCCTCGGA		
shAF9-1	TGCTGTTGACAGTGAGCGCCCGCTTTGATTATGACTTATTTAGTGAAGCCACAGATGTAAATAAGTCATAATCAAAGCGGATGCCTACTGCCTCGGA		
shAF9-2	TGCTGTTGACAGTGAGCGCACACACTGCCTTATTACATAATAGTGAAGCCACAGATGTATTATGTAATAAGGCAGTGTGTTTGCCTACTGCCTCGGA		
shBAT3-1	TGCTGTTGACAGTGAGCGAGCAGCAGCAGCTCCGGTCTGATATTAGTGAAGCCACAGATGTAATATCAGACCGGAGCTGCTGCCTGC		
shBAT3-2	TGCTGTTGACAGTGAGCGCCCTTCACAGTATTTAAGAAATTAGTGAAGCCACAGATGTAATTTCTTAAATACTGTGAAGGATGCCTACTGCCTCGGA		
shSIRT1-1	TGCTGTTGACAGTGAGCGCGCGCATCTTGCCTGATTTGTAAATAGTGAAGCCACAGATGTATTTACAAATCAGGCAAGATGCTTGCCTACTGCCTCGGA		
shSIRT1-2	TGCTGTTGACAGTGAGCGACCATGGAGGATGAAAGTGAAATAGTGAAGCCACAGATGTATTTCACTTTCATCCTCCATGGGTGCCTACTGCCTCGGA		
shSTAT1-1	TGCTGTTGACAGTGAGCGCCAGCTGTTACTCAAGAAGATGTAGTGAAGCCACAGATGTACATCTTCTTGAGTAACAGCTGTTGCCTACTGCCTCGGA		
shSTAT1-2	TGCTGTTGACAGTGAGCGCGGCCCTAAAGGAACTGGATATTAGTGAAGCCACAGATGTAATATCCAGTTCCTTTAGGGCCATGCCTACTGCCTCGGA		
shHNRNPM-1	TGCTGTTGACAGTGAGCGCGGCATAGGATTTGGAATAAATTAGTGAAGCCACAGATGTAATTTATTCCAAATCCTATGCCTTGCCTACTGCCTCGGA		
shHNRNPM-2	TGCTGTTGACAGTGAGCGCGGATGTATAAAGATGTTTAAATAGTGAAGCCACAGATGTATTTAAACATCTTTATACATCCATGCCTACTGCCTCGGA		

Table 4. List of shRNA oligo sequences

shNPM1-1	TGCTGTTGACAGTGAGCGGGAGGAAGTCTCTTTAAGAAAGTAGTGAAGCCACAGATGTACTTTCTTAAAGAGACTTCCTCTGCCTACTGCCTCGGA
shNPM1-2	TGCTGTTGACAGTGAGCGAAAGGTTCCACAGAAAAAAGTATAGTGAAGCCACAGATGTATACTTTTTTCTGTGGAACCTTGTGCCTACTGCCTCGGA
shCDK9-1	TGCTGTTGACAGTGAGCGCCCGCTGCAAGGGTAGTATATAATAGTGAAGCCACAGATGTATATATA
shCDK9-2	TGCTGTTGACAGTGAGCGAGCACAGTTTGGTCCGTTAGAATAGTGAAGCCACAGATGTATTCTAACGGACCAAACTGTGCCTGCC
shMLL1-1	TGCTGTTGACAGTGAGCGCGGGCCTTATTCGCAAACCAATATAGTGAAGCCACAGATGTATATTGGTTTGCGAATAAGACCTTGCCTACTGCCTCGGA
shMLL1-2	TGCTGTTGACAGTGAGCGCTGGGATCTAGTTCCAGAGATATAGTGAAGCCACAGATGTATATCTCTGGAACTAGATCCCATTGCCTACTGCCTCGGA
shMLL1-3	TGCTGTTGACAGTGAGCGGGACCGCTACTGATCTTGAATGTAGTGAAGCCACAGATGTACATTCAAGATCAGTAGCGGTCCTGCCTACTGCCTCGGA
shWDR5-1	TGCTGTTGACAGTGAGCGCGGCAAGTTCATCTGCTGATAATAGTGAAGCCACAGATGTATTATCAGCAGATGAACTTGCCATGCCTACTGCCTCGGA
shWDR5-2	TGCTGTTGACAGTGAGCGCCCTCAACAGCTTGTCACCCAATAGTGAAGCCACAGATGTATTGGGTGACAAGCTGTTGAGGTTGCCTACTGCCTCGGA
shRBBP5-1	TGCTGTTGACAGTGAGCGCCCATTTAAACCGAAACTCTACTAGTGAAGCCACAGATGTAGTAGAGGTTTCGGTTTAAATGGATGCCTACTGCCTCGGA
shRBBP5-2	TGCTGTTGACAGTGAGCGATGGGCACAGAATCAAGTAGAATAGTGAAGCCACAGATGTATTCTACTTGATTCTGGCCCAGTGCCTACTGCCTCGGA
shASH2L-1	TGCTGTTGACAGTGAGCGCCCGAGTAACTAACTTATTTAATAGTGAAGCCACAGATGTATTAAATAAGTTAGTT
shASH2L-2	TGCTGTTGACAGTGAGCGATCCAAAGATAAGGATAATTATAATAGTGAAGCCACAGATGTATATAATATCCTTATCTTTGGAGTGCCTACTGCCTCGGA
shDPY30-1	TGCTGTTGACAGTGAGCGCCCAAATCCCATTGAATTTCTATAGTGAAGCCACAGATGTATAGAAATTCAATGGGATTTGGTTGCCTACTGCCTCGGA
shDPY30-2	TGCTGTTGACAGTGAGCGCGGGTTAACATATTTCCCTTATTTAGTGAAGCCACAGATGTAAATAAGGGAAATATGTTAACCTTGCCTACTGCCTCGGA
shMEN1-1	TGCTGTTGACAGTGAGCGACCGAGTACAGTCTGTATCAAATAGTGAAGCCACAGATGTATTTGATACAGACTGTACTCGGGTGCCTACTGCCTCGGA
shMEN1-2	TGCTGTTGACAGTGAGCGACCGGGAAGACGAGGAGATCTATAGTGAAGCCACAGATGTATAGATCTCCTCGTCTTCCCGGCTGCCTACTGCCTCGGA
shWDR82-1	TGCTGTTGACAGTGAGCGCCCAAATGATCTTAATTGTTATTAGTGAAGCCACAGATGTAATAACAATTAAGATCATTTGGTTGCCTACTGCCTCGGA
shWDR82-2	TGCTGTTGACAGTGAGCGCACACAGTTGTTTACAGCTCTATAGTGAAGCCACAGATGTATAGAGCTGTAAACAACTGTGTTTGCCTACTGCCTCGGA
shHCFC1-1	TGCTGTTGACAGTGAGCGAGCCCATGTCCTCTCCAGAAATTAGTGAAGCCACAGATGTAATTTCTGGAGAGGACATGGGCCTGCCT
shHCFC1-2	TGCTGTTGACAGTGAGCGAACCGTTCACTATTGTAGAGTATAGTGAAGCCACAGATGTATACTCTACAATAGTGAACGGTGTGCCTACTGCCTCGGA
shMLL2-1	TGCTGTTGACAGTGAGCGAGCAGTTTGGCTAGTGAACTTATAGTGAAGCCACAGATGTATAAGTTCACTAGCCAAACTGCCTGC
shMLL2-2	TGCTGTTGACAGTGAGCGAAAGGTGTGTGGGCTGACAGAAATAGTGAAGCCACAGATGTATTTCTGTCAGCCACACCCTCTGCCTACTGCCTCGGA
shMLL3-1	TGCTGTTGACAGTGAGCGCAAGCAAGATAAGTTTAGATAATAGTGAAGCCACAGATGTATTATCTAAACTTATCTTGCTTTGCCTACTGCCTCGGA
shMLL3-2	TGCTGTTGACAGTGAGCGACAGGAGGTAGATAGACAAAGATAGTGAAGCCACAGATGTATCTTTGTCTATCTA
shMLL4-1	TGCTGTTGACAGTGAGCGCGGGCCAGAAACACATTGTTATTAGTGAAGCCACAGATGTAATAACAATGTGTTTCTGGCCCTTGCCTACTGCCTCGGA
shMLL4-2	TGCTGTTGACAGTGAGCGCTACCGGAAGTGTGACAAAATATAGTGAAGCCACAGATGTATATTTTGTCACACTTCCGGTATTGCCTACTGCCTCGGA
shCXXC1-1	TGCTGTTGACAGTGAGCGATCAGAGCAAAACATACTGTAATAGTGAAGCCACAGATGTATTACAGTATGTTTTGCTCTGAGTGCCTACTGCCTCGGA
shCXXC1-2	TGCTGTTGACAGTGAGCGATCCCTGGGTTTTGTTAATAAATA
shSET1B-1	TGCTGTTGACAGTGAGCGCCGTCCTCATCCGCGTCATCATTAGTGAAGCCACAGATGTAATGATGACGCGGATGAGGACGATGCCTACTGCCTCGGA
shSET1B-2	TGCTGTTGACAGTGAGCGCGGAGATTACCTATGACTATAATAGTGAAGCCACAGATGTATTATAGTCATAGGTAATCTCCTTGCCTACTGCCTCGGA
shFF	TGCTGTTGACAGTGAGCGCCCGCCTGAAGTCTCTGATTAATAGTGAAGCCACAGATGTATTAATCAGAGACTTCAGGCGGTTGCCTACTGCCTCGGA

2.1.3 gRNA cloning into lentiCRISPRv2 vector

gRNAs that are targeting AF10 gene are gifts from Or Gozani Lab (**Table** 5)¹³⁰. gRNAs are targeting MLL1 and DOT1L were cloned into lentiCRISPRv2 (Addgene # 52691) vector (**Figure 6**). Cloning of these gRNA plasmids were performed by members of the Önder lab. gNT1, gNT2 (non-targeting control) and gDOT1L (targets exon1) were cloned by Can Aztekin; gDOT1L-1 & gDOT1L-2 (targets exon 5) were cloned by Eray Enüstün; gMLL1-1, gMLL1-2 & g-MLL1-3 were cloned by Kenan Sevinç (**Table 5**). Cloning protocol of these gRNAs were carried out as described (Sanjana *et. al.*, 2014)¹³¹. This cloning procedure was confirmed with sequencing of gRNAs with U6 promoter sequencing primer in **Table 8**.



Figure 6. Sketch of gRNA cloned lentiCRISPRv2 plasmid

gRNA Name	5' to 3' Targeting Sequence
sgControl	CTTCGAAATGTCCGTTCGGT
sgAF10-1	TGCAGCGTCGCGGTGCATCA
sgAF10-2	ATAAATAGTCCTTACCACTC
gNT1	ACGGAGGCTAAGCGTCGCAA
gDOT1L-1 (exon5)	GTCCACAAACAGGTCGTCGT
gDOT1L-2 (exon5)	GGTCTCCCCGTACACCTCGG
gNT2	CGCTTCCGCGGCCCGTTCAA
gDOT1L (exon1)	CTGAGCCCGCCGTCTACCCG
gMLL1-21	TTGTAGGATGAGCAATTCTT
gMLL1-22	CCACCCTGAGTGCCTTACCA
gMLL1-753	CAGCAGCCTTTAGATCTAGA

Table 5. List of gRNA targeting sequences

2.1.4 T7-endonuclease assay

gRNA infected dH1f cells were harvested and genomic DNA were isolated using MN Nucleospin Tissue kit. gRNA targeting sites were amplified with specific primers that are listed in *Table 6*. PCR clean up (MN, PCR clean up and gel extraction kit) was performed. 400 ng from cleaned PCR products were mixed with NEB 2 buffer and shuffled via heteroduplex formation protocol (5 minutes at 95°C and ramp down to 85°C at -2°C/sec and ramp down to 25°C at -0.1°C/sec). After heteroduplex formation, samples were treated with T7 endonuclease (NEB) for 1-2 hours at 37°C. Control samples were not treated with T7 endonuclease. Cut samples were immediately loaded on 2% agarose gel. Instead of loading buffers, 5% glycerol was added and gels were visualized via Gel Doc XR System (Bio-Rad).

Table 6. List of T7 specific Primers

T7 Primer Name	5' to 3' Sequence
sgAF10-1 T7 fwd	CAACTCCCTCTTAGATGGTCTC
sgAF10-1 T7 rev	GCGGAATCACATGACAGTCC
sgAF10-2 T7 fwd	GTGACAGGTGGATTAATAGGGCT
sgAF10-2 T7 rev	TCTGAAATAAGGTAACCACCCAAGT
gMLL1-1 T7 fwd	TTGGGGCTGTATGTTTCTGC
gMLL1-1 T7 rev	ATGCCCCAAGTAGTTCCCAG
gMLL1-2 T7 fwd	GATCCTCTTGTCCCAGCCTC
gMLL1-2 T7 rev	ACACAGTCTGACAGCTCTCC
gMLL1-3 T7 fwd	CCGCATGGATCACTTTACCTC
gMLL1-3 T7 rev	ACCCTTCTTCTGAAACACAAAGC

2.1.5 AF10 overexpression plasmids cloning

pBp-AF10 overexpression plasmid is a gift from Or Gozani Lab¹³⁰. However, this plasmid did not overexpress AF10 to sufficient levels upon retroviral packaging and infection of dH1f cells (data not shown). Therefore, AF10

cDNA was cloned from pBp backbone into lentiviral, CMV promoter driven expression plasmid. Also, Hygromycin selectable plasmid backbone was used, because sgAF10 plasmids have puromycin selection and for rescue experiments, another antibiotic selection was needed.

For this purpose, AF10 cDNA was amplified with AF10 cloning primers (**Table 3**). For PCR amplification, Phusion polymerase was used with conditions depicted in **Table 7**.

	Temperature	Period	Cycle
1	$(^{\circ}C)$	(min:sec)	number
	98°C	00:30	1
	98°C	00:10	
	53°C	00:20	30
	72°C	01:00	
	72°C	10:00	1
	4°C	∞	

Table 7. PCR cycling conditions of AF10 cloning experiment

PCR product was digested with XhoI (NEB) enzyme for 3 hours at 37° C. pENTR1A no ccDB (Addgene # 17398) was cut with XhoI (NEB) enzyme for 2 hours at 37° C and treated with AP enzyme 30 min at 37° C. Digested DNA samples were run on an agarose gel and expected bands were excised from gel and purified (Gel extraction kit, MN). Gel extracted DNAs were ligated (T4 DNA Ligase, NEB) into pENTR1A backbone. Ligation product was transformed into Stbl3 competent bacteria. The resulting plasmid was confirmed with sequencing of the entire AF10 sequence with primers in **Table 8.** In the last step, AF10 sequence cloned into an expression plasmidpLentiCMV/TOHygroDEST(Addgene # 17291)viaLRcloning(Invitrogen).

2.1.6 Cloning of GFP Plasmids

Green Fluorescent Protein (GFP) cloned into different backbone plasmids to serve as a control in different experiments. For this purpose, GFP coding sequence was firstly cloned into pENTR1A vector. pBp GFP puro plasmid was cut with EcoRI (NEB) enzyme to excise eGFP. pENTR1A no ccDB (Addgene # 17398) was cut with EcoRI (NEB) enzyme and treated with AP enzyme for 30 min at 37°C. Digested pENTR1A was gel purified (Gel extraction kit, MN) and ligated (Quick Ligase, NEB) with eGFP insert. Ligation products were transformed into Stbl3 competent bacteria. The resulting plasmid sequence was confirmed by sequencing with pENTR1A sequencing primer (**Table 8**). In the last step, eGFP sequence was recombined into variety of destination plasmids including, pLenti CMV/TO Hygro DEST (Addgene # 17291) and pLEX-307 (Addgene # 41392) via LR cloning (Invitrogen).

2.1.7 Sequencing of samples

All sequencing samples were analyzed in Macrogen Europe Laboratories (Netherlands) by Sanger sequencing method (EZ-Seq). Samples were shipped by mixing 500 ng plasmid sample and 25 pmole sequencing primers that are listed in **Table 8**. Shipping was performed according to UN3373 regulations for Category B. Sequencing results were stored as .ab1, .txt and pdf file formats.

Table 8. List of sequencing primers

Primer Name	5' to 3' Sequence
pENTR1A fwd seq	CTACAAACTCTTCCTGTTAGTTAG
pENTR1A rev seq	ATGGCTCATAACACCCCTTG
shRNA sequencing (MSCV) fwd	CCCTTGAACCTCCTCGTTCGACCT
U6 promoter fwd seq	ACTATCATATGCTTACCGTAAC
DOT1L sequencing rev	CGGGATTTCTTCACAGACCCA
DOT1L sequencing fwd-1	CACGATGCTGCTCATGAAAT
DOT1L sequencing fwd-2	AATTTTGCCTTTGGTCCTGA
DOT1L sequencing fwd-3	GATGCCTACAGATCCCCTCA
DOT1L sequencing fwd-4	CTGCAGCTCAAGTCCTGTGT
DOT1L sequencing fwd-5	CAGTGAGAAGGGCCTGAGAG
DOT1L sequencing fwd-6	ATTCCGGCTTCTCAGATCCT
DOT1L sequencing fwd-7	CAACCTCAACTCCATGGTCA
DOT1L sequencing fwd-8	GTGCTTCTCTCTCCCCACAAG
DOT1L sequencing fwd-9	CAGTCGCTGTTCAGCTCTGT
AF10 sequencing rev	GGGACAAAGTTCACATCTCACTC
AF10 sequencing fwd-1	GCGTCGCGGTGCATCAAG
AF10 sequencing fwd-2	AGCTGAAAAAGAGCAAACGGG
AF10 sequencing fwd-3	CTGGCAGACCCAAAGGAAACA
AF10 sequencing fwd-4	AGAGGCAGTGGAGTGAAGGA

2.2 Cell Culture

Cells are grown at 37°C with 5% CO₂. HEK293T cells, mouse embryonic fibroblasts (MEF) and dH1f¹³² cells were grown in D10 medium composed of 1X DMEM (Gibco) and 10% fetal bovine serum (FBS, Gibco) and 1% Penicillin/Streptomycin (Pen/Strep, Gibco). Prior to MEF seeding, plates were incubated with 0.1% Gelatin (Sigma) solution for 10 min at room temperature (RT). Induced pluripotent stem cells (iPSCs) were grown in ES (hES) medium composed of DMEM/F12 human (Stem Cell Technologies), 20%knock-out serum replacement (KOSR, Gibco), 10 ng/ml bFGF, 0.1 mM β -mercaptoethanol, 1% Non-essential amino acids (neaa), 1% Pen/Strep. For iPSC culture, MEFs were seeded at least one day before. Cells were observed with Nikon Eclipse TS100 inverted microscope and fluorescence was detected with Nikon C-SHG Mercury lamp.

2.2.1 Cell dissociation, freezing and thawing procedures

HEK293T cells, dH1fs and MEFs were washed with DPBS solution (Gibco) and dissociated with 0.05% Trypsin-EDTA (Gibco) at 37°C for 4 min. Trypsin was inactivated with D10 medium and cells were passaged into new plate. To freeze cells, dissociated cells were collected in a tube and centrifuged for 5 min at 1500 rpm. Freezing medium was prepared by mixing 10% DMSO (Sigma Aldrich) with 90% FBS and filtering with 0.20 μ m regenerated cellulose (RC) syringe filters (Corning). After centrifugation, supernatant was removed and cell pellet was dissolved within freezing

medium. Then, cells were transferred into externally threaded cryovials (Corning) and stored in isopropanol filled Mr. Frosty freezing containers (Thermo Scientific) at -80°C for 1-2 days. After cells were completely frozen, cryovials were transferred into a liquid nitrogen tank for long-term storage. For thawing, cryovials were quickly defrosted in 37°C water bath until half melted then transferred immediately into growth medium. The mixture was centrifuged for 5 min at 1500 rpm for quick removal of DMSO. After centrifugation, supernatant was removed and cell pellet was dissolved within fresh growth medium.

2.2.2 Generation of Mitomycin-c treated MEFs

MEFs were obtained from pregnant mice at day 13 post coitum. Each embryo was separated from its placenta and surrounding membranes. Brain and dark red colored organs were removed and washed with PBS. Rest of the embryo was minced with razor blades within PBS. Minced tissue was incubated with 1-2 ml Trypsin per embryo on gentle shake at 37°C for 15 min. At the end of incubation, suspended cells were transferred into falcon tube and waited a few minutes for large pieces to settle down. Then, supernatant was carefully transferred to a falcon tube and centrifuged for 5 min at 1100 rpm. Pellet of cells were resuspended within fresh D10 medium and cells were plated as 1 embryo into 10 cm tissue plate. Fibroblasts attached to the plate and cells were passaged for 4 times and resulting cells were frozen. This procedure was performed by Dr. Tamer Önder. Previously frozen MEFs were thawed to make a Mitomycin-c treatment. MEFs were grown in tissue culture plates that were incubated with 0.1% gelatin (Sigma) solution for 10 min. Cells were passaged within 1-2 days and waited for them to reach confluency. Prior to Mitomycin-c treatment, medium was replaced with fresh D10 medium (10 ml medium for 15 cm plates). Mitomycin-c was added at a final concentration of 10 μ g/ml into medium (Millipore 475820-10mg - dissolved in 10 ml dH₂O and filtered). Cells were incubated with Mitomycin-c for 2 hours at 37°C. Medium was removed and cells were washed with PBS, twice. Then, cells were trypsinized and frozen.

2.2.3 Generation of iPSCs from dH1fs (Reprogramming assays)

For reprogramming experiments, dH1fs were counted and 50.000 cells were seeded per well into 12-well plates. Every experiment was performed in triplicate wells. Next day, dH1fs were transduced with 200-250 μ l O2S and K2M viruses and 8 μ g/ml protamine sulfate (Sigma Aldrich) in 700 μ l total volume. After overnight incubation, medium was replaced with fresh D10 medium and every two days thereafter. On post-infection day 6 or day 7, cells were trypsinized and transferred onto wells containing Mitomycin-c treated MEFs (75.000 cells/well of 12-well tissue plate) at a ratio of 1/6. Next day, medium was switched to hES medium and replaced every other day till day 14 of reprogramming. Between days 14 and 21, medium was replaced everyday with fresh hES medium. At the end of reprogramming experiments, cells were fixed and stained with Tra-1-60 antibody (**Figure 7**).



Figure 7. Timeline of reprogramming experiment

In experiments where the small molecule inhibitor of DOT1L (iDOT1L), EPZ004777 (Tocris Bioscience), was used, the final concentration of the compound in cell culture medium was 3 μ M. Cells were treated with iDOT1L or DMSO as control on days 1, 3 and 5.

2.2.4 Tra-1-60 staining of iPSC colonies

At day 21 of reprogramming experiments, cells were stained with Tra-1-60 antibody to count the iPSC colonies. Cells in 12-well plates were washed with 1X PBS and fixed with 500 μ l 4% paraformaldehyde (PFA) solution. Fixation was performed at room temperature for 20 min on gentle shaking. Then, PFA solution was removed and fixed cells were washed with 1X PBS solution for 3-4 times. Then, cells were incubated with 300 μ l biotin conjugated Tra-1-60 antibody (BioLegend #330604) which was diluted 1:200 within staining solution (3% FBS, 0.3% Triton X in PBS). Primary antibody incubation was

performed overnight at cold room on gentle shaking. Next day, cells were washed 5 times with 1X PBS and incubated with secondary antibody solution: Streptavidin-HRP (BioLegend #405210) that was diluted within staining solution 1:500. Incubation was performed for 2 hours at room temperature on gentle shaking. Cells were washed 5 times with 1X PBS and colonies were visualized with DAB solution (1% DAB -3,3 diaminobenzidine-, 1% Nickel Ammonium Sulfate, 0.3% H₂O₂). Staining was performed at room temperature for 20 min on gentle shaking. Then, DAB solution was removed and cells were washed with 1X PBS solution for 2 times. Plates were developed for 1 day at room temperature before imaging. Then, PBS was decanted and wells were filled with cream (SEK or Tikveşli) to make a background on DAB stained blackish-brownish iPSC colonies. Plates were scanned to digitalize the colony images. Scanned plate images were quantified well by well via ImageJ software. While quantifying the wells, threshold for intensity was adjusted to 150 and colonies that were bigger than 20 pixels were counted as an iPSC colony.

2.2.5 Generation of DOT1L-KO single cell clone

HEK293T cells were transfected with either non-targeting (gNT2) or guideDOT1L (gDOT1L) containing lenticrisprV2 plasmids and transfected cells were selected with puromycin (2 μ g/ml) for 2-3 days. After selection, cells were trypsinized, diluted to a single cell suspension and seeded onto 96well plates. Probability of events for a Poisson distribution was used to calculate the optimal cell number per plate. Accordingly, 26 cells were placed in 100-wells. For both NT and gDOT1L samples 3 plates were prepared and their growth medium was changed within 2-3 days intervals. At the end for 1 week of growth, single cell clones were identified and transferred to 48-well plates.

As expected, not all wells had a single cell clones. Many wells had no colonies at all while 30 of them had single colonies and in 7 wells there were multiple colonies. Selected single clones were passaged and half of the each colony was deposited as frozen stock. Other half of single cell clones was expanded for histone acid extraction to check the H3K79me2 levels. Proliferated single cell clones were pelleted and histone acid extraction was performed from 19 colonies. All single clones were tested for their H3K79me2 levels via immunoblotting. As a result of this experiment single clone #10 was picked as a DOT1L-KO HEK293T cell line for following experiments.

2.2.6 Transient Transfection

Transfection of HEK293T cells were performed with Fugene (Promega) transfection reagent. 2.5×10^6 cells were counted into each 10 cm cell culture plate. Transfection was performed the following day after cells were seeded. For transfection, 500 µl DMEM was mixed with 20 µl Fugene and incubated at RT for 5 minutes. 5 µg plasmid was added to DMEM/Fugene mixture and incubated at RT for 30 min. At the end of incubation, mixture was added dropwise onto HEK293T cells. Next day, medium was replaced with fresh D10 medium. At this point, fluorescent protein expression was detected with fluorescence microscope (Nikon) to determine the transfection efficiency. For

this purpose, following plasmids were used: pLenti CMV/TO-GFP-Hygro, pLenti PGK GFP puro (Addgene # 19070), pBp GFP puro, pLEX-307_GFP and RRL_GFP.

2.2.7 Virus production

Viruses were produced using HEK293T cells. Viruses can be produced in different scales from 6-cm cell culture plates to 15-cm plates. In this section, 10 cm cell culture plates will be explained but quantifications for different scales are depicted in **Table 9**. 2.5×10^6 HEK293T cells were counted for 10 cm cell culture plates. Transfection of viral plasmids was performed the following day. For transfection, 250 µl DMEM was mixed with 20 µl Fugene and incubated at RT for 5 min. In another tube, 250 µl 1xDMEM was mixed with 2.5 µg viral transfer vector and 2.5 µg viral packaging plasmids (2250ng PUMVC for retroviruses or pCMV-dR8.2 Δ VPR for lentiviruses and 250 ng pCMV-VSV-G). The two mixtures were combined and incubated at RT for 30 min. At the end of incubation, mixture was added dropwise onto HEK293T cells. Cells were grown with viral transfection mixture overnight and next day, medium of cells were changed with 8 ml of fresh D10.

48 hours after transfection, medium was collected in a falcon tube and stored at 4°C. 8 ml of fresh D10 medium was added on HEK293T cells for one more batch of virus production. 72 hours after transfection, medium was collected again and mixed with primary collected medium in falcon tube. All collected viral supernatants (16 ml in total) were centrifuged at 1500 rpm for 5 min to avoid any detached HEK293T cells and then filtered through a 0.45 μ m syringe filters (Corning). Filtered viral medium was aliquoted and stored at - 80°C for long-term usage. To concentrate the viral supernatants, 50% PEG-8000 (Sigma) was dissolved (w/v) in 1xPBS (Gibco) and used as 5X. Filtered viral medium was mixed 1X PEG solution and incubated at 4°C for at least overnight or at most 2 or 3 days. At the end of PEG precipitation, tubes were centrifuged at 4°C at 2500 rpm for 20 min and most of the supernatant was decanted into 10% bleach containing bottle. Rest of the precipitate was resuspended with 160 μ l cold 1X DPBS and aliquoted to store at -80°C for long-term usage.

Seele	6-cm	10-cm	15-cm
Scale	plate	plate	plate
HEK293T seeding amount (cells)	$1 \mathrm{x} 10^{6}$	$2.5\mathrm{x}10^6$	$6.5 \mathrm{x10}^{6}$
$1X \text{ DMEM } (\mu l)$	100	250	500
FuGene (µl)	8	20	60
Amount of plasmid (ng)	1000	2500	7500
Amount of pUMVC or 8.2- Δ vpr (ng)	900	2250	6750
Amount of pCMV-VSV-G (ng)	100	250	750
Collection medium amount (ml)	3 + 3 = 6	8 + 8 = 16	20 + 20 = 40
Addition of 5X PEG amount (ml)	1.5	4	10
Amount of PBS to resuspend (μl)	60	160	400

Table 9. Table of viral transfection information for different scales

2.2.8 Transduction of cells

Viral transductions were performed with the addition of 8 μ g/ml protamine sulfate. Cells were incubated with transduction mixture overnight. This transduction step was repeated one more time to increase infection efficiency. After 48 hours of transduction, cells were observed for their fluorescent emission or selected with antibiotics. For HEK293T cells, 2 μ g/ml puromycin was added for 2-3 days and 300 μ g/ml Hygromycin was used for 4-5 days to complete antibiotic selection. For dH1f cells, 1 μ g/ml puromycin was added for 2-3 days and 200 μ g/ml Hygromycin was used for 4-5 days to complete antibiotic selection.

2.3 Western Blots

Three different protein isolation methods were used in this thesis: whole cell lysis, cytosolic-nuclear fractionation and histone acid extraction. For all these methods, cells were prepared similarly: Cells were trypsinized and pelleted by centrifugation at 1500 rpm for 5 min. Supernatants were removed and pellets were washed with 1X PBS. Pellets were immediately frozen and stored at -80°C. For protein extraction, cells were thawed on ice with lysis buffer.
WHOLE CELL LYSIS BUFFER	CYTOSOLIC LYSIS BUFFER	NUCLEAR LYSIS BUFFER	TRITON EXTRACTION BUFFER
50mM Tris pH 8.0	10mM HEPES pH 7.9	20mM HEPES pH 7.9	0.5% Triton X 100
250mM NaCl	10mM KCl	0.4M NaCl	2mM PMSF
5mM EDTA	0.1mM EDTA	1mM EDTA	0.02% (w/v) NaN ₃
1% NP-40	0.4% NP-40	10% Glycerol	
Protease Inhibitor Coctail	Protease Inhibitor Coctail	Protease Inhibitor Coctail	
dH2O	dH2O	dH2O	PBS

Table 10. Recipes of protein lysis buffers

2.3.1 Whole cell lysis method

Whole cell lysis buffer was prepared with recipe in **Table 10** with the addition of cOmplete ULTRA protease inhibitor Tablets (Roche). Cell pellets were resuspended with whole cell lysis buffer and incubated for 45 min on ice with gentle shaking. At the end of incubation, tubes were centrifuged at 4°C for 10 min at 14000 rpm. Supernatant was removed into new tube and used as a whole cell lysis protein. Protein concentrations were determined via BCA assay (Thermo Scientific).

2.3.2 Nuclear protein extraction

Cytosolic and nuclear lysis buffers were prepared with recipe in **Table 10** with the addition of cOmplete ULTRA protease inhibitor Tablets (Roche). Cell pellets were resuspended with cytosolic lysis buffer and incubated for 15 min on ice on 50 rpm shaking plate. At the end of incubation, tubes were centrifuged at 4°C for 3 min at 3000*g*. Supernatant was removed into new

tube and centrifuged again at 4°C for 5 min at 3000g. This supernatant was reserved as the cytosolic protein fraction. The pellet was washed with half volume of cytosolic lysis buffer and centrifuged at 4°C for 3 min at 3000g. Supernatant was discarded and the pellet was resuspended in nuclear lysis buffer and sonicated 2 times for 10 seconds at 40 amplitude with a 10 second interval in between (QSONICA Q700 with microtip). After sonication, tubes were centrifuged at 4°C for 5 min at 15000g. Supernatant was removed into new tubes as a nuclear protein fraction. Both cytosolic and nuclear protein concentrations were determined via BCA assay (Thermo Scientific).

2.3.3 Histone acid extraction

Cell pellets were resuspended with triton extraction buffer (**Table 10**) and incubated for 10 min on ice on 50 rpm shaking plate. At the end of incubation, the tubes were centrifuged at 4°C for 10 min at 2000rpm. Supernatant was discarded and the pellet was washed with half volume of triton extraction buffer and centrifuged at 4°C for 10 min at 2000rpm. Supernatant was discarded and the pellet was resuspended in 0.2N HCl. Tubes were incubated at 4°C for overnight on rotating wheel at 10 rpm. At the end of incubation, tubes were centrifuged at 4°C for 10 min at 2000rpm and supernatant was collected in new tube. Acid extractions were neutralized with the addition 0.1M NaOH for 1/5 volume of HCl solution. Protein concentrations were determined via BCA assay (Thermo Scientific).

2.3.4 Western Blotting

Equal amounts of proteins were boiled for 10 min with loading buffer (4X Laemmli sample buffer, Bio-Rad) and loaded onto 4–15% Mini-PROTEAN TGX Precast Protein Gels (Bio-Rad). Gels were run with TGS buffer (diluted from 10X stock, Bio-Rad). Precision Plus Protein Dual Color Standards (Bio-Rad) were used a molecular weight ladder. Proteins were transferred onto Immun-Blot PVDF Membrane (Bio-Rad) via semi-dry or wet transfer technique.

For semi-dry transfer method, Trans-Blot Turbo Transfer System (Bio-Rad) was used. As a transfer buffer, 10% Ethanol added TGS buffer (Bio-Rad) was used with standard transfer protocol. Semi-dry transfer method was preferred for all the western blot methods unless the detected protein's size was more than 100 kDa. For larger proteins, wet transfer method was used (Mini Trans-Blot Electrophoretic Transfer Cell -Bio-Rad). As a transfer buffer, Towbin Buffer (25 mM Tris, 192 mM Glycine, 20% methanol (v/v) -pH 8.3) was used with 15 volt for overnight incubation in cold room.

After transfer of proteins on membrane, membrane was incubated with 5% blotting grade blocker (Bio-Rad) dissolved in TBS-T (20 mM Tris, 150 mM NaCl, 0.1% Tween 20 –pH 7.6) for 1-2 hours at room-temperature with gentle stirring. However, membranes to be incubated with Streptavidin-HRP antibody were blocked with 2% bovine serum albumin (BSA, Sigma) in TBS-T. After blocking step, membranes were incubated with primary antibody solution (1:200-1:1000 primary antibody in 2% BSA, 0.02% NaN₃ in TBS-T) at 4°C for 16 hours. Concentration of primary antibodies is depicted in **Table**

11. After primary antibody incubation, membranes were washed with TBS-T solution for 3 times with 15 min intervals on 50 rpm shaker at room temperature and then incubated with secondary antibody solution (1:5000 secondary antibody in 5% blotting grade blocker in TBS-T) at room temperature for 1-2 hours. Secondary antibodies were depicted in **Table 11**. Streptavidin-HRP blotted membranes were not incubated with a secondary antibody. After secondary antibody incubation, membranes were washed with TBS-T solution for 3 times with 15 min intervals on 50 rpm shaker at room temperature. Then, proteins were visualized with Pierce ECL Western Blotting Substrate (Thermo Scientific) and Odyssey Fc Imaging systems (LiCor).

Table 11. Table of antibody information that were used for western blots

Antibody	Catalog	Concentration
mame	number	
Streptavidin-HRP	405210	1:10,000
${ m H3K79me2}$	ab3594	1:1000
H3 total	ab1791	1:1000
H3K4me1	ab8895	1:1000
H3K4me3	ab8580	1:1000

2.4 Pull down experiments

HEK293T cells were infected with BirA*-DOT1L wt or mut concentrated viruses and selected with puromycin (2 μ g/ml) for 2-3 days. After selection, cells were treated with 50 μ M D-Biotin (Sigma, 47868) for 24 hours and cells were collected for protein isolation. Proteins were obtained via nuclear fractionation method. As a control, uninfected HEK293T cells were treated similarly. Pull-down was performed with Streptavidin beads (Thermo Scientific, 53117) as previously described¹³³. Briefly, equal amount of nuclear fration was incubated with Streptavidin beads at 4°C for 16 hours on rotating wheel at 10 rpm. Then supernatants were collected and beads were washed twice in 2% SDS; once with wash buffer 1 (0.2% deoxycholate, 1% Triton X, 500 mM NaCI, 1 mM EDTA, 50 mM HEPES, pH 7.5), once with wash buffer 2 (250 mM LiCI, 0.5% NP-40, 0.5% deoxycholate, 1% Triton X, 500 mM NaCI, 1 mM EDTA, 10 mM Tris, pH 8.1) and twice with wash buffer 3 (50 mM Tris, pH 7.4, and 50 mM NaCI). Eluted proteins were analyzed with Streptavidin-HRP antibodies to observe the efficiency of pull-down.

2.5 Mass-Spectrometry Analysis

For mass spectrometry analysis, control (uninfected) and BirA*-DOT1L wt or mut infected HEK293T cells were treated with 50 µM D-biotin for 24 hours and harvested. Following nuclear protein isolation, biotinylated proteins were pulled down with Streptavidin beads (Thermo Scientific, 53117). For mass-spectrometry analysis, beads were washed and bound proteins were digested with on-bead tryptic proteolysis method as previously described¹³⁴. Briefly, beads were washed (8 M urea in 0.1 M Tris-HCl, pH 8.5) and reduction and alkylation steps performed. Then beads were washed again with 50 mM ammonium bicarbonate and incubated with trypsin in 50 mM ammonium bicarbonate at 37 °C overnight. Beads were pulled-down at 1000g for 5 min and peptides were collected. Beads were rinsed with 50 mM ammonium and the supernatant was added to previously collected peptides. Peptides were acidificated and desalted. Then, all three samples were analyzed with reversed-phase nLC (NanoLC-II, Thermo Scientific) combined with orbitrap mass spectrometer (Q Exactive Orbitrap, Thermo Scientific) with data acquisition and processing steps that were as previously described¹³⁴. Each sample was run for twice. On bead tryptic digestion of biotinylated proteins and their LC-MS/MS analysis was performed by Nazh Ezgi Özkan Küçük in Nurhan Özlü Lab.

To discriminate the DOT1L-specific biotinylation, proteins detected in HEK293T control samples were subtracted from BioID samples. Rest of the proteins was selected only if they exist in both runs of mass-spectrometry. Among these common proteins, nuclear localized ones are determined via GO annotation (<u>http://www.geneontology.org/</u>) via cellular compartment analysis. UniProt protein names were converted via ID mapping tool (<u>https://www.uniprot.org/uploadlists/</u>). Determined proteins were sorted with their coverage percentage and then with PSM (peptide spectrum matches) numbers.

2.6 RNA isolation, cDNA synthesis and qPCR

Cells were trypsinized and pelleted by centrifugation at 1500 rpm for 5 min. Supernatant was removed and pellet was washed with 1X PBS. Resulting pellet was immediately frozen and stored at -80°C. RNA isolation kit (MN) was used to isolate total RNA. Concentrations of RNA samples were determined with Nanodrop 2000 (Thermo scientific). For cDNA synthesis, 1 μ g RNA solution was mixed with 200 μ M dNTP (Thermo Scientific) and 4 μ M random hexamer (invitrogen) with dH₂O up to 16.5 μ l total volume. This mixture was incubated at 65°C for 5 min and then quickly chilled on ice. 5X first strand buffer (invitrogen), 8 mM DTT (invitrogen) and 20 U Rnasin (promega) was added to the mixture for up to 24 μ l total volume and incubated for 10 min at room temperature. Then, 1 µl of M-MLV reverse transcriptase enzyme (200 U, Invitrogen) was added to the reaction and incubated at 37°C for 1 hour. Reaction was ended with inactivation at 70°C for 15 min. cDNA solutions were diluted with 75 μ l nuclease free water (NEB). From diluted cDNA mixture, 2 µl sample was used for 1 reaction of quantitative real-time PCR (qPCR) and the rest of the cDNA was stored at -20°C for long term.

For qPCR, 2 μ l of cDNA sample was mixed with 2.5 μ M forward and reverse primers, 10 μ l LightCycler 480 SYBR Green I Master (2X, Roche) and dH₂O up to 20 μ l total volume. Forward and reverse primers are listed in **Table 13**. Every sample was prepared in duplicates and loaded into 96-well opaque plates (Roche). Reaction was run in LightCycler 480 Instrument II (Roche) with conditions depicted in **Table 12**. For every sample, endogenous β -actin levels were used as controls. Expression values were calculated by the formula "2^{-(Ct-Cc)}", where Ct and Cc are the average of threshold cycles after normalization to β -actin. The relative quantification value for a target gene was compared to the control sample.

Temperature	Period	Cycle
$(^{\circ}C)$	(min:sec)	number
95°C	03:00	1
95°C	00:10	
60°C	00:30	40
72°C	00:30	
72°C	05:00	1
4°C	8	

Table 13.	List of	qRT-PCR	Primers
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qRT-PCR Primer Name	5' to 3' Sequence
RT Primer AF10 forward	GCGTCGCGGTGCATCAAG
RT Primer AF10 reverse	GGGACAAAGTTCACATCTCACTC
RT Primer NONO forward	CATCAAGGAGGCTCGTGAGAAG
RT Primer NONO reverse	TGGTTGTGCAGCTCTTCCATCC
RT Primer KAISO forward	TAGCAGAGCTTGGTGTCCCATTG
RT Primer KAISO reverse	CACCAGAATCAGGAGGTAAAGGC
RT Primer SIN3B forward	TCTGAGGACTCCACGTTCGTCA
RT Primer SIN3B reverse	AGGTTCGTCTCCAGGACAACGT
RT Primer AF17 forward	CTGCGTATGTTCGGACGGAGAG
RT Primer AF17 reverse	ACCTGAACGATGCCATAGCAA
RT Primer MRE11 forward	CAGCAACCAACAAAGGAAGAGGC
RT Primer MRE11 reverse	GAGTTCCTGCTACGGGTAGAAG
RT Primer ENL forward	GGTGAGGTTAGAGCTGGGG
RT Primer ENL reverse	TGGATGTCACATTGCTCGGG
RT Primer NUMA1 forward	GGTTCCAGGAAGAGAGGCAGAA
RT Primer NUMA1 reverse	CTTGCTGGCTTGGTCAGAGTCA
RT Primer TPR forward	GCTCAGGTTGAGAGTCTGCGTT
RT Primer TPR reverse	CAGTTCTTCATGCTGAGCCATTG
RT Primer DDX21 forward	TGCACGTGGGTTAGACATCC
RT Primer DDX21 reverse	CGCCCGGATCGATGAATGTA
RT Primer AF4 forward	TGCATTGCAAGCACAGGCAC
RT Primer AF4 reverse	AAGGTCAAAGGCGGTAAGAACAT
RT Primer AF9 forward	TGCAGCAGATCGTGAACCTT
RT Primer AF9 reverse	ACTGTGGTTTTGTCCAGCGA
RT Primer BAT3 forward	CAGTGGTATGCCTGCCAAGA
RT Primer BAT3 reverse	AGCTCTCCTGAACCTCTGGT
RT Primer SIRT1 forward	ACAGGTTGCGGGAATCCAAA
RT Primer SIRT1 reverse	GTTCATCAGCTGGGCACCTA
RT Primer STAT1 forward	ACTCCAGGCCAAAGGAAGC
RT Primer STAT1 reverse	GACATGGGGAGCAGGTTGTC
RT Primer HNRNPM forward	TGGACGCTGAAGGAAAGTCA
RT Primer HNRNPM reverse	CATACCCATCCCACCAGTCG
RT Primer NPM1 forward	CGGTTGTGAACTAAAGGCCG
RT Primer NPM1 reverse	TTTGCACCAGCCCCTAAACT
RT Primer CDK9 forward	TGCACGTGGGTTAGACATCC
RT Primer CDK9 reverse	CGCCCGGATCGATGAATGTA

RT Primer MLL1 forward	AAGCGGAAGGTGAAGGACAG
RT Primer MLL1 reverse	GGTCGGACCAGAAGAAGTCG
RT Primer WDR5 forward	AATTCAGCCCGAATGGAGAGT
RT Primer WDR5 reverse	AGGCTACATCGGATATTCCCAG
RT Primer RBBP5 forward	CATCTTTTGATAGGCGAGGGG
RT Primer RBBP5 reverse	GTTCCAGTTGTCACTCTGAAGG
RT Primer ASH2L forward	AGAATGGCCGACAGTTGGG
RT Primer ASH2L reverse	CCTTCAAGTTTGCTTGCTTCC
RT Primer DPY30 forward	GGAGGGACAAACGCAGGTT
RT Primer DPY30 reverse	GGTAGGCACGAGTTGGCAA
RT Primer MEN1 forward	GCCTGGGTAGTGTTTGGGC
RT Primer MEN1 reverse	AGCGCATGTATGATCCTTTCAG
RT Primer WDR82 forward	TTTCCTGGACATAGCAAAAGGG
RT Primer WDR82 reverse	TCCCAGAGTCGAATGGTCTTAT
RT Primer HCFC1 forward	GCAATGACCTCTACGAACTCC
RT Primer HCFC1 reverse	ACCTTGGAATGTTGTTCTTTGGG
RT Primer MLL2 forward	CTCTAAGATGTTGGTTTGCGAGA
RT Primer MLL2 reverse	GCCTTGCCTTCCAAGAGTGA
RT Primer MLL3 forward	GGACAGAGAAAAGAACGATCTCC
RT Primer MLL3 reverse	GGCATACTCCTAGTG
RT Primer MLL4 forward	ACCCCGGCGATTTATGGATG
RT Primer MLL4 reverse	CTTCTCAGGGAGTGGAACTGG
RT Primer CXXC1 forward	GCAAACCGGACATCAACTGC
RT Primer CXXC1 reverse	GCACTCCCGACAGTACCAC
RT Primer SET1B forward	TGAGTTTGAGTCAAGCTCCGA
RT Primer SET1B reverse	ATGCCCAACGAGTCCACTG
RT Primer βACTIN forward	TGAAGTGTGACGTGGACATC
RT Primer βACTIN reverse	GGAGGAGCAATAGATCTTGAT
RT Primer NANOG forward	TGATTTGTGGGCCTGAAGAAA
RT Primer NANOG reverse	TGGTGGTAGGAAGAGTAAAG

2.7 Microarray analysis

Differential gene expressions between pluripotent stem cells and fibroblast cells were computed by affy and limma packages from R. Samples of dH1f and BJ fibroblasts were compared to their respective iPSCs and embryonic stem cells from GEO data series GSE55679. Genes that had a log2 fold change value of 3 or more in all fibroblasts compared pluripotent cells were categorized as the fibroblast related gene set. Genes that have a log2 fold change value of -3 or less in all fibroblasts compared pluripotent cells were categorized as the pluripotency related gene set. This analysis was performed by Tunc Morova (Nathan Lack lab, Koc University).

2.8 RNA sequencing and analysis

RNA isolation was performed on previously harvested cell pellets (Day 0 and Day 6 samples) with Direct-zol kit (Zymo Research). Isolated RNAs were separated into tubes as; 1 µg for RNA-sequencing sample, 1 µg for cDNA synthesis and the rest was stored at -80°C as a long term backup. NEBNext Poly(A) mRNA Magnetic Isolation Module from NEBNext Ultra Directional RNA Library Prep Kit for Illumina was used to enrich mRNA from RNAsequencing samples. Samples were then validated on a Tapestation (Agilent) to determine library size and quantification prior to paired-end (2×41 bp) sequencing on a NextSeq 500 (Illumina) platform. Reads were mapped to hg19 built-in genome by Hisat2 after assessing their quality by FastQC. DeSeq2 package was used to find differentially expressed genes between samples. Genes were considered to be differentially regulated based on log2 fold change 0.5 and adjusted p-value 0.05. Gene Set Enrichment Analysis (GSEA) was performed on a pre-ranked gene list based on log2 fold change¹³⁵. Pluripotency- related, fibroblast-related gene sets and Wang_MLL_Targets¹³⁶ was used as a control for MLL knockout.



Chapter 3

3 Finding proximal-protein interactions of DOT1L via BioID method and shRNAmediated screen of DOT1L-proximity interactors for reprogramming efficiency

3.1 Introduction

3.1.1 Biotinylation based detection of protein-protein interaction methods

Finding protein-protein interactions (PPIs) is crucial for understanding the mechanistic properties of the proteins of interest. Different methods have been developed to detect PPIs, such as co-immunoprecipitation (co-IP) to detect direct interactions or yeast two hybrid to investigate in vivo binding of two proteins. Even though these approaches are important methods to identify PPIs, it is challenging to identify a large set of interactors with these types of experiments. Biotinylation based methods have emerged to fill this gap. Biotinylation is a naturally occurring reaction that takes place in very low abundance when compared with methylation, acetylation or ubiquitination. Therefore, ectopic biotinylation can be detected via massspectrometry analysis and specific proteins can be determined via comparison with control background. Biotin ligase protein, originated from E. coli (BirA) was utilized for such assays¹³⁷. BirA enzymes can biotinylate specific peptide

chain (GGGLNDIFEAQ<u>K</u>IEWHE) from its lysine residue. This method is a powerful tool when there is no high quality antibody against the protein of interest or to detect a protein interaction profile at a specific time. Biotinylation-based methods are powerful since they can capture biotinylated proteins efficiently via Streptavidin pull-down. Streptavidin-biotin binding is very strong when it is compared with antibody-protein binding. Conventional antibodies bind to a protein with K_d values in nanomolar range whereas high affinity antibodies can bind with K_d values in picomolar range; in contrast, Streptavidin binds to biotin with K_d values in femtomolar range ($K_d \sim 10^{-14}$ M)¹³⁸. This method still depends on the strong binding of interacting proteins, since their detection is possible only if they are strongly bound to target protein. But this method is insufficient to detect transient interactions and functional interactions of a protein. To solve this problem, R118G mutation was generated in BirA enzyme and this mutant BirA (BirA*) can promiscuously biotinylate proteins that bind in close proximity¹³⁹. To identify binding partners of a particular protein, BirA^{*} can be fused, and introduced to cells so that all proximal proteins whether they are strongly interacting or transiently form a complex, will be biotinylated by BirA^{*}. This method was initially called BioID. Later, a smaller BirA* enzyme was designed from Aquifex aeolicus with R40G mutation and referred as $BioID2^{140}$. Both methods require excess amount of supplemented biotin, however BioID2 needs less¹⁴¹. There are various other methods that make use of biotinylation such as proximity labeling with ascorbate peroxidase (APEX) and in vivo proximal labeling (IPL). APEX can be utilized in live cells which BioID cannot¹⁴². Also, BioID cannot be applied for shorter periods of time because it requires 16-24 hours of biotinylation incubation. However, recently

proposed TurboID method only requires 10 minutes of biotinylation which is developed from a mutant biotin ligase¹⁴³.

3.1.2 BioID is a powerful method to detect proximal protein interactions

Proximity dependent biotin identification (BioID) method is a powerful tool to identify proximal protein interaction¹³⁹. For BioID assay, fusion protein with BirA* and protein of interest is cloned. Then, fusion protein expressing cells are incubated with excess biotin for biotinylation of proximal proteins. Later, cells are lysed and biotinylated proteins are pulled-down with streptavidin conjugated beads. Biotinylated proteins eluted from beads and identified via mass spectrometry analysis. These steps are summarized in **Figure 8**.

Previous studies showed that BioID method is an effective way of identification of proximal proteins and protein complexes^{133,139,144}. BirA* fusion with LaminA¹³⁹, cytoskeletal protein bilobe¹⁴⁴ and centrosome proteins¹³³ showed that BioID can detect even transient protein interactions in diverse cellular compartments. BioID can be used for insoluble proteins and it can detect proteins that are in a very low abundance. Since candidate protein interactions are labeled with biotin, extremely stringent conditions can be applied during purification which can decrease contaminants.



Figure 8. Promiscuous biotin-ligase (BirA*) selectively biotinylates the proximal proteins

BioID also has some drawbacks that should be considered before designing any proximity interaction assay. To begin with, BioID approach relies on exogenous expression of fusion protein. Also, fusion proteins need to be generated and this will increase the size, and fusion may interfere with biological function of target protein. In BioID method, biotin is added to the lysines of proximal proteins and their biotinylation may hinder the biological modifications of that protein normally has. These limitations should be taken into account when proximity identification is planned.

3.1.3 AF10 is an important member of DOT1L-containing elongation complex

There are several elongation complexes reported to date such as EAP^{104} , AEP^{107} , SEC^{106} , DotCom^{105} and AF4-mediated complex¹⁰³. Among these elongation complexes AF10 was identified within DotCom^{105} and AF4-mediated complex¹⁰³. DOT1L was also identified within these complexes. It was also known that DOT1L and AF10 interact through AF10's OM-LZ (octapeptide motif and leucine zipper) motif at C-terminus (**Figure 9**). It was hypothesized that AF10 recruits the elongation complex to the chromatin site since it has also a unmodified H3K27 reader domain, and this binding is abrogated by H3K27 modification¹⁴⁵. The cross-talk between different epigenetic modifications can be explained with such cooperation within an elongation complex. Together with other protein components (AF9, AF17, ENL, p-TEFb) of the elongation complex, AF10 and DOT1L have a role in transcriptional regulation.



Figure 9. Schematic representation of the AF10 protein.

A PZP domain (PHD1-Zn-Knuckle-PHD2) is located at N-terminus of AF10, Octamer motif-leucine zipper (OM-LZ) motif interacts with $DOT1L^{145}$.

In human acute myeloid leukemia (AML), MLL-AF10 fusion proteins can be generated as a result of MLL translocation $t(10:11)(p12;q14)^{146}$. Main reason for transformation ability of MLL-AF10 fusion was claimed as AF10's interaction with DOT1L by recruiting DOT1L aberrantly to MLL-target sites¹⁴⁶. In those cells, DOT1L actives genes that are supposed to be silent such as *Hoxa* cluster genes and *Meis1* through H3K79 methylation¹⁴⁶. Aberrant expression of those genes causes transformation of MLL-AF10 fusion expressing cells. Therefore, many studies have suggested that a small molecule inhibitor that inhibits DOT1L-AF10 interaction can be used for leukemia therapy. Recently, the crystal structure of DOT1L-AF10 binding was reported (**Figure 10**)¹⁴⁷. This progress may improve the drug designation that targets DOT1L-AF10 interaction.

Af10 knock out in mice can cause developmental defects such as development of midline facial cleft due to the reduced levels of AP2 α gene¹⁴⁸. When they use chemical inhibitor of Dot1L (EPZ-5676), they also observed similar defects in embryos¹⁴⁸. Dot1L knock out mouse embryo is lethal after day 10^{119} and Af10-KO mice are lethal after embryonic day 16 and they are exhibiting severely decreased H3K79 methylation levels¹⁴⁸.



Figure 10. Representative structure of the DOT1L-AF10 interaction (Adapted from Zhang *et.al.* with permission presented in Appendix-III¹⁴⁷)

A, AF10 OM-LZ (octamer motif-leucine zipper) structure was represented as cyan and green color depicts for two chains. Dimer interface of two peptides was demonstrated as stick representation. **B**, Cartoon representation of DOT1L-CC2 (coiled-coil domain#2) interaction with AF10-OM-LZ.

3.1.4 AF10 regulates histone code

AF10 protein has two important domains: PZP and OM-LZ. PZP domain consists of Zn-knuckle in between two PHD (plant homeodomain) fingers. It was previously known that OM-LZ was the DOT1L-interaction domain¹²¹. PZP domain was identified as a reader of H3K27 residue by recognition of 2227 amino acids of $H3^{145}$. It was demonstrated that PZP domain of AF10 can bind to unmodified H3K27 therefore it can recruit DOT1L, leading to H3K79 methylation¹⁴⁵. On the other hand, AF10 cannot bind to methylated H3K27, hence DOT1L cannot recruited to methylated H3K27 sites via AF10; which promotes transcriptional silencing¹⁴⁵. It was previously claimed that AF10 was required for aberrant expression of *HOX* genes in AML cases (acute myeloid leukemia)^{146,149,150}. Even though it was claimed that continuous expression of *HOX* gene is dependent on AF10^{146,149,150}, in another study it was claimed that AF10's activity was required in cytoplasm rather than gene expression regulation^{151,152}. These controversial views need to be supported with further experiments to find out the mechanism of AF10.

AF10 was also thought to regulate H3K79 methylation through H2B ubiquitination¹⁵³. *C. elegans* homolog of AF10, ZFP-1 was demonstrated to negatively regulate essential highly expressed genes via interacting with DOT- 1.1^{153} . They claimed that H2Bub1 modification was read by ZFP-1 and recruitment of DOT-1.1 to the actively transcribed site results in negative feedback via Pol-II pausing¹⁵³. Since there are different hypotheses on how AF10 regulates gene expression, further studies are required to understand the mechanism and consequences of AF10 - DOT1L interaction.

In this chapter, novel DOT1L interactors were identified using the BioID method in which a promiscuous BirA ligase (BirA^{*}) was employed to biotinylate DOT1L-proximal proteins, *in vivo*. Biotinylated proteins were pulled-down by Streptavidin and identity of the proteins was determined by LC-MS/MS. The resulting novel interaction candidates were investigated for their effects on reprogramming. Candidate genes were knocked-down in

human fibroblasts via shRNAs followed by reprogramming. Our results indicated that knock-down of AF10, significantly increased the iPSC generation efficiency, suggesting that it acts as a barrier to reprogramming similar to DOT1L. This finding was verified by CRISPR/Cas9 mediated knockout of AF10. Combining DOT1L inhibition or knockout, with AF10 suppression did not result in an additive enhancement of reprogramming, suggesting that these two chromatin factors act in the same pathway.



3.2 Results

3.2.1 BirA*-DOT1L fusion protein successfully methylates H3K79 residue

DOT1L is an established barrier of reprogramming⁵⁵. However, what role, if any, its interaction partners play in reprogramming is not known. Therefore, we wanted to identify protein interactions of DOT1L. A biotinylation-based proteomics approach, BioID¹³⁹, was used in this study to investigate the protein interaction network of DOT1L. In this method, promiscuous biotin ligase (BirA*) was fused to DOT1L with the assumption that it will biotinylate proteins that come into close proximity (10 nm radius) with DOT1L (BirA*-DOT1L). Fusion proteins were generated with either wildtype DOT1L (DOT1L wt) or a catalytically inactive mutant (DOT1L mut). Mutant DOT1L has 3 point mutations (**Figure 11**) that renders it unable to bind the methyl donor S-adenosylmethionine (SAM) and blocks the H3K79 methyltransferase activity¹²¹. Both wt- and mut- constructs were cloned into a mammalian lentiviral expression vector (pLEX_307) which contains an E1Falpha promoter and puromycin antibiotic resistence gene (**Figure 11**).



Figure 11. Schematic of BirA*-DOT1L fusion proteins in pLEX 307 vectors

Catalytically inactive DOT1L was created by 3 point mutations¹²¹. Both inserts were cloned into pLenti-pLEX-307 vector which has $EF1\alpha$ promoter and puromycin resistance gene.

To confirm the fusion proteins did not affect DOT1L, the catalytic activity was tested. To do this, DOT1L knockout (DOT1L-KO) cells were generated. Since DOT1L is the sole enzyme that catalyzes H3K79 methylation, functionality of DOT1L can be tested via investigating the H3K79me2 levels. Aim of this experiment was to express BirA*-DOT1L fusion plasmids in DOT1L-deficient cells and observe the rescue phenotype by H3K79 methylation. DOT1L-KO cells are devoid of H3K79me2 and if ectopically expressed DOT1L fusion proteins are functional, H3K79me2 levels is expected to increase.

DOT1L-KO HEK293T cells were generated by CRISPR-Cas9 mediated genome editing. The first exon of *DOT1L* was targeted with a guideDOT1L plasmid which also contains a Cas9 protein (LentiCRISPRv2). HEK293T cells were transiently transfected with either non-targeting (NT) or guideDOT1L containing Cas9 plasmids and selected with puromycin. After selection was completed, cells were trypsinized and diluted to single cells. Then, single cells were seeded onto 96-well plates (**Figure 12**). Proliferated single cell clones were pelleted and histone acid extraction was performed for 19 colonies.



Figure 12. Time-line for the generation of DOT1L-KO HEK293T cells

HEK293T cells were transfected with gDOT1L along with Cas9. After puromycin selection, cells were diluted as single cells and transferred to 96well plates. Single clones were expanded for histone extraction to test their H3K79me2 levels.

All single clones were tested for their H3K79me2 levels via immunoblotting to select a single cell clone that is H3K79me2-deficient. Out of 19 clones, 4 clones retained high levels of H3K79 methylation similar to gNT transfected cells while H3K79me2 levels were significantly downregulated in 15 clones (Figure 13). As a result of this experiment, single clone #10 was selected as DOT1L-KO 293T cells for further experiments since it has the lowest levels of H3K79me2 (Figure 13). Residual H3K79me2 levels are most likely due to the early passage of the clones, as H3K79me2 bands were invisible in cells passaged 2-3 additional times (Figure 14).



Figure 13. H3K79me2 levels in DOT1L gRNA transfected HEK293T single cell clones

Immunoblot results of selected clones. Histone extracted protein lysates were incubated with either H3K79me2 antibody or H3 total antibody. Colony #10 was picked as DOT1L-KO HEK293T due to the drastically decreased H3K79me2 levels. NT is a non-targeting gRNA used as a control.

Having generated DOT1L-KO cells, BirA*-DOT1L fusion constructs could be tested for their ability to rescue diminished H3K79me2 levels. To test the functionality of the BirA*-DOT1L fusion proteins; DOT1L-KO HEK293T clone and gNT transfected HEK293T clones were transduced with BirA*-DOT1L-wt or mutant expressing lentiviral vectors. As a control, untransduced cells were included as well. After puromycin selection, cells were pelleted and histone acid extraction was performed. All samples were tested for their H3K79me2 levels via immunoblotting and H3 total immunoblot was performed as a loading control (Figure 14).



Figure 14. Rescue of H3K79 methylation by BirA*-DOT1L_wt fusion protein in DOT1L-KO cells

Both wt and mutant fusion protein expressing plasmids were packed into lentiviruses. HEK293T-NT (non-targeting) and DOT1L-KO cells were infected with wt and mutant fusion protein expression vectors. After puromycin selection, cells were collected for histone extraction. Histone extracts were incubated with either H3 total antibody or H3K79me2 antibody.

As a result of this assay, BirA*-DOT1L-wt could rescue the H3K79me2 levels in DOTL1-KO cells while BirA*-DOT1L-mut had no effect (**Figure 14**). Interestingly, overexpression of the mutant protein caused a decrease in H3K79 methylation in gNT transfected cells, suggestive of a dominant negative effect. This experiment shows that wt DOT1L in BirA*-DOT1L-wt fusion is enzymatically active, whereas mut-DOT1L fusion is inactive as expected.

3.2.2 Pull-down of biotinylated proteins via Streptavidin beads

Next, biotinylation activity of BirA*-DOT1L fusion proteins were tested to ensure that BirA* in fusion proteins can successfully biotinylate. Pull-down experiments were performed to test the biotinylation activity of BirA* in fusion proteins. For pull-down experiments, HEK293T cells were infected with BirA*-DOT1L wt or mutant viruses and selected with puromycin for 3 days. Cells were treated with 50 μ M D-Biotin for 24 hours and biotinylated cells were collected for protein isolation. Proteins were obtained via nuclear fractionation method as DOT1L is a nuclear protein. As a control, uninfected HEK293T cells were treated similarly. Pull-down was performed with Streptavidin beads since Streptavidin can strongly bind to biotin.

After pull-down, eluted proteins were analyzed with Streptavidin-HRP antibodies to visualize biotinylated proteins and observe the efficiency of pulldown. Total nuclear fraction and unbound proteins (supernatant) were also analyzed (**Figure 15A**). As a result, it was shown that BirA* in fusion protein can biotinylate proteins, since many different protein bands were observed in the eluate lane of fusion protein infected cells (**Figure 15B**). In contrast, there were only a few bands present in the eluate of HEK293T control cells which are naturally biotinylated proteins in the cell (**Figure 15B**). In addition, the absence of bands in the corresponding supernatants indicated that biotinylated proteins were efficiently captured by beads and pull-down protocol worked successfully (**Figure 15B**). This experiment shows that BirA* in fusion proteins can successfully carry out biotinylation reactions. In conclusion, BirA*-DOT1L fusion proteins can be used for BioID assay since functionality of both DOT1L and BirA* have been successfully demonstrated.



Figure 15. Biotinylated proteins in BirA*-DOT1L expressing HEK293T cells in comparison to uninfected cells.

A, Nuclear proteins were isolated from uninfected and BirA*-DOT1L wt and mut infected HEK293T cells. Equal amounts of nuclear lysate were incubated with Streptavidin-agarose beads. Unbound proteins (supernatant) were cleared from tube and the pelleted beads were washed. Biotinylated proteins were eluted from beads. **B**, Biotinylated protein levels were analyzed with Streptavidin-HRP antibody.

3.2.3 Proximal-protein interactions of DOT1L was identified after LC-MS/MS analysis of biotinylated proteins

For mass spectrometry analysis, uninfected control HEK293T cells and BirA*-DOT1L wt or mut infected HEK293T cells were treated with 50 μ M biotin for 24 hours and harvested. Following nuclear protein isolation and over-night incubation with Streptavidin beads, biotinylated proteins were captured as explained in section 3.2.2. Biotinylated proteins were released from beads via on-bead trypsin proteolysis and identified by LC-MS/MS. As a result of LC-MS/MS analysis, DOT1L protein was detected with the highest PSM (peptide spectrum matches) values and very high coverage percentage (~30%) in BioID samples; whereas none was detected in control samples (**Table 14**). This results shows that DOT1L was successfully overexpressed and biotinylated only in fusion vector transduced cells.

Table	14.	DOT1	L detection	values	after	\mathbf{mass}	spectrometr	y ana	lysis
from t	wo i	reads c	of each sam	ple (nd	, not	detect	(\mathbf{ed})		

Sample	Coverage %	PSM
Uninfected HEK293T	nd	nd
	nd	nd
HEK293T BirA*-DOT1L WT	28.12	101
	35.02	145
HEK293T BirA*-DOT1L mut	25.13	87
	26.74	101

The biotinylated proteins detected in HEK293T control samples were excluded from BioID samples to obtain the list of DOT1L-proximal proteins specifically biotinylated by BirA*-DOT1L fusions. These eliminated proteins are either naturally biotinylated proteins or non-specifically bound to Streptavidin beads. Among remaining proteins, common ones from two readings of LC-MS/MS results were determined. Then, common proteins in wt- and mut-DOT1L samples were selected according to their localization in the cell via GO annotation. Extra-nuclear proteins were disregarded with the assumption that they were contaminants from nuclear fractionation. Remaining proteins were sorted according to their coverage % and PSM (peptide spectrum matches) values. The analysis process is summarized in **Figure 16**.





Figure 16. Flowchart for identifying proteins specifically biotinylated by BirA*-DOT1L in LC-MS/MS analysis

As a result of LC-MS/MS analysis, 160 and 251 proteins were detected in HEK293T cells from 2 readings. When 2 readings of LC-MS/MS were combined, 118 proteins were common in both readings and in total 224 proteins were identified in control cells as non-specific background. When these background proteins were omitted from list of fusion protein infected samples, there were 35 and 89 proteins remaining in 2 readings of wt-DOT1L whereas there were 171 and 324 proteins in 2 readings of mut-DOT1L. When 2 readings of each sample were combined, 14 proteins were common in wt-DOT1L and 129 proteins in mut-DOT1L sample. Among these proteins, extranuclear ones were eliminated and 12 proteins remained in wt-DOT1L and 99 proteins in mut-DOT1L sample. 9 of these proteins are common in wt- and mut-DOT1L samples (Figure 17A). Among these 9 common proteins, AF17 and DDX21 were previously reported to interact with DOT1L¹²⁵. AF10 and ENL were detected in only wt-DOT1L samples and their direct interaction with DOT1L was previously reported¹²⁵. Novel interactions of DOT1L were also detected. WT-DOT1L sample had 7 novel interactions (TPR, KAISO, NUMA1, MRE11, NONO, SIN3B, Histone H1) whereas mut-DOT1L samples had 96 novel-proximal interactions (Figure 17). Whether these novel proteins are directly interacting with DOT1L requires further investigation but these proteins can be referred as DOT1Lproximal proteins.



Figure 17. Novel proximal interactions of DOT1L were revealed via BioID along with known direct interactions of DOT1L.

A, Wt and mut DOT1L's proximal interactors. **B**, Possible novel interaction partners of WT DOT1L that are ranked according to their PSM (peptide spectrum matches) and coverage% scores. Red arrows indicate previously known interactions of DOT1L.

In conclusion, BioID analysis identified five proteins (AF10, AF17, ENL, Histone1 and DDX21) that were previously reported as direct interactors of DOT1L. In addition, novel proximal proteins such as TPR, KAISO, NUMA1, MRE11, NONO and SIN3B were identified as potential interaction partners of DOT1L. On the other hand, mut-DOT1L had dozens of proximal protein interactions. This may be due to a defect in chromatin localization of the mutant protein, a notion that needs further experimental verification.

3.2.4 shRNA-mediated knock-down of DOT1L-proximal proteins

To determine the effect of DOT1L-interacting proteins on reprogramming, a loss-of-function based reprogramming screen was designed using short hairpin RNAs (shRNAs). Potential DOT1L-interacting proteins were curated from the BioID screen (**Figure 17**B). 12 proteins were found as potential interactors of wt-DOT1L including 4 proteins that were previously known to directly interact with DOT1L. Among 12 proteins, one of them was DOT1L protein itself and another one was histone protein, Histone H1.0, therefore no shRNA was targeted for it. For the remaining 10 proteins in DOT1L's interaction network (AF10, NONO, KAISO, SIN3B, AF17 MRE11 ENL, NUMA1, TPR, DDX21); 2 shRNAs were designed to target each gene. All shRNAs were cloned into puromycin resistance gene containing retroviral pSMP vector.

Successfully cloned shRNAs were packaged into retroviral particles and transduced to dH1f human fibroblast cells¹³². As a control (shControl), firefly luciferase targeting pSMP_sh-Luc (shFF) was used. Upon completion of puromycin selection, RNA isolation was performed and the expression levels of shRNA targeted genes were quantified by qRT-PCR. mRNA levels of each gene was normalized to shControl (shFF) infected cells.

All shRNAs achieved at least 50% knock-down of their respective target genes, except shTPR#2 (Figure 18). As a result, 2 functional shRNAs were designed, cloned and tested against 10 proximal proteins of DOT1L except TPR [*it has only 1 functional shRNA*].



Figure 18. mRNA expression levels of shRNA-targeted genes

qRT-PCR was performed as duplicate samples and β -actin was used as an internal control gene. Every genes expression level is normalized to shControl (shFF) infected cells. (n=2; error bars represents s.d.)

3.2.5 shRNA-mediated screen of DOT1L proximal interactors for reprogramming efficiency

To test the loss-of function effects of DOT1L proximal proteins on reprogramming, dH1f cells were infected with shRNA viruses and reprogrammed with OSKM (Figure 19).



Figure 19. Timeline of reprogramming experiments for shRNA infected fibroblasts

Seven days after OSKM transduction, cells were transferred onto MEFs. At the end of the reprogramming procedure, cells were stained with Tra-1-60 (embryonic cell surface marker) antibody to identify iPSC colonies. Quantifications were carried out with Image-J and results were compared with shControl sample with respect to Tra-1-60 positive colony number (**Figure 20**).



Figure 20. Fold change in reprogramming efficiency as a result of shRNA-mediated gene silencing

Reprogramming experiment for shRNA screen was performed. Average colony number of each experiment was calculated and normalized to shControl to calculate fold change. Average of fold change from different experiments was calculated and standard error is depicted in error bars. (*P* values were determined by a one sample t-test. *, P < 0.05; n is indicated above the bars and denotes independent biological replicates) Representative Tra-1-60 stained well images are displayed underneath the bar graph.

As a result of this shRNA screen, it was observed that knock-down of AF10 and NONO significantly increased the number of iPSC colonies, resulting in 1.5 to 2 fold greater reprogramming efficiency. (Figure 20). On the other hand, knock-down of MRE11 and TPR decreased reprogramming drastically while knock-down of KAISO, SIN3B and AF17 did not significantly affect reprogramming (Figure 20). In the case of ENL, NUMA and DDX21, one of the shRNAs did not affect the reprogramming whereas other shRNA decreased the iPSC colony numbers.

Effect of AF10 and NONO on reprogramming has not been studied in the literature and in this screen it was demonstrated that knock down of AF10 and NONO increase reprogramming. In this project, molecular mechanism behind AF10's effect on reprogramming was further investigated. However, effect of NONO on reprogramming would also warrant further investigation since its knock-down increases reprogramming significantly.

3.2.6 Knock-out of AF10 via CRISPR increases reprogramming efficiency similar to knock-down of AF10 via shRNA

The strongest candidate protein identified from the shRNA-mediated reprogramming screen was AF10, which is known to be a well-established direct interactor of DOT1L^{154} . Follow up experiments were performed to better understand the mechanism of action of AF10 during reprogramming. First, CRISPR/Cas9-mediated knock-out of AF10 was tested to verify the increase in the reprogramming via shAF10. *AF10 (MLLT10)* genomic region
was targeted by 2 independent sgRNAs targeting exon 2 or exon 3 (Figure 21A). Non-targeting control gRNA (sgControl) and sgAF10-1 & -2 containing lentiviral vectors were transduced to dH1f cells which were then selected with puromycin. CRISPR/Cas9-mediated mutations of the sgAF10 target sites were demonstrated via T7 endonuclease assay (Figure 21B). In addition, sgAF10 expressing dH1fs had lower AF10 mRNA levels compared to sgControl dH1fs as assessed by q-RT-PCR (Figure 21C). These experiments demonstrate that sgAF10s disrupts the AF10 gene.

Next, sgAF10 infected dH1fs were reprogrammed with OSKM transduction. At the end of reprogramming, iPSC colonies were quantified with Tra-1-60 antibody staining and normalized to sgControl infected dH1fs (**Figure 21D**). sgAF10 expressing fibroblasts generated approximately 2-fold greater number of iPSC colonies compared to control cells indicating that loss of AF10 increases reprogramming efficiency (**Figure 21D**). This experiment shows that knock-out of AF10 increases reprogramming efficiency similar to knockdown of AF10.



Figure 21. CRISPR/CAS9 based suppression of AF10 and its effect on reprogramming

A, sgAF10 targeting sites on AF10 (*MLLT10*) gene. Green bars show gRNA targeting site and NGG shows the PAM sequence that Cas9 targets. Red arrows show the T7 assay primers and expected DNA fragments were depicted. **B**, T7-endonuclease assay for sgAF10 targeting sites. **C**, sgRNA-mediated AF10 knock-out decreases expression levels of AF10 mRNA. (n=2; error bars represents s.d.) **D**, sgRNA-mediated AF10 knock-out increases reprogramming. Tra-1-60 colony numbers were quantified and normalized to sgControl to calculate fold change. Representative Tra-1-60 stained well images are displayed underneath the bar graph. (*P* values were determined by a one sample t-test; * *P* < 0.05; n=5 and denotes independent biological replicates)

3.2.7 sgAF10s decreases H3K79 methylation

It has previously been reported that AF10 is responsible for the recruitment of DOT1L to most of its target genes¹⁴⁹ and that loss of AF10 decreases overall H3K79 methylation levels. To confirm these findings in our system, H3K79me2 levels were measured in sgAF10 infected dH1fs. dH1fs treated with a small molecule inhibitor of DOT1L (EPZ004777) were used as a positive control for H3K79me2 depletion. Since EPZ004777 was dissolved in DMSO, control dH1fs were treated with DMSO. Immunoblot with H3K79 dimethyl specific antibody demonstrated a reduction in total H3K79me2 levels in sgAF10 expressing cells though not as extensive as small molecule inhibition of DOT1L (**Figure 22**). This result indicates that AF10 expression is needed for H3K79 methylation.



Figure 22. gRNA mediated AF10 knock-out decreases H3K79me2 levels of dH1fs

EPZ004777, a small molecule inhibitor of DOT1L, was used as a positive control of H3K79me2 depletion. dH1f cells were treated with DMSO or 3 μ M EPZ004777 for 10 days. sgAF10 infected dH1fs were selected with puromycin and cultured for 1 week.

3.2.8 sgAF10's effect on reprogramming can be reversed via overexpression of AF10

It was shown that silencing of AF10 via shRNAs or sgRNAs can increase reprogramming efficiency. To prove that these results are due specifically to AF10's silencing and not to off-target effects, a rescue experiment was designed. For this purpose, AF10 cDNA was cloned into a mammalian expression plasmid that has Hygromycin resistance gene. Since sgAF10 plasmids have puromycin resistance, both plasmids can be sequentially infected and selected with different antibiotics. First, dH1f cells were transduced with sgControl and sgAF10 vectors and selected with puromycin. After puromycin selection was completed, cells were infected with AF10 overexpression plasmid and selected with Hygromycin. sgAF10s do not target the AF10 overexpression construct because they are complementary to the splice junctions of AF10 gene which are absent in exogenous AF10 cDNA. Successfully selected dH1f cells were used in histone extraction, RNA isolation or reprogramming experiments (Figure 23).

qRT-PCR confirmed that *AF10* mRNA levels were increased 5 to 7-fold upon AF10 overexpression in control and sgAF10 cells (Figure 23B). Histone extraction and H3K79me2 immunoblot indicated that AF10 overexpression increased the overall H3K79me2 levels in dH1fs (Figure 23A). When AF10 is overexpressed, the reprogramming efficiency decreased approximately by half (Figure 23C). Taken together, these experiments showed that the increased reprogramming phenotype upon AF10 silencing can be rescued by the overexpression of AF10 cDNA, which further strengthened the notion that AF10 is a barrier to reprogramming.



Figure 23. AF10 overexpression rescues sgAF10 phenotypes

A, H3K79me2 levels in sgAF10 infected cells and AF10 rescued cells. gRNA mediated AF10 knock-out decreases H3K79me2 levels of dH1fs. Conversely, overexpression of AF10 increases H3K79me2 levels. **B**, sgRNA-mediated AF10 knock-out decreases expression levels of AF10 mRNA whereas overexpression of AF10 increases AF10 expression. (n=2; error bars represents s.d.) **C**, Tra-1-60 colony numbers were quantified and normalized to sgControl to calculate fold change. sgRNA-mediated AF10 knock-out increases reprogramming while overexpression of AF10 significantly decreases reprogramming for both sgControl and sgAF10 infected cells. (*P* values were determined by a one sample t-test; *, P < 0.05; n=3 and denotes independent biological replicates)

3.2.9 Loss-of AF10 together with inhibition of DOT1L does not have an additive effect on reprogramming efficiency

After demonstrating that genetic suppression of AF10 expression via shRNA or sgRNAs increases reprogramming efficiency, we next considered the possibility that AF10 blocks reprogramming through interfering with DOT1L function. To test this hypothesis, shAF10 and sgAF10 treated cells were reprogrammed with or without addition of a DOT1L inhibitor (EPZ004777). sgAF10 or shAF10 infected dH1fs were treated with 3 µM EPZ004777 for 6 days after OSKM transduction and control cells were treated with DMSO. At the end of reprogramming, Tra-1-60 positive colonies were counted and their fold change over DMSO treated shControl/sgControl cells was calculated.

The results revealed that, consistent with previous experiments, AF10 knockdown or knock-out on their own increases reprogramming. However, this effect is lost upon Dot1L inhibition, suggesting that the AF10 phenotype is dependent on the presence of H3K79 methylation activity of DOT1L. In other words, in DOT1L-inhibited cells loss of AF10 does not increase reprogramming efficiency further (**Figure 24**). These results suggest that AF10 and DOT1L may be acting in the same pathway to block reprogramming.



Figure 24. Knock-down or Knock-out of AF10 does not further increase reprogramming efficiency in DOT1L-inhibited condition

A, shAF10 infected cells were reprogrammed with DMSO or 3 μ M EPZ004777 treatment for 6 days. Average colony number of each experiment was calculated and normalized to shControl to calculate fold change. Average of fold change from n=5 experiments was calculated and standard error is depicted in error bars. **B**, sgAF10 infected cells were reprogrammed with DMSO or 3 μ M EPZ004777 treatment for 6 days. Average colony number of each experiment was calculated and normalized to sgControl to calculate fold change. Average of fold change from n=4 experiments was calculated and standard error is depicted in error bars. (*P* values were determined by a one sample t-test; *, P < 0.05) Representative Tra-1-60 stained well images are displayed underneath the bar graph.

3.2.10 Double-KO of AF10 and DOT1L during reprogramming

Since AF10 and DOT1L may work together during reprogramming, AF10 and DOT1L double knock-outs were generated to test their effect on reprogramming. DOT1L-KO cells were generated by gDOT1L-1 & gDOT1L-2 CRISPR plasmids both targeting exon 5 of *DOT1L gene (KMT4)*. sgAF10s and sgControl infected cells were knocked-out with non-targeting gRNA (gNT1) and gDOT1Ls (gD1 and gD2). Double-KO cells were reprogrammed to compare the reprogramming efficiency.

First, dH1fs were infected with non-targeting gRNA (gNT1) and gDOT1Ls (gD1 and gD2) and selected with puromycin. To test the gRNAs efficiency on silencing DOT1L, H3K79me2 levels were measured. DMSO and 3 μ M EPZ004777 treated dH1fs were used as a control as in **Figure 22**. gDOT1L infected cells exhibited drastic reduction in H3K79me2 levels similar to EPZ004777 treated cells (**Figure 25**A). This experiment demonstrates that sgRNA-mediated DOT1L suppression causes depletion of H3K79me2.

For reprogramming experiment, dH1f cells were infected with sgAF10 and sgControl viruses and selected with puromycin. Successfully selected cells were then transduced with non-targeting gRNA (gNT1) and gDOT1Ls (gD1 and gD2) without further puromycin selection. Cells were passaged for 10 days and half of the cells were harvested for histone extraction and the other half of the cells were utilized for reprogramming experiments. To test double-KO dH1fs, collected cells were investigated for their H3K79me2 levels (**Figure 25**B).



Figure 25. H3K79me2 levels in gRNA-mediated AF10 & DOT1L knock-out dH1fs

A, gDOT1L infected cells have depleted H3K79me2 levels. EPZ (EPZ004777) is a small molecule inhibitor of DOT1L, used as a positive control of H3K79me2 depletion. dH1f cells were treated with DMSO or 3 μ M EPZ004777 for 10 days. gDOT1L infected dH1fs were selected with puromycin and cultured for 10 days. **B**, gDOT1L and sgAF10 double knock-out cells display decreased H3K79me2 levels. (H3 total immunoblot depicts histone loading)

We observed that sgAF10 transduced cells exhibited reduction in H3K79 methylation and gDOT1Ls caused a further decrease in H3K79 methylation (Figure 25B). The decrease in H3K79me2 levels are not as drastic as in Figure 25A since no puromycin selection was done after gDOT1L transduction.

Double-KO cell populations were reprogrammed with OSKM transduction. At the end of reprogramming experiment, Tra-1-60 positive colony numbers were quantified and normalized to the uninfected dH1fs (**Figure 26**). This reprogramming experiment demonstrated that AF10-KO cannot further increase the reprogramming when DOT1L was knocked-out even though sgAF10 and gDOT1L can increase reprogramming 3 to 4-fold, by themselves (**Figure 26**). These results suggest that silencing AF10 increases reprogramming through DOT1L.



Figure 26. gRNA mediated AF10 & DOT1L double knock-out does not have additive effect on reprogramming

sgAF10 and gDOT1L infected cells were reprogrammed. Average colony number of each experiment was calculated and normalized to uninfected dH1fs to calculate fold change. Average of fold change from n=3 experiments were calculated and standard error is depicted in error bars. (*P* values were determined by a one sample t-test; *, P < 0.05; n.s., not significant, P > 0.05)

Experimental work described in this chapter indicated that BioID analysis identified TPR, KAISO, NUMA1, MRE11, NONO and SIN3B as novel proximal proteins of DOT1L. Taken together, these data are the first to demonstrate that knock-down of AF10, significantly increased iPSC generation efficiency, suggesting that it acts as a barrier to reprogramming similar to DOT1L. This finding was verified by CRISPR/Cas9 mediated knockout of AF10. In addition we showed that combining DOT1L inhibition or knockout, with AF10 suppression did not result in an additive enhancement of reprogramming, suggesting that these two chromatin factors act in the same pathway.

Chapter 4

4 MLL1 silencing increases reprogramming efficiency

4.1 Introduction

Mixed Lineage Leukemia 1 (MLL1/KMT2A) gene was discovered by its association with leukemia through genetic analyses¹⁵⁵. Homozygous *Mll* knockout mice are embryonic lethal at day 11.5-14.5 and exhibit decreased amount of hematopoietic cells in the liver¹⁵⁶. Further investigations revealed that MLL1 regulates growth of hematopoietic precursors¹⁵⁶. MLL1 catalyzes H3K4 methylation and it mainly regulates *Hox* genes expression¹⁵⁷. MLL1 also regulates cell cycle through cyclins, CDK inhibitors and transcription factor GATA3^{158,159}. Therefore, MLL1 is a master regulator that has important roles in gene expression regulation during development, cell cycle and hematopoiesis.

4.1.1 MLL1 translocations in Acute Myeloid Leukemia (AML) patients

MLL1 (KMT2A) is a histone H3 lysine 4 (H3K4) methyltransferase and H3K4 methylation on chromatin is associated with active gene transcription. MLL1 enzyme is well-known for its translocations which leads to 70% of the infant acute leukemias¹⁶⁰. There are more than 60 fusion partners of MLL1¹⁶⁰. Among MLL1 translocations the top five subtypes are: MLL1-AF4, MLL1-ENL, MLL1-AF9, MLL1-AF10, MLL1-AF6¹⁶¹. In the MLL1 translocation, MLL1 loses its SET domain which is the H3K4 methyltransferase domain; however the fusion protein still causes increased expression of some target genes¹⁶². One of the most prominent outcomes of MLL1 translocations is that aberrant transcriptional regulation of HOX genes¹²³. Even though MLL1 loses its SET domain, HOX genes' expression is upregulated. It was shown that many of the fusion partners of MLL1 such as AF9, AF10, AF17 and ENL are direct interactors of DOT1L, the H3K79 methyltransferase. MLL fusion target genes were high in H3K79 methylation which supports the common interactor DOT1L as an important player of leukemia¹⁶³. Since H3K79 methylation is found in actively transcribed genes, DOT1L was found as a strongest suspect of HOX genes' aberrant transcriptional upregulation due to DOT1L's interaction with MLL1 fusion partners. Therefore, there have been many attempts to use small molecule inhibitors of DOT1L in AML patients to inhibit DOT1L methyltransferase activity¹²³. However, using these drugs might result in side effects such as disruption in normal hematopoiesis because DOT1L has a role during normal hematopoiesis as well¹²⁴. Therefore, inhibition of interactions between MLL fusion partners and DOT1L to block aberrant recruitment of DOT1L to MLL1 target genes could be an alternative route to ameliorate AML.

4.1.2 MLL complex in transcription

MLL1 has multiple functional domains including AT-hook domains and a CXXC motif that bind to DNA, plant homeodomains (PHDs), a bromo domain (BD), transactivation domain (TAD) and a SET domain that catalyzes the H3K4 methylation¹⁶⁴. MLL1 is cleaved by Taspase1 into N-320 kDa and C-180 kDa fragments that are forming heterodimers to stabilize complex¹⁶⁵. There are two phenylalanine-tyrosine rich regions (FYR) in MLL1 that re-associates the MLL1-N and MLL1-C fragments¹⁶⁶ (**Figure 27**). MLL1 has evolutionary conserved protein-binding sites such as MENIN binding motif (MBM), WDR5 interaction motif (Win) and LEDGF binding domain (LBD)¹⁶⁷. MLL1^{-/-} mice have a fetal liver hematopoiesis defect which is associated with decreased expression of HOX genes¹⁵⁶. Dysregulation of HOX genes resulted in acute myeloid leukemia (AML) where there are MLL1 translocations from its break point region¹⁶⁸. Therefore, MLL1 has a crucial role during development of hematopoietic precursors.



Figure 27. Multiple functional domains of MLL1 is depicted before and after its cleavage by Taspase1

DNA binding AT-hooks, zinc finger containing CXXC motif, plant homeodomain (PHD) fingers, bromodomain (BD), phenylalanine-tyrosine rich regions (FYR), transactivation domain (TAD), WDR5 interaction (Win) motif, and the histone methyltransferase SET domain are highlighted. The full-length MLL1 protein is cleaved by Taspase 1 into MLL-N (300 kDa) and MLL-C (180 kDa) fragments that then re-associate through FYRN and FYRC motifs to form stable complex. Adapted from *Dharmarajan and* $Cosgrove^{167}$.

MLL1 forms a dynamic complex that regulates H3K4 methylation. The core subunits of this complex are <u>WDR5</u>, <u>RBBBP5</u>, <u>ASH2L</u> and <u>DPY30</u> which are referred as WRAD¹⁶⁹. It has been demonstrated by structural biologists that RBBP5-ASH2L heterodimer activates the catalytic function of MLL family histone methyltransferases¹⁷⁰. In addition to core components there are accessory proteins in the complex which are CXXC1, WDR82, HCFC1 and MENIN¹⁷¹. These interactors of MLL proteins are important to recruit MLL complex to the specific gene sites therefore assist in regulation of H3K4 methylation. MENIN is thought to bind DNA directly and recruit MLL complex to specific sites¹⁷². Also MENIN binding domain (MBD) is retained in the translocated MLL1 fusion proteins therefore MENIN drives the aberrant recruitment of fusion partners of MLL1 at promoters of HOX genes¹⁷².

MLL1 can catalyze mono-, di-, tri-methylation of H3K4 residue with its SET domain. There are catalytic subunits other than MLL1 as a H3K4 methyltransferase in dynamic MLL complex such as SET1A, SET1B, MLL2, MLL3 and MLL4 which are all MLL family proteins¹⁷⁰. H3K4 methylation is correlated with transcriptionally active genomic sites. And each H3K4 methylation has distinct transcriptional outcomes: H3K4 tri-methylation found in actively transcribed genes, H3K4 di-methylation is associated with poised chromatin and H3K4 mono-methylation is enriched at enhancers, ribosomal DNA¹⁶⁷. H3K4 methylation is tightly regulated process since methylation degree has different functions in chromatin.

4.1.3 The role of MLL1 in pluripotency

During reprogramming, H3K4 methylation levels are increased globally^{173,174}. MLL complex is mainly responsible from H3K4 methylation. It was previously shown that Yamanaka factors are interacting with proteins in MLL complexes¹⁷⁵. SOX2 strongly binds ASH2L and WDR5 through its highmobility group (HMG) domain¹⁷⁵. DPY30 and RBBP5 knock-down in MEF decreases the OCT4 expressing cells ¹⁷⁵. In another study Wdr5 was shown as an essential protein for reprogramming and WDR5 is overexpressed during reprogramming process⁷⁶. On the other hand, it was shown that an inhibitor that blocks WDR5-MLL1 interaction is sufficient for reprogramming of epiblast stem cells (EpiSCs) into naïve pluripotency¹⁷⁶. They also showed that inhibition of WDR5-MLL1 interaction results in global redistribution of H3K4me1 marks on enhancers¹⁷⁶. This study shows the importance of H3K4 methylation mark on pluripotency however MLL1's role on somatic cell reprogramming is unknown.

In this chapter, known direct and functional interactors of DOT1L were curated from the literature and their effect on reprogramming was investigated through loss of function experiments. Suppression of *Mixed Lineage Leukemia 1 (MLL1)* expression via RNA interference or CRISPR/Cas9 significantly increased reprogramming efficiency. To determine how MLL1 prevents reprogramming, RNA-sequencing was performed. MLL1 suppression resulted in downregulation of fibroblast-specific genes and accelerated the activation of pluripotency-related genes.

4.2 Results

4.2.1 shRNA-mediated screen of DOT1L's previously known interactors for reprogramming efficiency

To test the loss of function effect of DOT1L's previously known interactors on reprogramming; an shRNA-mediated screen was carried out. For this purpose, proteins that are known to interact with DOT1L directly or functionally were curated from the literature. As a result, 13 proteins were found to be closely related with DOT1L, however among those proteins 4 of them (AF10, AF17, ENL and DDX21) have been already investigated, which were also identified in our BioID assay. For the 9 remaining proteins (MLL1, BAT3, NPM1, SIRT1, AF9, AF4, CDK9, STAT1 and HNRNPM) in the interaction network of DOT1L, 2 shRNAs were designed to target each gene. All shRNAs were cloned into puromycin resistance gene containing mammalian expression vector (pSMP) and verified by sequencing.

Successfully cloned shRNA plasmids were packaged into retroviruses. dH1fs were infected with each shRNA viruses twice and selected with puromycin for 2-3 days. As a control shRNA (shControl), firefly luciferase targeting pSMP_sh-Luc (shFF) was used. Successfully selected cells were collected for RNA isolation and q-RT-PCR was performed to quantify the expression levels of targeted genes. While quantifying the results, mRNA level of each gene was compared with shControl infected cells (**Figure 28**). As a result, every shRNA successfully knocked-down its target gene at least 40%.



Figure 28. mRNA expression levels of shRNA-target genes

qRT-PCR was performed as duplicate samples and β -actin was used as an internal control gene. Every genes expression level is normalized to shControl (shFF) infected cells. (n=2; error bars represents s.d.)

shRNA infected dH1f cells were reprogrammed as previously summarized in **Figure 19**. At the end of the reprogramming procedure, cells were stained with Tra-1-60 (embryonic cell surface marker) antibody. Quantifications were carried out with Image-J and results were compared to shControl sample with respect to Tra-1-60 positive colony number (**Figure 29**).

Both shRNAs targeting MLL1 and one shRNA targeting BAT3 significantly increased reprogramming efficiency in this screen (**Figure 29**). On the other hand, one shRNA of AF9, CDK9; and both shRNAs of HNRNPM significantly decreased reprogramming, while knock-down of other genes did not affect reprogramming significantly (**Figure 29**). MLL1 knock-down generated approximately 2-fold more iPSC colonies compared to shControl cells indicating that loss of MLL1 increases reprogramming (**Figure 29**). As a next step, the role of MLL1 on reprogramming was investigated.



Figure 29. Reprogramming efficiency change as a result of shRNAmediated gene silencing of DOT1L's previously known interactors.

Reprogramming experiment for shRNA screen was repeated for n=3 times and for each experiment, samples were in triplicates. Average colony number of each experiment was calculated and normalized to shControl to calculate fold change. Average fold change from independent n=3 experiments is shown and error bars indicate standard error. (*P* values were determined by a one sample t-test; *, P < 0.05) Representative Tra-1-60 stained well images are displayed underneath the bar graph.

4.2.2 MLL1 and DOT1L has independent roles during reprogramming

The strongest candidate protein identified from previous screen was MLL1 and it is known to be a functional interactor of DOT1L¹⁷⁷. Follow up experiments were performed to better understand the mechanism of MLL1 during reprogramming. First, we considered the possibility that MLL1 blocks reprogramming through DOT1L, similar to AF10. To test this hypothesis, shMLL1 treated cells were reprogrammed with or without DOT1L inhibitor (EPZ004777). shRNA infected dH1fs were treated with 3 μ M EPZ004777 for 6 days after OSKM transduction and control cells were treated with DMSO. At the end of reprogramming, total area of Tra-1-60 positive colonies was measured and their fold change over DMSO treated control cells was calculated (**Figure 30**). In this experiment, quantification was done by comparison of Tra-1-60 positive colonies total area instead of colony numbers; because EPZ004777 treated colonies had grown too much and were interfering with each other.

This result revealed that one of the shRNAs targeting MLL1 (shMLL1-1) significantly increased reprogramming 2-fold in DOT1L inhibitor-treated cells, while another shRNA (shMLL1-2) only slightly increased the efficiency (**Figure 30**). This result suggested that DOT1L and MLL1 may operate independently during the reprogramming process. Since we observed a strong phenotype in only one of the shMLL1s, this hypothesis was tested in alternative experimental set up. For this purpose, knock-out MLL1 cells were reprogrammed with DOT1L inhibitor treatment condition instead of shMLL1. 3 gRNAs were designed against *MLL1* to have more confident results.



Figure 30. Knock-down of MLL1 in DOT1L-inhibited condition further increases reprogramming efficiency

shMLL1 infected cells were reprogrammed with DMSO or 3 μ M EPZ004777 treatment for 6 days. Average Tra-1-60 positive colonies total area of each experiment was calculated and normalized to shControl to calculate fold change. Average of fold change from n=7 experiments were calculated and standard error is depicted in error bars. (n=7 indicates independent biological replicates; P values were determined by a one sample t-test; *, P < 0.05) Representative Tra-1-60 stained well images are displayed underneath the bar graph.

MLL1 knock-out reprogramming was performed to verify the increase in the reprogramming efficiency via shMLL1s. CRISPR/Cas9 method was used to knock-out MLL1. *MLL1* genomic region was targeted by 3 sgRNAs (**Figure 31**A). Non-targeting control gRNAs (gNT1 and gNT2) and gMLL1s (gMLL1-

1, gMLL1-2 and gMLL1-3) were cloned into lentiCRISPRv2 plasmids and packed into lentiviruses. CRISPR/Cas9-mediated mutation of gMLL1 target sites was demonstrated via T7 endonuclease assay (**Figure 31**B). T7 endonuclease assay of gMLL1 infected cells exhibited expected band sizes depicted in **Figure 31**A (**Figure 31**B). In addition, gMLL1 infected dH1fs had lower *MLL1* mRNA levels compared to gNT1 dH1fs as assessed by qPCR (**Figure 31**C). These experiments show that *MLL1* can be successfully targeted by gRNAs.

gMLL1 infected dH1fs were reprogrammed via OSKM transduction with or without DOT1L inhibitor (EPZ004777). gMLL1 infected dH1fs were treated with 3 μ M EPZ004777 for 6 days after OSKM transduction and control cells were treated with DMSO. At the end of reprogramming, Tra-1-60 positive colonies were measured and their fold change over DMSO treated control cells (gNT1) was calculated. Three replicates of this reprogramming experiment were performed by Gülben Gürhan in Tamer Önder's group. This result revealed that all of the gMLL1s significantly increased reprogramming in DMSO, control condition whereas 2 out of 3 gMLL1s were significantly increased (2 to 3-fold) iPSC colony number in the DOT1L inhibitor treated cells (**Figure 31**D). Thus, it supports the hypothesis that DOT1L and MLL1 independently operate during reprogramming functions of DOT1L and MLL1 since there is not any significant increase between DMSO and EPZ004777 treated gMLL1 samples.



Figure 31. Verification of MLL1 silencing experiments with knockout MLL1 experiments

A, gMLL1 targeting sites on *MLL1 (KMT2A)* gene. Green bars shows the gRNA targeting site. Red arrows show the T7 assay primers and expected DNA fragments were depicted. **B**, T7-endonuclease assay for gMLL1 targeting sites. **C**, gRNA-mediated MLL1 knock-out decreases expression levels of *MLL1* mRNA. (n=2; error bars represents s.d.) **D**, gRNA-mediated MLL1 knock-out increases reprogramming with or without treatment with 3 μ M EPZ004777. (*P* values were determined by a one sample t-test; *, *P* < 0.05; n is indicated above the bars and denotes independent biological replicates) Representative Tra-1-60 stained well images are displayed underneath the bar graph.

4.2.3 shRNA-mediated screen of MLL1 complex proteins for reprogramming efficiency

Having shown that MLL1 is a barrier to reprogramming, we next asked which proteins in MLL complex have an effect on reprogramming. MLL1 functions in large, multi-protein complexes in transcription regulation. We therefore sought to examine the role of MLL1-interacting proteins in reprogramming and investigated whether their inhibition would phenocopy MLL1 loss in reprogramming. An shRNA-mediated screen was planned to target MLL1 complex proteins in reprogramming. 12 proteins were curated as MLL1 complex proteins according to literature (ASH2L, RBBP5, DPY30, MENIN1, SET1B, CXXC1, MLL2, MLL3, MLL4, WDR82, WDR5, and HCFC1). Two shRNAs were designed to determined 12 proteins in MLL1 complex. All shRNAs were cloned into puromycin resistance gene containing, pSMP vector.

Successfully cloned shRNAs were packed with retroviral packaging plasmids to produce viruses. As a control shRNA (shControl), firefly luciferase targeting pSMP_sh-Luc (shFF) was used. Successfully selected cells were collected for RNA isolation and followed by q-RT-PCR to quantify the expression levels of shRNA targeting genes. While quantifying the results, mRNA levels of each gene was compared with shControl infected cells. As a result of qRT-PCR experiments, all shRNAs were successfully knocked-down their target gene (**Figure 32**).



Figure 32. mRNA expression levels of shRNA-targeted genes belonging to MLL1 complexes

qRT-PCR was performed as duplicate samples and β -actin was used as an internal control gene. Every genes' expression level is normalized to shControl (shFF) infected cells. (n=2; error bars represents s.d.)

shRNA infected dH1f cells were reprogrammed with OSKM to test the loss-of function effect of MLL complex proteins on reprogramming. At the end of the reprogramming, cells were stained with Tra-1-60 (embryonic cell surface marker) antibody. Quantifications were carried out with Image-J and results were compared to shControl sample with respect to Tra-1-60 positive colony number.

As a result of this shRNA screen, it has been concluded that some of the proteins in MLL1 complex (ASH2L, RBBP5, DPY30, MEN1, SET1B and CXXC1) act as a barrier of reprogramming similar to MLL1. Whereas, WDR5 and HCFC1 are essential for reprogramming since the reprogramming efficiency drastically decreases when they are knocked-down (**Figure 33**). These results can be interpreted as knock-down of MLL1 core complex

increases the efficiency, except WDR5 and HCFC1. These exceptions may be due to the differential functions of WDR5 and HCFC1 since WDR5 interacts with OCT4⁷⁶ and HCFC1 interacts with Sin3 histone deacetylase (HDAC)¹⁷⁸. This result reveals that MLL1 complex has an undeniable effect on reprogramming since the complex consist of both enhancers and barriers of reprogramming.



Figure 33. The effect of knocking down MLL1 complex members on reprogramming efficiency

Reprogramming experiment for shRNA screen was repeated for n=4 times and triplicate technical replicates for each experiment were used. Average of each experiment was calculated and normalized to shControl to calculate fold change. Average of fold change from different experiments was calculated and standard error was depicted in error bars. (*P* values were determined by a one sample t-test; *, P < 0.05; n=4 and denotes independent biological replicates) Representative Tra-1-60 stained well images are displayed underneath the bar graph.

4.2.4 gMLL1s change gene expression to accelerate fibroblast to iPSC transition

MLL complex is known to play an important role during transcriptional regulation¹⁵⁷. Since we have shown that MLL1 as a complex has a role during reprogramming, we next determined the global gene expression differences upon MLL1 downregulations. gMLL1-2 and gMLL1-3 were picked for further experiments since they increase reprogramming efficiency more than gMLL1-1 (Figure 31D). RNA-sequencing (RNA-seq) was performed on gMLL1 expressing cells with and without reprogramming factor transduction (OSKM).

dH1f cells were infected twice with gNT1, gMLL1-1 and gMLL1-2 and selected with puromycin. Successfully selected cells were passaged for 10 days and then seeded onto triplicate wells in two replicate plates. Samples in one of the plates were infected with OSKM while other samples were not reprogrammed and referred as Day 0 samples of RNA-seq experiment. At day 6 of reprogramming, infected cells were trypsinized and 1/6 of them were transferred on MEFs to continue the reprogramming experiment while the remaining cells were harvested as Day 6 samples of RNA-seq experiment. At the end of reprogramming, gMLL1's reprogramming efficiency was analyzed via Tra-1-60 staining (**Figure 34**A). As a result, almost 2-fold increase in Tra-1-60 positive colony number was observed. RNA isolation was performed on previously harvested cell pellets (Day 0 and Day 6 samples). Firstly, cDNA synthesis and q-RT-PCR analysis were performed for quality control of RNA samples. *NANOG* mRNA levels were checked to confirm that



isolated RNA samples represent the increase in reprogramming efficiency (Figure 34B).

Figure 34. Validation of reprogramming phenotype of cells used for RNA-sequencing analysis

A, Tra-1-60 colony numbers were quantified via Image J software. gRNA mediated MLL1 knock-out increases reprogramming. Representative Tra-1-60 stained well images are displayed underneath the bar graph. (error bars represents standard error of n=3 technical replicates) **B**, OSKM treated cells have increased expression levels of *NANOG* mRNA at Day 6. (n=2; error bars represents s.d.)

After quality control of RNA samples; RNA sequencing and its analysis were performed by Kenan Sevinç and Tunc Morova. After RNA sequencing result were obtained, differentially expressed genes among gMLL1 treated cells were identified via DESeq2 software. Significant genes were selected if their pvalue<0.05 and upregulated-downregulated genes were separated if their log2fold_change >0.5 or log2fold_change <-0.5, respectively. According to these cutoffs, upregulated and downregulated genes of gMLL1-3 are identified as a subset of gMLL1-2 results. At day 0, 36 genes out of 38 upregulated genes of gMLL1-3 were common with 191 upregulated genes of gMLL1-2; 76 genes out of 77 downregulated genes of gMLL1-3 were common with 307 downregulated genes of gMLL1-2. At day 6, 7 genes out of 8 upregulated genes of gMLL1-3 were common with 53 upregulated genes of gMLL1-2; all 4 downregulated genes of gMLL1-3 were common with 53 upregulated genes of gMLL1-2; all 4 downregulated genes of gMLL1-3 were common with 42 downregulated genes of gMLL1-2 (Figure 35). Similar comparison was also performed with p-adjusted values<0.05 and differentially expressed genes were separated if their log2fold_change >0 or log2fold_change <0 (Appendix-I; Figure 42).





Differentially expressed genes upon gMLL1 infection were analyzed with gene set enrichment analysis (GSEA) to investigate the statistically significant correlations of these genes with set of fibroblast-specific genes, pluripotencyspecific genes and MLL-target genes. First, a set of fibroblast and iPSC specific genes were determined by analyzing microarray data to compare fibroblasts with ESCs and iPSCs (Figure 36A). Then, established gene sets were related with differential genes between gNT1 and gMLL1 samples publically **36**B). available MLL (Figure Also, target gene set (Wang MLL Targets)¹³⁶ was compared with gMLL1 samples (Figure 36B). Same analysis was performed for samples that are induced with OSKM and these are referred as Day 6 samples (Figure 36C).



Figure 36. MLL1-KO accelerates the decrease in fibroblast gene sets and promotes the increase in pluripotency gene expression

A, Microarray analysis of fibroblasts and pluripotent cells to determine fibroblast related genes and pluripotency related gene sets. GEO data series GSE55679. **B**, RNA sequencing analysis by using MLL target genes, fibroblast related genes and pluripotency related gene sets. (NES, normalized enrichment score; FDR, false discovery rate)

As a result of RNA-sequencing experiments, gMLL1 infected cells display accelerated decrease in fibroblast gene sets and increase in pluripotency gene expression. When we compared differentially expressed genes of gMLL1 treatment with DOT1L inhibitor treated cells, only a small number of genes were appeared as common (RNA-sequencing data not shown for DOT1L inhibitor treated cells). To be exact; among 76 downregulated genes, 27 of them was common with 2543 downregulated genes of DOT1L inhibitor treated cells and among 36 upregulated genes, only 4 of them was common with 180 upregulated genes of DOT1L inhibitor treated cells (Figure 37). This result supports the hypothesis that DOT1L and MLL1 independently operate during reprogramming process. Similar analysis was performed with p-adjusted values<0.05 and differentially expressed genes were separated if their log2fold_change >0 or log2fold_change <0 (Appendix-I; Figure 43). In addition, each gMLL1 infected samples were compared with EPZ004777 samples (Appendix-I; Figure 44).





Differentially expressed genes were selected if their p-value<0.05. Upregulated genes were selected if their log2fold_change >0.5 and downregulated genes were selected if log2fold_change <-0.5.

To validate the RNA-sequencing results, a few commonly downregulated (FBLN5, PRRX1, and FOXF2) or upregulated (SERPINB9) genes were analyzed with q-RT-PCR (**Figure 38**). As a result of q-RT-PCR validation of RNA-sequencing samples, SERPINB9 demonstrated increasing levels of mRNA with gMLL1 samples and FBLN5, PRRX1 and FOXF2 exhibits decreasing levels as expected from RNA-sequencing results (**Figure 38**). These set of experiments validate the results of the RNA sequencing analyses.



Figure 38. RNA-sequencing validation with q-RT-PCR analysis to compare SERPINB9, FBLN5, PRRX1 and FOXF2 gene levels

qRT-PCR was performed as duplicate samples and β -actin was used as an internal control gene. Every genes' expression level is normalized to gNT1 infected cells. (n=2; error bars represents s.d.)

Taken together, experimental work described in this chapter indicated that these data are the first to demonstrate that knock-down of MLL1, significantly increased iPSC generation efficiency, suggesting that it acts as a barrier to reprogramming similar to DOT1L. This finding was verified by CRISPR/Cas9 mediated knockout of MLL1. In addition we showed that combining DOT1L inhibition with MLL1 knockout resulted in an increased enhancement of reprogramming, suggesting that these two chromatin factors act independently. Our findings suggest that MLL1 suppression resulted in downregulation of fibroblast-specific genes and accelerated the activation of pluripotency-related genes.


Chapter 5

5 Discussion

DOT1L is the sole H3K79 methyltransferase and it catalyzes mono-, di-, and tri-methylation¹⁷⁷. It is also known that H3K79 methylation is linked to active gene transcription¹⁷⁷. DOT1L catalyzes this modification during elongation of transcription and it works in a complex during transcriptional regulation¹⁰⁵. DOT1L is an established barrier of reprogramming⁵⁵. It is known that H3K79 methylation can affect lineage specific genes' expression; therefore, knock-down or inhibition of DOT1L increases reprogramming efficiency⁵⁵. However, other proteins in DOT1L complex have not been investigated for their roles on reprogramming. In this study, our aim was to identify novel interaction partners of DOT1L and investigate their effect on reprogramming. In this thesis, three main findings have been presented: (1) Novel proximal interactors of DOT1L were found via BioID assay, (2) AF10 was found as a barrier of reprogramming through regulation of H3K79 methylation with DOT1L, and (3) MLL1 was found as a barrier of reprogramming through regulation of gene expression.

5.1 Proximal interactors of DOT1L was identified by BioID method

AF9, AF10, and ENL are the proteins that were identified as direct interactors of DOT1L^{105,121,179}. Later, DOT1L's interactors were identified by affinity pull-down method and these interactions were verified by co-IP experiments¹²⁵. In that study¹²⁵, interaction of DOT1L with AF9, AF10 and ENL was verified and a few novel proteins were suggested as DOT1L interactors; including NPM1, HNRNPM, DDX21, etc. In our study, we focused on finding DOT1L's interactions as a complex rather than direct interactors. Therefore, we chose a method that will reveal proximal interaction partners: BioID.

BioID is a powerful method to find out proximal protein interactions of a particular protein¹³⁹. In our study, we aimed to identify DOT1L's proximal interactors, therefore, we cloned a fusion protein of BirA* (promiscuous biotin ligase) and DOT1L. This method allowed us to biotinylate proximal proteins that are in 10 nm radius so that we can pull-down these proteins with Streptavidin beads and identify via LC-MS/MS. As a result of this analysis, some of the known interactors (AF10, AF17, ENL, DDX21) of DOT1L were acquired as well as some novel interactions were suggested (TPR, NONO, NUMA, KAISO, MRE11, SIN3B, Histone H1.0).

Since BioID captured some of the known interactions of DOT1L, we can say that BioID method successfully worked in our experimental design. However, not all of the known interactions were found in LC-MS/MS analysis. This can be due to the algorithm that we used for identification of interactions. For example, NPM1 and HNRNPM proteins, which are also known interactions of DOT1L¹²⁵, were detected via LC-MS/MS in BirA*-DOT1L samples; however, they were eliminated from the list because they were also detected in control/background sample (Appendix: BioID raw data). In the case of NPM1, detected PSM values were similar in both samples and control. On the other hand, HNRNPM was highly enriched in both reads of BirA*-DOT1L-mut sample (1st reading 34 PSM, 2nd reading 37 PSM), whereas it was detected in only one reading of BirA*-DOT1L-wt sample and control sample with a low PSM value. This result suggests that HNRNPM might be an interaction partner of DOT1L when DOT1L is catalytically inactive. Another possibility is that, DOT1L mutant might have a different set of interactors in the cell as a result of an aberrant localization of mut-DOT1L on chromatin. Moreover, AF9 is a well-established interaction partner of DOT1L, but it was not in the final list of DOT1L-proximal interactors. In LC-MS/MS analysis, AF9 was detected in only one of the readings of BirA*-DOT1L-wt sample. Therefore, we eliminated this interaction when we selected the proteins that are common in both readings. This can be interpreted as follows: some of the novel interactions may be eliminated due to the stringent scanning that was used. On the other hand, we revealed 4 of the known interactions of DOT1L along with 7 possible novel proximal interactions, even though we used this stringent scanning. The scanning that we followed increased the confidence in our suggested novel interactions despite a few possible interactions might have eliminated during analysis.

When we analyze the BioID results, DOT1L was the top hit detected in samples and none was detected in control cells. This is the first step that shows the BioID method worked efficiently in our study. During BioID assay, proteins other than DOT1L were at their basal levels in the cell since they were not overexpressed. Therefore, we might have missed some of the low expressed proteins that are interacting with DOT1L. One way of overcoming this issue might be repeating the assay. In this study, we performed BioID assay once with 2 readings of each sample. When replicated, the confidence of detection could be increased.

In this study, we fused BirA^{*} to the N-terminus of DOT1L. Even though BirA^{*} is a relatively small protein with 35 kDa weight, it might interfere with the N-terminus specific interactions of DOT1L. Alternatively, another fusion protein could be used for BioID assay. If BirA^{*} was fused to the C-terminus of DOT1L, possible interactions of DOT1L that requires intact N-terminus structure could be captured. Similarly, BirA^{*} might interfere with the catalytic activity of DOT1L since the catalytic domain of DOT1L is on the N-terminus. However, we tested the catalytic activity of DOT1L and found that it did not lose its H3K79 methyltransferase activity. Since fusion of BirA^{*} was close to the catalytic domain, interactions of DOT1L that are important for its catalytic activity could be identified.

In future work, the novel proximal proteins identified here can be investigated to understand the interaction dynamics whether they directly interact or occupy the same complex or transiently interact at a certain time point. For this purpose, a few techniques can be performed such as coimmunoprecipitation (co-IP), mammalian two hybrid, proximity ligation assay, etc. It would be insightful to understand the details of interactions that DOT1L has.

5.2 AF10 blocks reprogramming through regulation of H3K79 methylation via DOT1L

Our shRNA-mediated screen against DOT1L-proximal proteins revealed that AF10 is a barrier of reprogramming. Although AF10's recruitment of DOT1L to the target genes¹³⁰ was known before, AF10's effect on reprogramming has not been investigated. In this study, we showed the increase in reprogramming when AF10 is silenced via shRNA or sgRNA. Rescue of AF10-KO with sgAF10-resistant overexpression plasmid indicates that the increase in reprogramming is indeed through AF10-loss and not via off-target effect of sgAF10s. When combinatory knock-down of AF10 with other DOT1L-interacting genes ENL and AF17 was tried, reprogramming efficiency was not increased more than only AF10 knock-down (Appendix-I, Figure 40). In addition, our results suggest that AF10's effect on reprogramming is through DOT1L. It was reported that DOT1L inhibition decreases H3K79 methylation and increases reprogramming⁵⁵. Previously, it was demonstrated that AF10 has an important role in the regulation of H3K79 methylation¹³⁰, as well. These findings are consistent with our observation that AF10 silencing increased reprogramming through DOT1L. On the contrary, sgAF10 treated cells does not exhibit decreased levels of expression in DOT1L-target genes (Appendix-I, Figure 41).

In shRNA-mediated screen of DOT1L-proximal interactions on reprogramming, knock-down of NONO was increased reprogramming significantly. In the future, effect of NONO on reprogramming can be investigated. Previously, it was reported that loss of Nono had a significant role in mouse ESC self-renewal through Erk pathway activation¹⁸⁰. Therefore, an evolutionarily conserved effect of NONO could be revealed since our reprogramming experiments were conducted with human fibroblasts. NONO is found in RNA regulatory paraspeckles in nucleus of differentiated cells¹⁸¹. However, paraspeckle formation is not observed in ESCs¹⁸². Therefore, it is correlated to observe that loss of NONO increasing the reprogramming. These observations and our results are consistent with the finding that NONO is a possible barrier in reprogramming. Thus, further investigation of NONO's effect on reprogramming could be a promising future project.

In this study, it was demonstrated that knock-down of MRE11 and TPR significantly decreased iPSC generation in shRNA-mediated screen of DOT1L-proximal interactions on reprogramming. TPR is a member of nuclear pore complex and its function is to regulate mRNA transportation to the cytoplasm via regulating the quality control of spliced mRNAs¹⁸³. However, TPR's effect on reprogramming or pluripotency had not been investigated before. MRE11 is a DNA damage repair protein that has a functional role in the cell against double stranded brakes (DSBs)¹⁸⁴. Another report shows that fibroblasts have lower levels of MRE11 while hESCs and iPSCs have elevated levels of MRE11¹⁸⁵. These observations are consistent with our finding that shows knock-down of MRE11 significantly decreased iPSCs generation.

Taken together, findings in our study suggest that knock-down of AF10 increases reprogramming through DOT1L by regulation of H3K79 methylation and knock down of NONO also facilitates reprogramming. Conversely, knock-down of MRE11 and TPR impede reprogramming, however we do not know by which mechanism these proteins operate during reprogramming. Nevertheless, interaction partners of DOT1L has a certain role during reprogramming, therefore, it was important to pursue their effect on reprogramming.

Recently, it was reported that KDM4D might be responsible for H3K79 demethylation¹²⁰. Before that study, H3K79 specific demethylase had not been identified. Since it is known that H3K79 methylation is important for reprogramming process and now, we are suggesting that regulation of H3K79 methylation has a role during reprogramming; it would be worthwhile to investigate the effect of KDM4D on reprogramming, as well.

5.3 MLL1 blocks reprogramming through regulation of gene expression independent from DOT1L

As result of BioID assay, a few known interactions of DOT1L were detected along with a few novel proximal interactions of DOT1L. However, in the literature there are a few more known interactions of DOT1L: some are direct interactions (AF4, AF9, HNRNPM, NPM1, STAT1, BAT3) and some of them are functional interactions (CDK9, MLL1, SIRT1). Since we have obtained crucial information by investigating the BioID-identified DOT1L proximal interactors on reprogramming; we decided to adopt a similar strategy with known interactions of DOT1L. As a result of this shRNAmediated screen of reprogramming, knock-down of MLL1 demonstrated a significant increase in iPSC generation. Knock-down of MLL1 was associated with the increased pluripotency for the first time; therefore, further investigation to find out how knock-down of MLL1 increased reprogramming was carried out. First, we tested whether MLL1 is functioning though DOT1L and the results indicated that MLL1 and DOT1L appear to have overlapping as well as distinct functions in reprogramming. Then, we investigated the effect of proteins in MLL1 complex during reprogramming process. Our findings indicated that knockdown of core components (ASH2L, DPY30, RBBP5) of MLL complex increased reprogramming. This finding contradicts with a previous study, where they demonstrated that knock-down of Rbbp5 and Dpy30 decreased reprogramming in MEFs¹⁷⁵. These adverse outcomes could be as a result of differential epigenetic regulations between mouse and human. Nevertheless, further investigation is required to make a definite conclusion on this issue. Knock-down of WDR5, another core protein of MLL complex, decreased reprogramming significantly. In fact, it was previously known that WDR5 is essential for self-renewal of ESCs and therefore it is also essential for reprogramming⁷⁶. It could be due to the fact that WDR5 interacts with OCT4⁷⁶. Knock-down of HCFC1 also decreased reprogramming significantly. This could be as a result of HCFC1's interaction with histone deacetylase, Sir3¹⁷⁸. Taken together, these findings suggest that MLL1 complex has an important role during reprogramming.

MLL1 complex is known to play an important role during transcriptional regulation. Catalytic function of MLL1 complex is associated with H3K4 methylation¹⁶⁹. In previous reports, H3K4 methylation was also associated with lineage specificity and demonstrated that down-regulation of H3K4 methylation promote pluripotency^{186,187}. In one study, H3K4 tri-methylation

was suggested as a barrier to efficient nuclear reprogramming due to its ability to maintain the memory of somatic cell identity¹⁸⁶. In another report, downregulation of H3K4 methylation via MLL1 inhibitor was associated with improved somatic cell nuclear transfer¹⁸⁷. However, in our study we did not observe a significant decrease in the global levels of H3K4me1, 2 or 3 when MLL1 is knocked-down (Figure 39). Therefore, we decided to investigate the action of MLL1 complex through comparing the gene expression dynamics.



Figure 39. MLL1 knock-down does not change global H3K4 mono- and tri-methylation in dH1fs

H3 Total was used as a loading control.

RNA sequencing was performed to gMLL1-2, gMLL1-3 and gNT1 infected cells, with or without OSKM transduction. As a result of RNA sequencing analysis, it was shown that gMLL1 treated cells exhibited down-regulated expression of MLL1-target genes which suggests that MLL1 silencing successfully achieved. When differentially expressed genes of gMLL1 treated cells were compared with fibroblast-specific gene sets, significant decrease was observed in the fibroblast-specific genes' expression. In addition, when gMLL1 infected cells were reprogrammed, pluripotency-specific genes' expression was significantly enriched in differentially expressed genes. These two observations suggest that MLL1 might promote reprogramming by accelerating the transition of fibroblasts to pluripotency state by downregulating the fibroblast-specific gene expression and accelerating the activation of pluripotency-related genes' expression. Furthermore, when down-regulated genes upon gMLL1 were compared with down-regulated genes upon DOT1L inhibition, only a subset of genes was common. This observation also supports our previous claim that MLL1 and DOT1L have distinct functions as well as overlapping functions.

Taken together, findings in this study suggest that silencing MLL1 increased reprogramming through regulation of fibroblast-specific genes expression. Similar to MLL1, knock-down of MLL1 complex proteins, especially ASH2L and DPY30, was demonstrated to facilitate reprogramming. Conversely, knock-down of WDR5 and HCFC1 was inhibited the iPSC generation. These results suggest that MLL1 as a complex has an important regulatory role during reprogramming. In the future, chromatin immunoprecipitation (ChIP) experiments can be performed to determine the localization of MLL1 marks, H3K4 methylation, during reprogramming.

5.4 Final conclusion

In this thesis, we showed that DOT1L's interaction partners have an effect on reprogramming. First, we identified NONO, KAISO, NUMA1, TPR, MRE11, and SIN3B as novel proximal interactions of DOT1L via BioID method. Several known interactions of DOT1L (AF10, AF17, ENL and DDX21) were detected via BioID method. Second, we investigated the effect of proximal interactions of DOT1L on reprogramming. As a result, AF10 was found as a barrier to reprogramming since shRNA or sgRNA-mediated silencing of AF10 increased reprogramming efficiency. Our findings suggest that AF10 increases reprogramming through DOT1L. Third, we tested the effect of known interaction partners of DOT1L on reprogramming. Consequently, MLL1 was identified as another barrier to reprogramming. It was also proposed that MLL1, as a complex, regulates gene expression of cells. sgRNA-mediated silencing of MLL1 decreased fibroblast-specific gene set and promoted pluripotency genes' expression. Taken together, we identified novel proximal interactors of DOT1L and revealed that AF10 and MLL1 are novel barriers to reprogramming.

APPENDIX-I



Figure 40. Fold change in reprogramming efficiency as a result of combination of shRNA-mediated silencing of ENL, AF10 and AF17

Reprogramming experiment for shRNA infected dH1fs were performed. Average colony number of each experiment was calculated and normalized to shControl to calculate fold change. Average of fold change from different experiments was calculated and standard error is depicted in error bars.



continues...



continues...



Figure 41. mRNA expression levels of AF10, AF17, DOT1L and DOT1L-target genes

qRT-PCR was performed as duplicate samples and β -actin was used as an internal control gene. Every genes expression level is normalized to sgCntrl cells. (n=2; error bars represents s.d.)



Figure 42. Commonly upregulated and downregulated gene numbers among gMLL1-2 and gMLL1-3 samples at Day 0 and Day 6 samples

Differentially expressed genes were selected if their p-adjusted-value <0.05. Upregulated genes were selected if their log2fold_change >0 and down regulated genes were selected if log2fold_change <0



Figure 43. Commonly upregulated and downregulated gene numbers among gMLL1 and EPZ004777 samples at Day 0

Genes that are commonly upregulated and downregulated in gMLL1-2 and gMLL1-3 samples were detrmined and compared with EPZ004777 sample. Differentially expressed genes were selected if their p-adjusted-value<0.05. Upregulated genes were selected if their log2fold_change >0 and downregulated genes were selected if log2fold_change <0.



Figure 44. Commonly upregulated and downregulated gene numbers among gMLL1-2&3 and EPZ004777 samples at Day 0

Differentially expressed genes were selected if their p-adjusted-value<0.05. Upregulated genes were selected if their log2fold_change >0 and downregulated genes were selected if log2fold_change <0.

APPENDIX-II

Table 15. Raw data of BioID experiment: HEK293T control cells, 1^{st} reading

Accession	Description	ΣCoverage	Σ# PSMs
P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	56.74	28
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	39.18	28
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	38.35	51
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	34.60	20
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	33.15	14
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	32.86	4
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	32.56	6
P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	32.21	12
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	31.94	17
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	31.65	15
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	31.52	11
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	30.72	17
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	29.72	18
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	29.13	8
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	28.64	11
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	28.30	10
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	27.78	9
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	26.96	4
P29372	DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 - [3MG_HUMAN]	26.85	10
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	26.52	13
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	26.38	41
P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10_HUMAN]	25.23	12
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	24.82	9
P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24_HUMAN]	23.57	7
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	23.53	9
P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A_HUMAN]	22.97	7
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	22.79	24
P62633	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 - [CNBP_HUMAN]	22.60	5
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	22.51	20
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16_HUMAN]	22.47	7
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	22.45	9
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	22.38	6
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	21.98	24
P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	21.43	3
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	21.14	5
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA_HUMAN]	20.42	74
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	20.12	43
P62891	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]	19.61	1
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	18.42	4
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	18.20	14
095232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]	17.82	16
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	17.82	14
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	17.57	15
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	17.39	2
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	16.95	2
O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	16.16	25
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	15.77	12
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	15.69	8

Accession	Description	ΣCoverage	Σ# PSMs
Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3 - [H2A1J_HUMAN]	14.84	1
P62910	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 - [RL32_HUMAN]	14.81	6
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	14.71	15
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	14.37	12
Q96EY4	Translation machinery-associated protein 16 OS=Homo sapiens GN=TMA16 PE=1 SV=2 - [TMA16_HUMAN]	14.29	5
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 - [GNL3_HUMAN]	13.84	16
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	13.62	6
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK_HUMAN]	13.61	7
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	13.10	4
P62273	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 - [RS29_HUMAN]	12.50	2
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	12.35	3
P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	12.24	2
Q5JTH9	RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	12.03	24
Q6NXT2	Histone H3.3C OS=Homo sapiens GN=H3F3C PE=1 SV=3 - [H3C_HUMAN]	11.85	3
E9PL08	Volume-regulated anion channel subunit LRRC8D (Fragment) OS=Homo sapiens GN=LRRC8D PE=4 SV=3 - [E9PL08_HUMAN]	11.76	1
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	11.64	6
P56270	Myc-associated zinc finger protein OS=Homo sapiens GN=MAZ PE=1 SV=1 - [MAZ_HUMAN]	11.32	10
P62847	40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1 - [RS24_HUMAN]	11.28	3
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	11.25	20
P62917	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]	10.51	4
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMAN]	10.41	5
P48730	Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D PE=1 SV=2 - [KC1D_HUMAN]	9.88	6
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	9.87	6
P61513	60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2 - [RL37A_HUMAN]	9.78	2
P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1_HUMAN]	9.58	6
P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 - [RL29_HUMAN]	9.43	2
H0YL99	28S ribosomal protein S11, mitochondrial OS=Homo sapiens GN=MRPS11 PE=1 SV=1 - [H0YL99_HUMAN]	9.32	1
015235	28S ribosomal protein S12, mitochondrial OS=Homo sapiens GN=MRPS12 PE=1 SV=1 - [RT12_HUMAN]	8.70	1
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	8.50	5
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	8.28	11
Q9GZV4	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3 - [IF5A2_HUMAN]	7.84	2
P62987	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]	7.81	1
Q9H5H4	Zinc finger protein 768 OS=Homo sapiens GN=ZNF768 PE=1 SV=2 - [ZN768_HUMAN]	7.78	8
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	7.69	1
G3V5X6	Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1 - [G3V5X6_HUMAN]	7.69	1
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	7.53	3
P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]	7.47	5
Q02543	60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 - [RL18A_HUMAN]	7.39	2
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_HUMAN]	7.39	12
P07477	Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1 - [TRY1_HUMAN]	7.29	13
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	7.28	1
P61927	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 - [RL37_HUMAN]	7.22	1
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	7.20	2
P62899	60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 - [RL31_HUMAN]	7.20	1
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	7.11	4
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	7.02	4
Q7Z3I7	Zinc finger protein 572 OS=Homo sapiens GN=ZNF572 PE=2 SV=1 - [ZN572_HUMAN]	6.81	1
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	6.21	2
Q5T280	Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 - [CI114_HUMAN]	6.12	3
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13 HUMAN]	5.96	1

Accession	Description	ΣCoverage	Σ# PSMs
Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3 - [MCCA_HUMAN]	5.93	7
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	5.93	5
Q16629	Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1 - [SRSF7_HUMAN]	5.88	2
P50914	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14_HUMAN]	5.58	2
Q9Y324	rRNA-processing protein FCF1 homolog OS=Homo sapiens GN=FCF1 PE=2 SV=1 - [FCF1_HUMAN]	5.56	2
P78549	Endonuclease III-like protein 1 OS=Homo sapiens GN=NTHL1 PE=1 SV=2 - [NTH_HUMAN]	5.45	2
Q9Y698	Voltage-dependent calcium channel gamma-2 subunit OS=Homo sapiens GN=CACNG2 PE=1 SV=1 - [CCG2_HUMAN]	4.95	1
Q8IWS0	PHD finger protein 6 OS=Homo sapiens GN=PHF6 PE=1 SV=1 - [PHF6_HUMAN]	4.93	3
Q9Y2R4	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3 - [DDX52_HUMAN]	4.34	3
Q5T440	Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 - [CAF17_HUMAN]	4.21	1
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	4.14	2
H0YKS4	Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=1 SV=1 - [H0YK54_HUMAN]	3.98	1
Q9BZE4	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1_HUMAN]	3.94	5
Q5H913-2	Isoform 2 of ADP-ribosylation factor-like protein 13A OS=Homo sapiens GN=ARL13A - [AR13A_HUMAN]	3.91	1
C9JK49	Protein LOC400891 (Fragment) OS=Homo sapiens GN=LOC400891 PE=4 SV=1 - [C93K49_HUMAN]	3.83	1
P22087	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2 - [FBRL_HUMAN]	3.43	2
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 - [UTP18 HUMAN]	3.24	1
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1 HUMAN]	3.20	3
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6 HUMAN]	3.13	2
P02768	Serum albumin OS=Homo sabiens GN=ALB PE=1 SV=2 - [ALBU HUMAN]	3.12	3
O9P016	Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1 - [THYN1 HUMAN]	3.11	2
I3L3U9	Ribosomal L1 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=RSL1D1 PE=1 SV=1 - [I3L3U9 HUMAN]	3.04	1
096EK4	THAP domain-containing protein 11 OS=Homo sapiens GN=THAP11 PE=1 SV=2 - [THA11 HUMAN]	2.87	2
05T6C4	Ataxin-7-like protein 2 OS=Homo sapiens GN=ATXN7L2 PE=4 SV=1 - [OST6C4 HUMAN]	2.87	7
M0OYT0	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [M0OYT0_HUMAN]	2.80	1
Q7L3S4	Zinc finger protein 771 OS=Homo sapiens GN=ZNF771 PE=1 SV=1 - [ZN771 HUMAN]	2.52	2
075475	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1 HUMAN]	2.45	2
G3V1A6	Gasdermin domain containing 1, isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 - [G3V1A6_HUMAN]	2.44	1
Q9H0S4	Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens GN=DDX47 PE=1 SV=1 - [DDX47_HUMAN]	2.42	2
Q6P087	RNA pseudouridylate synthase domain-containing protein 3 OS=Homo sapiens GN=RPUSD3 PE=1 SV=3 - [RUSD3 HUMAN]	2.28	2
000409-2	Isoform 2 of Forkhead box protein N3 OS=Homo sapiens GN=FOXN3 - [FOXN3 HUMAN]	2.14	1
P25205	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3 HUMAN]	2.10	3
043175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	2.06	1
O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR HUMAN]	2.05	2
000325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	1.93	1
Q96P11	Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens GN=NSUN5 PE=1 SV=2 - [NSUN5 HUMAN]	1.86	2
Q6ZN08	Putative zinc finger protein 66 OS=Homo sapiens GN=ZNF66 PE=5 SV=3 - [ZNF66 HUMAN]	1.57	2
08WYO5	Microprocessor complex subunit DGCR8 OS=Homo sapiens GN=DGCR8 PE=1 SV=1 - [DGCR8 HUMAN]	1.55	1
014684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 - [RRP1B HUMAN]	1.45	2
O9NVP1	ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DDX18 HUMAN]	1.34	2
A0A087WU	DNA polymerase alpha catalytic subunit OS=Homo sapiens GN=POLA1 PE=4 SV=1 - [A0A087WU64 HUMAN]	1.30	4
P49711	Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF HUMAN]	1.24	2
P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	0.73	2
08N2Y8	Iporin OS=Homo sapiens GN=RUSC2 PE=1 SV=3 - [RUSC2 HUMAN]	0.73	1
060241	Brain-specific angiogenesis inhibitor 2 OS=Homo sapiens GN=BAI2 PE=2 SV=2 - [BAI2 HUMAN]	0.69	1
000411	DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM HUMAN]	0.65	2
E9PPJ1	Protein CASC5 OS=Homo sapiens GN=CASC5 PE=1 SV=2 - [E9PPJ1 HUMAN]	0.57	1
H0Y7L2	Dedicator of cytokinesis protein 7 (Fragment) OS=Homo sapiens GN=DOCK7 PE=1 SV=1 - [H0Y7L2 HUMAN]	0.54	1
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC HUMAN]	0.44	3
H3BLS7	Vacuolar protein sorting-associated protein 13D (Fragment) OS=Homo sapiens GN=VPS13D PE=1 SV=1 - [H3B S7 HUMAN]	0.44	1

Accession	Description	ΣCoverage	Σ# PSMs
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	53.49	10
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	50.52	35
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	41.85	19
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	41.77	19
060814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	38.89	10
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	38.39	26
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	38.18	10
P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	37.64	22
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	36.50	18
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	36.18	51
P29372	DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 - [3MG_HUMAN]	34.23	17
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	33.73	24
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	33.06	49
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16 HUMAN]	30.14	14
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28 HUMAN]	29.93	11
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	29.41	14
P62805	Histone H4 QS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4 HUMAN]	29.13	6
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A HUMAN]	28.79	16
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A HUMAN]	28.30	14
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2 HUMAN]	27.65	18
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA HUMAN]	27.47	27
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35 HUMAN]	26.02	6
P62241	40S ribosomal protein S8 OS=Homo sabiens GN=RPS8 PE=1 SV=2 - [RS8 HUMAN]	25.00	12
P61927	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 - [RL37 HUMAN]	24.74	3
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1 HUMAN]	23.12	9
P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A HUMAN]	22.97	9
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23 HUMAN]	22.38	8
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1 HUMAN]	22.08	22
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA HUMAN]	21.48	88
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5 HUMAN]	21.17	17
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 [PYC_HUMAN]	21.14	50
P62633	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 - [CNBP_HUMAN]	20.90	7
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 - [GNL3_HUMAN]	20.77	21
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	20.69	15
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16_HUMAN]	20.22	7
Q96EY4	Translation machinery-associated protein 16 OS=Homo sapiens GN=TMA16 PE=1 SV=2 - [TMA16_HUMAN]	20.20	8
P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10_HUMAN]	20.09	11
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9 HUMAN]	20.06	24
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19 HUMAN]	20.00	5
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	19.72	10
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK_HUMAN]	19.65	12
P62891	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]	19.61	2
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	19.12	8
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	18.42	6
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	18.12	12
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	18.12	12
P84098	60S ribosomal protein I 19 OS=Homo sapiens GN=RPI 19 PE=1 SV=1 - [RI 19 HUMAN]	17.86	10

Table 16. Raw data of BioID experiment: HEK293T control cells, 2^{nd} reading

Accession	Description	ΣCoverage	Σ# PSMs
Q02543	60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 - [RL18A_HUMAN]	17.61	6
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	17.39	4
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	17.39	2
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	17.28	10
P32969	60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [RL9_HUMAN]	17.19	3
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	16.95	2
P22090	40S ribosomal protein S4, Y isoform 1 OS=Homo sapiens GN=RPS4Y1 PE=1 SV=2 - [RS4Y1_HUMAN]	16.35	9
015235	28S ribosomal protein S12, mitochondrial OS=Homo sapiens GN=MRPS12 PE=1 SV=1 - [RT12_HUMAN]	15.94	4
Q9H5H4	Zinc finger protein 768 OS=Homo sapiens GN=ZNF768 PE=1 SV=2 - [ZN768_HUMAN]	15.93	15
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	15.38	3
P62910	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 - [RL32_HUMAN]	14.81	6
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	14.81	21
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	14.55	16
P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	14.29	2
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	14.29	1
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	13.93	18
Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3 - [MCCA_HUMAN]	13.79	13
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	13.76	8
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	13.61	9
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	13.59	10
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	13.53	10
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMAN]	13.42	8
Q9GZV4	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3 - [IF5A2_HUMAN]	13.07	3
Q5JTH9	RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	12.57	28
P62273	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 - [RS29_HUMAN]	12.50	3
P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	12.24	2
000571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	11.78	19
P78549	Endonuclease III-like protein 1 OS=Homo sapiens GN=NTHL1 PE=1 SV=2 - [NTH_HUMAN]	11.54	4
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	11.52	8
Q8IYL3	UPF0688 protein C1orf174 OS=Homo sapiens GN=C1orf174 PE=1 SV=2 - [CA174_HUMAN]	11.52	4
P48730	Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D PE=1 SV=2 - [KC1D_HUMAN]	11.33	9
P62847	40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1 - [RS24_HUMAN]	11.28	4
095232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]	10.88	15
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	10.55	15
Q8N3J9	Zinc finger protein 664 OS=Homo sapiens GN=ZNF664 PE=2 SV=1 - [ZN664_HUMAN]	10.34	3
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	10.29	4
Q9BZE4	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1_HUMAN]	10.09	12
Q7L3S4	Zinc finger protein 771 OS=Homo sapiens GN=ZNF771 PE=1 SV=1 - [ZN771_HUMAN]	10.09	3
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN]	9.83	13
P61513	60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2 - [RL37A_HUMAN]	9.78	2
P56270-2	Isoform 2 of Myc-associated zinc finger protein OS=Homo sapiens GN=MAZ - [MAZ_HUMAN]	9.74	7
P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	9.52	2
P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 - [RL29_HUMAN]	9.43	2
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_HUMAN]	8.97	16
Q96P11-2	Isoform 2 of Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens GN=NSUN5 - [NSUN5_HUMAN]	8.58	4
P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 - [HNRPL_HUMAN]	8.15	10
F6QUH3	Actin filament-associated protein 1-like 2 (Fragment) OS=Homo sapiens GN=AFAP1L2 PE=1 SV=1 - [F6QUH3_HUMAN]	8.01	1
M0R2S1	Ubiquitin-60S ribosomal protein L40 (Fragment) OS=Homo sapiens GN=UBA52 PE=1 SV=1 - [MOR2S1_HUMAN]	7.97	2
P62854	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	7.83	2
P20719	Homeobox protein Hox-A5 OS=Homo sapiens GN=HOXA5 PE=1 SV=2 - [HXA5 HUMAN]	7.78	2

Accession	Description	ΣCoverage	Σ# PSMs
Q8IWS0	PHD finger protein 6 OS=Homo sapiens GN=PHF6 PE=1 SV=1 - [PHF6_HUMAN]	7.40	5
P07477	Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1 - [TRY1_HUMAN]	7.29	16
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	7.28	2
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	7.20	2
P62899	60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 - [RL31_HUMAN]	7.20	1
Q6P087	RNA pseudouridylate synthase domain-containing protein 3 OS=Homo sapiens GN=RPUSD3 PE=1 SV=3 - [RUSD3_HUMAN]	7.12	6
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	7.11	4
P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	7.03	2
043390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	6.95	7
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	6.93	4
E9PB28	Transcription factor HES-4 OS=Homo sapiens GN=HES4 PE=4 SV=1 - [E9PB28_HUMAN]	6.88	1
Q9Y3B4	Splicing factor 3B subunit 6 OS=Homo sapiens GN=SF3B6 PE=1 SV=1 - [SF3B6_HUMAN]	6.40	1
P62917	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8 HUMAN]	6.23	2
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	6.21	2
Q96I27	Zinc finger protein 625 OS=Homo sapiens GN=ZNF625 PE=2 SV=1 - [ZN625_HUMAN]	6.21	2
Q5T280	Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 - [C1114 HUMAN]	6.12	4
P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1 HUMAN]	6.01	4
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13 HUMAN]	5.96	4
014119	Vascular endothelial zinc finger 1 OS=Homo sapiens GN=VEZF1 PE=1 SV=2 - [VEZF1 HUMAN]	5.95	4
P61313	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2 - [RL15 HUMAN]	5.88	2
P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24 HUMAN]	5.73	2
09Y2R4	Probable ATP-dependent RNA helicase DDX52 QS=Homo sapiens GN=DDX52 PE=1 SV=3 - [DDX52 HUMAN]	5.68	4
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sabiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2 HUMAN]	5.67	4
P50914	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14 HUMAN]	5.58	2
09Y324	rRNA-processing protein FCE1 homolog OS=Homo saniens GN=FCE1 PE=2 SV=1 - [FCE1 HUMAN]	5.56	2
096EK4	THAP domain-containing protein 11 OS=Homo sapiens GN=THAP11 PE=1 SV=2 - [THA11 HUMAN]	5.41	2
O9P016	Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1 - [THYN1 HUMAN]	5.33	2
P35659	Protein DEK OS=Homo saniens GN=DEK PE=1 SV=1 - [DEK HUMAN]	5.07	4
016629	Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1 - [SRSF7 HUMAN]	5.04	2
007666	KH domain-containing. RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 - [KHDR1 HUMAN]	4.97	3
000059	Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1 - [TFAM HUMAN]	4.88	1
P27695	DNA-(apurinic or apyrimidinic site) vase OS=Homo sapiens GN=APEX1 PE=1 SV=2 - [APEX1 HUMAN]	4,72	2
P46778	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21 HUMAN]	4.38	1
O9BXK1	Krueppel-like factor 16 OS=Homo sabiens GN=KLF16 PE=1 SV=1 - [KLF16 HUMAN]	4.37	2
P50454	Servin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH HUMAN]	4.31	4
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU HUMAN]	4.27	4
F6TRA5	Soliceosome RNA helicase DDX398 (Fragment) OS=Homo sapiens GN=DDX398 PE=1 SV=1 - [F6TRA5 HUMAN]	4.20	1
05W52	Zinc finger protein 691 OS=Homo sapiens GN=ZNF691 PE=1 SV=1 - [ZN691 HUMAN]	4.17	2
O9Y383	Putative RNA-binding protein Luc2-like 2 OS=Homo sapiens GN=LUC2/2 PE=1 SV=2 - [LC2/2 HUMAN]	4.08	2
075475	PC4 and SERS1-interacting protein QS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1 HUMAN]	3.77	5
P26599	Polyovrimidine tract-binding protein 1 OS=Homo saniens GN=PTBP1 PE=1 SV=1 - [PTBP1 HUMAN]	3.58	4
P01891	HIA class L histocompatibility antigen. A-68 alpha chain OS=Homo sapiens GN=HIA-A PE=1 SV=4 - [1A68 HUMAN]	3.56	1
067NI 6-2	Isoform 2 of FYVE, RhoGEE and PH domain-containing protein 5 OS=Homo saniens GN=EGD5 - (EGD5 HUMAN)	3.52	1
076021	Ribosomal 11 domain-containing protein 1 OS=Homo saniens GN=RS11D1 PF=1 SV=3 - [R11D1 HUMAN]	3.47	4
095478	Ribosome biogenesis protein NSA2 homolog OS=Homo sapiers GN=ENSA2 PE=1 SV=1 - (NSA2 HumAn)	3.46	1
O9Y511	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo saniens GN=UTP18 PE=1 SV=3 - [UTP18 HIMAN]	3.24	2
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo saniens GN=GNR211 PE=1 SV=3 - [GBLP HLIMAN]	3.15	1

Accession	Description	ΣCoverage	Σ# PSMs
Q9Y4X4	Krueppel-like factor 12 OS=Homo sapiens GN=KLF12 PE=1 SV=2 - [KLF12_HUMAN]	2.99	2
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	2.99	2
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	2.96	2
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	2.89	2
Q15717	ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2 - [ELAV1_HUMAN]	2.76	1
P25205	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN]	2.72	5
Q9HC62	Sentrin-specific protease 2 OS=Homo sapiens GN=SENP2 PE=1 SV=3 - [SENP2_HUMAN]	2.72	2
P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15 HUMAN]	2.63	2
P33992	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5 HUMAN]	2.45	3
Q9H0S4	Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens GN=DDX47 PE=1 SV=1 - [DDX47 HUMAN]	2.42	2
012834	Cell division cycle protein 20 homolog OS=Homo sapiens GN=CDC20 PE=1 SV=2 - [CDC20 HUMAN]	2.40	1
P13797-3	Isoform 3 of Plastin-3 OS=Homo sapiens GN=PLS3 - [PLST_HUMAN]	2.39	1
P18754	Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [RCC1 HUMAN]	2.38	2
P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	2.37	6
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 - [LAP2B HUMAN]	2.20	2
014498	RNA-binding protein 39 OS=Homo sabiens GN=RBM39 PE=1 SV=2 - [RBM39 HUMAN]	2.08	1
014667-3	Isoform 3 of UPE0378 protein KIAA0100 OS=Homo sapiens GN=KIAA0100 - [K0100 HUMAN]	2.06	1
000325	Phosphate carrier protein, mitochondrial OS=Homo spagers GN=SI C25A3 PE=1 SV=2 - [MPCP_HUMAN]	1.93	2
050974	Nucleolar MIF4G domain-containing protein 1 OS=Homo saniens GN=NOM1 PE=1 SV=1 - [NOM1 HUMAN]	1.86	2
O9BRX2	Protein plata homolog OS=Homo sanjens (N=PFI 0 PE=1 SV=2 - IPFI 0 HUMAN)	1.82	1
P14618	Provide kinase PKM OS=Homo sapiens GN=PKM PF=1 SV=4 - [KPYM HUMAN]	1.69	2
086YZ3	Homerin OS=Horm saniens GN=HRNR PF=1 SV=2 - [HORN HIMAN]	1.68	2
Q00120	Nacylneuraminate outinkultransferase OS=Homo saniens GN=CMS PE=1 SV=2 - [NFIIA_HUMAN]	1.61	1
Q67N08	Putative zinc finger protein 66 OS=Horns sapiers GN=ZNE66 PE=5 SV=3 - [ZNE66 HIMAN]	1.57	2
O9LIPP1	Histone lusine demethylase PHFR 05=Horno saniens (0)=PHFR 0=1 (5)=3 - (PHFR HI MAN]	1.42	2
C91185	hidenic translation initiation factor 2-alpha kinasea 2 (Franment) OC=Hom series CM=EF2AK3 PE=1 SV=1 - [CQ1185_HIMAN]	1.12	2
O8NE71	Equation of the sub-family F member 1 Ω S=Horn canies O = ΔF (FI PE = 1 O = 1 E = 10 = 1 [25105_10^{-1}0^{-1}0^{-1}0^{-1}]	1.30	1
096T88	Et ubinitis ensource sub-transfer i OS-Horne series d'ar-bet i TE-TS-TE-T (Not 1-100 MR)	1.30	2
P49711	E doupduitr protein ligase or ki 1 os - homo saperis div-or ki 1 r L - 1 ov - 1 (or ki 1 - horwing)	1.20	2
096ME7	This type of the period of the type of type of the type of type of the type of typ	1.21	2
P52272	Lateringer protein 512 00 - Holis Brite Br	1.23	2
000411	Interclogeneous Induent Induedeplotein In Co-Hom Sapiens City-Internet I-1 Stars - [Internet Induedeplotein In Co-Hom Sapiens City-Internet I-1 Stars - [Internet Induedeplotein I-1 Stars - Internet I-1 Stars - [Internet Induedeplotein I-1 Stars - Internet I-1 S	1.25	2
0000111	Muk bidde particip 10 OC-Home carings OL-MORENTAL DE-1 C/C2 [MPDIA HIMAN]	1.17	
Q9DQG0	http://www.communication.com/communication/com	1.15	7
052700 4	Dreferre de Amorie de la classie i constructione andicte andicte andicita andicitate andicitat	0.00	
Q33130"4	Isoform 4 of Antyou opinic lateral sciences 2 chromosomal region candidate gene 11 protein OS=homo sapers On=ALS2CAT1 * (ALS3A_homAAV)	0.99	1
Q3NR02-3	Isoform of reasoning of coasting of the second seco	0.97	1
P40939	Initiatuolai eleyne subuniti elipila, initochonolai op-noino sepiens div-naora re-1 sv-2 * [cona_noi-ani]	0.92	1
P13039	Elongation raction 2 OS-monto sapients directed 2 FE-1 SV-4 * [EF2_montoin]	0.82	1
Q15740	My osini light chain kinase, shouti musue OS=horro sapieris GN=MTLX PE=1 SV=4 ([MTLnuMAN]	0.78	1
Q9NQ18		0.71	1
060241	prain-specific anglogenesis infinitor 2 OS=north saperis GN=BAL2 PE=2 SPE2 - [BAL2_nUMAN]	0.69	3
Q6WXEU	Cashir 2 OS=noinb sapletis Giv=CaShir2 PE-1 SV22 - [CSK12_HUMAN]	0.58	1
Q51200	zinc iniger cccn domain-contraining protein 13 US=Homo sapiens GN=2L3113 Pt=1 SV=1 - [ZC3HD_HUMAN]	0.42	1
Q5VYK3	Proceasome-associated protein ELM29 homolog US=Homo sapiens GN=ELM29 PE=1 SV=2 - [ELM29_HUMAN]	0.38	1
P46013	Antigen KI-b/ US=Homo saplens GN=MKIb/ HE=1 SV=2 - [KIb/_HUMAN]	0.28	2
Q5UIP0	reiomere-associated protein κ_{IT1} US=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN]	0.28	1
P/8527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	0.24	2

Table	17.	Raw	data	of	BioID	experiment:	BioID-DOT1L-wt	infected
HEK2	93T	cells,	$1^{ m st}$ rea	din	g			

Accession	Description	ΣCoverage	Σ# PSMs
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	41.86	7
P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	39.33	15
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	38.83	10
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	36.30	8
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	34.78	8
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	34.60	17
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	34.02	18
P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	32.21	12
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	31.01	13
P29372	DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 - [3MG_HUMAN]	30.87	13
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	28.81	12
Q8TEK3	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Homo sapiens GN=DOT1L PE=1 SV=2 - [DOT1L_HUMAN]	28.12	101
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	28.11	23
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	27.85	36
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	26.62	11
Q8N257	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3 - [H2B3B HUMAN]	26.19	7
060814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	26.19	8
P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10 HUMAN]	25.23	12
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC HUMAN]	24.62	45
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A HUMAN]	24.53	6
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17 HUMAN]	23.37	7
P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A HUMAN]	22.97	6
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20 HUMAN]	22.69	8
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA HUMAN]	20.61	4
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1 HUMAN]	20.10	6
P62891	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]	19.61	1
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5 HUMAN]	19.59	11
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1 HUMAN]	19.38	9
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28 HUMAN]	18.98	5
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	18.77	8
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2 HUMAN]	18.77	14
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1 HUMAN]	18.61	16
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	18.57	2
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	18.42	4
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA HUMAN]	18.24	57
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK HUMAN]	17.71	11
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C HUMAN]	17.59	13
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	17.52	13
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 - [GNL3 HUMAN]	17.49	12
F8W8C9	Immunoqlobulin iota chain OS=Homo sapiens GN=VPREB1 PE=1 SV=1 - [F8W8C9 HUMAN]	17.36	1
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30 HUMAN]	16.95	1
000571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X HUMAN]	16.92	19
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16 HUMAN]	16.29	4
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMAN]	15.89	6
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA HUMAN]	15.66	19
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35 HUMAN]	15.45	3
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	15.20	4
P62910	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 - [RL32 HUMAN]	14.81	5

Accession	Description	ΣCoverage	Σ# PSMs
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	14.69	4
P16403	Histone H1.2 OS=Homo sapiens GN=HISTIH1C PE=1 SV=2 - [H12 HUMAN]	14.08	8
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	14.06	10
095232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]	13.89	11
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19 HUMAN]	13.78	4
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	13.64	7
P62633	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 - [CNBP HUMAN]	13.56	3
P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24 HUMAN]	13.38	5
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2 HUMAN]	13.09	8
P62273	40S ribosomal protein S29 OS=Homo saniens GN=RPS29 PE=1 SV=2 - [RS29_HUMAN]	12.50	2
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1 HUMAN]	12.11	13
O6NXT2	Histone H3.3C OS=Homo saniens GN=H3F3C PE=1 SV=3 - [H3C, HUMAN]	11.85	2
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5 HUMAN]	11.76	6
P62847	40S ribosomal protein S24 OS=Homo saniens GN=RPS24 PE=1 SV=1 - [RS24 HI IMAN]	11.28	4
096FY4	Translation machinery-associated protein 16 OS=Homo sapiens GN=TMA16 PF=1 SV=2 - [TMA16 HUMAN]	10.84	3
092841	Probable ATP-dependent RNA helicase DDX17 OS=Homo saniens GN=DDX17 PF=1 SV=2 - (DDX17 HUMAN)	10.70	15
P62917	60S ribosonal protein I& OS=Homo saniens (N=RPI & PE=1 SV=2 - [RI & HIMAN]	10.51	4
P61927	605 ribosomal protein L37 OC-Homo canienc GN-RDI 37 PF-1 S/L-2 - [DI 37 HI MAN]	10.31	1
P12236	ADP/ATP transforces a 3 OS-Homo sapients GN-SI (2566 PE-1 SV-4 - [ADT3 HIJMAN]	9.73	6
P31043	Heteroneus nuclear ribonucleonartein H OS=Horm caniene CN=HNRNPHT PE=1 SV-4 - [HNRH1 HI MAN]	9.58	6
D00874	heterogeneous nacional horizationes i OS-Horizationes autoristationes and the second statement in the second statement is the	9.30	10
P03074		0.43	2
015325	2005 hbosonial protein E25 00-1 kiliko Sapieris Con-Kr E25 FE-1 54-2 (FRE25-1004Ki) 2905 hbosonial protein E12 pritochondrial OS-Morro scapions CAL-MDDC12 DE-1 0/-1 [DT12 HIMAN]	9.70	1
D79540	205 IDUSTINI PI UCEN 512, INCUMUNINI US-HOND SAPENS GIV-PIK-512 FL-1 SV-1 F [K12_HOMAN] Endoputesse III-like protein 105-Hond capiers 6N-HIH 10 FL-1 SV-2 F [K112_HOMAN]	8.70	3
008061	Lindonacease in fine protein 1 05-10 bapters dream the 1 PL-1 32-2 [trift_indonat]	7.05	1
000714		7.93	1
090204	Lucaryout of a ladouth initiation ratio of Area constrained on the constraints of the con	7.04	2
P02987	Durquium-ous Industrial protein L40 US=nomo sapiens GN= UBAS2 PE=1 SV=2 - [KL40_n0MAN]	7.81	4
P33327		7.70	2
P49207		7.09	2
002070	Neurexophilini - 1 (rraginent) OS=norto septens div=NXPT1 PE=4 SV=1 - [C92PUD_normali]	7.69	1
Q02878	Supering protein to US=monto sapients GN=RPL0 PE=1 SV=3 - [Ltc_moveAu]	7.04	4
Q90504	Zilic Iniger protein 766 OS=norito Sapieris GN=Z/NF706 PC=1 SV=2 - [Z/NonOriAN]	7.59	/
P22087	rkiva 2-0-methyltransferase fibrillarin OS=Homo saplens GN=FbL PE=1 SV=2 - [FBKL_HUMAN]	7.48	2
P48730	Casein kinase I isorom deita US=Homo sapiens Giv=USINKLD PE=I SV=2 - [KCID_HUMAN]	7.47	5
P60709	Actin, cytoplasmc 1 OS=Homo sapiens GN=ACIB PE=1 SV=1 - [ACIB_HUMAN]	7.4/	4
Q86124	Iranscriptional regulator Kalso OS=Homo saplens GN=ZBI B33 PE=1 SV=2 - [KALSO_HUMAN]	7.44	8
Q02543	605 ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 - [RL18A_HUMAN]	7.39	2
P07477	Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1 - [TRY1_HUMAN]	7.29	9
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	7.28	2
Q8NC51	Plasmnogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	/.11	4
Q86UA1-2	Isoform 2 of Pre-mRNA-processing factor 39 OS=Homo sapiens GN=PRPF39 - [PRP39_HUMAN]	6.99	1
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	6.90	1
Q9NSQ0	Putative ribosomal RNA-processing protein 7 homolog B OS=Homo sapiens GN=RP7B PE=5 SV=1 - [RRP7B_HUMAN]	6.80	1
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEFIG PE=1 SV=3 - [EFIG_HUMAN]	6.41	3
Q03111	Protein ENL US=Homo sapiens GN=MLLT1 PE=1 SV=2 - [ENL_HUMAN]	6.26	4
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	6.21	2
Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3 - [MCCA_HUMAN]	5.79	7
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	5.78	3
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_HUMAN]	5.70	10
P84103-2	Isoform 2 of Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 - [SRSF3_HUMAN]	5.65	1
Q9Y324	rRNA-processing protein FCF1 homolog OS=Homo sapiens GN=FCF1 PE=2 SV=1 - [FCF1_HUMAN]	5.56	2
Q5JTH9	RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	5.55	10
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	5.38	3

Betergenesa nuclar robuschopeters A/210 CS=Horo spins (GH=HRR/ADI (F=1 SV-2 - [ROA2_HIMM]) 5.8 3 Cols Zer Confergenetar 71.05=Horo spins (GH=HRR/ADI (F=1 SV-1 - [ROA2_HIMM]) 5.22 1 Statistics Statistics Statistics 1 1 5.22 1 Statistics Statistics Statistics Statistics 1 <th>Accession</th> <th>Description</th> <th>ΣCoverage</th> <th>Σ# PSMs</th>	Accession	Description	ΣCoverage	Σ# PSMs
20,154 Size (Finger potent 7.1) Co-Homo sapers OR-129777 [FE-159-1 [DV7_1MMAN] 5.2 1 DV7055 Hatone HL 0. OS-Homo sapers OR-19872 PE-159-1 [PV7_1MMAN] 5.2 1 DV7055 Hatone HL 0. OS-Homo sapers OR-19872 PE-159-1 [PV7_1MMAN] 4.82 4 DV7055 Hatone HL 0. OS-Homo sapers OR-19872 PE-159-1 [PV7_1MMAN] 4.82 4 DV7055 Hatone HL 0. OS-Homo sapers OR-19872 PE-159-1 [PV7_1MMAN] 4.82 4 DV7055 Hatone HL 0. OS-Homo sapers OR-19872 PE-159-1 [PV7_1MMAN] 4.80 1 DV7055 Hatone HL 0. OS-Homo sapers OR-19872 PE-159-1 [PV7_1MMAN] 4.80 1 DV7057 Hatone Hutphanofrees Control Sol Homo sapers OR-19874 PE-159-1 [PV7_1MMAN] 4.80 1 DV7058 Hatone Hutphanofrees Control Sol Homo sapers OR-19974 PE-159-1 [PV7_1MMAN] 3.72 2 DV8109 No.PV7_1MMAN_100 3.72 2	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HINRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	5.38	3
98995 Hoton IG-Hons agens GH-HPES PE 1 SY-1 (PDO, HAMAI) 5.15 22 95270 Hoton IL, OS-Hons agens GH-HZPE 1 SY-1 (PDZ, HAMAI) 6.22 44 95270 AF Bynthes suburt algh, microbardia IG-Hons agens GH-HZPE 1 SY-1 (FDZ, HIAMAI) 4.70 44 95270 AF Bynthes suburt algh, microbardia IG-Hons agens GH-HZPE 1 SY-1 (FDZ, HIAMAI) 4.70 44 95271 AFT Bynthes suburt algh, microbardia IG-Hons agens GH-IZEZ ISFS 2 SY-1 (SZZ, HIAMAI) 4.20 11 95275 AFT Bynthes suburt algh, microbar Solven sagens GH-CHZP HF-1 SY-3 (FOLLHAMAI) 3.77 44 95276 AFT Bynthes Solven sagens GH-CHZP HF-1 SY-3 (FOLLHAMAI) 3.77 44 95170 Pathte methyltrametrase. Chrolin Gielson sagens GH-CHZP HF-1 SY-3 (FOLLHAMAI) 3.22 22 97100 Marke methyltrametrase. Introbundia GH-Intra sagens GH-INTR FE-1 SY-1 (FXPL JHAMAI) 3.24 12 97110 Small method Solven sagens GH-INTR FE-1 SY-1 (FXPL JHAMAI) 3.24 12 97110 Small method Solven sagens GH-INTR FE-1 SY-1 (FXPL JHAMAI) 3.24 12 97111 Small method Solven sagens GH-INTR FE-1 SY-1 (FXPL JHAMAI) 3.24 12 12	Q7L3S4	Zinc finger protein 771 OS=Homo sapiens GN=ZNF771 PE=1 SV=1 - [ZN771_HUMAN]	5.36	3
PixPa05 Hittone HL, DOS-Horon Sapiers GM-HER (PE-13/S-1-[H02,LMMAN] 4.82 PixPa05 Mix associated an Engreg roution GS-Horon Sapiers GM-HER (PE-13/S-1-[H02,LMMAN] 4.82 PixPa05 Mix associated an Engreg roution GS-Horon Sapiers GM-HER (PE-13/S-1-[H02,LMMAN] 4.82 PixPa05 Mix associated an Engreg roution Sapiers GM-HER (PE-13/S-1-[SD2,FJLMAN] 4.64 PixPa05 Discher Carrier funk 22 merche 15 OS-Horon Sapiers GM-HER (PE-13/S-1-[SD2,FJLMAN] 3.94 PixPa05 PixPa05 Discher Carrier funk 22 merche 15 OS-Horon Sapiers GM-HER (PE-15/S-1-[ND2,LLMAN] 3.72 PixPa05 PixPa05 Discher Carrier funk 32 merche 15 OS-Horon Sapiers GM-HER (PE-15/S-1-[ND2,LLMAN] 3.72 PixPa05 MixPa05 Discher Carrier Sapiers GM-HER (PE-15/S-1-[ND2,LLMAN] 3.72 PixPa05 MixPa05 Discher Carrier Sapiers GM-HER (PE-15/S-1-[ND2,LLMAN] 3.72 PixPa05 MixPa05 Discher Carrier Sapiers GM-HER (PE-15/S-1-[ND2,LLMAN] 3.72 PixPa05 MixPa05 Discher Carrier Sapiers GM-HER (PE-15/S-1-[ND2,LLMAN] 3.72 PixPa05 MixPa05 Discher Carrier Sapiers GM-HER (PE-15/S-1-[ND2,LLMAN] 3.72 PixPa05 PixPa05 <	Q9NP85	Podocin OS=Homo sapiens GN=NPHS2 PE=1 SV=1 - [PODO HUMAN]	5.22	1
P59270 MY-associated atcr floge protein OS-throm sapers GM-MX2 PE-1 SV-1 (FMX_HMAN) 4.70 P6277 MY-associated atcr floge protein OS-throm sapers GM-RX2 PE-1 SV-1 (FMX_HMAN) 4.70 P6277 MY-associated atcr floge protein IS OS-throm sapers GM-RX2 SV-1 (FSX_HMAN) 4.70 P6278 MX-associated atcr floge protein IS OS-throm sapers GM-RX2 SV-1 (FSXE_HMAN) 3.77 P6278 MY-associated atcr floge protein IS OS-throm sapers GM-CRXP FFS-1 SV-2 (FXXE_HMAN) 3.77 P6278 MY-associated atcr floge protein IS OS-throm sapers GM-CRXP FFS-1 SV-1 (FXXE_HMAN) 3.72 P2780 PAthiev methyltraneterse. rhothoridi GS-throm sapers GM-HMXP FE-1 SV-1 (FXXE_HMAN) 3.24 P3710 Small models PMA-associated atcr floge protein GS-throm sapers GM-HMXP FE-1 SV-1 (FXXE_HMAN) 3.34 P40(A) RMA polymerase, rhothoridi GS-throm sapers GM-HMXP FE-1 SV-1 (FXXE_HMAN) 3.32 22 P3710 Polyman Charling are grade grade to floge protein GS-throm sapers GM-HMXP FE-1 SV-1 (FXXE_HMAN) 3.34 1.31 P40(A) RMA polymerase, rhothoridi GS-throm sapers GM-HMXP FE-1 SV-1 (FXXE_HMAN) 3.32 2.24 2.25 1.33 1.32 2.34 1.34 1.34 3.35 2.35 1.35 1.35 1.35	P07305	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3 - [H10_HUMAN]	5.15	2
92505 ATP synthase suburd spins, metochordial OS+Horn sapiers GM-ATFAL PE-15V-1 (ATPA, HUMAI) 4,0 1 92505 ATP synthase suburd spins, metochordial OS+Horn sapiers GM-SU22X15 FF2-32V-1 (252X-JUMANI) 4,64 1 92670 ATS bound inprotent S13-OS-Horn sapiers GM-SU22X15 FF2-32V-1 (252X-JUMANI) 4,64 1 92670 Attracket DF-hording protein SO-Horn sapiers GM-SU2X15 FF2-32V-1 (252X-JUMANI) 3,74 4 92671 Attracket DF-hording protein SO-Horn sapiers GM-FRAPE FE-15V-1 (PDE-JUMANI) 3,72 2 92672 Nucleice MRN associated protein SO-Horn sapiers GM-FRAPE FE-15V-1 (PDE-JUMANI) 3,72 2 926731 Ut small nucleice RMN associated protein 18-horndig OS-Horn sapiers GM-FRAPE FE-15V-1 (PDE-JUMANI) 3,44 11 927535 Protein A-Horn sapiers GM-FRAPE FE-15V-1 (FIDE-JUMANI) 3,33 22 921535 Protein A-TF OS-Horn sapiers GM-FRAPE FE-15V-2 (FIDE-JUMANI) 3,34 11 11 921537 Phothinger protein GS-Horn sapiers GM-FRAPE FE-15V-2 (FIDE-JUMANI) 3,34 12 12 921537 Phothinger protein GS-Horn sapiers GM-FRAPE FE-15V-2 (FIDE-JUMANI) 3,34 13 13 13 13	P56270	Myc-associated zinc finger protein OS=Homo sapiens GN=MAZ PE=1 SV=1 - [MAZ HUMAN]	4.82	4
165 Description 4.64 1 165 Description 1.65 4.64 1 165 Description 1.65 4.64 1 168 Description 1.65 4.64 1 177 174 175 </td <td>P25705</td> <td>ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA HUMAN]</td> <td>4.70</td> <td>4</td>	P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA HUMAN]	4.70	4
58.0.82 Solate carrier family 22 methor 15 05—bitons agenes GN=C22ALS PE=2 Vi=1 (52.0.4 ; PLMAN] 4.20 69.226 Abcelor GPP holding protein 05—bitons agenes GN=CPBP PE=1 Vi=1 - (52.0.4 ; PLMAN] 3.77 742 Add SPRS1-interacting potein 05—biton sagenes GN=CPBP PE=1 SV=1 - (50.712, PLMAN) 3.77 7257 Putable methytraniferance (SOF1140 GS=bitons agenes GN=CPBP PE=1 SV=1 - (20.712, PLMAN) 3.52 7257 Putable methytraniferance (SOF1140 GS=biton sagenes GN=CPBP PE=1 SV=1 - (20.712, PLMAN) 3.44 7297 113 small nucleals PM-bitosciente bita/summa GS=bitos PE=1 SV=1 - (20.712, PLMAN) 3.21 7297 113 small nucleals PM-bitosciente bita/summa GS=bitos PE=1 SV=1 - (20.712, PLMAN) 3.21 7291 123 small nucleals PM-bitosciente SM=CHI (PE PE SV=2 - (20.712, PLMAN) 3.21 7210 123 small nucleals PM-bitosciente SM=CHI (PE PE SV=2 - (20.721, PLMAN) 3.21 7211 123 small nucleals PM-bitosciente SM=CHI (PE PE SV=2 - (20.721, PLMAN) 3.21 7212 124 124 124 7214555 Protein DE (Smeltans agenes GM=PHE PE SV=2 - (20.721, PLMAN) 3.21 7214555 Protein DE (Smeltans agenes GM=PHE PE SV=2 - (10.721, PLMAN) 3.21 72145555	P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13 HUMAN]	4.64	1
20223 Nucksier GTP-inding protein 10.5—from sapers GM=GTP8 PF E-1 SV-3 [NG2], HUMAN] 3.77 9743 PC4 and SPRS.interacting protein GS-from sapers GM=GTP8 PF E-1 SV-3 [NG2], HUMAN] 3.72 9743 PC4 and SPRS.interacting protein GS-from sapers GM=GTP8 PF E-1 SV-3 [NG2], HUMAN] 3.72 97440 PN(A) RNA polymerase, micchordial OS-from sapers GM=GTP8 PF E-1 SV-1 [PARD_], HUMAN] 3.44 97110 Usang mode and sapers GM=MTR PF E-1 SV-1 [PARD_], HUMAN] 3.44 97103 Usang mode and sapers GM=MTR PF E-1 SV-1 [PARD_], HUMAN] 3.44 97110 Usang mode and sapers GM=MTR PF E-1 SV-2 [NRP, HUMAN] 3.21 97212 Dama containing sapers GM=MTR PF E-1 SV-2 [NRP, HUMAN] 3.21 975198 Protein AF-17 OS-from sapers GM=MTR PF E-1 SV-1 [PK F HUMAN] 3.20 975103 Dama containg sapers GM=MTR PF E-1 SV-1 [PK F HUMAN] 3.21 976104 Dama containg sapers GM=MTR PF E-1 SV-1 [PK F HUMAN] 3.20 976105 Dama containg sapers GM=MTR PF E-1 SV-1 [PK F HUMAN] 3.21 976106 Dama containg sapers GM=MTR PF E-1 SV-1 [PK F HUMAN] 3.20 97611 Dama containg sapers GM=MTR PF E-1 SV-1 [PK F HUMAN] 3.21 97612 <td>O8IZD6</td> <td>Solute carrier family 22 member 15 OS=Homo sapiens GN=SLC22A15 PE=2 SV=1 - [S22AF HUMAN]</td> <td>4.20</td> <td>1</td>	O8IZD6	Solute carrier family 22 member 15 OS=Homo sapiens GN=SLC22A15 PE=2 SV=1 - [S22AF HUMAN]	4.20	1
PC4 and SPR3-immediate potent OS-Hom Saples GH-EXP1 PE-1 (V-1 [PSP], HAMAN] 3.77 4 PC180 Puttor methytonarisance SOF114 OS-Hom Saples GN-EXP0114 (HAMAN) 3.72 2 PR2167 Lamas associated polyopitit 2, isoforms beth/gumma OS-Hom Saples GN-EXP0114 (HAMAN) 3.42 1 PV2167 U3 small nucleals RN-associated protein 18 homolog OS-Homo Saples GN-EXP121 FE-15V-1 - [KUT18, HAMAN] 3.23 2 PV3167 U3 small nucleals RN-associated protein SI-Homo Saples GN-EXP121 FE-15V-1 - [KUT18, HAMAN] 3.23 2 PV3157 Hamole SI-Homo Saples GN-HUT18 FE-15V-2 - [KUT1, HAMAN] 3.21 2 PV3158 Protein AFT / OS-Homo Saples GN-HUT18 FE-15V-2 - [KUT1, HAMAN] 3.21 2 PV3158 Protein AFT / OS-Homo Saples GN-HUT18 FE-15V-2 - [KUT1, HAMAN] 3.21 2 PV3158 Protein AFT / OS-Homo Saples GN-HUT18 FE-15V-2 - [KUT1, HAMAN] 3.01 11 PV3168 Homo Saples GN-HUT18 FE-15V-2 - [KUT1, HAMAN] 3.01 12 PV3159 Protein AFT dependent GN Makez DOV CS-Homo Saples GN-HUT18 FE-15V-2 - [CDV2, HAMAN] 2.87 11 PV3159 Protein AFT dependent GN Makez DOV CS-Homo Saples GN-HUT18 FE-15V-2 - [CDV2, HAMAN] 2.87	O9BZE4	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1 HUMAN]	3.94	4
Diable methylanardense Clorif Li OS-Horn saplers GN-Clorif Li PE-15V-3 - (CLI Li HUMA) 3.72 2 Diable methylanardense Clorif Li OS-Horn saplers GN-TDOP (PE-15V-3 - (CLI Li HUMA)) 3.44 1 Diable Methyland Clorif Diable Methyland Clorif Diable Signes GN-TDDE PE-15V-3 - (CLI PL JLMAN) 3.44 1 Diable Methyland Clorif Diable Methyland Clorif Diable Signes GN-TDTE PE 15V-3 - (CLI PL JLMAN) 3.20 2.21 Diable Methyland Clorif Diable Signes GN-TDTE PE 15V-3 - (MRX, HUMA) 3.21 2.21 Diable Methyland Clorif Diable Signes GN-TDTE PE 15V-3 - (MRX, HUMA) 3.21 2.21 Diable Methyland Clorif Diable Signes GN-TDTE PE 15V-3 - (MRX, HUMA) 3.20 4.41 Diable Methyland Diable Signes GN-TDTE PE 15V-1 - (MRX, HUMA) 3.21 2.21 Diable Methyland Diable Signes GN-TDTE PE 15V-1 - (MRX, HUMA) 3.01 1.11 Diable Methyland Diable GN-TDTE Diable Signes GN-CMP (PE 15V-1 - (MMA)) 3.01 1.11 Diable Signes GN-TDTE Diable Signes GN-CMP (PE 15V-1 - (MRX, HUMA)) 3.01 1.11 Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Signe GN-TDTE Diable Signes GN-TDTE Diable Signes GN-TDTE Diable Sign	075475	PC4 and SERS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1 HUMAN]	3.77	4
Part 157 Iamma-associated polyceptide 2, soforms beta/gamm 025-thom sapiers GM-TNPO PE-1 SV-2 / [LAPLB_HUMM] 3.52 2 QPV511 U3 small nucleolar RNA-associated protein 18 homolog 05-thom sapiers GM-TNPAP PE-1 SV-2 / [NRRINAMA] 3.24 11 QPV511 U3 small nucleolar RNA-associated protein 18 homolog 05-thom sapiers GM-TNRAPP. PE-1 SV-2 - [NRRINAMA] 3.21 22 QPV514 Heterogeneous nucleon robot appen GM-TNRAPP. PE-1 SV-2 - [NRRINAMA] 3.20 44 V1535 Appen the Internant GS-thomo sapiers GM-TNRAPP. PE-1 SV-2 - [NRRINAMA] 3.11 11 V1536 Appen the Internant GS-thomo sapiers GM-TNRAPP. PE-1 SV-2 - [NRRINAMA] 3.01 11 V1537 Appen the Internant GS-thomo sapiers GM-TNRAPP. PE-1 SV-2 - [INAMA] 3.01 11 V1576 Atach - TAbe protein GS-thomo sapiers GM-ADAR PE-1 SV-2 - [GSP_LHMAN] 3.01 11 V1576 Atach - Tabe protein GS-thomo sapiers GM-ENARD PE-1 SV-2 - [GSP_LHMAN] 2.07 12 V1576 Atach - Tabe protein GS-thomo sapiers GM-ENARD PE-1 SV-2 - [GSP_LHMAN] 2.07 12 V1577 ELAV-Hete protein ID S-thomo sapiers GM-ENARD PE-1 SV-2 - [GDXJ_LHMAN] 2.07 12 V1576 Atach ATh	O5T280	Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 - [CI114 HUMAN]	3.72	2
Q9MVM PAy(A) RNA polymerase, mitochordnil QS-Horo spaces GN-MTXP PE=15V-1 (PAPDL HUMAN) 3.44 Q9T511 U3 amail nucleair RNA-associated protein 18 homolog GS-Horo spaces GN-HITXP PE=15V-2 (INTR_HUMAN) 3.22 Q1532 Aptha-Interment Donucleoprotein 1.05-Horo spaces GN-HITXP PE=15V-2 (INTR_HUMAN) 3.21 Q1532 Aptha-Interment Donucleoprotein 1.05-Horo spaces GN-HITXP PE=15V-2 (INTR_HUMAN) 3.20 Q1533 Non-POU domin-containing octame-inding protein OS-Horo spaces GN-HITXP PE=15V-2 (INTR_HUMAN) 3.11 Q1533 Non-POU domin-containing octame-inding protein OS-Horo spaces GN-HITXP PE=15V-2 (INTR_HUMAN) 3.01 Q15434 Non-POU domin-containing octame-inding protein OS-Horo spaces GN-EATXPUT2 PE=15V-2 (INTR_HUMAN) 3.01 Q157054 Atxxh-Yile protein 2.05-Horo spaces GN-EATXPUT2 PE=45V-1 (IQSTC4-HUMAN) 2.67 Q15717 EAV-Med protein 1.05-Horo spaces GN-EATXPUT2 PE=45V-1 (IQSTC4-HUMAN) 2.67 Q15717 EAV-Med DS-Horo spaces GN-EATXPUT2 PE=45V-1 (IQSTC4-HUMAN) 2.67 Q1717 EAV-Med DS-Horo spaces GN-EATXPUT2 PE=45V-1 (IQSTC4-HUMAN) 2.67 Q1717 EAV-Med DS-Horo spaces GN-EATXPUT2 PE=45V-1 (IQSTC4-HUMAN) 2.67 Q1717 EAV-Med DS-Horo spaces GN-EATXPUT2 PE=45V-1 (ICST-HUMAN) 2.67 <td>P42167</td> <td>lamina-associated polypeptide 2, isoforms beta/gamma QS=Homo sapiens GN=TMPO PE=1 SV=2 - [IAP2B_HUMAN]</td> <td>3.52</td> <td>2</td>	P42167	lamina-associated polypeptide 2, isoforms beta/gamma QS=Homo sapiens GN=TMPO PE=1 SV=2 - [IAP2B_HUMAN]	3.52	2
13 amil nucleater RNA-associated protein 18 homelog GS-Home agiess GN-LITP18 PE-1 SV-3 - [UTP18_HUMAN] 3.24 19466 Hetergeness nuclear intonucleoprotein LOS-Home agies GN-LITP18 PE-1 SV-2 - [INVR_HUMAN] 3.22 2016352 Alpha-Internexin OS-Home agiess GN-LINA FE-1 SV-2 - [AIDX_HUMAN] 3.20 44 155198 Protein AF-17 OS-Home agiess GN-BITM1 PE-1 SV-2 - [INVR_HUMAN] 3.18 33 12533 Non-Home agiess GN-BITM1 PE-1 SV-1 - [INVL_HUMAN] 3.11 11 12534 Non-Home agiess GN-BITM1 PE-1 SV-1 - [INVL_HUMAN] 3.01 11 125716 Taxim FR FE ST SV-1 - [INVL_FIRE - [INVL_HMAN] 3.01 11 125717 EAV-Kike protein 10 S-Home agiess GN-EGAPIN FE-1 SV-3 - [G3P_HUMAN] 2.67 11 125717 EAV-Kike protein 10 S-Home agiess GN-EGAPIN FE-1 SV-3 - [G3P_HUMAN] 2.42 22 125717 EAV-Kike protein 10 S-Home agiess GN-EGAPIN FE-1 SV-3 - [CD37_HUMAN] 2.44 24 125717 EAV-Kike protein 10 S-Home agiess GN-EGAPIN FE-1 SV-3 - [CD37_HUMAN] 2.42 22 125717 EAV-Kike protein 10 S-Home agiess GN-EGAPIN FE-1 SV-3 - [CD37_HUMAN] 2.44 22 125717 EAV-Kike protein 10 S-Home agies	09NW4	Poly(A) RNA polymerase, mitochondrial QS=Homo sapiens GN=MTPAP PE=1 SV=1 - [PAPD1 HUMAN]	3.44	1
Pareson Heterogeneous nuclear ribonuclesportabil L05-Horn sapiers GN-HNRPL PE1 SV-2 - [HNRPL_HUMAN] 3.21 Q16352 Alpha-Internetin OS-Horn sapiers GN-INA FE-1 SV-2 - (AIDX, HUMAN] 3.21 2 Q16353 Angha-Internetin OS-Horn sapiers GN-INA FE-1 SV-2 - (AIDX, HUMAN] 3.20 4 Q16352 Non-FOU domini-containing octame-inding protein OS-Horn sapiers GN-INATOR FE-1 SV-1 - (INATU, HUMAN) 3.11 1 Q16352 Mon-FOU domini-containing octame-inding protein OS-Horn sapiers GN-INATOR FE-1 SV-1 - (INATU, HUMAN) 3.01 1 Q17054 Ataxin - Yake protein 2 OS-Horn sapiers GN-INATOR 2 FE-1 SV-1 - (IGST C4_LHUMAN) 2.67 1 Q17057 Ataxin - Yake protein 2 OS-Horn sapiers GN-INATOR 2 FE-4 SV-1 - (QST C4_LHUMAN) 2.76 1 Q17057 Ataxin - Yake protein 2 OS-Horn sapiers GN-INATOR 2 FE-1 SV-1 - (DST C4_LHUMAN) 2.76 1 Q17057 Ataxin - Yake protein 2 OS-Horn sapiers GN-INTOR 2 FE-1 SV-1 - (DST C4_LHUMAN) 2.40 1 Q17057 Ataxin - Yake protein 2 OS-Horn sapiers GN-INTOR 2 FE-1 SV-1 - (DST C4_LHUMAN) 2.40 1 Q17058 Protein DSO-S-Horn sapiers GN-INTOR 2 FE-1 SV-1 - (DST L4 MUMA) 2.40 1 Q17058 Protein DSO-S-Hor	09Y511	13 small nucleolar RNA-associated protein 18 homolog OS=Homo saniens GN=107P18 PE=1 SV=3 - [107P18 HUMAN]	3.24	1
20,1352 Abba-Internets OS-Hom sapies GN-IBA FE-1 SV-2 - [ABX, HUMAN] 3.21 22 Protein AF-17 OS-Hom sapies GN-IBA FE-1 SV-2 - [ABX, HUMAN] 3.20 44 PS138 Protein AF-17 OS-Hom sapies GA-IBALTG FEE SV-2 - [AFL7, HUMAN] 3.18 3 US133 Non-POU domini-containing cotame inding protein GS-Hom sapies GN-IATANI PE-1 SV-1 - [IPANI, HUMAN] 3.11 11 D1990 DEVENDMENT PHO TIPATE SN-1 - [IPANI, HUMAN] 3.01 11 D1990 Gycarabidityde Jnospheta deflydrogenase GS-Hom sapies GN-GAPBH FE-1 SV-3 - [GSP_LHUMAN] 2.67 11 D1991 ELAV-Hile protein I OS-Hom sapies GN-EADANI 2FE-4 SV-1 - [CICAU, HUMAN] 2.67 11 D1991 ELAV-Hile protein I OS-Hom sapies GN-EADANI 2FE-4 SV-1 - [CICAU, HUMAN] 2.42 22 PS559 Protein EAT-Generate CNN holicace DDS2 CS-Hom sapies GN-EADANI 2FE-4 SV-3 - [CD2X], HUMAN] 2.43 2.44 Q972M Probable ATH-dependent RNA holicace DDS2 CS-Hom sapies GN-EADDISP E-1 SV-3 - [CD2X], HUMAN] 2.43 2.24 Q972M Probable ATH-dependent RNA holicace DDS4 FEE SV-3 - [REFLHUMAN] 2.44 2.44 2.44 2.44 2.44 2.44 2.44 2.44	P14866	Heterogeneous nuclear ribonucleoprotein LOS=Homo saniens GD=HIRNPI PE=1 SV=2 - [HIRPI HUMAN]	3.23	2
Protein AF-17 OS-Homo sapiens GN=MLITS PE=1 SV=2 - [AF17_HUMAN] 3.20 4 21233 Non-POU domain-containing octame-inding protein OS-Homo sapiens GN=NON DE-1 SV=4 - [NONO_HUMAN] 3.18 3 21233 Non-POU domain-containing octame-inding protein OS-Homo sapiens GN=PON DE-1 SV=1 - [TH/NL_HUMAN] 3.11 1 21303 PHO finger protein COS-Homo sapiens GN=PHF6 PE-1 SV=1 - [TH/NL_HUMAN] 3.01 1 21404 PHO finger protein 2 OS-Homo sapiens GN=ADMP IP E-1 SV=1 - [TH/NL_HUMAN] 2.99 2 21571 ELAVHE protein 2 OS-Homo sapiens GN=ADMP IP E-1 SV=1 - [CDX47_HUMAN] 2.87 1 21571 ELAVHE protein 2 OS-Homo sapiens GN=ADMP IP E-1 SV=1 - [CDX47_HUMAN] 2.40 1 294054 Probable ATP-dependent RNA helicase DX2 OS-Homo sapiens GN=DXXF PE=1 SV=1 - [DXX2_HUMAN] 2.40 1 29724 Probable ATP-dependent RNA helicase DX2 OS-Homo sapiens GN=DXXF PE=1 SV=2 - [DXX2_HUMAN] 2.40 1 21766 BTM/DOZ domain-containing protein 3 OS-Homo sapiens GN=DXXF PE=1 SV=2 - [DXX2_HUMAN] 2.40 1 21761 BTM becontaining protein 3 OS-BON SAPER SCHOMO SAPERIS DE-1 SV=2 - [LDX3_HUMAN] 2.40 1 21762 Brotymathase domain-containing protein 3	016352	Alpha-internexin OS=Homo saniens GN=TNA PF=1 SV=2 - [ATNX HIJMAN]	3.21	2
1 1	P55198	Protein AF-17 OS-Homo samine GN-MITG PF-1 SV-2 - [AFT7 HIMAN]	3.20	4
22225 Inter-Odd Structure and the Analy process prime (AIR - IPA IN PERT Style (THNU , HUMAN) 3.11 1 280106 Timmocyte nuclear protein 6 OS-Horo sagiens (AIR - IPA IN PERT Style (THNU , HUMAN) 3.01 1 280105 Timmocyte nuclear protein 6 OS-Horo sagiens (AIR - IPA IN 2, FUMAN) 2.99 2 257562 Ataxin - Yake protein 2 OS-Horo sagiens (AIR - ATAX) 2 EE-4 Svil - (10757C4 , HUMAN) 2.87 1 201717 ELAVIKe protein 2 OS-Horo sagiens (AIR - ATAX) 2 EE-4 Svil - (10757C4 , HUMAN) 2.86 1 201717 ELAVIKe protein 2 OS-Horo sagiens (AIR - DEK / PE 1 Svil - (100X47 / HUMAN) 2.40 1 201717 ELAVIKe protein 2 OS-Horo sagiens (AIR - DEK / PE 1 Svil - (100X47 / HUMAN) 2.40 1 201708 TBR / DS - Moro sagiens (AIR - DEK / PE 1 Svil - (100X47 / HUMAN) 2.43 2 201708 TBR / DS - Moro sagiens (AIR - DEK / PE 1 Svil - (100X1 / HUMAN) 2.88 1 121207 Nucleoprotein TR OS - Horo sagiens (AIR - DD SVIL SV - 2 (DIX1 / HUMAN) 2.07 66 201746 DS - Horo sagiens (AIR - DD SVIL SV - 2 (DIX1 / HUMAN) 1.92 1 121207 Nucleoprotein TR N S - Horo sagiens (AIR - DD SV - 5 (DOX1 / HUMAN)	015233	Non-POLI domain-root bings of the the total of total of the total of total	3.19	3
Protocyte 111 111 111 111 111 PR4406 Glyceradehyde-3-phosphate dehydrogenase OS=Horos sapers GN=CAPDN FE=1 SV=3 [G3P_HUMAN] 2.99 2 SCFC4 AtaX** Proto Sapers GN=CM=TWS Zepress GN=CAPDN FE=1 SV=3 [G3P_HUMAN] 2.87 11 D15717 ELAV-like protein 1 OS=Horos sapers GN=CAPTOR Zepress GN=CAPDN FE=1 SV=1 - [D3XC2 - HUMAN] 2.76 11 D15717 ELAV-like protein 1 OS=Horos sapers GN=CAPTOR Zepress GN=D3XC2 FE=1 SV=3 - [D3X52_HUMAN] 2.40 11 D15716 AtaX** Protein DEK OS=Horos sapers GN=D3X2 GS=Horos sapers GN=D3X2 PE=1 SV=3 - [D3X52_HUMAN] 2.84 2 D17806 Protein DEK OS=Horos sapers GN=D3X1 PE=1 SV=3 - [D3X52_HUMAN] 2.84 2 2 D17806 BTB/P02 domain-containing protein 3 GS=Horos sapers GN=CMCTD19 FE=3 SV=3 - [DX32_HUMAN] 2.84 2 2 D17806 D153-Hee sonuclease 1 OS=Horos sapers GN=D321 PE=1 SV=2 - [DX1_HUMAN] 2.97 1 D17810 E18 D153-Hee sonuclease 1 OS=Horos sapers GN=D321 PE=1 SV=2 - [DX1_HUMAN] 2.97 1 D17810 D153-Hee sonuclease 1 OS=Horos sapers GN=D121 PE=1 SV=2 - [DX1_HUMAN] 1.92 1 <	Q13233	Norroot de nuclear parties 1.05 - Home casines Children US-1 of THVN1 ID-1 SUPER INFORMATION OF 1-1 SUPER INFORMATION OF	3.10	1
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Q210C4 PLASH Prime protein 10S=Hord Supers GN=ERAULI PE-15V=2 - [EUX]_HUMAN] 2.67 1 Q210C4 Probable ATP-dependent RNA helicase D0X47 OS=Horn sapiers GN=D0X47 PE-15V=1 - [D0X47_HUMAN] 2.42 2 Q210C4 Probable ATP-dependent RNA helicase D0X47 OS=Horn sapiers GN=D0X52 PE-15V=3 - [D0X52_HUMAN] 2.34 22 Q40004 Probable ATP-dependent RNA helicase D0X52 OS=Horn sapiers GN=RPUS32 PE-15V=3 - [D0X52_HUMAN] 2.28 1 Q40047 RNA pseudourlylate synthase domain-containing protein 30G=Horn sapiers GN=RPUS32 PE-15V=3 - [RCD19_HUMAN] 2.27 1 Q40047 RNA pseudourlylate synthase domain-containing protein 30G=Horn sapiers GN=RPUS32 PE-15V=3 - [RCD19_HUMAN] 2.07 66 Q40146 DS=Horn sapiers GN=ED0X21 PE-15V=3 - [TRP_1HUMAN] 2.07 66 Q40147 DSHe domain-containing protein XCD5=Horn sapiers GN=D0X21 PE-15V=2 - [RCD1_HUMAN] 1.99 1 Q40147 DSHe domain go notein 10S=Horn sapiers GN=D0X21 PE-15V=2 - [RED1_HUMAN] 1.92 1 Q40149 Nucleolar RNA helicase 2 OS=Horn sapiers GN=MER1PE-15V=2 - [RED1_HUMAN] 1.88 1 Q40149 DSHe domain go notein 1 OS=Horn sapiers GN=MER1PE-15V=2 - [RED1_HUMAN] 1.81 2 Q51	OFTEC4		2.99	2
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Product AT Producting Intervention 2.42 QPRIDSH Product AT Producting Intervention 2.40 936569 Protecting DKC OS-Horns sepres GN=DDXS2 PE=1 SV=3 - [DXS2_HUMAN] 2.40 1 QPR2R4 Probable ATP-dependent RNA helicase DDXS2 OS-Horns sepres GN=DDXS2 PE=1 SV=3 - [DXS2_HUMAN] 2.28 1 QPR2R4 Probable ATP-dependent RNA helicase DDXS2 OS-Horns sepres GN=PDDXS2 PE=1 SV=3 - [RUS03_HUMAN] 2.27 1 Q17RG1 BTR/POZ domah-containing protein KCTD19 OS=Horns sepres GN=PDDX3 DE=1 SV-3 - [RUS03_HUMAN] 2.27 1 Q17RG1 BTR/POZ domah-containing protein KCTD19 DE=1 SV=3 - [RUS11_HUMAN] 2.07 66 Q17RG1 BTR/POZ domah-containing protein COS-Horns sepres GN=DSD21_HUMAN] 1.92 1 Q20NS3 Nucleolar RNA helicase 2 OS-Horns sepres GN=DSD3 DE1 SV=1 - [RUB1_HUMAN] 1.84 2 Q20S182 Paired amphipatric helix protein MRE11A OS=Horns sepres GN=DSV=2 [RUB1_HUMAN] 1.84 2 Q39NS9 Double-strand break repair protein MRE11A OS=Horns sepres GN=DSV=2 [RUB1_HUMAN] 1.81 2 Q8WNVB Accytricity/itransfrase GN=DSHOR Sepres [SV=2 - [SV=1 - [CRC8_HUMAN] 1.81 2 Q8WNVB Ac	Q15/1/	ELAV-IKE PROLEIT I OS=ROUTO SAPETS GN=ELAVLI PE=T SI=2 - [ELAVI_HUMAN]	2.76	1
Protein DEX.OSSPRINT SUPERING SQUECK PET SQUES OS-Floron sapiers (N=DDXS2 PET SV=3 - [DDXS2_HUMAN] 2.44 2 Q6P087 Probabe ATP-depenter RNA helicas DDXS2 OS-Floron sapiers (N=RDXD3 PET SV=3 - [RUSD3_HUMAN] 2.28 1 Q17RG1 BTB/PO2 domain-containing protein 3 OS-Horon sapiers (N=RDXD19 PET SV=1 - [RCD19_HUMAN] 2.27 1 Q17RG1 BTB/PO2 domain-containing protein RCTD19 OS-Horon sapiers (N=RDXD19 PET SV=1 - [RCD19_HUMAN] 2.07 6 Q18TF6 DISS-Hike exonuclose 1 OS-Horon sapiers (N=DDS12 PET SV=2 - [D12L_HUMAN] 1.99 1 Q18T80 Nucleoprotein TRR OS-Horon sapiers (N=DDS12 PET SV=2 - [D12L_HUMAN] 1.88 1 Q18T80 Duble-strand break repair protein NRE11A OS-Horon sapiers (N=DDX1 FET SV=5 - [D12L_HUMAN] 1.88 1 Q18T950 Double-strand break repair protein NRE11A OS-Horon sapiers (N=DCR8 PE 1 SV=2 - [NELA_HUMAN] 1.61 1 Q18T940 N-scyheuraminate cytidylythransferase OS-Horon sapiers GN=MPEP5 - [FA_HUMAN] 1.61 1 Q8W705 Microprocessor complex subunit DOCR8 OS-Horon sapiers GN=MPEP5 - [FA_HUMAN] 1.55 2 Q48W705 Microprocessing protein 1 horolog BOS-Horon sapiers GN=MPEP5 - [FA_HUMAN] 1.55 2 Q49U705	Q90054	Probable AIP-dependent kina heikase bDX47 OS=horto Sapieris GI=DDX47 PE=1 SV=1 - [UDX47_numAn]	2.42	2
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QARDB/ NMA pseudourdyate synthase doman-contaning protein 3 US=Horno sapiens (M=KPUSU) H=1 SVS=1 (KCD19 J+UMAN) 2.27 11 P12270 Nucleoprotein TPR OS=Horno sapiens GN=DTRR_HUMAN) 2.07 66 Q8TF46 DIS3-like exonuclease 1 OS=Horno sapiens GN=DDX21 FE=1 SV=2 (DIS1_LHUMAN) 1.99 11 P01873 Nucleoprotein TPR OS=Horno sapiens GN=DDX21 FE=1 SV=2 (DIS1_LHUMAN) 1.92 11 P01873 Nucleoprotein TPR OS=Horno sapiens GN=DDX21 FE=1 SV=2 (DIS1_HUMAN) 1.88 11 P01879 Polypyrindline tract-binding protein 1 OS=Horno sapiens GN=PDB21 FE=1 SV=1 (PTB2_HUMAN) 1.88 11 P01895 Polybyrindline tract-binding protein 1 OS=Horno sapiens GN=DE11 PE=1 SV=3 (RE11_HUMAN) 1.81 22 Q8NPVG Moreprocessor computes valumit DSCHB SO S=Horno sapiens GN=RCMS PE=1 SV=2 (SIN3B PE=1 SV=2 - [COCR8_HUMAN] 1.55 11 Q14684 Rbosomal RNA processing bes GN=MEIT10 PE=1 SV=2 - [CICCR_PLIMAN] 1.55 11 Q14595 Polyber valumit DSCHB SO S=Horno sapiens GN=CMEXCR8 PE=1 SV=2 - [CNCR8_HUMAN] 1.15 11 Q14504 Rbosomal RNA processing computein 1 hornolg B OS=Horno sapiens GN=SNCR1P PE=1 SV=2 - [HNR0P_HUMAN] 1.15 11 Q14504	Q9Y2R4	Probable AIP-dependent KIVA neicase DUX52 US=Homo sapiens GN=DUX52 PE=1 SV=3 - [DUX52_HUMAN]	2.34	2
QLINGL BIR/ND2 domain-domain-domain-domain-domain-spiens GN=RC IDJ PE-2 SVE1 - [KLD19_HUMAN] 2.27 QRITE4 DIS3-like exonuclease 1 OS=Homo sapiens GN=DIS3L PE=1 SV=2 - [DI3L_HUMAN] 1.99 QRITE4 DIS3-like exonuclease 1 OS=Homo sapiens GN=DIS3L PE=1 SV=2 - [DIXL_HUMAN] 1.92 QRITE4 DIS3-like exonuclease 1 OS=Homo sapiens GN=DIS3L PE=1 SV=2 - [DIXL_HUMAN] 1.88 QRITE4 Dis3-like exonuclease 1 OS=Homo sapiens GN=DIS3L PE=1 SV=2 - [PITB1_HUMAN] 1.84 Q25599 Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=2 - [NEIA_HUMAN] 1.61 QRIV08 N-acylneuramiate cytidylytransferase OS=Homo sapiens GN=DCRS PE=1 SV=2 - [NEIA_HUMAN] 1.55 QRIV09 Microprocessor complex subunit DCCR8 OS=Homo sapiens GN=MCREPS PES - [SA_HUMAN] 1.55 QRIV04 Microprocessor complex subunit DCCR8 OS=Homo sapiens GN=MCREPS PES - [SA_HUMAN] 1.31 QRIV09 Microprocessor protein I nomolog BOS=Homo sapiens GN=MCREPS PE=1 SV=2 - [HURAN] 1.45 QRIV04 Microprocessor complex subunit DCCR8 OS=Homo sapiens GN=MCREPS PE=1 SV=2 - [NEPA_HUMAN] 1.55 QRIV09 Microprocessor protein I nomolog BOS=Homo sapiens GN=MCREPS PE=1 SV=2 - [NEPA_HUMAN] 1.31 QRIV04 Microprocessor CTCF OS=Homo sapiens GN=C	Q6P087	RNA pseudoundylate synthase domain-containing protein 3 05=Homo sapiens GAT=RPUSD3 PE=1 SV=3 - [RUSD3_HUMAN]	2.28	1
P12270 Nucleoprotein THR US=Homo sapiens GN=11R PET=1 SV=2 - [INR_HUMAN] 1.99 1 Q9RTF6 DIS3 Mee concludes 1 OS=Homo sapiens GN=128 PET=1 SV=2 - [DI3L] HUMAN] 1.92 1 Q9RR30 Nucleolar RNA helicase 2 OS=Homo sapiens GN=128 PET=1 SV=2 - [DI3L] HUMAN] 1.92 1 P0599 Polyprimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PET=1 SV=3 - [NRE11_HUMAN] 1.84 2 Q0T5182 Paired amphipathic heak protein Sin3b OS=Homo sapiens GN=SCHS PET=3 V=2 - [SIN3B_HUMAN] 1.61 1 Q0WVOS Microprocessor Complex suburt DCGR8 OS=Homo sapiens GN=CMAS PE =1 SV=2 - [DGCR8_HUMAN] 1.55 2 Q1F562 Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NEPPS - [PSA_HUMAN] 1.55 1 Q1684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=SYRCRIP PET=1 SV=2 - [HUNAN] 1.31 2 Q60506 Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYRCRIP PE=1 SV=2 - [HUNAN] 1.24 1 Q12786 Serum aburin OS=Homo sapiens GN=CPCP PE=1 SV=2 - [NRAP_HUMAN] 1.24 1 Q12879 Gutarnate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=CRIN2A PE=1 SV=2 - [NRAP_HUMAN] 1.09 1 Q12879	Q1/RGI	BIB/PO2 domain-containing protein KLIDIJ OS=Homo sapiens GN=KLIDIJ PE=2 SV=1 - [KCD19_HUMAN]	2.2/	1
QBT+6 DIS3-like exonuclease 1 OS-Homo sapiens GN-DIS1P, PE-1 SV-2 - [DIS1L_HUMAN] 1.99 1 QPNR30 Nucleolar RNA helicase 2 OS-Homo sapiens GN-DIS21P, PE-1 SV-5 - [DIS2L_HUMAN] 1.88 1 P0599 Polypyrimidine tract-binding protein 1 OS-Homo sapiens GN-PTBP1 PE-1 SV-1 - [PTBP_1HUMAN] 1.88 1 P0599 Double-strand break repair protein MRE11A OS-Homo sapiens GN-MRE11A PE-1 SV-2 - [SIN3B_HUMAN] 1.81 2 Q8NFW8 N-acylneuraminate cytidylyltransferase OS-Homo sapiens GN-SINSB PE-1 SV-2 - [SIN3B_HUMAN] 1.61 1 Q8WFW8 N-acylneuraminate cytidylyltransferase OS-Homo sapiens GN-PEPEPS - [PSA_HUMAN] 1.55 2 Q8WFW8 N-acylneuraminate cytidylyltransferase OS-Homo sapiens GN-PEPEPS - [PSA_HUMAN] 1.55 1 Q14684 Ribosomal RNA processing protein 1 homolog BOS-Homo sapiens GN-PEPEPS - [PSA_HUMAN] 1.31 2 Q41694 Ribosomal RNA processing protein 1 homolog BOS-Homo sapiens GN-SYNCRIP PE-1 SV-2 - [HNRPQ_HUMAN] 1.45 1 Q51764 Ptoretin AF-10 OS-Homo sapiens GN-MENDE PE-1 SV-2 - [NRAP_HUMAN] 1.24 1 Q51764 Ptoretin AF-10 OS-Homo sapiens GN-RCRIP PE-2 SV-2 - [INRAP_HUMAN] 1.09 1 Q5176	P122/0	Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN]	2.07	6
VPN/E30 NUCleoiar KNA helicase 2 US=homo sapiens GN=DUX21_PUPAN] 1.92 1 P25599 Polyprimidie tract-binding protein I OS=homo sapiens GN=PIBP FE=1 SV=2 - [PTBP1_HUMAN] 1.88 1 P49959 Double-strand break repair protein MRE11A OS=homo sapiens GN=PIBP FE=1 SV=2 - [STB3_HUMAN] 1.81 2 OVENDE Paired amphipathic helix protein Sn²b OS=homo sapiens GN=CMAS PE=1 SV=2 - [NEUA_HUMAN] 1.61 11 Q8WVQS Microprocessor complex subunit DGCR8 OS=Homo sapiens GN=MCRS PE=1 SV=2 - [NEUA_HUMAN] 1.55 2 Q8WVQS Microprocessor complex subunit DGCR8 OS=Homo sapiens GN=RRP1BPE=1 SV=3 - [DCCR8_HUMAN] 1.55 1 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 - [RPIB_HUMAN] 1.45 1 Q55197 Protein AF-10 OS=Homo sapiens GN=HLIT10 PE=1 SV=2 - [AF10_HUMAN] 1.24 1 Q60506 Heterogeneous nuclear ribonuckoprotein Q OS=Homo sapiens GN=SNCRIP PE=1 SV=1 - [INRPQ_HUMAN] 1.24 1 Q12677 Nebulin-related-anchoring protein OS=Homo sapiens GN=RRP PE=2 SV=2 - [NRAP_HUMAN] 1.04 1 Q12679 Glutamate receptor inoncipic, MNDA 2A OS=Homo sapiens GN=MCR1 PE=1 SV=2 - [DIX18_HUMAN] 0.67 1	Q81F46	DIS3-like exonuclease 1 OS=Homo sapiens GN=DIS3L PE=1 SV=2 - [DI30HUMAN]	1.99	1
P20599 Polypyrmäline tract-binding protein 1 OS=Homo sapiens GN=PI BP1 Fe 1 SV=3 [PI BP1, HUMAN] 1.88 1 P09595 Double-strand break repair protein NRE11A OS=Homo sapiens GN=SIN3B PE=1 SV=2 [SIN3B_HUMAN] 1.81 22 Q8NFW8 Nacyheuraminate cytidylytransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 [NEAL_HUMAN] 1.61 1.61 Q8WTQS Microprocessor complex subunit OGCR8 OS=Homo sapiens GN=CMAS PE=1 SV=2 [NEAL_HUMAN] 1.55 2 SPST86-2 Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=RPEPS [PSA_HUMAN] 1.55 1 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RPIB PE=1 SV=3 - [RKP1B_HUMAN] 1.45 1 Ob1506 Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SMPEPS - [PSA_HUMAN] 1.28 2 P49711 Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=2 - [HNRPQ_HUMAN] 1.24 1 P02768 Serum alburin OS=Homo sapiens GN=GNRAP PE=2 SV=2 - [NRAP_HUMAN] 1.10 1 Q80VF7 Nebulin-related-anchoring protein OS=Homo sapiens GN=GRIN2A PE=1 SV=1 - [MMAN] 1.04 1 Q12876 Gluamate receptor inortorpic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=1 - [NMAN] 0.67 1	Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DUX21 PE=1 SV=5 - [DUX21_HUMAN]	1.92	1
P49959 Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1SV=3 - [NRE11_HUMAN] 1.84 2 Paired amphipathic helix protein SIB3 OS=Homo sapiens GN=SIN3B PE=1 SV=2 - [INEUA_HUMAN] 1.61 1 QRNFWB N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 - [INEUA_HUMAN] 1.61 1 QRNFWB N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 - [INEUA_HUMAN] 1.65 1 QRNFWB N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=NEPEPS - [PSA_HUMAN] 1.55 2 955786-2 Isoform 2 of Puronycin-sensitive aminopeptidase OS=Homo sapiens GN=NEPEPS - [PSA_HUMAN] 1.45 1 914684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [RIRPQ_HUMAN] 1.45 1 906050 Heterogeneous nuclear ribonuckoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [INRPQ_HUMAN] 1.28 2 9171 Transcriptional repressor CTCP CS =Isomo sapiens GN=RIN2A PE = I SV=2 - [CTCF_HUMAN] 1.15 1 928077 Nebulin-related-anchoring protein OS=Homo sapiens GN=RIN2A PE = I SV=2 - [NRAP_HUMAN] 1.09 1 921879 Glutamate receptor ionotropic, MNDA 2A OS=Homo sapiens GN=ERIN2A PE=1 SV=2 - [NCHA]_HUMAN] 1.04	P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=P1BP1 PE=1 SV=1 - [P1BP1_HUMAN]	1.88	1
D75182 Paired amphipathic helix protein Sn3b OS=Homo sapiens GN=SIN3B PE=1 SV=2 - [INEUA_HUMAN] 1.81 2 Q8NFW8 N-acylneuraninate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 - [INEUA_HUMAN] 1.61 1 Q8NFW8 N-acylneuraninate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=1 - [IDGCR8_HUMAN] 1.55 2 P55786-2 Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=RP1B PE=1 SV=3 - [RP1B_HUMAN] 1.55 1 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RP1B PE=1 SV=3 - [RP1B_HUMAN] 1.15 1 Q14684 Ribosomal INA processing protein 1 homolog B OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN] 1.28 2 Q60506 Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN] 1.24 1 P02768 Serum albumin OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN] 1.15 1 Q142879 Glutamate receptor ionotropic, NMAD 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=2 - [NRAP_HUMAN] 1.09 1 Q12879 Glutamate receptor ionotropic, NMAD 2A OS=Homo sapiens GN=GN2A PE=1 SV=1 - [NCM3_HUMAN] 0.67 1 Q12879 Glutamate receptor ionotropic, NMAD 2A OS=Homo sapiens GN=GMCM3 PE=1 SV=2 - [DXLB_HUMAN]	P49959	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3 - [MRE11_HUMAN]	1.84	2
Q8NFW8 N=acylneuraminate cyticly/ltransferase 0S=Homo sapiens GN=CMAS PE=1 SV=2 - [NL0A,HUMAN] 1.61 1 Q8WYQ5 Microprocessor complex subunit D6CR8 0S=Homo sapiens GN=D6CR8 PE=1 SV=1 - [DGCR8,HUMAN] 1.55 2 S5786-2 Esoform 2 of Puromycin-sensitive aninopeptidase OS=Homo sapiens GN=NPEPPS - [PSA_HUMAN] 1.45 1 Q14684 Rbosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=NPEPPS - [PSA_HUMAN] 1.45 1 OS0506 Heterogeneous nuclear nbonuckoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN] 1.24 1 OS0506 Heterogeneous nuclear nbonuckoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN] 1.24 1 P02768 Serum alburnin OS=Homo sapiens GN=CTCF PE=1 SV=2 - [ALBU_HUMAN] 1.05 1 Q80VF7 Nebulin-related-anchoring protein OS=Homo sapiens GN=RAP PE=2 SV=2 - [NRAP_HUMAN] 1.09 1 Q80VF7 Nebulin-related-anchoring protein OS=Homo sapiens GN=CDNL9 PE=1 SV=2 - [DX18_HUMAN] 1.04 1 Q12879 Gutamate receptor ionotropic, MMDA 2A OS=Homo sapiens GN=EDX18_0 ST=1 SV=3 - [DX18_HUMAN] 0.67 1 Q14980 DAA replication licensing factor MCM3 OS=Homo sapiens GN=EDX18_0 ST=1 SV=3 - [DX18_HUMAN] 0.67 1 <td>075182</td> <td>Paired amphipathic helix protein Sin3b OS=Homo sapiens GN=SIN3B PE=1 SV=2 - [SIN3B_HUMAN]</td> <td>1.81</td> <td>2</td>	075182	Paired amphipathic helix protein Sin3b OS=Homo sapiens GN=SIN3B PE=1 SV=2 - [SIN3B_HUMAN]	1.81	2
QBWYQ5 Microprocessor complex subunit DGCR8 05=Homo sapiens (N=DGCR8 PE=1 SV=1 - [CGCR8_HUMAN] 1.55 2 Q14684 Ribosoral RNA processing protein 1 homolog BOS=Homo sapiens (N=MPEPFS - [PSA_HUMAN] 1.45 1 Q14684 Ribosoral RNA processing protein 1 homolog BOS=Homo sapiens (N=MPEPFS - [PSA_HUMAN] 1.45 1 Q14684 Ribosoral RNA processing protein 1 homolog BOS=Homo sapiens (N=RP1B PE=1 SV=2 - [RNPQ_HUMAN] 1.31 2 Q60506 Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [RNRQ_HUMAN] 1.24 1 P02768 Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] 1.15 1 Q12879 Qlutamate receptor ionotropic, IMOX 2A OS=Homo sapiens GN=RR1P2 PE=1 SV=2 - [DX18_HUMAN] 1.09 1 Q12879 Qlutamate receptor ionotropic, IMOX 2A OS=Homo sapiens GN=ERIV2 PE=1 SV=2 - [DX18_HUMAN] 1.04 1 Q12879 Qlutamate receptor ionotropic, IMOX 2A OS=Homo sapiens GN=ADX18 PE=1 SV=2 - [DX18_HUMAN] 0.87 1 Q14879 Liburater teceptor ionotropic, IMOX 2A OS=Homo sapiens GN=ERDX18 PE=1 SV=3 - (MCM3_HUMAN] 0.87 1 Q14879 Liburater teceptor ionotropic, IMOX 2A OS=Homo sapiens GN=EGRIPA PE=1 SV=3 - (DX18_HUMAN] 0.87 <t< td=""><td>Q8NFW8</td><td>N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 - [NEUA_HUMAN]</td><td>1.61</td><td>1</td></t<>	Q8NFW8	N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 - [NEUA_HUMAN]	1.61	1
P55786-2 Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=MPEPPS - [PSA,LHUMAN] 1.55 1 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 · [RRP1B_HUMAN] 1.45 1 Protein AF-10 OS=Homo sapiens GN=MLIT10 PE=1 SV=2 · [AF10_HUMAN] 1.31 22 D60506 Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=CTCF PE=1 SV=2 · [HNRPQ_HUMAN] 1.28 22 P49711 Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=2 · [RRP_HUMAN] 1.24 11 P02768 Serumalbumin OS=Homo sapiens GN=ALB PE=1 SV=2 · [ALBU_HUMAN] 1.10 11 Q280F7 Nebulin-related-anchoring protein OS=Homo sapiens GN=GNEARA PE=2 SV=2 · [NRAP_HUMAN] 1.09 11 Q14879 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIAZA PE=1 SV=1 · [MDBE1_HUMAN] 1.04 11 Q280F7 Nebulin-related-anchoring protein OS=Homo sapiens GN=MCM3 PE=1 SV=2 · [DXIB_HUMAN] 0.87 11 Q14838 Elongation factor 2.05=Homo sapiens GN=DXIB PE=1 SV=2 · [DXIB_HUMAN] 0.87 11 Q280F7 Nuclear mitox pecific adenosine dearmisee OS=Homo sapiens GN=LOXIB PE=1 SV=2 · [DXB_A_HUMAN] 0.82 11 P35205 DNu replaction factor 2.05=Homo sapiens GN=MCM3 PE=1 SV=2 · [DKMA_HUMAN]	Q8WYQ5	Microprocessor complex subunit DGCR8 OS=Homo sapiens GN=DGCR8 PE=1 SV=1 - [DGCR8_HUMAN]	1.55	2
Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens (N=RRP1B PE=1 SV=3 - [RRP1B_HUMAN] 1.45 1 P55197 Protein AF-10 OS=Homo sapiens (N=MLIT10 PE=1 SV=2 - [AF10_HUMAN] 1.28 22 O65056 Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SVNCRIP PE=1 SV=2 - [HNRPQ_HUMAN] 1.24 11 P02768 Serum alburnin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] 1.15 11 P02768 Serum alburnin OS=Homo sapiens GN=RDE PE=2 SV=2 - [NRAP_HUMAN] 1.10 11 Q80K97 Nebulin-related-anchoring protein OS=Homo sapiens GN=RDE PE=2 SV=2 - [NRAP_HUMAN] 1.09 11 Q12879 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=2 - [NCAP_HUMAN] 1.04 11 Q280VF1 NE-polacient RNA helicase DX18 OS=Homo sapiens GN=GMEXI3 PE=1 SV=2 - [DX18_HUMAN] 0.87 1 Q280VF2 Iongation factor 20 S=Homo sapiens GN=EE7 PE=1 SV=4 - [E72_HUMAN] 0.87 1 Q12839 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=ADAR PE=1 SV=2 - [DX18_HUMAN] 0.87 1 Q14940 NA replication licensing factor MCM3 OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSAD_HUMAN] 0.87 1 P5265 Doubl	P55786-2	Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS - [PSA_HUMAN]	1.55	1
Protein AF-10 OS=Homo sapiens GN=MLIT10 PE=1 SV=2 - [AF10_HUMAN] 1.31 2 ObdStof Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN] 1.28 2 P49711 Transcriptional repressor CTC OS =Homo sapiens GN=CTCP PE=1 SV=1 - [CTCF_HUMAN] 1.24 1 P02768 Serum ablumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] 1.15 1 Q80VF7 Nebulin-related-anchoring protein OS=Homo sapiens GN=RAP PE=2 SV=2 - [NRAP_HUMAN] 1.09 1 Q12879 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=1 - [MOE1_HUMAN] 1.04 1 Q280VF1 ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=EGN2AB PE=1 SV=2 - [DX18_HUMAN] 0.87 1 Q9NVP1 ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=EDX18 PE=1 SV=3 - [MCM3_HUMAN] 0.87 1 P13639 Elongation factor 2 OS=Homo sapiens GN=EEP 2 FE=1 SV=4 - [DSRAD_HUMAN] 0.73 1 P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=EQGAP1 PE=1 SV=4 - [DSRAD_HUMAN] 0.66 1 P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2 APE IS SV=3 - [TOP2A_HUMAN] 0.65 1 Q14980 Nuclear mitotic appariatus	Q14684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 - [RRP1B_HUMAN]	1.45	1
D60506 Heterogeneous nuclear inbonucleoprotein Q OS=Homo sapiens GN=SYWCRIP PE=1 SV=2 - [HNRPQ_HUMAN] 1.28 2 P49711 Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN] 1.24 1 P49711 Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN] 1.15 1 Q80VF7 Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2 - [NRAP_HUMAN] 1.09 1 Q12870 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GNIXA2 PE=1 SV=2 - [DDX18_HUMAN] 1.09 1 Q9NVP1 ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=GNIXA2 PE=1 SV=2 - [DDX18_HUMAN] 0.87 1 Q125205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN] 0.82 1 P13639 Elongation factor 2 OS=Homo sapiens GN=EEP2 PE=1 SV=4 - [EF2_HUMAN] 0.82 1 P55255 Double-stranded RN4-specific adenosine dearmase OS=Homo sapiens GN=LQGAP1 PE=1 SV=4 - [DSRAD_HUMAN] 0.66 1 P13689 IDA topoisomerase 2-alpha OS=Homo sapiens GN=NDRAP PE=1 SV=3 - [IOPA_HUMAN] 0.65 1 D040411 DNA-depended RN4-specific adenosine dearmase OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 0040411 DNA-depended RN4 sopemeras	P55197	Protein AF-10 OS=Homo sapiens GN=MLLT10 PE=1 SV=2 - [AF10_HUMAN]	1.31	2
P49711 Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN] 1.24 1 P02768 Serum albumin OS=Homo sapiens GN=CTCF PE=1 SV=2 - [RAP_HUMAN] 1.15 1 P02768 Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN] 1.10 1 Q12879 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=1 - [NMDE1_HUMAN] 1.09 11 Q12879 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=2 - [DXL8_UHMAN] 1.04 1 Q50VF1 ATP-dependent RNA helicase DX18 OS=Homo sapiens GN=GM2K03 PE=1 SV=3 - [MCM3_HUMAN] 0.87 1 Q5055 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN] 0.82 1 P55265 Double-stranded RNA-specific adenosine dearniase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSAD_HUMAN] 0.66 1 P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=QGAP1 PE=1 SV=1 - [IQGA1_HUMAN] 0.65 1 Q1138 DNA-drected RNA polymerase, mtochondrial OS=Homo sapiens GN=QGAP1 PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 Q14980 Nuclear mtotic apparatus protein 1 OS=Homo sapiens GN=PO2A PL=2 - [RVAL1_HUMAN] 0.57 2 Q90QG0 Myb-binding protein 6 OS=Homo sapiens GN=CMCAP PE=1 SV=2 - [RDM_HUMAN] 0.53 1 Q9174 Protein AHNAK2 OS=Homo sapiens GN=CHMAP PE=1 SV=2 -	O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_HUMAN]	1.28	2
P02760 Serum albumin OS=Homo sapiens GN=ALB PE=1 SV-2 - [ALBU_HUMAN] 1.15 1 Q86VF7 Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2 - [NRAP_HUMAN] 1.00 1 Q86VF7 Nebulin-related-anchoring protein OS=Homo sapiens GN=GNIA2 PE=2 SV=2 - [NRAP_HUMAN] 1.09 1 Q98VF1 ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=GNIA2 PE=1 SV=2 - [DDX18_HUMAN] 1.04 1 Q98VF1 ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=EMCM3 PE=1 SV=3 - [MCM3_HUMAN] 0.87 1 P13039 Elongation factor VCM3 OS=Homo sapiens GN=EEP EF=1 SV=4 - [EF2_HUMAN] 0.82 1 P55265 Double-stranded RNA-specific adenosine dearninase OS=Homo sapiens GN=EEP EF=1 SV=4 - [ICGA1_HUMAN] 0.66 1 P46940 Ras GTPase-activating-Ikke protein IQGAP1 OS=Homo sapiens GN=EQAP1 EF=1 SV=2 - [ICGA1_HUMAN] 0.65 1 01411 DNA dropcide RNA oppimerase, mitochondrial OS=Homo sapiens GN=EQAP1 EF=1 SV=2 - [RPOM_HUMAN] 0.65 1 014980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUM1 PE=1 SV=2 - [RPOM_HUMAN] 0.57 2 0280GQ Myb-binding protein 6 OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [RPOM_HUMAN] 0.53 1 02419	P49711	Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN]	1.24	1
Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2 - [NRAP_HUMAN] 1.00 1 Q12879 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=1 - [NMDE1_HUMAN] 1.09 1 Q12879 Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=2 - [DOX18_HUMAN] 1.04 1 Q12879 DNA replication licensing factor MCM3 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DOX18_HUMAN] 0.67 1 P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=EMCM3 PE=1 SV=3 - [MCM3_HUMAN] 0.82 1 P55265 Double-stranded RNA-specific ademosine dearniase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] 0.66 1 P13639 Elongation factor 2 OS=Homo sapiens GN=TOP2A PE=1 SV=1 - [IQGA1_FUMAN] 0.66 1 P14580 DNA topoisomerase 2-alpha OS=Homo sapiens GN=CDP2A PE=1 SV=2 - [NDA1_HUMAN] 0.65 1 Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=CDRMT PE=1 SV=2 - [NUMAN] 0.65 1 Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=CDRMT PE=1 SV=2 - [NUMAN] 0.57 2 Q9GQG0 Myb-binding protein 1 OS=Homo sapiens GN=CMCHO PE=1 SV=2 - [NUMAN] 0.53 1 Q5TD26 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CMCHO PE=1 S	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	1.15	1
Q12879 Glutamate receptor ionotropic, MMDA 2A OS=Homo sapiens GM=GRIN2A PE=1 SV=1 - [MMEL_HUMAN] 1.09 1 Q9NVP1 ATP-dependent RNA helicase DXI8 OS=Homo sapiens GN=DXI8 PE=1 SV=2 - [DDX18_HUMAN] 1.04 1 Q9NVP1 ATP-dependent RNA helicase DXI8 OS=Homo sapiens GN=DXI8 PE=1 SV=2 - [DDX18_HUMAN] 0.87 1 P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN] 0.82 1 P55255 Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] 0.73 1 P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN] 0.66 1 D0141 DNA topoisomerase 2-alpha OS=Homo sapiens GN=NDRAP PE=1 SV=2 - [TOP2A_HUMAN] 0.65 1 000411 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 0149400 Kuckear mitotic apparatus protein 1 OS=Homo sapiens GN=NUM1 PE=1 SV=2 - [RPOM_HUMAN] 0.57 2 020400 Mycheinding protein 1A OS=Homo sapiens GN=NUM1 PE=1 SV=2 - [RUMAL_HUMAN] 0.53 1 021705 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CM29 PE=1 SV=4 - [CH05_HUMAN] 0.38 1 021704 Protein AHNAK2 OS=Homo sapiens GN=	Q86VF7	Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2 - [NRAP_HUMAN]	1.10	1
Q9NVP1 ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DX18, JUMAN] 1.04 1 P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=EDX18 PE=1 SV=3 - [MCM3_HUMAN] 0.87 1 P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN] 0.82 1 P55265 Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN] 0.73 1 P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=EQGAP1 PE=1 SV=1 - IQGA1_HUMAN] 0.66 1 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN] 0.65 1 DN4 drected RNA polymerase, mitochondrail OS=Homo sapiens GN=NUM1 PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 Q149800 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [RVMA1_HUMAN] 0.57 2 Q80C00 Myb-binding protein 1A OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [RVMA1_HUMAN] 0.53 1 Q817D26 Chromodonain-Heidese-DNA-binding protein 6 OS=Homo sapiens GN=CM29 PE=1 SV=4 - [CHO6_HUMAN] 0.38 1 Q8VK3 Protein AHNAK2 OS=Homo sapiens GN=CM29 PE=1 SV=2 - [EMB1A_HUMAN] 0.38 1 Q8VK4 Pr	Q12879	Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=1 - [NMDE1_HUMAN]	1.09	1
P25205 DNA replication licensing factor MCM3 0S=Homo sapiens GN=MCM3 BE=1 SV=3 - [MCM3_HUMAN] 0.87 1 P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN] 0.82 1 P55265 Double-stranded RNA-specific adenosine deamiase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] 0.66 1 P55265 Double-stranded RNA-specific adenosine deamiase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] 0.66 1 P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=IOP2A PE=1 SV=3 - [TOP2A_HUMAN] 0.65 1 D00411 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NDLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.57 2 Q80C00 Myb-binding protein 1 OS=Homo sapiens GN=NDRAI PE=1 SV=2 - [NUMA1_HUMAN] 0.53 1 Q81D26 Chromodomin-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=4 - [CHD6_HUMAN] 0.41 1 Q81VK3 Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN] 0.38 1 Q81VK2 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNC2_HUMAN] 0.35 1 Q81VK3 Protein AHNAK2 OS=Homo sapiens GN=A	Q9NVP1	ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DDX18_HUMAN]	1.04	1
P13639 Elongation factor 2 OS=Homo sapiens GN=EEP2 PE=1 SV=4 - [EF2_HUMAN] 0.82 1 P55265 Double-stranded RNA-specific adenosine dearninase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] 0.73 1 P55265 Double-stranded RNA-specific adenosine dearninase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN] 0.66 1 P65265 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN] 0.66 1 P01388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN] 0.65 1 Q04011 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 Q04900 Mychear mitotic apparatus protein 1 OS=Homo sapiens GN=VMLA1 PE=1 SV=2 - [NUMAL] HUMAN] 0.57 2 Q80Q00 Myb-binding protein 1 A OS=Homo sapiens GN=MURA1 PE=1 SV=2 - [NUMAL] HUMAN] 0.53 1 Q817D26 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CM29 PE=1 SV=2 - [CHO5_HUMAN] 0.41 1 Q5VYK3 Protein AHNAK2 OS=Homo sapiens GN=MEM29 FE=1 SV=2 - [ECM29_HUMAN] 0.38 1 Q5VYK3 Protein AHNAK2 OS=Homo sapiens GN=CM29 PE=1 SV=2 - [ECM29_HUMAN] 0.35 1 Q5VYK3 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNC_HUMAN]<	P25205	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN]	0.87	1
P55265 Double-stranded RNA-specific adenosine dearninase OS-Homo sapiens GN=ADAR PE-I SV=4 - [DSRAD_HUMAN] 0.73 1 P46940 Ras GTPase-activating-like protein IQGAPI OS=Homo sapiens GN=IQGAPI PE-I SV=1 - [IQGA1_HUMAN] 0.66 0.1 P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=DP2A PE=I SV=1 - [IQGA1_HUMAN] 0.65 0.1 000411 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=POLAMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 0.1 004011 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=POLAMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 0.1 004011 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=VDLAMT PE=1 SV=2 - [RVMA1_HUMAN] 0.57 22 09BQG00 Myb-binding protein 1A OS=Homo sapiens GN=NUBBP1 PE=1 SV=2 - [RUMA1_HUMAN] 0.53 1 09DVX3 Proteomodamin-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CM29 PE=1 SV=4 - [CHO6_HUMAN] 0.38 1 05VX3 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [ALWA2 FEI SV=2 - [ECM29_HUMAN] 0.38 1 04UES5 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 10S=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.38 1 04UES5 Sushi, von Willebrand fact	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	0.82	1
P46940 Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - IQGA1_HUMAN] 0.66 1 P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN] 0.65 1 00111 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=NURMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 0141980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [RPOM_HUMAN] 0.57 22 029BQG0 Myb-binding protein 1A OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN] 0.53 11 029BQG0 Myb-binding protein AO S=Homo sapiens GN=NUMA1 PE=1 SV=2 - [MBBLA_HUMAN] 0.53 11 029DQ0 Myb-binding protein 6 OS=Homo sapiens GN=CHOE PE=1 SV=4 - [CHOE, HUMAN] 0.38 11 02VYK3 Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN] 0.38 11 02VYK3 Protein AHUAK2 OS=Homo sapiens GN=AHUAK2 PE=1 SV=2 - [AHUK2_HUMAN] 0.35 11 024LDE5 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 10S=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.31 22 04D12 Sushi, von Willebrand factor type A, EGF and pentraxin domain-contatoning protein 10S=Homo sapiens GN=SVEP1 PE=1 SV=3	P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	0.73	1
P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN] 0.65 11 D00411 DNA-drected RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 11 Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.57 22 Q80Q00 Myb-binding protein 1 AOS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN] 0.53 21 Q80Q02 Myb-binding protein 1 AOS=Homo sapiens GN=CHD6 PE=1 SV=4 - [CHD6_HUMAN] 0.41 11 Q81V26 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=4 - [CHD6_HUMAN] 0.41 11 Q5VYK3 Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN] 0.38 11 Q8IVF2 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNC2_HUMAN] 0.35 11 Q4LDE5 Sushi, von Wilebrand factor type A, EGF and pentraxin domain-containing protein 10 S=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.31 22 Q4E013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] 0.28 11	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	0.66	1
000411 DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.65 1 014980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN] 0.57 2 029BQG0 Myb-binding protein 1 A OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1, HUMAN] 0.53 1 029BQG0 Myb-binding protein 1 A OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1, HUMAN] 0.53 1 028U706 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CH06 PE=1 SV=4 - [CH06_HUMAN] 0.41 1 025VK3 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [ECM29_HUMAN] 0.38 1 028U7C2 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CM29 PE=1 SV=2 - [ECM29_HUMAN] 0.38 1 028VK3 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHIK2_HUMAN] 0.35 1 024UE55 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.38 1 04D125 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.38 1	P11388	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN]	0.65	1
QL4980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1, HUMAN] 0.57 2 Q9BQG0 Myb-binding protein 1 A OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMAN] 0.53 11 Q9BQG0 Myb-binding protein 1 A OS=Homo sapiens GN=NUBP1A PE=1 SV=2 - [RUBB1A_HUMAN] 0.41 11 Q8TD26 Chromodonain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHCP0 PE=1 SV=4 - [CH05_HUMAN] 0.38 11 QSVTK3 Protein AHUMAX OS=Homo sapiens GN=AHUMA2 PE=1 SV=2 - [ALH0X_2_HUMAN] 0.38 11 QSVTK3 Protein AHUMAX OS=Homo sapiens GN=AHUMA2 PE=1 SV=2 - [ALH0X_2_HUMAN] 0.35 11 Q4UDE5 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.31 22 Q4UDE5 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.31 21	000411	DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN]	0.65	1
Q9BQG0 Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 · [MBB1A_HUMAN] 0.53 11 Q8TD26 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=4 · [CHD6_HUMAN] 0.41 11 QSVYK3 Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=CHD6 PE=1 SV=2 · [ECM29_HUMAN] 0.38 11 Q8IVF2 Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 · [ECM29_HUMAN] 0.35 11 Q8IVF2 Proteasome-associated protein SCN=AHNAK2 PE=1 SV=2 · [AHNK2_HUMAN] 0.35 11 Q4LDES Sushi, von Wilebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 · [SVEP1_HUMAN] 0.38 12 Q4LDES Sushi, von Wilebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 · [SVEP1_HUMAN] 0.38 12 Q46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 · [KI67_HUMAN] 0.28 11	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	0.57	2
Q8TD26 Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=4 - [CHD6_HUMAN] 0.41 1 QSVVK3 Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=CHD6 PE=1 SV=2 - [ECM29_HUMAN] 0.38 1 Q8IVF3 Proteasome-associated protein SCM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN] 0.38 1 Q8IVF3 Proteasome-associated protein SCM28 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN] 0.35 1 Q4LDE5 Sushi, von Wilbrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.38 2 P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] 0.28 1	Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]	0.53	1
QSVYK3 Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN] 0.38 11 QSUYF3 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNC2_HUMAN] 0.35 11 Q4LDES Sushi, von Wilebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.31 22 P40113 Antigen K1-67 OS=Homo sapiens GN=MK167 PE=1 SV=2 - [K167_HUMAN] 0.28 11	Q8TD26	Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=4 - [CHD6_HUMAN]	0.41	1
Q8IVF2 Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNK2_HUMAN] 0.35 1 Q4LDE5 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.31 22 P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] 0.28 11	Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	0.38	1
Q4LDE5 Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN] 0.31 2 P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] 0.28 1	Q8IVF2	Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNK2_HUMAN]	0.35	1
P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN] 0.28 1	Q4LDE5	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3 - [SVEP1_HUMAN]	0.31	2
	P46013	Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN]	0.28	1

Table	18.	Raw	data	of	BioID	experiment:	BioID-DOT1L-wt	infected
HEK2	93T	cells,	$2^{ m nd}~ m rea$	adir	ıg			

Accession	Description	ΣCoverage	Σ# PSMs
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	47.83	1
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	46.91	33
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	45.35	1
P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	43.26	30
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	41.85	1
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	39.81	2
P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	37.98	1
Q8TEK3	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Homo sapiens GN=DOT1L PE=1 SV=2 - [DOT1L_HUMAN]	35.02	14
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	34.93	1
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11_HUMAN]	34.81	1
060814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	33.33	
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	32.41	
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	32.16	1
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]	31.52	1
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	31.40	1
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	30.88	
P29372	DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 - [3MG_HUMAN]	30.87	1
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	30.86	1
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	30.52	2
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	30.43	
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16_HUMAN]	30.34	1
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	29.93	1
F2Z2W6	Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=1 - [F2Z2W6_HUMAN]	29.55	
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	29.41	1
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	29.13	
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	28.50	4
P62633	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 - [CNBP_HUMAN]	27.68	
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	27.27	1
Q5TEC6	Histone H3 OS=Homo sapiens GN=HIST2H3PS2 PE=1 SV=1 - [Q5TEC6_HUMAN]	27.21	
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	26.83	
Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	26.74	2
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	26.42	1
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	26.02	1
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	25.61	1
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	25.50	1
P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10_HUMAN]	25.23	1
P62910	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 - [RL32_HUMAN]	25.19	
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	24.36	5
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	24.29	
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	24.16	1
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA_HUMAN]	23.36	8
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMAN]	23.29	1
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK_HUMAN]	23.11	2
P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A_HUMAN]	22.97	
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	22.81	1
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	22.66	2
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	22.38	1
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 - [GNL3_HUMAN]	22.22	2
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	21.12	3
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	20.56	1
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	20.47	1
P62987	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]	20.31	
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	19.72	1
P62891	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]	19.61	
P62847	40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1 - [RS24_HUMAN]	19.55	
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	19.38	1

Accession	Description	ΣCoverage	Σ# PSMs
000571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	18.88	29
Q9H5H4	Zinc tinger protein 768 OS=Homo sapiens GN=ZNF768 PE=1 SV=2 - [ZN768_HUMAN]	17.78	15
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	17.05	13
P62861	405 ribosomal protein S30 US=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	16.95	2
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	16.80	9
P62263	405 ribosomal protein S14 05=Homo sapiens GN=RP514 PE=1 SV=3 - [KS14_HUMAN]	16.56	4
015235	285 ribosomal protein S12, mtochondrial OS=Homo sapiens GN=MIR/S12 PE=1 SV=1 [[R112_HUMAN]	15.94	2
P04264	Keratin, type II cytoskeletal I US=Homo sapiens GN=KKII PE=I SV=0 - [K2C1_HUMAN]	15.84	15
P05204	Non-histone chromosomal protein HMG-17 OS=Homo sapiens GN=HMGN2 PE=1 SV=3 - [HMGN2_HUMAN]	15.56	2
P49207	605 ribosomal protein L34 OS=Homo sapiens GN=RPL34 Pt=1 SV=3 - [RL34 HUMAN]	15.38	2
P62851	405 ribosomai protein S25 US=Homo sapiens GN=RPS25 PE=1 SV=1 - [KS25_HUMAN]	15.20	3
P09874	Poly (AUP-TROSE) polymerase 1 US=nomo sapiens GN=PARP1 PE=1 SI=4 - [PARP1_numan]	15.09	2/
P78549	Endonuclease III-like protein I OS =Homo saplens GN =N(HL) PE=1 SV =2 ($P(H)$ =HUMAN)	14.42	/
ESKHH/	ADP-mossiation factor Girase-activating protein 1 (Fragment) US=homo Saplens Gira-AkrGAP1 PE=1 Sv=1 - [ESKHH/_HUMAN]	14.38	1
P62829	605 tiposomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	14.29	2
Q96EY4	Iranslation machinery-associated protein 16 US=Homo sapiens GN=IMA16 PE=1 SV=2 - [IMA16_HUMAN]	14.29	/
P26641	Elongation factor 1-gamma OS=Homo saplens GN=EEFIG PE=1 SV=3 [EFIG_HUMAN]	13.50	8
095232	Luc/-like protein 3 OS=Homo sapiens GN=LUC/L3 PE=1 SV=2 - [LC/L3_HUMAN]	13.43	11
Q96RQ3	Methykrotonoyi-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCCI PE=1 SV=3 - [MCCA_HUMAN]	13.38	14
Q9GZV4	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3 - [IF5A2_HUMAN]	13.07	3
Q02543	60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 - [RL18A_HUMAN]	13.07	4
C9JDJ7	U2 snRNP-associated SURP motif-containing protein (Fragment) OS=Homo sapiens GN=U2SURP PE=1 SV=3 - [C9JDJ7_HUMAN]	12.98	1
Q5JTH9	RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	12.95	29
Q86T24	Transcriptional regulator Kaiso OS=Homo sapiens GN=ZBTB33 PE=1 SV=2 - [KAISO_HUMAN]	12.65	16
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 - [LAP2B_HUMAN]	12.56	6
P62273	405 ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 - [RS29_HUMAN]	12.50	3
P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	12.50	3
000483	Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 - [NDUA4_HUMAN]	12.35	1
P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	12.24	2
Q5T280	Putative methyltransterase C9ort114 OS=Homo sapiens GN=C9ort114 PE=1 SV=3 - [C1114_HUMAN]	11.97	7
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	11.52	7
P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	11.48	6
P62269	405 ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	11.18	2
Q16629	Serine/arginine-rich splicing factor 7 OS=Horno sapiens GN=SRSF7 PE=1 SV=1 - [SRSF7_HUMAN]	10.92	2
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	10.88	8
P10599-2	Isoform 2 of Thioredoxin OS=Homo sapiens GN=TXN - [THIO_HUMAN]	10.59	1
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_PL0MAN]	10.42	5
P50990	I-complex protein 1 subunit theta US=Homo sapiens GR=CC I8 PE=1 SV=4 - [ICPQ_HUMAN]	9.85	9
Q9P016	Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYNI PE=1 SV=1 - [THYN1_HUMAN]	9.78	3
P61513	60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2 - [RL37A_HUMAN]	9.78	2
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	9.55	4
P42677	405 ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	9.52	2
P47914	bus ribosomai protein L29 US=Homo sapiens GN=RPL29 PE=1 SV=2 - [RL29_HUMAN]	9.43	2
P61927	bus ribosomai protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 - [RL37_HUMAN]	9.28	2
P62314	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMD1_HUMAN]	9.24	1
P62917	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]	8.95	3
Q19T08	Endothelial cell-specific chemotaxis regulator OS=Homo sapiens GN=ECSCR PE=1 SV=1 - [ECSCR_HUMAN]	8.78	1
P48730	Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D PE=1 SV=2 - [KC1D_HUMAN]	8.67	7
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	8.51	7
P56270	Myc-associated zinc finger protein OS=Homo sapiens GN=MAZ PE=1 SV=1 - [MAZ_HUMAN]	8.39	9
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	8.27	3
P63167	Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 - [DYL1_HUMAN]	7.87	1
P62854	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	7.83	1
C9JPD0	Neurexophilin-1 (Fragment) OS=Homo sapiens GN=NXPH1 PE=4 SV=1 - [C9]PD0_HUMAN]	7.69	1
Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 - [NONO_HUMAN]	7.64	4
P22087	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2 - [FBRL_HUMAN]	7.48	4
Q8IYL3	UPF0688 protein C1orf174 OS=Homo sapiens GN=C1orf174 PE=1 SV=2 - [CA174_HUMAN]	7.41	2
Q8IWS0	PHD finger protein 6 OS=Homo sapiens GN=PHF6 PE=1 SV=1 - [PHF6_HUMAN]	7.40	5
P55197	Protein AF-10 OS=Homo sapiens GN=MLLT10 PE=1 SV=2 - [AF10_HUMAN]	7.30	10

Accession	Description	ΣCoverage	Σ# PSMs
P32969	60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [RL9_HUMAN]	7.29	2
P62899	60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 - [RL31_HUMAN]	7.20	2
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	7.11	4
Q9P2Y5-2	Isoform 2 of UV radiation resistance-associated gene protein OS=Homo sapiens GN=UVRAG - [UVRAG_HUMAN]	6.73	1
P07305	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3 - [H10_HUMAN]	6.70	1
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	6.59	9
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNRPC_HUMAN]	6.54	3
Q9Y3B4	Splicing factor 3B subunit 6 OS=Homo sapiens GN=SF3B6 PE=1 SV=1 - [SF3B6_HUMAN]	6.40	1
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	6.21	2
Q96I27	Zinc finger protein 625 OS=Homo sapiens GN=ZNF625 PE=2 SV=1 - [ZN625_HUMAN]	6.21	2
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	6.18	3
P62244	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2 - [RS15A_HUMAN]	6.15	1
P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1_HUMAN]	6.01	5
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_HUMAN]	5.94	10
P61313	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2 - [RL15_HUMAN]	5.88	1
Q9BZE4	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1_HUMAN]	5.84	8
P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24_HUMAN]	5.73	3
C9JGC1	Zinc finger protein neuro-d4 (Fragment) OS=Homo sapiens GN=DPF1 PE=4 SV=1 - [C9JGC1_HUMAN]	5.71	1
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	5.67	3
Q9Y324	rRNA-processing protein FCF1 homolog OS=Homo sapiens GN=FCF1 PE=2 SV=1 - [FCF1_HUMAN]	5.56	2
P49959	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3 - [MRE11_HUMAN]	5.51	6
Q96EK4	THAP domain-containing protein 11 OS=Homo sapiens GN=THAP11 PE=1 SV=2 - [THA11_HUMAN]	5.41	3
043390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	5.37	4
Q07020	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 - [RL18_HUMAN]	5.32	2
P07355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN]	5.31	3
P12270	Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN]	5.25	21
Q9Y4X4	Krueppel-like factor 12 OS=Homo sapiens GN=KLF12 PE=1 SV=2 - [KLF12_HUMAN]	5.22	3
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 - [KHDR1_HUMAN]	5.19	3
P20719	Homeobox protein Hox-A5 OS=Homo sapiens GN=HOXA5 PE=1 SV=2 - [HXA5_HUMAN]	5.19	2
Q16527	Cysteine and glycine-rich protein 2 OS=Homo sapiens GN=CSRP2 PE=1 SV=3 - [CSRP2_HUMAN]	5.18	1
076021	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3 - [RL1D1_HUMAN]	5.10	4
Q6HA08	Astacin-like metalloendopeptidase OS=Homo sapiens GN=ASTL PE=1 SV=4 - [ASTL_HUMAN]	5.10	1
P14866	Heterogeneous nuclear ribonucleoprotein LOS=Homo sapiens GN=HNRNPL PE=1 SV=2 - [HNRPL_HUMAN]	5.09	4
P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]	5.07	3
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	4.99	6
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	4.85	6
P27695	DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2 - [APEX1_HUMAN]	4.72	2
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	4.70	3
Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 - [ILKAP_HUMAN]	4.59	2
P35637	RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN]	4.56	1
Q96P11	Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens GN=NSUN5 PE=1 SV=2 - [NSUN5_HUMAN]	4.43	3
Q14119	Vascular endothelial zinc finger 1 OS=Homo sapiens GN=VEZF1 PE=1 SV=2 - [VEZF1_HUMAN]	4.41	2
Q9ULJ8-2	Isoform 2 of Neurabin-1 OS=Homo sapiens GN=PPP1R9A - [NEB1_HUMAN]	4.39	1
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 - [SFPQ_HUMAN]	4.38	3
Q9Y2R4	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3 - [DDX52_HUMAN]	4.34	3
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	4.29	4
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	4.27	4
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	4.24	1
P55265	Double-stranded RNA-specific adenosine dearninase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	4.16	10
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	4.14	3
P46109	Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1 - [CRKL_HUMAN]	3.96	2
Q9BQ75	Protein CMSS1 OS=Homo sapiens GN=CMSS1 PE=1 SV=2 - [CMS1_HUMAN]	3.94	1
P25205	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN]	3.84	7
Q6PK04	Coiled-coil domain-containing protein 137 OS=Homo sapiens GN=CCDC137 PE=1 SV=1 - [CC137_HUMAN]	3.81	2
Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]	3.77	9
075475	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1_HUMAN]	3.77	5
Q9UQR0	Sex comb on midleg-like protein 2 OS=Homo sapiens GN=SCML2 PE=1 SV=1 - [SCML2_HUMAN]	3.71	5
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	3.70	2
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]	3.62	3

Accession	Description	ΣCoverage	Σ# PSMs
P33992	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5_HUMAN]	3.54	4
Q9UNQ2	Probable dimethyladenosine transferase OS=Homo sapiens GN=DIMT1 PE=1 SV=1 - [DIM1_HUMAN]	3.51	1
095478	Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens GN=NSA2 PE=1 SV=1 - [NSA2_HUMAN]	3.46	1
Q8N3J9	Zinc finger protein 664 OS=Homo sapiens GN=ZNF664 PE=2 SV=1 - [ZN664_HUMAN]	3.45	2
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 - [UTP18_HUMAN]	3.24	2
P55198	Protein AF-17 OS=Homo sapiens GN=MLLT6 PE=1 SV=2 - [AF17_HUMAN]	3.20	7
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	3.07	2
Q8IZJ6	Inactive L-threonine 3-dehydrogenase, mitochondrial OS=Homo sapiens GN=TDH PE=2 SV=1 - [TDH_HUMAN]	3.04	2
P39023	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 - [RL3_HUMAN]	2.98	2
P52655	Transcription initiation factor IIA subunit 1 US=Homo sapiens GN=GIF2A1 PE=1 SV=1 - [1F2AA_HUMAN]	2.93	1
Q14684	Ribosomal RNA processing protein 1 nomolog B OS=Hormo sapiens GN=RRP1B PE=1 SV=3 - [RRP1B_HUMAN]	2.90	5
Q13148	TAK DIVA-binding protein 43 OS-Honto sapiens GN=TAKDBY PE=1 SV=1 - [TADBY-TIUMAN]	2.90	2
Q14960	Nuclear mixture apparatus protein i OS=noinis sapienis on=noimai re=1 svz - r [noimai_noimani]	2.00	/
P27340	14-3-3 protein tricted OS=horito Soprets Give TWHAQ YEE1 SV=1 - [14-53]_HOVAND	2.00	1
QJ17492	Putative defisience of 17, interforming context (ALMOYR) Experies (H=10437 FE-1 SV-1 FGAT (D=10444)	2.01	1
09HC62	Total course processing of the set of the se	2.00	1
000712	Schein specine process 2 Schein scheinen Scheinen Structure 2 (Schein Zhonen)	2.62	1
071354	The fine protein 721 OS=Homo sapiens (SN=ZNF721 PF=1 SV=1 - 72N721 HUMAN)	2.52	2
075182	Paired amphinathic helix protein Sin3b OS=Homo saniens GN=SIN3B PE=1 SV=2 - [SIN3B HUMAN]	2.50	2
094900	Thymocyte selection-associated high mobility group box protein TOX OS=Homo sapiens GN=TOX PE=2 SV=3 - [TOX HUMAN]	2.47	2
P18754	Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [RCC1 HUMAN]	2.38	2
000148	ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 - [DX39A_HUMAN]	2.34	1
Q03111	Protein ENL OS=Homo sapiens GN=MLLT1 PE=1 SV=2 - [ENL_HUMAN]	2.33	2
Q8WVM0	Dimethyladenosine transferase 1, mitochondrial OS=Homo sapiens GN=TFB1M PE=1 SV=1 - [TFB1M_HUMAN]	2.31	1
P42568	Protein AF-9 OS=Homo sapiens GN=MLLT3 PE=1 SV=2 - [AF9_HUMAN]	2.29	2
Q6P087	RNA pseudouridylate synthase domain-containing protein 3 OS=Homo sapiens GN=RPUSD3 PE=1 SV=3 - [RUSD3_HUMAN]	2.28	1
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	2.20	2
Q8HWS3	DNA-binding protein RFX6 OS=Homo sapiens GN=RFX6 PE=1 SV=2 - [RFX6_HUMAN]	2.16	2
P43246	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1 - [MSH2_HUMAN]	2.14	3
P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	2.11	1
Q14498	RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39_HUMAN]	2.08	2
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	2.08	e
Q9NPA5-2	Isoform 2 of Zinc finger protein 64 homolog, isoforms 1 and 2 OS=Homo sapiens GN=ZFP64 - [ZF64A_HUMAN]	1.91	1
Q8WWY3	U4/U6 small nudear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2 - [PRP31_HUMAN]	1.80	1
000541	Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 - [PESC_HUMAN]	1.70	2
Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN]	1.66	1
Q8WYQ5-3	Isoform 3 of Microprocessor complex subunit DGCR8 OS=Homo sapiens GN=DGCR8 - [DGCR8_HUMAN]	1.62	1
060264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 - [SMCA5_HUMAN]	1.62	2
Q8NFW8	N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 - [NEUA_HUMAN]	1.61	2
Q86V48	Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV=2 - [LUZP1_HUMAN]	1.58	2
Q6ZN08	Putative zinc finger protein 66 OS=Homo sapiens GN=ZNF66 PE=5 SV=3 - [ZNF66_HUMAN]	1.57	2
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KH-SRP PE=1 SV=4 - [FUBP2_HUMAN]	1.55	1
P/852/	DNA-dependent protein kinase catalytic subunit OS=Horm sapiens GN=PKKUC PE=1 SV=3 - [PKKUC_HUMAN]	1.53	11
P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GIR=RANBP2 PE=1 SV=2 - [RBP2_HUMAN]	1.52	/
Q8WWV6	High attinity immunogiobulin alpha and immunogiobulin mu Fc receptor OS=Homo sapiens GN=FCAMR PE=1 SV=1 - [FCAMR_HUMAN]	1.50	1
Q999959	Praconfinite 2 US= Homo saperis GN=PR/2 PE=1 SI=2 - $[PR/2, HUMAN]$	1.48	4
000567	Nucleolar protein 50 US=Horto Sapiens Gir=NUP56 PE=1 SV=4 - [NUP56_HUP4N]	1.35	2
AUAU8/WU6	LIVA polymerase alpha datalytic subunit US=homo saplens GR=PULA1 PE=4 SV=1. [AUAUS/WUO4_HUMAN]	1.30	
D/5400	Pre-mkiva-processing raccor 440 homolog a OS=homo saplens GN=PKP+40A PE=1 SV=2 - [PK+40A_HUMAN]	1.25	1
P49/11 DE2272	Trainscriptional repression CTCF USERIDING appendix GNEETCOF PEETS VETE 1 2 (CTCF_DOMAN)	1.24	
P322/2	Tectorgeneous nuclear nuoniceophoteni in OSE-nonio sapieris dire=niktakim PEET 3943 - [nikkrin_noimaki TIMTI Bio sankala OC-Hama asalana OL-TIMTI DE 1 OC-2. [TIMTI HI MAN]	1.23	
Q72215 014920	IRMITENE PROTEIN OSENNIK SAKET KMILL KEET SKEZ (IRMITENDARMIN)	1.25	
Q14035	Circumbuohathetaisasethive-binding protein + too-include spirets site-circut-to-to-to-to-to-to-to-to-to-to-to-to-to	1.20	
000411	Integrated 20 Software applicate one-index (==1.59-2) [Integrational [Integrated PMA directed PM	1.17	
P11387	DNA transferação 10.54bm saniens (N=TOPI PE=1 SV=2 - ITOPI HIMANI	1.05	2
O9NVP1	ATD-dependent RNA helizase DDX18 OS=Horm saniers (SH=DDX18 PE = SV=2 - IDDX18 HIMAN]	1.05	1
O96T88	Subjuitin-protein ligase UHRF1 OS=Homo saplese GN=UHRF1 PE=1 SV=1 - (UHRF1 HIMANI	1.01	1
E7EPI0	Lo balance processing and environmentation appendix of a statistic field of the first statistic field of the stati	0.97	1
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9 HUMAN]	0.94	2
Q8IZX4	Transcription initiation factor TFIID subunit 1-like OS=Homo sapiens GN=TAF1LPE=1 SV=1 - ITAF1L HUMANI	0.93	2
Q8NEB9	Phosphatidylinositol 3-kinase catalytic subunit type 3 OS=Homo sapiens GN=PIK3C3 PE=1 SV=1 - [PK3C3 HUMAN]	0.90	1
Q9NZM1	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 - [MYOF_HUMAN]	0.87	1
Q3KQU3	MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1 - [MA7D1 HUMAN]	0.83	2
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	0.82	2
O60885	Bromodomain-containing protein 4 OS=Homo sapiens GN=BRD4 PE=1 SV=2 - [BRD4_HUMAN]	0.73	2
Q9ULM3	YEATS domain-containing protein 2 OS=Homo sapiens GN=YEATS2 PE=1 SV=2 - [YETS2_HUMAN]	0.70	2
060241	Brain-specific angiogenesis inhibitor 2 OS=Homo sapiens GN=BA12 PE=2 SV=2 - [BA12_HUMAN]	0.69	2
Q5SW79	Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1 - [CE170_HUMAN]	0.57	1
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]	0.38	1
P46013	Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN]	0.28	2
Q5UIP0	Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN]	0.28	1

Table	19.	Raw	data	of BioID	experiment:	BioID-DOT1L-mut	infected
HEK2	93T	cells,	$1^{\rm st}$ rea	ading			

Accession	Description	ΣCoverage	Σ# PSMs
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	55.65	
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]	44.64	4
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	42.27	3
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	41.86	
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17 HUMAN]	41.85	
P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11 HUMAN]	41.57	
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 - [RS11 HUMAN]	41.14	
08N257	Histone H2B type 3-B OS=Homo saniens GN=HIST3H2BB PF=1 SV=3 - [H2B3B_HUMAN]	39.68	
060814	Histone 1-K OS=Homo saniens GN=HIST1H2BK PE=1 SV=3 - [H2B1K HIIMAN]	39.68	
P62805	Historic Historic Host Honoranians Graduate Historic Hi	38.83	1
P22626	Historicanaous purdear ribonurdeira del 1971 DE 1972 [Includent]	38.24	
P22020	The elogeneous index a monitore up of each x_2 bit 03 - non 3 spheric $3n$ - non $3n$ - $2n$	25.16	
P02307	Output Postick is the compared and the sphere scheme sphere Sub-Dut Age 100-21 (LT-02-100-44)	25.10	
P02937	Pepudy-provide Castralis Bollied ase A DS=Roll D salperts GN=PPTA PE=1 SV=2 - [PTA_nonani]	35.15	
P20373	oos huosoniai protein Ets OS=mono sapiens div=RPELS PE=1 SV=4 + (RELS_mon#id)	33.07	2
P04406	Gyceraidenyde-3-phosphate denydrogenase OS=homo sapiens Gyl=GAPUH PE=1 Sys3 - [G3P_HUMAN]	34.93	4
P15880	40s hibosomal protein S2 0S=Homo sapiens GN=RFS2 PE=1 SV=2 - [RS2_HUMAN]	33.45	1
P62/01	4US ribosomal protein S4, X isoform US=Homo sapiens GN=RPS4X PE=1 SV=2 - [KS4X_HUMAN]	33.08	2
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	32.96	2
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	32.82	2
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_HUMAN]	32.53	3
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	32.12	
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16_HUMAN]	30.90	1
P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	30.29	1
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]	30.26	
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK_HUMAN]	30.24	2
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	29.49	
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1 HUMAN]	28.64	1
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20 HUMAN]	28.57	1
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	28.11	2
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo saplens GN=DDX5 PE=1 SV=1 - [DDX5 HUMAN]	27.85	4
P29372	DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 - [3MG_HUMAN]	27.85	1
P60709	Actin. cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	27.73	2
P61247	405 ribosomal protein S3a OS=Homo saniens GN=RPS3A PF=1 SV=2 - [RS3A H IMAN]	27.65	1
P39019	40S ribosomal protein S19 OS=Horm saniens (N=RPS19 PE=1 SV=2 - [RS19 HIMAN]	27.59	
P62240	Also sitilogeneral protections is to the statistical of the statistical statistica	27.40	1
0062215		27.10	
05000		27.54	
P02029		27.14	
P03207	Actin, gamma-enteric smooth muscle US=monto sapiens GV=AL (12 PE=1 SV=1 - [ACTH_HUMAN]	27.13	4
P0/43/	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	26.35	1
P04075	Fructose-bispnosphate adolase A US=Homo sapiens GN=ALDUA Pt=1 SV=2 - [ALDUA_HUMAN]	25.2/	1
Q8TEK3	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Homo sapiens GN=DOTIL PE=1 SV=2 - [DOTIL_HUMAN]	25.13	8
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	24.53	
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	24.29	
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	24.03	2
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	23.90	2
P62318	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1 - [SMD3_HUMAN]	23.81	
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	23.57	1
P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2 - [H13_HUMAN]	23.08	1
P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A_HUMAN]	22.97	
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNRPC_HUMAN]	22.88	
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	22.79	
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	22.65	
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 - [GNL3 HUMAN]	22.59	
- P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA HUMAN]	22.58	
P52272	Heterogeneous nuclear ritopuckeoprotein M OS=Homo saliens GN=HINRNPM PE=1 SV=3 - [HINRPM_HUMAN]	22,50	
D62266	All of physical participants (\$3,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0	22.1/	
002543	ACC shoes and partial 188 CC-Ham sphere CH-PD182 PE-154-5 [R422-5 FD184 HIMAN]	22.30	
202343	uos nuosonai procente toa uos-tonino sabietis diverte talo PEET SPEZ - [RELOA_TIUPAN]	22.16	
Q99023	Promodule 2 OS=nono saprension=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	22.07	

Accession	Description	ΣCoverage	Σ# PSMs
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	21.84	14
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	21.83	21
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	21.48	16
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_HUMAN]	20.11	11
P27635	605 ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 - [RL10 + UMAN]	20.09	9
P62910	605 ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 - [RL32_HUMAN]	20.00	7
P08107	Heat shock /U kua protein 1A/1B/OS=Hormo sapiens GN=HSPAIA PE=1 SV=5 [HEP/1_HUMAN]	19.81	25
P11498	Pyruvate carboxylase, mtochondrial OS=Homo sapiens GN=PC PE=1 SV=2 [PVC, HUMAN]	19.69	38
P62891	605 nbosomal protein L39 05=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]	19.61	2
P62847	405 ndosomai protein 524 05=nomo sapiens Gv=kr524 Pt=1 5V=1 - [K524_numVAN]	19.55	4
Q15505 Q12151	POV(C)-DURING protein LOS=HORD September 304=PCDP1 PE=1 SP2 - [PCPP_HORDMIN] Hotoprogenus puedes ribonucleoperatin AO Co-Horp conjung CAL-HUNDIAO DE=1 S/21 - [PCA0. HUMAN]	19.56	10
Q13131 P30050	Intercogeneous induced induced induced induced induced and a second	19.02	10
P83731	GS ribosomal protein E2 GO-Finite series GV-RUE2EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	18.47	6
P62269	dos nicosonia protein 518 OS=Hom sanjens GN=RP518 PT=1 V=3 : [R518 HIMAN]	18.42	6
096FY4	Transition machinery-associated protein 16 05=Homo salens GN=TMA16 PF=1 SV=2 - [TMA16 HUMAN]	18.23	7
P12236	ADP/ATP transforces 3 OS=Horm satisfies GH=SI (2566 PE=1 SV=4 - FADT3 HUMAN)	18.12	14
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3 HUMAN]	18.11	6
P62244	40S ribosomal protein S15a OS=Homo sabiens GN=RPS15A PE=1 SV=2 - [RS15A HUMAN]	17.69	4
P62314	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMD1 HUMAN]	17.65	2
P61927	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 - [RL37 HUMAN]	17.53	4
P29692	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5 - [EF1D HUMAN]	17.44	3
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA_HUMAN]	17.39	67
P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]	17.39	1
095232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]	17.36	13
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	17.35	5
A8MWD9	Putative small nuclear ribonucleoprotein G-like protein 15 OS=Homo sapiens GN=SNRPGP15 PE=5 SV=2 - [RUXGL_HUMAN]	17.11	2
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	16.95	2
O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	16.47	22
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	16.37	19
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	15.97	8
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMAN]	15.89	7
P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1_HUMAN]	15.81	12
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	15.69	8
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	15.45	4
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	15.36	21
P84103	Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [SRSF3_HUMAN]	15.24	4
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 - [RS25_HUMAN]	15.20	4
P62306	Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1 - [RUSF_HUMAN]	15.12	2
P0/900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP9UA1 Pt=1 SV=5 - [HS9UA_HUMAN]	14.89	1/
PUCUS5	NISTORE MLA, Z USS-FINITO SAPIENTS GIVER MLARZ Y EFE I SIYEZ - [HCAZ_ MUMAN]	14.84	4
P10809	ou kua neat snock protein, mitochononali US=homo sapiens GN=HISPU IYE=1 SV=2 [CHoU_HUMAN]	14.66	15
P23703	AT Synthase subunit dipling, introductional operations adjusters on early start start start and adjusters and adjusters and adjusters and adjusters and adjusters and adjusters and adjusters and adjusters adjust	14.03	13
P23240	Spicing raction, provide and guidantine-incli OS=holito Sates SPR2 PEE 1 SPR2 [Company]	14.43	1/
COND30	Subscripts protein Lit to 2 hours septents diverter till 1 5 4 - 1 (Litter 1 in the set of the set	14.20	10
000830	NUCLEURI NVA HERKABE 2 CO-HIND SEPTIS ON-DOZET FL-1 SI-5 (DAAL_I OVINI)	14.18	23
007020	According to the second s	13.83	4
P78549	Second Second Process Control of the Second Se	13.78	4
096E39	Endomaceuse III mac processing of Annual III and Annual IIII and Annual III annual III annual III annual III annual III annual III annual III annual III annual III annual III annual III annual III annual III annual III annual III annual III annual II	13.59	9
015233	Non-POLI domain-containing octamer-hinding protein OS=Homo springers (N=NONO PE-I Sv=4 - TWNO HUMAN]	13.59	15
Q10255	Persing one activator inhibitor 1 RNA-binding protein OS-Homo sanjens GN-SERRPI PE-1 SV-2 - [ROHE_HOMIN]	13.48	7
P62917	60S ribosomal protein 18 OS=Homo saniens GN=RPI 8 PE=1 SV=2 - [RI 8 HLIMAN]	13.23	5
092522	Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1 - [H1X HUMAN]	13.15	3
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1 HUMAN]	13.05	9
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	12.94	9
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	12.81	11
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	12.78	6
P62273	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 - [RS29_HUMAN]	12.50	2
Q9NY12	H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens GN=GAR1 PE=1 SV=1 - [GAR1_HUMAN]	12.44	3
P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	12.41	3
H0YAQ1	KH domain-containing, RNA-binding, signal transduction-associated protein 3 (Fragment) OS=Homo sapiens GN=KHDRBS3 PE=1 SV=1 - [H0YAQ1_HUMAN]	12.31	1
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	12.28	6
O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	12.16	12
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	11.89	19
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	11.86	11
043175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	11.63	9
P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HINRNPL PE=1 SV=2 - [HNRPL_HUMAN]	11.38	12
P22087	rPNA 2-0-methyltraneforase fibrillaria OS-Home capions GN-ERL DE-1 SV-2- [ERRL HI IMAN]	11.21	6

Accession	Description	ΣCoverage	Σ# PSMs
P18077	60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2 - [RL35A_HUMAN]	10.91	2
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	10.88	7
Q6NW1	Putative 60S ribosomal protein L13a protein RPL13AP3 OS=Homo sapiens GN=RPL13AP3 PE=5 SV=1 - [R13P3_HUMAN]	10.78	2
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	10.61	4
P62277	405 ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13_HUMAN]	10.60	3
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	10.43	2
P37108	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 - [SRP14_HUMAN]	10.29	1
P61313	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2 - [RL15_HUMAN]	10.29	3
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E HUMAN]	10.20	6
P62826	GIP-binding nuclear protein kan OS=Homo Sapiens GN=RAN PE=1 SV=3 - [KAn_HUMAN]	10.19	4
P35268	605 nbosomal protein 122 05=Homo sapiens (xH=RPL22 PE=1 5V=2 - [RL22_HUMAN]	10.16	2
P27695	DNA-(apunnic or apyrimidinic site) lyase US=Homo sapiens (N=APEX1 PE=1 SV=2 - [APEX1_HUMAN]	10.06	4
B2KPKU	Putative nigh mobility group protein B1-like 1 OS=homo sapiens GN=HMGBIP1PE=5 SV=1 - [HGBLA_HUMAN]	9.95	4
F8VWV4	bus addr. rbosomal protein v0 (Fragment) US=Horno sapiens GN=KPLV VE=1 SV=1 - [F8VWV4_HUMAN]	9.91	1
P32909 D61E12	BOS increases protein 1272 OCENTRIA CARDED SAPIENTS GARANTER CAN BE STORE AND AND AND AND AND AND AND AND AND AND	9.90	1
P01515	DOS filosofial protein E27 OS=nono salpers GV=RYE37A PC=1 SV=2 + KE37A_normAN]	9.76	2
P47014	To show the process of the second sec	9.32	2
P55760	NUPD-like protein 125 03-1000 September 34 - Kr 25 FL-1 3V-2 [RC25] TOMMU]	9.38	2
060506	NUTEZINCE (INCLUSION CONTEXT C	9.30	10
0517H9	nectogeneous nuclear inducer proceeding 03-none septens on-sinceur re-13-22 [newrog_non-Aw] DDD12.like nortain 05-Hom caning CM-DDD12 DE-15(P-2, FDDD12 HillMAN] DDD12.like nortain 05-Hom caning CM-DDD12 DE-15(P-2, FDDD12 HillMAN]	9.51	20
P50000	Technick in the protein of scheme scheme and the term of the term of the term of the term of the term of the term of the term of the term of the term of the term of the term of the term of the term of the term of the term of the term of t	9.12	20
014103	Heterogeneus nuclear ribonucleonoratein D0 OS=Horm saniers GN=HINRNPD PE=1 SV=1 - [HIRPD HUMAN]	9.01	3
P39748	Flap endonuclease 1 OS=Homo spriens GN=FEN1 PF=1 SV=1 - [FEN1 HUMAN]	8.95	5
P43243	Matrin-3 OS=Homo sabiens GN=MATR3 PE=1 SV=2 - [MATR3 HUMAN]	8.85	13
016629	Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1 - [SRSF7 HUMAN]	8.82	3
Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2 HUMAN]	8.72	6
015235	28S ribosomal protein S12, mitochondrial OS=Homo sapiens GN=MRPS12 PE=1 SV=1 - [RT12 HUMAN]	8.70	2
P56270	Myc-associated zinc finger protein OS=Homo sapiens GN=MAZ PE=1 SV=1 - [MAZ_HUMAN]	8.60	9
P62633	Cellular nudeic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 - [CNBP_HUMAN]	8.47	1
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	8.36	8
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	8.29	10
F8WBB8	Cullin-associated NEDD8-dissociated protein 2 OS=Homo sapiens GN=CAND2 PE=1 SV=1 - [F8WB88_HUMAN]	8.18	1
P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	7.89	3
Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3 - [MCCA_HUMAN]	7.86	10
Q9GZV4	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3 - [IF5A2_HUMAN]	7.84	4
P14174	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 - [MIF_HUMAN]	7.83	1
P62854	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3 - [RS26_HUMAN]	7.83	2
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	7.79	8
Q9BZE4	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1_HUMAN]	7.73	9
Q13148	TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 - [TADBP_HUMAN]	7.73	6
P49207	60S fibosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	7.69	2
P18124	60S ribosomal protein L7 OS=Horro sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	7.66	2
P35637	RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN]	7.60	4
D6R9P3	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=1 - [D6R9P3_HUMAN]	7.50	2
P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]	7.47	6
Q15691	Microtubule-associated protein RP/EB ramily member 1 OS=Homo sapiens GN=MAPRE1 PE-1 SV=3 - [MARE1_HUMAN]	7.46	1
P23284	Peptoyi-provides-trans somerase bios=homo saplens dui=PPIB PE=1 SV=2 - [PPIB_HUMAN]	7.41	4
Q9H5H4	Zinc ringer protein 768 US=homo sapiens GN=ZNP768 PE=1 SV=2 - [ZV765_HUMAN]	7.41	/
PU/4//	INVPSIINT USERUID SUPERSSTREET SUERCESTREET SUER SUPERSSTREET SUERCESTREET SUERCE	7.29	9
P02203	Host incostrial protein Str OS=norib saperts over KrStr FE=1 SV=5 - [KS14, morekn]	7.20	1
P02099	Tooshidusonal procent D31 03=holito saperis dat=krC11 re=1 3v=1 - [rC3	7.20	2
000149	ATE departs PNA belieze DDV20A OCHAMIC CALL CALL CALL CALL CALL CALL CALL CA	7.10	7
P13645	ATF-respondent two Telescope OS-Homo Sopiets GTV-EDACSA FE-1 SV-2 (DASA_TIONAN) Keratin two Lovtokeletal 10.05-Homo Sones GN-KT10 PE-1 SV-6 - [K1C10 HUMAN]	7.03	10
008211	Activity cycle of oscience and occurrence of the control of the co	6.85	16
A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2 - FAXA21 HUMAN1	6.78	2
012906	Interleukin enhancer-binding factor 3 OS=Homp sapiens GN=ILF3 PE=1 SV=3 - [11 F3 HUMAN]	6.71	10
P49006	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2 - [MRP_HUMAN]	6.67	10
P61353	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27 HUMAN]	6.62	2
076021	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3 - [RL1D1 HUMAN]	6.53	7
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 - [HNRPF HUMAN]	6.27	4
P14678	Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=2 - [RSMB HUMAN]	6.25	2
Q15717	ELAV-like protein 1 OS-Homo sapiens GN=ELAVL1 PE=1 SV=2 - [ELAV1 HUMAN]	6.13	6
Q5T280	Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 - [C1114 HUMAN]	6.12	4
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	5.99	3
P18754	Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [RCC1_HUMAN]	5.94	2
Q9UKM9	RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN]	5.88	4
P06576	ATP synthese subunit beta mitochondrial OS-Homo sanians GN-ATPSR DE-1 SV-3 [ATDR HUMAN]	5.86	4

Accession	Description	ΣCoverage	Σ# PSMs
P25205	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN]	5.69	6
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	5.60	4
Q9Y324	rRNA-processing protein FCF1 homolog OS=Homo sapiens GN=FCF1 PE=2 SV=1 - [FCF1_HUMAN]	5.56	1
P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	5.49	5
Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	5.43	9
Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]	5.42	12
Q96EK4	THAP domain-containing protein 11 OS=Homo sapiens GN=THAP11 PE=1 SV=2 - [THA11_HUMAN]	5.41	2
Q9Y4X4	Krueppel-like factor 12 OS=Homo sapiens GN=KLF12 PE=1 SV=2 - [KLF12_HUMAN]	5.22	2
P39023	bUS ribosomal protein L3 US=Homo sapiens GN=KPL3 PE=1 SV=2 - [KL3_HUMAN]	5.21	4
P0/305	Histone HI. U OS=Homo sapiens GN=H110 PE=1 SV=3 - [H10_HUMAN]	5.15	1
P20700		5.12	2
000567	Caselli Miase Li solominuella OSERDIDE DEL SINCO P.C.E. 1992 - (N.C.ID, ROMAN]	5.06	5
D17097		5.05	2
060097	Promptex protein Fishbarra applie commission and the second state of the second state	4.00	1
Q0F007	Niki paeduolinky jale synthiase donianing molecular user initia spleti o direkti observe 1 3 - 5 - [Kusbu] tohinki] Creating kinase Buhung OS-Horm servicing (M-CKR DE-1 SU-1 - [K/CRB HIIMAN]	4 72	4
P08621	Lit small nuclear ribonuckonzotein 70 k/a 0.5 - Kom zaniane GN - SNDND70 DE - 1 SV-2 - [D117 H1MAN]	4.58	4
K7ETTO	Staffild attachment factor B1 (Frammeth) OS=Hom saliens (N=SAEP DF=1 SV=1 - [K7FII) HI (MAN)	4.50	1
P36578	Solition discrete in the OSE-Home scalars of Sile RP14 PEET Sile Sile H HIMANI	4.50	4
P61204	ADP-rihosvistion factor 3 OS=Homo scalence GN=ARE3 PE=1 SV=2 - [ARE3 HIIMAN]	4 42	1
08IWS0	PHD finger protein 6 OS=Homo saniens GN=PHF6 PE=1 SV=1 - [PHF6 HIMAN]	4.38	2
A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1 - [RP1BL HUMAN]	4.35	1
09Y2R4	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3 - [DDX52 HUMAN]	4.34	4
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	4.24	3
Q5T440	Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 - [CAF17_HUMAN]	4.21	2
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	4.14	5
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 - [GRP75_HUMAN]	4.12	5
P35232	Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1 - [PHB_HUMAN]	4.04	1
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	4.00	32
P46109	Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1 - [CRKL_HUMAN]	3.96	1
P15259	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3 - [PGAM2_HUMAN]	3.95	1
075475	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1 - [PSIP1_HUMAN]	3.77	3
Q13642	Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4 - [FHL1_HUMAN]	3.72	2
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	3.69	1
P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	3.67	10
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]	3.62	3
P01891	HLA class I histocompatibility antigen, A-68 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=4 - [1A68_HUMAN]	3.56	1
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	3.55	3
075533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	3.53	5
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN]	3.53	2
P49368	T-complex protein 1 subunt gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 - [TCPG_HUMAN]	3.49	4
P00918	Carbonic annyorase 2 US=homo sapens GN=LA2 $PE=1$ SV=2 - [CAH2_HUMAN]	3.46	1
HU1414	Lentrosomai protein or 170 kula (Fragment) US=homo sapiens GN=CE170 PE=1 SV=1 - [hUY414_hUMAN]	3.42	1
P33992 D21222	Diva replication incertaing ratio mumo operations adjects one-mumo pre-1 SV=3 - [mumo_momany]	2.41	12
001091	PlainterA OS=nullo Sopietis Giver Duk PC=1 SV=+ [[LTukDUkN] Sulens Extern [DAE 2: AD a glubal OC=Horse Sopies CA_UITAE1 DE=1 SV=2 [[12AE1, k] [MAN]	3.30	15
Q01001 D18846	spicing factor between solution of actor ATE I OS-Hom service OAA TEL DE-1 (JCAF I _ 1004M) Cyclic AMD-dependent transcription factor ATE I OS-Hom service OAA TEL DE-1 (JCAF I _ 1004M)	3.33	1
A8M736	Cyclic Ammungenetic anisological and an internet source in the source of	3.32	1
014078	Envipelant and collections in the second science of the second sci	3.32	2
Q11570	Historial uniced body prosproprotein 1 00-100 september 201-101-2 (10-101-2) (10-100-2) (10-101-2)	3.25	1
015084	Protein disulfide-isomerase A6 OS-Hom saniens GN=PDIA6 PE-1 - (PDIA6 HIMAN]	3.18	2
007666	KH domain-containing RNA-hinding signal transduction-associated protein 1 OS=Horn saniers GN=KHDRBS1 PE=1 SV=1 - [KHDR1 HI IMAN]	3.16	2
P78347	General transmitting, retrieved and considered account of the second process of the second of the second process of the second proce	3.11	- 5
O9P016	Thymocyte nuclear protein 1 OS-Homo sapiens GN=THYN1 PE=1 SV=1 - [THYN1 HUMAN]	3.11	2
Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B HUMAN]	3.11	4
P36873	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1 - [PP1G HUMAN]	3.10	2
Q8IZJ6	Inactive L-threonine 3-dehydrogenase, mtochondrial OS=Homo sapiens GN=TDH PE=2 SV=1 - [TDH_HUMAN]	3.04	1
Q7L190	Developmental pluripotency-associated protein 4 OS=Homo sapiens GN=DPPA4 PE=1 SV=2 - [DPPA4. HUMAN]	2.96	1
Q15061	WD repeat-containing protein 43 OS=Homo sapiens GN=WDR43 PE=1 SV=3 - [WDR43 HUMAN]	2.95	4
043615	Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2 - [TIM44_HUMAN]	2.88	1
Q5T6C4	Ataxin-7-like protein 2 OS=Homo sapiens GN=ATXN7L2 PE=4 SV=1 - [Q5T6C4_HUMAN]	2.87	1
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN]	2.83	4
P12004	Proliferating cell nuclear antigen OS=Homo saplens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	2.68	1
Q86T24	Transcriptional regulator Kaiso OS=Homo sapiens GN=ZBTB33 PE=1 SV=2 - [KAISO_HUMAN]	2.53	2
Q14684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 - [RRP1B_HUMAN]	2.51	2
09H054	Prohable ATE-dependent PNA beirase DDY47 OS-Hom saniens GN-DDY47 PE-1 SV-1 - [DDY47 HI IMAN]	2 42	2
Accession	Description	ΣCoverage	Σ# PSMs
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Q9NVP1	ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DDX18_HUMAN]	2.39	4
Q9Y2X3	Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 - [NOP58_HUMAN]	2.27	2
P15170	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1 - [ERF3A_HUMAN]	2.20	1
P11908	Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2 - [PRPS2_HUMAN]	2.20	1
Q9NQ29	Putative RNA-binding protein Luc7-like 1 OS=Homo sapiens GN=LUC7L PE=1 SV=1 - [LUC7L_HUMAN]	2.16	1
P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	2.16	1
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	2.13	16
P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	2.11	2
Q13247	Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2 - [SRSF6_HUMAN]	2.03	1
060832	H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3 - [DKC1_HUMAN]	1.95	2
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]	1.91	1
014979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3 - [HNRDL_HUMAN]	1.90	1
Q14498	RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39_HUMAN]	1.89	1
P61619	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2 - [S61A1 HUMAN]	1.89	1
P49959	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3 - [MRE11 HUMAN]	1.84	2
P35520	Cvstathionine beta-svnthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	1.81	1
012874	Solicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1 - [SF3A3 HUMAN]	1.80	1
O8WWY3	14/16 small nuclear ribonucleoprotein Pro31 OS=Homo saniens GN=PRPE31 PE=1 SV=2 - [PRP31 HUMAN]	1.60	1
09U0R0	Sex comb on midleo-like protein 2 OS=Homo saniens GN=SCMI2 PF=1 SV=1 - [SCMI2 HUMAN]	1.57	1
08WY05	Micronroessor combes the protein to CR AS Statem sames (N=DCCR PE=1 SV=1 - FOCCR HEIMAN)	1.55	1
092945	Far unstream element-hinding nortein 2 OS-Homo sanjens (A)=KHSRP PF=1 SV=4 - [EHR2 + IIIMAN]	1.55	1
09BZZ5	An opticient enter of any process consistence of the optical of th	1.53	1
Q35570	Applead an and a specific definition of the spec	1.53	2
042142	Provide Section Section Section Field Section And Section And Section And Section Sect	1.55	1
006799	Public provide per linker place in a construction reaction of the provide per linker per linker place in the per per linker place in the per per per per linker per l	1.51	1
004776	LS dupduit protein ingise of int 1 03-1 non saperis Green in 1 1 1 1 - 1 3 - 1 - [UTIN 1] 10 int 1] 10 int 1 - 10 int 3	1.51	1
094770	metastasts-dssoulated protein mitaz openoin sapients one-mitaz PEET system (mitaz normania)	1.50	1
P12950	Artay repair cross-complementaring proceed to 05-monto sapients one-ArcCorPet SVE2 - [ArcCo_monwing]	1.40	2
Q90M54	Pre-mixiva-processing factor 19 US=Horno Sapiens GN=PKP+19 PE=1 SV=1 - [PKP19_HUMAN]	1.39	1
P27816	microtubue-associated protein 4 US=Homo Saplens GN=mAP4 PE=1 SV=3 - [mar44_HUMAN]	1.30	1
Q9H0D6	5-3 exonibonuclease 2 US=Homo sapiens GN=XKN2 PE=1 SV=1 - [XKN2_HUMAN]	1.26	2
P49711	Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN]	1.24	2
Q14839	Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2 - [CHD4_HUMAN]	1.20	4
P43246	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1 - [MSH2_HUMAN]	1.18	2
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	1.15	2
E9PDR5	Inhibitor of Bruton tyrosine kinase OS=Homo sapiens GN=IBTK PE=1 SV=1 - [E9PDR5_HUMAN]	1.13	1
J3KNJ3	N-acetylated-alpha-linked acidic dipeptidase 2 OS=Homo sapiens GN=NAALAD2 PE=4 SV=1 - [J3KNJ3_HUMAN]	1.13	1
Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	1.13	2
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	1.10	1
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	1.05	1
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	1.01	2
P05129	Protein kinase C gamma type OS=Homo sapiens GN=PRKCG PE=1 SV=3 - [KPCG_HUMAN]	1.00	1
Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	0.99	2
Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN]	0.97	1
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	0.94	1
P58215	Lysyl oxidase homolog 3 OS=Homo sapiens GN=LOXL3 PE=2 SV=1 - [LOXL3_HUMAN]	0.93	2
P55198	Protein AF-17 OS=Homo sapiens GN=MLLT6 PE=1 SV=2 - [AF17_HUMAN]	0.91	1
Q8NEM7	Transcription factor SPT20 homolog OS=Homo sapiens GN=SUPT20H PE=1 SV=2 - [SP20H_HUMAN]	0.90	1
Q15477	Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=1 SV=3 - [SKIV2_HUMAN]	0.80	1
Q00858	Epithelial cell-transforming sequence 2 oncogene-like OS=Homo sapiens GN=ECT2L PE=2 SV=2 - [ECT2L HUMAN]	0.77	1
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 - [RAD50_HUMAN]	0.76	2
060264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 - ISMCA5 HUMANI	0.76	1
Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205 HUMAN]	0.75	2
P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 - [RBP2 HUMAN]	0.71	4
060241	Prain-specific angiogenesis inhibitor 2 OS-Homo saniens GN=BA12 PF=2 SV=2 - IBA12 HUMAN1	0.69	2
P11388	DNA tonokomerase 2-alnha OS=Hom sanjens GN=TOP2A PF=1 SV=2 ST TOP2A HIJMANI	0.65	2
000411	DNA-directed RNA notwersse infliction drial OS-Hom sanices (N=POHTPE=1 SV=2 _ 100 AH (HIMAN)	0.65	1
000111	Cardio 2. O C-Mann payments, intercenting 00-18/103 appendix 00-10000 appendix 00-1000 appendix 00-1000 appendix 00-10000 appendix 0	0.05	1
Q0WAEU	Lashirz 0.3- Iruin saprins (3)DirC Der 15 V-2 - (LSNL_NUPAN) Dirtin OC-Homs sains (3)DirC Der 15 V-2 - (DirC HillMAN) Dirtin OC-Homs sains (3)DirC Der 15 V-2 - (DirC HillMAN)	0.38	2
D12270		0.30	1
05/0/2	INUCCUPITER TO USE INTO A SUBJECTS STATE IF K YESTS / [IPK_TOURN]	0.30	1
012111		0.30	1
PIZIII	L DIADED ADDA-SUVU CUARU USEDOUD SADIEDS GIVEL OLIDA S PEEL SVES - LL UBA S PEUMANI	11//	1

Accession	Description	ΣCoverage	Σ# PSMs
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	56.09	53
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA HUMAN]	47.88	17
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30 HUMAN]	46.96	9
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9 HUMAN]	46.91	41
P46779	60S ribosomal protein 128 OS=Homo sapiens GN=RPI 28 PE=1 SV=3 - [RI 28 HUMAN]	43.07	13
P15880	40S ribosomal protein S2 OS=Horm saniens (N=RPS2 PF=1 SV=2 - [RS2 HIIMAN]	41.64	21
P23306	Als ribosonal protein 52 OS-Homo canient GN-DDS2 EF1 SV-2 [IOS-1004N]	41 15	20
P62290	405 ribosomal protein 51 0 CS-100 sapietis Giv-Ar55 FL-1 5V-2 (CS-100-Mit)	41.13	2.
P02200	HUS INDUSTRIAL PROCEEDING ALL AND ADDRESS AND AND AND ADDRESS AND	41.14	
P49458	Signal recognition particle 9 KDa protein US=Homo Sapiens GN=SKP9 PE=1 SV=2 - [SkP09_HUMAN]	40.70	
P62249	405 ribosomal protein 516 OS=Homo sapiens GN=RP516 PE=1 SV=2 - [R516_HUMAN]	40.41	10
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	40.22	1
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	40.00	2.
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	39.81	13
060814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	38.89	15
P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	38.20	20
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HINRNPK PE=1 SV=1 - [HNRPK_HUMAN]	37.15	34
P22392	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]	36.84	10
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	36.79	70
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	36.36	2
P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31 HUMAN]	36.03	10
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HINRNPA1 PE=1 SV=5 - [ROA1 HUMAN]	36.02	34
P08670	Vimentin QS=Homo sapiens GN=VIM PE=1 SV=4 - [VIMF_HUMAN]	35.84	4(
P62701	40S ribosomal protein S4_X isoform OS=Homo saniens GN=RP54X PF=1 SV=2 - [R54X_HIIMAN]	34.60	15
P26373	60 schosomal protein 113 OS-Homo schiare GN-DD13 DF-1 STATE [10 AN]	34.60	20
D60700	Acting and appreciate Construction of the CPT December 2011 Constructi	22.22	2.
00005	Acting cytopication 1 00-1 total september 2017-2017 (Acting Total Park)	33.33	
QONZ57		33.33	10
P62857	405 noosonnai protein 528 OS=nomo sapiens Gui=kr528 PE=1 SV=1 - [K528_nUMAN]	33.33	
Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIS11H2AH PE=1 SV=3 - [H2A1H_HUMAN]	32.81	9
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	32.55	26
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNRPC_HUMAN]	31.70	21
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	31.40	30
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	31.26	30
P84103	Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [SRSF3_HUMAN]	31.10	9
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	30.52	19
Q9Y3C1	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16_HUMAN]	30.34	12
P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	29.81	10
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	29.41	13
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_HUMAN]	29.37	21
P05204	Non-histone chromosomal protein HMG-17 OS=Homo sapiens GN=HMGN2 PE=1 SV=3 - [HMGN2 HUMAN]	28.89	4
P04264	Keratin, type II cytoskeletal 1 OS=Homo sabiens GN=KRT1 PE=1 SV=6 - [k2C1 HUMAN]	28.73	30
015366-7	Soform 7 of Poly(r()-binding protein 2 OS=Homo saniens GN=PCRP2 - [PCRP2 HIMAN1	28.62	
P07437	Tuhulin beta chain OS-Homo caniang GO-TI IBR DE-1 SV-2 , TTRRS HI MANI	28.60	3(
D62947	All scheme in protein Scheme scheme scheme S	20.00	50
D0E16E	TO TRUSTING PICEL 2CT OST MID SERVICE ON TRUSTIC IN TRUSTICE INTERVICE INCOMENTATION OF TRUSTICE INTERNO IN TRUSTICE IN TRUSTICE IN TRUSTICE IN TRUSTI	20.57	20
PU5105	Propiety-CoA carboxylase alpita citalit, intocionidiai OS=horito sapieto six=PCCA PE=1 Sv=4 - [PCCA_horitait]	20.37	50
P46/82	405 nbosonal protein 55 05=homo sapiens GN=RP55 PE=1 SV=4 - [K55_HUMAN]	27.94	1.
Q13885	Iubuin beta-2A chan OS=Homo sapiens GN=IUB82A PE=1 SV=1 - [IB82A_HUMAN]	27.87	30
P29372	DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 - [3MG_HUMAN]	27.85	12
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2 - [IF5A1_HUMAN]	27.27	6
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	27.23	26
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	27.20	20
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	27.14	13
P63267	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]	27.13	2
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	26.90	
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	26.83	
Q8TEK3	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Homo sapiens GN=DOT1L PE=1 SV=2 - [DOT1L HUMAN]	26.74	10
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RI 19 HIJMAN]	26.53	1
P52272	Heterogeneous nuclear ritionucleonrotein M OS=Homo saniens GN=HIRRIPM PF=1 SV=3 - [HIRRIPM HI IMAN]	26.65	3.
D69104	Expertion Sector 1 alpha 1 Oct Hom controls Child EE104 DE 1 (1-1) [EE104 DE 1 HIMAN]	20.11	21
100104	Longation ractor 1 albua 1 00-notio pabletis diversi 141 LE-1 3V-1 - [El 141 LIONAIA]	20.19	53

Table 20. Raw data of BioID experiment: BioID-DOT1L-mut infected HEK293T cells, 2^{nd} reading

Accession	Description	ΣCoverage	Σ# DSMc
ALLESSION	Non-DOL domin-containing octamer binding protein OS-blom caping: Ch=NONO_BE_1_S/=4ENONO_BLIMANI	200Verage	2# 13115
Q13233	Ren too dollar too tabinding occurre transing processing appendix of a non-rest of the rent 25.87	25	
Q5DVF2	Qualinite inducedute/unituity protectifike a OGE- Mining sequence of the Control	25.87	2.
P1/044	Provable A P-dependent kniw fieldase Duxo OS=nonitio sapietis OLAS - DUXS-TO-LANG - DUX-TO-LANG - DU	25.75	41
P08107	Heat snok / vka protein 1A/15 US=homo sapiens GN=H5/ALA PE=1 SV=5 - [Th5P/1_HUMAN]	25.43	
P02033	Cellular nucleic acid-binding protein OS=homo sapients Gv=CNBP PE=1 SV=1 - [UNRP_HOMAN]	25.42	6
P2/635	Sous moissing protein Liu OS=Homo sapiens GH=RPLIU FE=1 SV=4 - [KLLQ_HUMAN]	25.23	14
P62910	605 filosomai protein 132 (5=Homo sapiens GN=KP132 /F=1 SV=2 - [R132 - [NI32]	25.19	10
P83881	bus nosomal protein L36a US=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]	24.53	10
P63173	605 ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	24.29	-
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	24.19	23
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1HIC PE=1 SV=2 - [H12_HUMAN]	23.94	14
P62244	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2 - [RS15A_HUMAN]	23.85	6
P62318	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1 - [SMD3_HUMAN]	23.81	3
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	23.63	18
P38159	RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3 - [RBMX_HUMAN]	23.53	19
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	23.26	5
P05114	Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=3 - [HMGN1_HUMAN]	23.00	4
P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	22.62	2
P29692	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5 - [EF1D_HUMAN]	22.42	1
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	22.38	11
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA_HUMAN]	22.25	9
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	21.63	12
P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23 HUMAN]	21.43	
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB HUMAN]	21.26	1
P10809	60 kDa heat shock protein, mitochondrial OS-Homo sablens GN=HSPD1 PE=1 SV=2 - ICH60 HUMANI	20.94	2
P62854	40S ribosomal protein S26 OS=Homo saniens GN=RPS26 PF=1 SV=3 - IRS26 HUMAN1	20.97	-
076021	Ribosonal I domain-containing protein 1 OS Hom spring GN=8 (1D) PF (10PF (10 PF (10PF (10 PF (10PF (10 PF (10PF (1	20.37	10
P25705	All South at domain original protein a OS-HATD Salperis of A-NELDI FE-1 SY-2 [RED2_HOPM]	20.01	1
016620	Air syntaise subunit aping introduction of 3-inform september 2014 AIR Section 2014 AIR Sec	20.01	2.
010029	Cellina (Cellina Cellina Ce	20.39	
P23528	Comin-1 US=Homo saplens GN=C+LI PE=1 SV=3 - [COFI_HUMAN]	20.48	
P12236	ADP/AIP translocase 3 US=Homo sapiens GR=SLC25A6 PE=1 SV=4 - [AD13_HUMAN]	20.47	18
P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	20.31	6
P62987	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]	20.31	6
Q96EY4	Translation machinery-associated protein 16 OS=Homo sapiens GN=TMA16 PE=1 SV=2 - [TMA16_HUMAN]	20.20	9
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	20.06	22
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	19.95	11
P62891	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]	19.61	2
P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 - [RL27A_HUMAN]	19.59	8
P27695	DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2 - [APEX1_HUMAN]	19.50	8
Q99623	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	19.06	9
Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	19.02	12
000571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X HUMAN]	18.58	26
P23246	Solicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPO PE=1 SV=2 - [SFPO HUMAN]	18.39	26
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP2C_HUMAN]	18.27	26
P22087	RNA 2'-O-methyltransferace fibrillarin OS=Homo saniens GN=EBI PE=1 SV=2 - [EBR] HUMANI	18.07	1
002543	60S ribosomal protein 18a OS=Horno sanjans GN=RPI 18a PE=1 SV=2 - [R1 18a HIIMAN]	17.61	
P06748	Nucleonaria DS-Homo saniare GN-NDMI DF-1 SU-2 - [NDM H] MMN]	17.01	1
D22060	Accorptionary protein 0.0 C= Marca Particle Part (C= 200, C= 10,	17.33	1
014102	Judzi Judzinia ji judzini 5 03-1 kili bi spjenis dv-Art 5 rL-1 3v-1 * [LC5_1 kili privit]	17.19	12
Q14105	neterogeneous induced nooninduce/protein bolos=noinb sapients direminikative pre=1 sv=1 - [nikePb_noinain]	17.10	13
P62269	405 noosomai protein 518 OS=Homo sapiens GN=KP518 PE=1 SV=3 - [K518_HUMAN]	17.11	
A8MWD9	Putative small nuclear ribonucleoprotein G-like protein 15 US=Hormo sapiens GM=SNRPGP15 PE=5 SV=2 - [RUXGL_HUMAN]	17.11	4
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	16.97	4
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	16.96	2
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	16.95	2
Q99729-3	Isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB - [ROAA_HUMAN]	16.49	
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	16.38	1
P84090	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1 - [ERH_HUMAN]	16.35	2
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	16.32	23
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]	16.27	10
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN]	16.17	7
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	16.16	21
P50990	T-complex protein 1 subunit theta OS=Homo saniens GN=CCT8 PE=1 SV=4 - [TCPO_HUMAN]	16.06	15
O9H5H4	Zinc finger protein 768 OS=Homo sabiens GN=ZNF768 PE=1 SV=2 - [ZN768 HUMAN]	15.74	13
000839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HINRNPU PE=1 SV=6 - [HNRP1] HIJMANI	15.64	25
015717	FIAV-like protein 1 OS=Homo soniens (N=FI AVI 1 PF=1 SV=2 - [FI AVI 1 HJMAN]	15.64	
O8IWS0	PHD finger protein 6 OS=Homo spaciens GN=PHF6 PE=1 SV=1 - [PHF6 HUMAN]	15.62	
D31043	Heterogeneine nickasterine to the term caning COLIMINATION COLIMINAT	15.02	11
D62851	All choored installing Store-Home series (Share) Store (Sh	15.35	
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F 32119		15.15	t
r1480b	The Druk Halder anti-the ADC LOS=HORD Saplers GN=HINKINFLFE_L SVZ- [HNKPL_HUMAN]	15.11	18
Q13148	TAK DIVA-DINGING PROTEIN 45 OS-HOMO SAPIENS GN=TAKUBH YE=1 SV=1 - [TAUBH HUMAN]	14.98	10
P06576	A IP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	14.74	10
043175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	14.45	12
P50914	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 - [RL14_HUMAN]	14.42	4
Q8N726	Cyclin-dependent kinase inhibitor 2A, isoform 4 OS=Homo sapiens GN=CDKN2A PE=1 SV=2 - [CD2A2_HUMAN]	14.39	2
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	14.35	8
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	14.22	7
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	13.91	
B2RPK0	Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 - [HGB1A_HUMAN]	13.74	(
4			

Description Distance and an introduction (Dis France ageins (Dis Distance ageins (Distance ageinc) (Distance ageins (Distance ageins (Distance ageins	Accorcion	Description	5Covorago	5# DCMc
0222 Lic / He pricht 0.5-Henn space 0.6-LUCL 19.4-92. [LCL 19.4490] 1.23 1.23 10211 Glef facoral prichts	O60506	Leternoeneous nuclear rihonucleonrotein O. OS=Homo saniens GN=SYNCRIP PF=1 Sv=2 - THNRPO. HI IMAN1	13.64	2# PSPIS
CHACL 2015 Disk chacking product 3.1. Includence 0.5-inter sages 0.6-inter 1.124. [URA] MANU 1.2.8 1.2.9 CHACL 2015 Set chacking product 3.1. Set chacking 0.6-inter 1.124. [URA] MANU 1.2.1 1.2.1 CHACL 2015 Set chacking product 3.1. Set chacking 0.6-inter 1.124. [URA] MANU 1.2.1 1.2.1 CHACL 2015 Set chacking product 3.1. Set chacking 0.6-inter sages 0.6-inter 1.124. [URA] MANU 1.2.0 1.2.1 CHACL 2015 Set chacking product 3.1. Set chacking 0.6-inter sages 0.6-inter 1.124. [URA] MANU 1.2.0 1.2.1 CHAL 2015 Set chacking product 3.1. Set chacking product 3.1. Set chacking 0.1. Set product 3.1. Set prod	095232	Lucz-like protein 3 OS=Homo sapiens GN=11/C7/3 PF=1 SV=2 - [I/C7/3 HUMAN]	13.43	16
PMD21 602 rboost prode 1.44 Sol-line spaces Gl-MR M = 1.94 - [1921. [1940] 1.31 OHS Service product of bard for a factor space GL-MR M = 1.94 - [1921. [1940] 1.32 OHS Dering and production spector for factor space GL-MR M = [1941. [1941. [1941] 1.32 OHS Dering and production spector for factor space GL-MR M = [1941. [1941. [1940] 1.32 OHS Dering and production spector for factor space GL-MR M = [1941. [1941. [1940] 1.32 OHS Dering and production factor 4.10 Service space GL-MR M = [1941. [1940] 1.23 OHS Dering and production factor 4.10 Service space GL-MR M = [1941. [1940] 1.24 OHS Dering and production factor 4.10 Service space GL-MR M = [1941. [1940] 1.24 OHS Dering and production factor 4.10 Service space GL-MR M = [1941. [1940] 1.24 1.24 OHS Dering and production factor 4.10 Service space GL-MR M = [1941. [1941] 1.24 1.24 1.24 OHS Dering and production factor 4.10 Service space GL-MR M = [1941. [1941] 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24 1.24	Q96EL3	39S ribosomal protein L53, mitochondrial OS=Homo sapiens GN=MRPL53 PE=1 SV=1 - [RM53 HUMAN]	13.39	2
00095 Semulophism on discription 1.05-brow space 0.0-8207 (m ⁻¹ , Se ¹ , S	P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24 HUMAN]	13.38	4
OHB00 Charge and palesdrophic hashes and Society and palesdrophic hashes (Society and Society and	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	13.31	5
00287 Börhessen jereten IGS-riters agere GH-BBR Fr.1 Str [FBA, JURAN] 11.0 11.0 00287 Börhessen jereten IGS-riters agere GH-BBR Fr.1 Str [FBA, JURAN] 12.6 1 00270 Bork in Edu Coll-sters agere GH-BBR Fr.1 Str [FBA, JURAN] 12.6 1 00270 Bork in Edu Coll-sters agere GH-BBR Fr.1 Str [FBA, JURAN] 12.6 1 12.10 Environment Str [FBA, JURAN] 12.6 1 12.11 Environment Str [FBA, JURAN] 12.6 1 12.11 Environment Str [FBA, JURAN] 12.6 1 12.12 Environment Str [FBA, JURAN] 12.6 1 12.13 Environment Str [FBA, JURAN] 12.6 1 12.14 Environment Str [FBA, JURA JURAN] 12.6 1 12.15	O43809	Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1 - [CPSF5_HUMAN]	13.22	4
Note: Elaryon: Intern face 4-00-term space 01-FERM 11-FERM 11-	Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	13.19	10
PA1010 Match in Sterbars and Control IP(14) 1.2.9 2.2.9.9 2.2.9	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [IF4A1_HUMAN]	13.05	9
20019 Introduct proton line Add Construct agene Gill-Place (FMAX (LAMA)) 11.5 11.5 20019 Introduct proton line Add Construct agene Gill-Place (FMAX (LAMA)) 12.4 12.5 20019 Introduct proton line Add Construct agene Gill-Place (FMAX (LAMA)) 12.4 12.5 20019 INTRACE Add Construct agene Gill-Place (FMAX (LAMA)) 12.4 12.5 20019 Introduct agene Gill-Place (FMAX (LAMA)) 12.4 12.5 20019 Introduct agene Gill-Place (FMAX (LAMA)) 12.4 12.5 20019 Introduct agene Gill-Place (FMAX (LAMA)) 12.6 12.5 20019 Introduct agene Gill-Place (FMAX (LAMA)) 11.6 12.5 20139 Introduct Agene Gill-Place (FMAX (LAMA	P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	12.99	24
(Photo B) Bit Adda (Dis-Letter spaces (Di-BOMA) (LEA) 11.1 11.1 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 2 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 1 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 1 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 1 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 1 / Sol-tree spaces (Di-BOMA) 12.4 12.4 (Photo B) Designed for 1 / Sol-tree space (Di-BOMA) <td>P20719</td> <td>Homeobox protein Hox-AS OS=Homo sapiens GN=HOXAS PE=1 SV=2 - [HXA5_HUMAN]</td> <td>12.96</td> <td>4</td>	P20719	Homeobox protein Hox-AS OS=Homo sapiens GN=HOXAS PE=1 SV=2 - [HXA5_HUMAN]	12.96	4
PL10: Units add/ord (0) PL00: // END/NE Example Co-PUPOR Example Co-PUPOR 2007 (2004) 1.2.6 1.2.6 PL12: Units add/ord (0) PL00: // END/NE Example Co-PUPOR 2007 (2004) 1.2.4 1.2.4 PL12: EGG reasoning protein LGG Co-PUPOR agenes (0) PL02 (4004) 1.2.4 1.2.5 PL12: EGG reasoning protein LGG Co-PUPOR agenes (0) PL02 (4004) 1.2.5 1.2.5 PL12: EGG reasoning protein LGG - Fortons agenes (0) PL02 (4004) 1.2.5 1.2.5 PL12: EGG reasoning protein LGG - Fortons agenes (0) PL02 (4004) 1.2.5 1.2.5 PL12: EGG reasoning protein LGG - Fortons agenes (0) PL02 (4004) 1.2.6 1.2.6 PL12: P	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	12.94	10
1.0007 BM20 dim Name download from the bulk of GA-MATH, 15-1 (RAL, HANA) 1.0 </td <td>P42167</td> <td>Lamina-associated polypeptide 2, isoforms beta/gamma US=Homo sapiens GN=I MPO PE=1 SV=2 - [LAP2B_HUMAN]</td> <td>12.56</td> <td>8</td>	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma US=Homo sapiens GN=I MPO PE=1 SV=2 - [LAP2B_HUMAN]	12.56	8
00125 05:31:00 (S-bron seques (0.89/23/FE 159:1-1902, 1904) 1.2 1.2 1.2 00126 05:00 (S-bron codes ub. htt /OVA (AS-bron seques (0.89/23/FE 159:1-1902, 1904) 1.3 1.2 00126 05:00 (S-bron codes ub. htt /OVA (AS-bron seques (0.49/27/FE 159:1-1902, 1904) 1.3 1.1 01126 05:00 (S-bron codes (0.49/07/FE 159:1-1902, 1904) 1.16 1.0 01126 05:00 (S-bron codes (0.49/07/FE 159:1-1902, 1904) 1.16 1.0 01126 05:00 (S-bron codes (0.49/07/FE 1159:1-1902, 1904) 1.16 1.0 01126 05:00 (S-bron codes (0.49/07/FE 1159:1-1904) 1.16 1.0 01126 05:00 (S-bron codes (0.49/07/FE 149:1-1904) 1.16 1.0 01126 10:00 (S-bron codes (0.49/07/FE 149:1-1904) 1.16 1.0 01126 </td <td>P13639</td> <td>Exongation factor 2 US=Homo Sapiens GH=EEF2 VF=1 SV=4 + [EF2_HUMAN]</td> <td>12.47</td> <td>20</td>	P13639	Exongation factor 2 US=Homo Sapiens GH=EEF2 VF=1 SV=4 + [EF2_HUMAN]	12.47	20
000000 Cychoteme cycles wheth UD244/05-40m squere (D-HU244F1; SA-1 (PULA)(HAN)) 12.35 012000 Nethoder (D-Hosing preto 10-50m squere (D-HU274F1; SA-1 (PULA)) 11.97 01200 Methoder enhances that (D-Hosing preto 10-50m squere (D-HU274F1; SA-1 (PULA)) 11.97 01200 Methoder enhances that (D-Hosing preto 10-50m squere (D-HU274F1; SA-1 (PULA)) 11.87 01200 Methoder enhances that (D-Hosing preto 10-50m squere (D-HU274F1; SA-1 (PULA)) 11.48 01200 Methoder enhances that (D-Hosing preto 10-10m squere (D-HU274F1; SA-2 (PUL2, MANA)) 11.48 11.44 01200 Methoder enhances that (D-Hosing Preto 10-10m squere (D-HU274F1; SA-2 (PUL2, MANA)) 11.45 11.45 11.45 01200 Methoder Enhances (D-HU274F1; SA-2 (PUL2, MANA) 11.45	Q9N112 D612E4	TAACA TIDOTICLE CUPTOLETING TO SETUDIO SALETING AND THE TO	12.44	3
00200 Nackskir CPI background 12.0 11 01201 Intersite information of the start start of the constraint	000483	Cytochrome covidase subunt NDI F64 O S=Home sainers (SH=NDI F64 PE=1 SV=1 - (NDI 64 HI MAN)	12.11	2
0.2906 Internation enhance advance data 3 CS-1000 agains GH-197 E-1 SP-3 [UP3_HAMM] 11.92 11.92 0.2105 Strain-generation advance monocompares GN-1978 E-1 SP-3 [UP3_HAMM] 11.62 11.62 N223 Strain-generation advance monocompares GN-1978 E-1 SP-3 [UP3_HAMM] 11.63 11.63 N233 Strain-generation advance monocompares GN-1978 E-1 SP-3 [UP3_HAMM] 11.64 11.64 N234 Strain-GN-1978 E-1 SP-3 [UP3_HAMM] 11.53 11.64 N234 Strain-GN-1978 E-1 SP-3 [UP3_HAMM] 11.64 11.64 N234 Strain-GN-1978 E-1 SP-3 [UP3_HAMM] 11.64 11.61 11.61 N234 Strain-GN-1978 E-1 SP-3 [UP3_HAMM] 11.64 11.61<	0987F4	Systematic transfer and the second seco	12.30	16
(1)210 Strendpringer, charge factor, factor, 6 Co-Horn segiers (0-HSRF (FF 19-2-; [SRF (JHMA)] 11.69 11.76 C (1)210 Hetrogeneons index information pairs (0-HMRR (FF 19-2-; [SRF (JHMA)] 11.69 C (1)210 Interestal methods (-Interestapes (0-HMRR (FF 19-2-; [I/12, JHMA)] 11.54 C (1)200 Interestal methods (Interestapes (0-HMRR (FF 19-2-; [I/12, JHMA)] 11.64 C (1)200 Interestation methods (Interestapes (0-HMRR (FF 19-2-; [I/12, JHMA)] 11.64 C (1)200 Interestation methods (Interestapes (0-HMRR (FF 19-2-; [I/12, JHMA)] 11.16 C (1)200 Interestation methods (Interestapes (0-HMRR (FF 19-2-; [I/12, JHMA)] 11.10 C (1)200 Interestation frame proteon Seleme SIGH (INTER (INT	Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3 HUMAN]	11.97	18
Pi-32 protein epake On-throw appres ON-WARE PE-1 Syn - 1 (1982), HUMM) 11-69 11 PM-50 protein syn action to So-throw appres ON-WARE PE-1 Syn - 1 (1982), HUMM) 11-69 11 PM-50 protein Co-throw appres ON-WARE PE-1 Syn - 1 (1982), HUMM) 11-64 11 PM-50 protein Co-throw appres ON-WARE PE-1 Syn - 1 (1982), HUMM) 11-54 11 PM-50 protein Co-throw appres ON-SERVID HER Syn - 1 (1982), HUMM) 11-54 11 PM-50 protein Co-throw appres ON-SERVID HER Syn - 1 (1982), HUMM) 11-16 11	Q13247	Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2 - [SRSF6_HUMAN]	11.92	8
0.0339 Heterogeneon nacker thouckeyords (0.1-bitms agene (0.H-MWR) RE-1.94-2. (10.2, UMAN] 11.54 0.0 0.1396 Endendation ethnoc agenes (0.H-L107 Her.1.94-2. (10.2, UMAN] 11.54 0.0 0.1396 Endendation ethnoc agenes (0.H-U107 Her.1.94-2. (10.2, UMAN] 11.52 0.0 0.1391 Endendation ethnoc agenes (0.H-U107 Her.1.94-2. (10.2, UMAN] 11.52 0.0 0.1391 Endendation ethnoc agenes (0.H-U107 Her.1.94-2. (10.2, UMAN] 11.12 11.12 0.1391 Endendation ethnoc agenes (0.H-U107 Her.1.94-2. (10.02, UMAN) 11.10 11.10 12.0 0.1391 Endendation from genes (0.H-U107 Her.1.94-2. (1002, UMAN) 11.10 12.0 12.0 0.1391 Endelation from genes (0.H-U107 Her.1.94-2. (1002, UMAN) 11.10 12.0 12.0 0.1391 Endelation from genes (0.H-U107 Her.1.94-1. (1002, UMAN) 10.0 12.0 12.0 0.1392 Endelation from genes (0.H-U107 Her.1.94-1. (1002, UMAN) 10.0 10.0 12.0 0.1392 Endelation from genes (0.H-U107 Her.1.94-1. (1002, UMAN) 10.0 10.0 10.0 10.0 10.0 10.0 10.0	P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	11.76	6
PISSE Endounchase III Regrete Indo- Hom segies GH-PITH IF S-V-2 [INZ - HOW] 11.54 61 Ditto Batteria Homoro Work (Factor 20 Serbon segies GH-2017 H K-1 SV-2 [INZ - HOW] 11.64 61 GRID A Disto Homoro Work (Factor 20 Serbon segies GH-2017 H K-1 SV-2 [INZ - HOW] 11.64 61 GRID A Disto Homoro Moro Segies GH-2017 H K-1 SV-2 [INZ - HOW] 11.15 11.15 GRID A Disto Homoro Moro Segies GH-2017 H K-1 SV-1 [INZ - HOW] 11.11 11.10 GRID A Personacities G Inter Trans segies GH-2017 H K-1 SV-1 [INZ - HOW] 11.11 11.10 GRID A Personacities G Inter Trans segies GH-2017 H K-1 SV-1 [INZ - HOW] 11.10 12.22 GRID A Disto Homoro Moro Segies GH-2017 H K-1 SV-1 [INZ - HOW] 10.65 12.22 GRID A Disto Homoro Moro Segies GH-2017 H K-1 SV-1 [INZ - HOW] 10.65 12.22 GRID A Disto Homoro Moro Segies GH-2017 H K-1 SV-1 [INZ - HOW] 10.55 12.22 GRID A Disto Homoro Moro Segies GH-2017 H K-1 SV-1 [INZ - HOW] 10.63 12.22 GRID A Disto Homoro Moro Segies GH-2017 H K-1 SV-1 [INZ - HOW] 10.63 12.22 GRID A Disto Homo	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	11.69	16
QL200 Interleader enhance sheefing factor 2.05-free superior Science 2.102-2,1004N] 11.54 11.54 QL200 UPRO86 protect (Ch17) ACC 1000 superior SC-1001 PAE 1.347-2,1247A, JURAN] 11.64 6 QL200 Septem 10.05-free superior SC-1007 PAE 1.347-2, ISBN JURAN] 11.65 11.65 QL200 Maximum NM Indiana CDX00 Septem Science ADX00 PAE 1.574-1 [DX01A, JURAN] 11.10 11.11 QL200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 11.01 12.02 QU200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 11.01 12.02 QU200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 10.51 12.02 QU200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 10.53 12.02 QU200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 10.63 12.02 QU200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 10.63 12.02 QU200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 10.03 12.02 QU200 Maximum SC 10-5-free superior SC-1002 PAE 1.574-1 [DX01A, JURAN] 10.02 12.0	P78549	Endonuclease III-like protein 1 OS=Homo sapiens GN=NTHL1 PE=1 SV=2 - [NTH_HUMAN]	11.54	6
QBU10 UPROBE predm.10174 (G-shron sagers GH-CLOT14 FE-13V-2 (CA174, HUMA) 11.42 11.42 Q1388 Spiconcome NM Alexae DDCMI0 G-hron sagers GM-CLOXPH FE-13V-2 (DCM) HUMA) 11.22 11. Q1388 Spiconcome NM Alexae DDCMI0 G-hron sagers GM-CLOXPH FE-13V-2 (DCM) HUMA) 11.22 11. Q1388 Spiconcome NM Alexae DDCMI0 G-hron sagers GM-CHOXP FE-13V-2 (DCM, HUMA) 11.11 11.11 Q1070 Alexabar NM Indexae DDCMI0 G-hron sagers GM-CHOXP FE-13V-2 (DLSM, HUMA) 10.69 10.71 Q1070 Alexabar Rube spices GM-CHOXP FE-13V-1 (DOSE HUMA) 10.69 10.71 Q1070 Alexabar Rube spices GM-CHOXP FE-13V-2 (DLSM, HUMA) 10.63 10.71 Q1070 Alexabar Rube spices GM-CHOXP FE-13V-2 (DLSM, HUMA) 10.63 10.71 Q1070 Alexabar Rube spices GM-CHOXP FE-13V-2 (DLSM, HUMA) 10.63 10.71 Q1070 Alexabar Rube spices GM-CHOXP FE-13V-2 (DLSM, HUMA) 10.63 10.71 Q1070 Alexabar Rube spices GM-CHOXP FE-13V-2 (DLSM, HUMA) 10.63 10.71 Q1070 Alexabar Rube spices GM-CHOXP FE-13V-2 (RDZ, HUMA) 10.64 10.72 Q1070 Alexabar Rube spices GM-	Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2_HUMAN]	11.54	10
numbes bergin if Los-itom sagers (ht-SRPRint Pice 1, 292-7, LBRPH, LUMM) 11.48 64 102188 Sciences RN Medicas DOS do-itom sagers (ht-RCXP Her 1, 594-1 [DOSR, HUMM) 11.12 11.12 102100 India Markanz / DS-itom sagers (ht-RCXP Her 1, 594-1 [DOSR, HUMM) 11.11 11.12 102100 India Markanz / DS-itom sagers (ht-RCXP Her 1, 594-1 [DOSR, HUMM) 11.11 11.12 102100 India Markanz / DS-itom sagers (ht-RCXP Her 1, 594-1 [DOSR, HUMM) 10.90 12.12 102100 Markanz protein SD OS-itom sagers (ht-RCXP Her 1, 594-1 [DOSR, HUMM] 10.90 12.12 10207 Markanz protein SD OS-itom sagers (ht-RCXP Her 1, 594-1 [PDR J, HUMM] 10.61 12.12 10207 Markanz protein SD OS-itom sagers (ht-RCXP Her 1, 594-1 [PDR J, HUMM] 10.63 12.12 10208 Markanz protein SD OS-itom sagers (ht-RCXP Her 1, 594-1 [PDR J, HUMM] 10.64 12.12 10209 Phylymid (ht stark hing protein SD OS-itom sagers (ht-RCXP HZ Her 1, 594-1 [PDR HER 1, 594-1	Q8IYL3	UPF0688 protein Clort174 OS=Homo sapiens GN=Clorf174 PE=1 SV=2 - [CA174_HUMAN]	11.52	4
(1,135) Spectratome non-nackie UAU-990 (S-H100 Spectra (MAV) [1,14] [1,15] [1,15] (1,15) Machedie TRin Mendee 2 (S-H100 Spectra (MAV) (F-1 SV-1 (MAV)) [1,11] [1,11] (1,11) Machedie TRin Mendee 2 (S-H100 Spectra (MAV) (F-1 SV-1 (MAV)) [1,11] [1,11] (1,11) Machedie TRin Mendee 2 (S-H100 Spectra (MAV) [1,12] [1,11] [1,11] (1,11) Machedie TRin Mendee 2 (S-H100 Spectra (MAV)) [1,12] [1,11] [1,11] (1,11) Machedie TRin Mendee 2 (S-H100 Spectra (MAV)) [1,12] [1,11] [1,11] (1,11) Machedie TRin Mendee 2 (S-H100 Spectra (MAV)) [1,12] [1,11] [1,12] (1,11) Machedie TRin Mendee 2 (S-H100 Spectra (MAV)) [1,12] [1,11] [1,12] (1,12) Machedie Trin Spectra (MAV) [1,12] [1,12] [1,12] [1,12] (1,12) Machedie Trin Spectra (MAV) [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12] [1,12]	P50454	Serpin H1 US=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	11.48	8
rescuence set ingle placet 0-5 mus agenes GN-PDR 12 = 3x-1 (metUNW) 11.10 11.20 Q2119 RAV2.24e protein Stop Chrono segnes GN-PDR 21 = 5x-5 : [CDR 21, UNWN] 11.10 12.20 Q2119 RAV2.24e protein Stop Chrono segnes GN-PDR 21 = 5x-5 : [CDR 21, UNWN] 10.50 11.10 22 Q2119 RAV2.24e protein Stop Chrono segnes GN-PDR 21 = 5x-5 : [CDR 21, UNWN] 10.50 11.10 22 Q2119 RAV2.24e protein Stop Chrono segnes GN-PDR 21 = 5x-1 : [CDR 21, UNWN] 10.55 11.50 12 Q2207 RAV5.24e protein Stop Chrono segnes GN-PDR 21 = 5x-1 : [CDR 21, UNWN] 10.43 12 Q2207 Tansgebr- 20 = 51-bron segnes GN-PDR 21 = 5x-1 : [CDR 21, UNWN] 10.43 12 Q2208 RAV5.24e protein Chrono segnes GN-PDR 21 = 5x-1 : [CDR 21, UNWN] 10.42 12 Q2208 Stop Interpot protein Stop Chrono segnes GN-PDR 21 = 5x-1 : [CDR 21, UNWN] 10.64 22 Q2208 Stop Interpot protein Stop Chrono segnes GN-PDR 21 = 15x-2 : [CDR 14, UNWN] 10.65 22 Q2208 Stop Interpot protein 1 : Constrain segnes GN-PDR 21 = F1 > 5x-2 : [CDR 14, UNWN] 10.65 22 Q2208 Stop Interpot PDR 14 : Interpot PDR 14 : Int	Q13838	Spiceosome kiva neikase bukasib usenomo sapiens (N=UX398 PE=1 SV=1 - [LX398_HIMAN]	11.45	10
control mecode number based 6 Ad=Land Megnes On-HOUZ PE (Ad=) (LANAN) 11.10 12. (2017) BR32.248 prodets 3-45 mode 3.04	P562/U	Improcessource unit initiate protein US=monto septents unit=mark PE=1 v=1 (mark_HUMAN]	11.32	13
000000 Nuckear practs 19 GS-Horo spins OI-NOPS PET 15-11 [DDPS] HEMM] 10.66 10.7 PR077 667 checomal protein 153 OS-Horo spins OI-NOPS PET 15-27 [ES3, LUMM] 10.61 10.7 PR027 467 checomal protein 153 OS-Horo spins OI-NOPS PET 15-72 [ES3, LUMM] 10.55 10.7 PR027 467 checomal protein 153 OS-Horo spins OI-NOPS PET 15-12 [FS1, LUMM] 10.55 10.7 PR028 Protein Distribution Control Control Spins OI-NOPS PET 15-12 [FS1, LUMM] 10.43 20.7 PR029 Payouth Control Spins OI-NOPS PET 15-12 [FS1, LUMM] 10.43 20.7 PR029 Payouth Control Spins OI-NOP Spins OI-NOPS PET 15-12 [FS1, LUMM] 10.42 10.42 PR029 Payouth Control Spins OI-NOPS PET 15-12 [FS1, LUMM] 10.42 10.16 20.7 PR029 Spinal reconption partice 142 Pay artering PET 15-12 [FS1, LUMM] 10.63 20.7 10.63 20.7 10.63 20.7 10.63 20.7 10.63 20.7 10.63 20.7 10.63 20.7 10.63 20.7 10.63 20.7 10.7 20.7 10.7 20.7 10.7 20.7 10.7	Q9NK30	Nucleolar Kiva Heikase 2 OS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein CS-Hornolin Sapletis GV=DA21 PE-1 SV=3 - [LOX21_HOVIN] PD1212ile protein SAPLETIS [LOX21_HOVIN] PD1212 PD1212 PD121 PD121 PD121 PD121 PD121 PD121 PD121 PD121 PD121 PD121	11.11	26
PB077 465 rbscored priords 132 65-shore agains (Sh-RP335 JF = 15v-2 (R15.1) LUNAN) 10.64 P2077 465 rbscored priords 132 05-shore agains (Sh-RP31 JF = 15v-2 (R15.1) LUNAN) 10.63 P3082 Transpite C3-shore agains (Sh-RP31 JF = 15v-2 (R15.1) LUNAN) 10.43 P3082 Transpite C3-shore agains (Sh-RP31 JF = 15v-1 (R12.2) LUNAN) 10.43 P3087 65 addir rbscored protein 120 05-shore agains (Sh-RP31 JF = 15v-1 (R12.2) LUNAN) 10.43 P3086 Paddy-rold c+rans accomma RNM-kinecular (4 fragment) O5-shore agains (Sh-RP11 JF = 15v-1 (R12.2) HUNAN) 10.43 P3086 Paddy-rold c+rans accomma RNM-kinecular (4 fragment) O5-shore agains (Sh-RP11 JF = 15v-2 (R12.1) HUNAN) 10.67 P3086 Poddy-rold c+rans accomma RNM-kinecular (Harganet) O5-shore agains (Sh-RP11 HP = 15v-2 (R12.1) HUNAN) 10.67 P3086 Poddy-rold kines (Sh adura) that 05-shore agains (Sh-RP11 SV-2 (R12.1) HUNAN) 10.67 P3070 Lam-Sh 20 S-shore agains (Sh-RP12 HF = 15v-2 (R12.1) HUNAN) 9.80 11 P4730 Lam-Sh 20 S-shore agains (Sh-RP12 HF = 15v-2 (R12.1) HUNAN) 9.81 12 P3070 Lam-Sh 20 S-shore agains (Sh-RP12 HF = 15v-2 (R12.1) HUNAN) 9.83 12 P3070 Lam-Sh 20 S-shore agains (Sh-RP12 H	09Y2X3	NAPTIZINE (FUCE) COSTICUTS SUPERIOR CONTEXT LET 2012 (CONTEXT)	10.96	20
Piezzz 40% rbscorni prices SLI 05-hons sages GN-PERP IF SLV - [FDE_HIMM] 10.65 Piezzy Piezzy Tansgele 2 O5-hons sages GN-PERP IF SLV - [FDE_HIMM] 10.55 Piezzy Tansgele 2 O5-hons sages GN-FERD IF SLV - [FDE_HIMM] 10.43 Piezzy Tansgele 2 O5-hons sages GN-FERD IF SLV - [FDE_HIMM] 10.43 Piezzy Tansgele 2 O5-hons sages GN-FERD IF SLV - [FDE_HIMM] 10.42 Piezzy Spain tencopit on artic 1 4 Hap preto 05-hons sages GN-FERD IF SLV - [FDE_LIMM] 10.42 Piezzy Spain tencopit on artic 1 4 Hap preto 05-hon sages GN-FERD IF SLV - [FDE_LIMM] 10.61 Piezzy Spain tencopit On artic 1 5 Hap D5-hons sages GN-FERD IF SLV - [FDE_LIMM] 10.63 Piezzy D30/creat Hase 1 O5-hons sages GN-FERD IF SLV - [FDE_LIMM] 10.03 60 Piezzy D40/creat Hase 1 O5-hons sages GN-FERD IF SLV - [FDE_LIMM] 9.0 11 Piezzy D40/creat Hase 1 O5-hons sages GN-FERD IF SLV - [FDE_LIMM] 9.8 66 Piezzy LMMA] 9.0 11 9.8 66 Piezzy LMMA] 9.8 66 9.2 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.0	P18077	Additional production by the solution of the s	10.91	2
Phytyminithe instability graden 10 selects (0+-Hom segiers (0+-HP2P (F=1, Sy-1, FTP2 (-LHUAN)) 10.55 10.55 P12002 Transgele 2 Co-Hom segiers (0-HADU PE (F) 30-1, TAD2, JHUAN) 10.43 10.43 P03587 P624404 (PA) (d-Statis Services RIM-HARCE PE (-1) (PL 2, PLANA) 10.43 10.43 P03586 Perdothypolic charts Services RIM-HARCE PE (-1) (PL 2, PLANA) 10.43 10.43 P0468 Perdothypolic charts Services RIM-HARCE PE (-1) (PL 2, PLANA) 10.42 10.33 P03586 Perdothypolic charts Services RIM-HARCE PE (-1) (PL 2, PLANA) 10.63 10.67 P03586 Perdothypolic charts Services RIM-HARCE PE (-1) (PL 2, PLANA) 10.63 10.67 P03586 Perdothypolic charts Services RIM-HARCE PE (-1) (PL 2, PLANA) 10.63 10.67 P03586 Perdothypolic charts Services RIM-HARCE PE (-1) (PL 2, PLANA) 9.86 11.17 P03598 Perdothypolic charts Services RIM-HARCE PE (-1) (PL 2, PLANA) 9.86 11.17 P03598 Perdothypolic charts Services RIMA PE (-1) (PL 2, PLANA) 9.86 12.17 P03598 Perdothypolic charts Services RIMA PE (-1) (PL 2, PLANA) 9.86 12.17 P03598	P62277	dos ribosonal protein 513 OS=Homo sapiens GN=RF513 PE=1 SV=2 - (R513 HUMAN)	10.60	6
172822 Tansgebra C5-Horns ageins G4-TAGU2 FE-1SV-3 [TAGL2 HMVN] 10.55 05387 655 addr hosonin protein 120 S5-Horns ageins GV-FINI FE1 SV-1 [HV3FM] 10.43 179786 Pedddylprolyd chrans kornsake IMVA Hreatding 4 (Tagment) O5-Horn ageins GV-FINI FE1 SV-1 [HV3FM5 HJVMN] 10.43 1797106 Spall recogreton partice 14 K4D protein O5-Horns ageins GV-FINI FE1 SV-2 [SGB1 HVMN] 10.64 1797106 Spall recogreton partice 14 K4D protein O5-Horns ageins GV-FR12 FE1 SV-2 [SGB1 HVMN] 10.67 170753 Ameen A C5-Horns ageins GN-FR122 FE1 SV-2 [RC12 HVMN] 10.03 00 170753 Ameen A C5-Horns ageins GN-FR122 FE1 SV-2 [RC12 HVMN] 9.90 111 170700 Lamin-B1 C5-Horns ageins GN-FR122 FE1 SV-2 [RC12 HVMN] 9.80 10.7 170700 Lamin-B1 C5-Horns ageins GN-FR122 FE1 SV-2 [RC12 HVMN] 9.80 10.7 170700 Lamin-B1 C5-Horns ageins GN-FR122 FE1 SV-2 [RC12 HVMN] 9.78 37 170710 Softward MC12 S0 S-Horns ageins GN-FR122 FE1 SV-2 [RC12 HVMN] 9.78 37 170714 G5 Tobosoming Totein L120 GS-Horns ageins GN-FR122 FE1 SV-2 [RC12 HVMN] 9.78 37 170714 G5 Tobosoming Totein L120 GS-Horns ageins GN-FR122 FE1	P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	10.55	12
19538 655 addr. Hossenil protein 120 C5+Hore saglers G1+BPL2 FE-1 SV-2 [SCB1_HUMAN] 10.43 10.47 19766 Pedity (hord) & trans sources NNA+ retexting (4 (Fragment) C5-Hore saglers G1+SUPL 14, HUMAN] 10.42 10.43 19716 Spail for transport protein Seci. Suburi beta O5-Hore saglers G1+SUPL 14, HUMAN] 10.42 10.43 19716 Spail for control L2 C5-Hore saglers G1+SUPL 14, HUMAN] 10.03 66 197355 Hossenity C5-Hore saglers G1+SUPL 14, HUMAN] 10.03 66 197055 Pedity C5-Hore saglers G1+SUPL 15V-2 - [NCL, HUMAN] 9.00 111 197356 Saglers G1+SUPL 12, S2-Hore Saglers G1+SUPL 14, FE-1 SV-2 - [NCL, HUMAN] 9.93 10.33 197050 Larrisk G1-Hore saglers G1+SUPL 15V-2 - [NCL, HUMAN] 9.88 66 197051 G1-Hore saglers G1+SUPL 15V-2 - [NCL, HUMAN] 9.88 66 197052 Kerathy, type II ordskeltal 2 epidermal G5-Hore saglers G1-GCGP FE 15V-2 - [NCL, HUMAN] 9.88 62 197054 Hore saglers G1+SUPL 15V-1 - [NCL, HUMAN] 9.43 10.43 197054 Hore saglers G1+SUPL 15V-1 - [NUPL 14, MUMA] 9.43 10.43 197054 Hor	P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 - [TAGL2_HUMAN]	10.55	4
HYDB6 Petbd/pind/starts isomerase. NRM-viteracting 4 (Fragmert) Co-Horon sapiers CAI-PIM PEI SV-1 - [NV246], HUMAN] 10.43 PPG466 Protest inangot protes Sec1 Jubot 14 Edo Sc-Horon sapiers CAI-SPP14/FE-1SV-2 - [SCB14_HUMAN] 10.29 P3708 Signal recognitor particle 14 KBb protein OS-Horon sapiers GN-SPP14/FE-1SV-2 - [SCB14_HUMAN] 10.07 P0538 Pinos phong Portal L22 (SCB14_HUMAN) 10.07 P0735 Amene AD OS-Horon sapiers GN-WARE / FE-1SV-2 - [N22_HUMAN] 9.00 P10700 Lamis-B1 OS-Horon sapiers GN-WARE / FE-1SV-2 - [N22_HUMAN] 9.00 P10700 Lamis-B1 OS-Horon sapiers GN-WARE / FE-1SV-2 - [N22_HUMAN] 9.07 P10710 Lamis-B1 OS-Horon sapiers GN-WARE / FE-1SV-2 - [N22_HUMAN] 9.78 P10710 Lamis-B1 OS-Horon sapiers GN-WARE / FE-1SV-2 - [C22_HUMAN] 9.45 P10710 Cond Pinot L22 OS-Horon sapiers GN-WARE / FE-1SV-2 - [C22_HUMAN] 9.45 P1071 Cond Pinot Pinot Sapiers GN-WARE / FE-1SV-2 - [C22_HUMAN] 9.45 P1071 Cond Pinot Pinot Sapiers GN-WARE / FE-1SV-2 - [C20_HUMAN] 9.45 P1071 Cond Pinot Pinot Sapiers GN-WARE / FE-1SV-2 - [C20_HUMAN] 9.21 P1071 Cond Pinot Pinot Sapiers GN-WARE / FE-1SV-2 - [C20_HUMAN]	P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	10.43	2
Piodes Protein transport protein Secial submit beta OS-Horns agalers GN-SERDI PE-1 SV-2 - [SCB14, HUMM] 10.42 11 P3708 Signal tecopitatin particle 14 Kao protein OS-Horns agalers GN-SERDI PE-1 SV-2 - [SR21, HUMM] 10.6 22 P3708 Boot Incompto protein 122 OS-Horns agalers GN-SERDI PE-1 SV-2 - [RE21, HUMM] 10.03 66 P0705 Principation Status 10.03 66 P0705 Annecin A2 OS-Horns agalers GN-MADA 2FE-1 SV-2 - [RADA, JHMAN] 90 111 P4700 Lamin-B OS-Horns agalers GN-SERDI (SPE-1 SV-2 - [RADA, JHMAN] 9.8 66 P1513 GS Frons agalers GN-MADA 2FE-1 SV-2 - [RADA, JHMAN] 9.8 66 P1513 GS Frons agalers GN-MARD 2FE-1 SV-2 - [RADA, JHMAN] 9.8 67 P1514 GS Frons agalers GN-CRAP 2FE - SV-2 - [RADA, JHMAN] 9.3 7 P1519 Frons agalers GN-ER32 FE - SV-2 - [RADA, JHMAN] 9.3 7 P1519 Frons agalers GN-ER32 FE - SV-2 - [RADA, JHMAN] 9.2 7 P1511 Exit for Status Status 7 7 P1511 Exit for Status Status 7 7 <t< td=""><td>H0Y8P6</td><td>PeptidyI-prolyl cis-trans isomerase NIMA-interacting 4 (Fragment) OS=Homo sapiens GN=PIN4 PE=1 SV=1 - [H0Y8P6_HUMAN]</td><td>10.43</td><td>1</td></t<>	H0Y8P6	PeptidyI-prolyl cis-trans isomerase NIMA-interacting 4 (Fragment) OS=Homo sapiens GN=PIN4 PE=1 SV=1 - [H0Y8P6_HUMAN]	10.43	1
P37108 Signal recognitor particle 14 Kba protein OS-Homo sagiers GN-SRP14 PE-15V-2-[RR214,HUMM] 10.29 P3526 BOS foromal protein 12.05 S-Homo sagiers GN-RR212 FE-15V-2- [RR21,HUMM] 10.07 P00575 Ameent A2 OS-Homo sagiers GN-HORZ (FE-15V-2- [RR22,HUMM] 9.09 P10700 Lamin-B1 OS-Homo sagiers GN-HORZ (FE-15V-2- [RR22,HUMM] 9.09 P10700 Lamin-B1 OS-Homo sagiers GN-HORZ FE-15V-2- [RR21,HUMM] 9.05 P10700 Case Homo sagiers GN-HORZ FE-15V-2- [RR22,HUMM] 9.07 P00700 Case Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM] 9.07 P00700 Case Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM] 9.07 P00710 CGS triplet repeat-binding protein 17.0 GS-Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM] 9.43 P00711 CGS triplet repeat-binding protein 12.0 GS-Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM] 9.28 P01714 GS for bomoral protein 12.0 GS-Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM] 9.21 P01714 Heat robunckepent DS nD LG-Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM] 9.22 P01714 Heat robunckepent DS nD LG-Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM] 9.22 P10714 Heat robunckepent DS nD LG-Homo sagiers GN-HORZ FE-15V-2- [RZ2,HUMM]	P60468	Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2 - [SC61B_HUMAN]	10.42	1
605 Rbosomal protein 122 OS+horm sapiers GN+RR12 RF: 15V-2 (R122_HUMAN) 10.07 6058 Phosphycrote kinas disc I GS+horm sapiers GN+R02 RF: 15V-2 (R122_HUMAN) 10.03 607058 Phosphycrote kinas disc I GS+horm sapiers GN+R02 RF: 15V-2 (R121_HUMAN) 9.90 60737 Guardian Bio CS+horm sapiers GN+R02 RF: 15V-2 (R121_HUMAN) 9.90 60738 Phosphylane Bio CS+horm sapiers GN+R02 RF: 15V-2 (R121_HUMAN) 9.83 6075 Rbosomal protein L23 OS-horm sapiers GN+R02 RF: 15V-2 (R122_HUMAN) 9.78 71508 Kerstin, type II optoskelda J 2 optiermal OS-horm sapiers GN-R02 RF: 15V-2 (R22E_HUMAN) 9.43 71914 GS rbosomal protein L23 OS-horm sapiers GN-R02 RF: 15V-2 (R122_HUMAN) 9.43 71924 Heit repeat-binding protein 1 (Fragment) OS-horm sapiers GN-R02 RF: 15V-2 (R22E_HUMAN) 9.43 71924 Heit repeat-binding protein 1 Gragment) OS-horm sapiers GN-R02 RF: 15V-2 (R24HUMAN) 9.22 71924 Heit repeat-binding protein 10 S-horm sapiers GN-R02 RF: 15V-2 (R24HUMAN) 9.22 71924 Heit repeat-binding protein 10 S-horm sapiers GN-S0RPD FE-15V-2 (R54HUMAN) 9.22 71924 Heit repeat-binding protein 10 S-horm sapiers GN-S0RPD FE-15V-2 (R54HUMAN) 9.22 71924 Heit repeat-binding protein 10 S-horm sapiers GN-S0RPD FE-15V-2 (R54HUMAN) 9.22 71924 Heit repeat-binding protein 10 S-horm sapiers GN-S0RPD FE-15V-2 - (R54HUMAN)	P37108	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 - [SRP14_HUMAN]	10.29	1
Phosphagh/center kinase 1 05-Horon sapiers QH=DKI PE-1 SV3 - [PGK1_HUMAN] 10.07 60 P0355 Annexh 2 OS-Horon sapiers CN=UMKRI PE-1 SV2 - [PGK1_HUMAN] 9.00 111 P2070 Lamin-B1 CG-Horon sapiers CN=UMKRI PE-1 SV2 - [PGK1_HUMAN] 9.88 60 P0355 Annexh 160 Treffent SD S-Horon sapiers CN=CNEXUD EP 1 SV2 - [PGK1_HUMAN] 9.78 52 P0350 Kerath, hype II dystaketal 2 adjerteril OS-Horon sapiers CN=CRCE DP 1 Fe-1 SV2 - [PGZ HUMAN] 9.43 11 P0391 Tcompile protein 1320 GS-Horon sapiers CN=CRCE DP 1 Fe-1 SV2 - [PGZ HUMAN] 9.43 21 P0391 Tcompile protein 1320 GS-Horon sapiers CN=CRCE DP 1 Fe-1 SV2 - [PGZ HUMAN] 9.28 22 P0391 Tcompile protein 1320 GS-Horon sapiers CN=CRE DP 1 Fe-1 SV2 - [PGRH_HUMAN] 9.28 22 P13942 Heterogeneous nuclear robouckeportein B10 CS-Horon sapiers CN=HUMAN] 9.24 22 P13943 Hadle Arbouckeportein B10 CS-Horon sapiers CN=HUMAN] 9.22 21 P13944 Heterogeneous nuclear robouckeportein B10 CS-Horon sapiers CN=HUMAN] 9.22 21 P13945 Fall Arbouckeportein B10 CS-Horon sapiers CN=HUMAN] 9.22 21 22	P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	10.16	2
PM235 Annexin A2 OS-Horon saplers GN-LANXAZ PE-1 SV-2 - [MANA] 9.00 111 PM200 Lamin BC OS-Horon saplers GN-LANXAZ PE-1 SV-2 - [MANA] 9.80 111 PM230 Lamin BC OS-Horon saplers GN-LANXAZ PE-1 SV-2 - [KI2L, HUMAN] 9.80 111 PM230 Lamin BC OS-Horon saplers GN-RE73 ZPE -1 SV-2 - [KI2L, HUMAN] 9.78 25 PM230 Kerath, type I cytoskeletal 2 epidemal OS-Horon saplers GN-RE73 ZPE -1 SV-2 - [KI2L, HUMAN] 9.43 27 PM291 Complex protein 1 200 OS-Horon saplers GN-CHC60P IE-1 SV-1 - [CU2L, HUMAN] 9.43 27 PM291 Complex protein 1 200 OS-Horon saplers GN-CHC60P IE-1 SV-1 - [CU2L, HUMAN] 9.43 27 PM291 Complex protein 1 200 OS-Horon saplers GN-CHC60P IE-1 SV-1 - [CU2L, HUMAN] 9.25 27 PM214 Heterogeneous nuclear ribonucleoprotein IB OS-Horon saplers GN-FMRPD IE-1 SV-1 - [RM1L, HUMAN] 9.22 11 PM2131 Erni Complex protein 1 subunt alpha OS-Horon saplers GN-FMRP PE-1 SV-1 - [RM1L, HUMAN] 9.21 66 PM214 Februard DS-Horon saplers GN-FRM PE-1 SV-1 - [RM2L, HUMAN] 9.21 66 PM214 Straft Intucker thonucleoprotein saduel GS I-HORO saplers GN-FM2R PE-1 SV-1 - [RM2L, HUMAN]	P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	10.07	6
Image: Part of the share is a formed at the shar	P0/355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN]	10.03	6
Photo Case In Notes I Isolari Indux Provide Sixtu Dr E 1 SV-2 (RL 2), HUMAN] 9.56 P1513 GIS Inbosomi protein L27a OS=Hom sapiers GN=RR12 PE 1 SV-2 (R23, HUMAN] 9.75 12 P3508 Keratin, type II cytoskietal 2 epidemia OS=Hom sapiers GN=RR12 PE 1 SV-2 - (R22, HUMAN] 9.43 2 P47914 GIS Tobosomi protein 1 (200 S=Hom sapiers GN=RR12 PE 1 SV-2 - (R22, HUMAN] 9.43 2 P47914 GIS Tobosomi protein 1 20 OS=Hom sapiers GN=CRE PE 1 SV-1 - (CD2, HUMAN] 9.25 2 P1992 Heterogeneous nuclear ribonucleoprotein 18 OS=Hom sapiers GN=CRE PE 1 SV-1 - (SMD_HUMAN] 9.22 21 P1914 Interogeneous nuclear ribonucleoprotein 30 OS=Hom sapiers GN=CRE PE 1 SV-1 - (FDD, HUMAN] 9.22 21 P311 Exit Observes appiers GN=RE PE 1 SV-1 - (FEN_L HUMAN] 9.22 21 P3786 Fige endonuclears 10 OS=Hom sapiers GN=CRE PE 1 SV-2 - (FEN_L HUMAN] 9.21 66 P17897 Toomplex protein 1 subunt alpha OS=Hom sapiers GN=CRE PE 1 SV-2 - (FEN_L HUMAN] 8.99 11 P6217 GOS chosonal protein 1 S0 S=Hom sapiers GN=CRE PE 1 SV-2 - (FEN_L HUMAN] 8.95 22 P17897 Toomplex protein 1 subunt alpha OS=Hom sapiers GN=CRE PE 1 SV-1 - (FEN_L J	P20700	Lamin-51 US=Homb saplens Giv=Unitis1 Pt=1 SV=2 - [Unitis1_HUMAN]	9.90	11
19350 March International application Data Park Data March 2014 (2014) 9.55 12 19350 Keratin, type II (robasketal 2 paldemal Os-Homo sapiers GN-KRT2 PE 15 V2 - [122 JUD, HJMAN] 9.43 12 19350 Keratin, type II (robasketal 2 paldemal Os-Homo sapiers GN-KRT2 PE 15 V2 - [122 JUD, HJMAN] 9.43 12 19350 Keratin, type II (robasketal 2 paldemal Os-Homo sapiers GN-KCT4 PE 15 V2 - [122 JUD, HJMAN] 9.26 12 19351 Complex protein 1 subunt delta Os-Homo sapiers GN-KCT4 PE 15 V2 - [120 JUD, HJMAN] 9.25 72 19324 Hetrogeneous nucleas GN-KERZ PE 15 V2 - [122 HJMAN] 9.24 22 11 19374 Fib pendonuclease 1 Os-Homo sapiers GN-KERZ PE 15 V2 - [120 JUL, HJMAN] 9.21 62 19374 Fib pendonuclease 1 Os-Homo sapiers GN-KERZ PE 15 V2 - [120 JUL, HJMAN] 9.21 62 19374 Fib pendonuclease 1 Os-Homo sapiers GN-KERZ PE 15 V2 - [120 JUL, HJMAN] 8.55 52 19374 Fib pendonuclease 1 Os-Homo sapiers GN-KERZ PE 15 V2 - [120 JUL, HJMAN] 8.55 52 19375 Complex protein 1 subunt abla OS-Homo sapiers GN-KERZ PE 15 V2 - [120 JUL, HJMAN] 8.56 52 19415 Small nuclear nhonuclep	P40730 P61513	Cabell Nildse i sulutilituela US=holitu sapleris GN=CNNLD PC=1 SP=2 · [N.1D_molekni] (SC shoeppal protein] 273 OS=Homo sanjare (SN=DPI) 270 PC=1 SV=2 · [N.1D_molekni]	9.00	3
CG5 triplet repeat-binding protein 1 (Fragment) OS=Homo sapiens GN=CGGBP1 PE=1 SV=1 - [CSUUD, HUMAN] 9,43 1 P47914 605 rbosomal protein L29 OS=Homo sapiens GN=ERPL29 FE=1 SV=2 - [RL29_HUMAN] 9,43 2 P6991 T-complex protein 1 subuti dela OS=Homo sapiens GN=CREP PE=1 SV=2 - [RD2_HUMAN] 9,28 62 P21942 Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNIPE PE=1 SV=2 - [RNH1_HUMAN] 9,22 7 P15311 Errin OS=Homo sapiens GN=CRE R=1 SV=4 - [EZRI, HUMAN] 9,22 11 P39748 Fäp endonuclease 1 OS=Homo sapiens GN=CRE R=1 SV=4 - [EZRI, HUMAN] 9,21 62 P16311 Errin OS=Homo sapiens GN=CRE R=1 SV=4 - [EZRI, HUMAN] 9,21 63 P17987 T-complex protein 1 subunt alpha OS=Homo sapiens GN=TCPI PE=1 SV=2 - [REV_HUMAN] 8,55 52 P17987 T-complex protein 1 subunt alpha OS=Homo sapiens GN=CIFP N=2 - [REV_HUMAN] 8,85 52 P39141 Eborgation factor 4A-H1I OS=Homo sapiens GN=CIFP N=2 - [REV_HUMAN] 8,85 52 P39141 Eborgation factor 70.m thotohontial OS=Homo sapiens GN=CIFP N=2 - [REV_HUMAN] 8,85 52 P3145 Karath, type 1 cytoskabet 10 OS=Homo sapiens GN=CIFP N=2 - [SV=4 - [FUV_H MAN]	P35908	Seratin hydrogen Euro Gost nun general Selferen Sante Er Serat Se	9.70	12
PM7914 605 rbosomal protein L29 OS=Homo sapiens GN=CPL29 FE=1 SV=2 - [RL29_HUMAN] 9,43 2 P5091 T-complex protein 1 subunt deta OS=Homo sapiens GN=CCT4 FE=1 SV=4 - [TCPD_HUMAN] 9,28 6 P50914 Hetergeneous nuclear inbouckopprotein 18 OS=Homo sapiens GN=KNPRIDP FE=1 SV=2 - [NRHL]_HUMAN] 9,24 22 P62314 Small nuclear robonuckopprotein 18 OS=Homo sapiens GN=SNPED PE=1 SV=2 - [NRHL]_HUMAN] 9,22 111 P39748 Flap endonuclease 1 OS=Homo sapiens GN=SNPED PE=1 SV=2 - [RSM_PLUMAN] 9,21 605 P19757 T-complex protein 1 subunt alpha GS=Homo sapiens GN=SNPE PE=1 SV=2 - [RSM_PLUMAN] 9,21 605 P19767 T-complex protein 1 subunt alpha GS=HOMO sapiens GN=SNPE PE=1 SV=2 - [RSM_PLUMAN] 8,95 92 P19767 T-complex protein 1 subunt alpha GS=HOMO sapiens GN=ERPLB PE=1 SV=2 - [RSM_PLUMAN] 8,85 92 P19767 T-complex protein 1 subunt alpha GS=HOMO sapiens GN=ERPLB PE=1 SV=2 - [FULUMAN] 8,85 92 P19761 Eurgation factor 10, mtchohodial OS=Homo sapiens GN=ERPLB PE=1 SV=4 - [IFA3_PLIMAN] 8,85 92 P19781 Eurgation factor 11, mtchohodial OS=Homo sapiens GN=ERPLB PE=1 SV=4 - [IFA3_PLIMAN] 8,60 44 P1345 Kerath, type 1 cytoskeletal 10 OS=Homo sapiens GN=ERPLB PE=	C91U10	CGG triplet repeat-binding protein 1 (Fragment) QS=Homo sapiens GN=CGGP1 PE=1 SV=1 - (CG)110 HUMAN1	9.43	1
p50991 T-complex protein 1 suburt deta OS=Horo sapiers GN=CFT4 PE=1 SV=2 [FINRH3_HUMAN] 9.28 57 P31942 Heterogeneous nuclear ribonucleoprotein H3 OS=Horo sapiers GN=SNRPD PE=1 SV=1 [SND_1_HUMAN] 9.24 22 P1511 Exrin OS=Horo sapiers GN=EZR R=1 SV=4 - [EXR_HUMAN] 9.22 11 P3746 File pendonucleas ribonucleoprotein S and B OS=Horo sapiers GN=EXPLP_TSV=1 - [FILH_HUMAN] 9.21 68 P14678 Small nuclear ribonucleoprotein s and B OS=Horo sapiers GN=EXPLP_TSV=1 - [FELL_HUMAN] 9.21 68 P14678 Small nuclear ribonucleoprotein s and B OS=Horo sapiers GN=EXPLP_FEL_SV=1 - [TEA_HUMAN] 8.99 100 P14787 T-complex protein 1 suburt alpha OS=Horo sapiers GN=EXPLP_FEL_SV=2 - [TEA_HUMAN] 8.99 100 P6217 GGs rbosomal protein L8 OS=Horo sapiers GN=EXPLP FE_1 SV=2 - [TEU_HUMAN] 8.85 52 P3441 Ebongation Factor Tu, mbochondrial OS=Horo sapiers GN=EXPLP FE_1 SV=2 - [CHL_HUMAN] 8.85 52 P3445 Keratin, type 1 cytoskeletal 10 OS=Horo sapiers GN=EXPLP FE SV=2 - [CHL_HUMAN] 8.66 64 P13454 Keratin, type 1 cytoskeletal 10 OS=Horo sapiers GN=EXPLP FE SV=1 - [SV=2 - [GHL_HUMAN] 8.66 52 P3445	P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 - [RL29 HUMAN]	9.43	2
P13192 Heterogeneous nuckear ribonuckoprotein H3 OS=Horn sapiers GN=INNPH5 PE-1 SV=2 - [HMRH3_HUMAN] 9.25 72 P62314 Small nuckear ribonuckoprotein Sm DI OS=Horn sapiers GN=SNRPD1 PE-1 SV=1 - [SMD1_HUMAN] 9.24 72 P3734 Fage and nuckear ribonuckase 10 S=Horn sapiers GN=SNRPD1 PE-1 SV=1 - [SMD1_HUMAN] 9.21 62 P3748 Fage and nuckear ribonuckase 10 S=Horn sapiers GN=SNRP PE-1 SV=2 - [RSME_HUMAN] 9.21 62 P14767 Small nuckear ribonuckase 10 S=Horn sapiers GN=SNRP PE-1 SV=2 - [RSME_HUMAN] 9.17 60 P14768 Small nuckear ribonuckeo protein 3 saccide protein 8 and B1 OS=Horn sapiers GN=SNRP PE-1 SV=2 - [RSME_HUMAN] 8.99 100 P62917 Complex protein 1 a solunt alpha OS=Horn sapiers GN=GNRPL1 PE-1 SV=2 - [REU_HUMAN] 8.83 52 P62944 Guanne nucleotide brinding protein solunt beta-2-like 1 OS=Horn sapiers GN=GNR21 PE-1 SV=2 - [GEU_HUMAN] 8.83 52 P63145 Keratin, type 1 cytoskeletal 10 OS=Horn sapiers GN=SNR52 PE =1 SV=2 - [SEU_HUMAN] 8.60 44 P13454 Keratin, type 1 cytoskeletal 10 OS=Horn sapiers GN=SNR52 PE =1 SV=4 - [SRS2_HUMAN] 8.47 31 P13464 Reatin, type 1 cytoskeletal 10 OS=Horn sapierS GN=KR52 PE-1 SV=4 - [REUZ_HUMAN]	P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	9.28	8
PR2214 Small nuclear rbonuckeportein Sm D1 OS-Homo sapiens GM-SNRPD1 PE=1 SV=1 - [SMD1_HUMAN] 9.24 22 P15311 Ezrin OS=Homo sapiens GM=EZR PE=1 SV=4 - [EZR_HUMAN] 9.21 26 P14678 Small nuclear rbonuckeportein-associated proteins B and B 'OS=Homo sapiens GM=SNRPB PE=1 SV=2 - [RSMB_HUMAN] 9.21 26 P14678 Small nuclear rbonuckeportein-associated proteins B and B 'OS=Homo sapiens GM=SNRPB PE=1 SV=2 - [RSMB_HUMAN] 8.99 100 P14787 T-complex protein 1 SO=Homo sapiens GM=RIB PE=1 SV=2 - [RETU_HUMAN] 8.95 23 P49411 Elongation factor Tu, mtochondrial OS=Homo sapiens GM=TUM PE=1 SV=2 - [RETU_HUMAN] 8.85 29 P3244 Guaine nucleotide-binding protein subunk beta2-WERTI D FE=1 SV=2 - [RETU_HUMAN] 8.85 29 P33919 Eukaryotic initiation factor 4A-III OS=Homo sapiens GM=SIRSP PE=1 SV=4 - [IF43_HUMAN] 8.86 42 P13455 Kerath, type I cytoskeltal 10 OS=Homo sapiens GM=SIRSP PE=1 SV=4 - [IF43_HUMAN] 8.60 42 P13455 Kerath, type I cytoskeltal 10 OS=Homo sapiens GM=SIRSP PE=1 SV=4 - [IF43_HUMAN] 8.61 42 P13455 Kerath, type I cytoskeltal 10 OS=Homo sapiens GM=SIRSP PE=1 SV=4 - [ISF3_HUMAN] 8.61 42 <tr< td=""><td>P31942</td><td>Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]</td><td>9.25</td><td>7</td></tr<>	P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	9.25	7
PI5311 Exin OS=homo sapiers GN=EZR PE-1 SV=4 - [EZRL_HUMAN] 9.22 111 P39748 Flap endonuclease 1 OS=Homo sapiers GN=FENI PE=1 SV=1 - [FENI_HUMAN] 9.21 62 P14787 Small nuclear ribonuckoprotein-associated proteins B and 9 CS=Homo sapiers GN=SNPB PE=1 SV=2 - [RSMB_HUMAN] 9.21 62 P17987 T-complex protein 1 subunt alpha OS=Homo sapiers GN=TCPL PE=1 SV=2 - [RLM_HUMAN] 8.95 53 P62917 60S ribosomal protein subunt beta-2-like 1 OS=Homo sapiers GN=CREL PE=1 SV=2 - [FLM_HUMAN] 8.85 55 P63244 Guanne nucleotide-binding protein subunt beta-2-like 1 OS=Homo sapiers GN=GREL PE=1 SV=3 - [GBLP_HUMAN] 8.60 64 P3919 Eukaryotic initiation factor 4A:III OS=Homo sapiers GN=SREP2 PE=1 SV=4 - [KF43_HUMAN] 8.60 64 P13454 Kerath, type I cytoskeital 10 CS=Homo sapiers GN=SREP2 PE=1 SV=4 - [KF43_HUMAN] 8.61 64 P13454 Kerath, type I cytoskeital 10 CS=Homo sapiers GN=SREP2 PE=1 SV=4 - [KF02_HUMAN] 8.47 111 P13464 Ribosomal RNA processing protein 1 homolg B OS=Homo sapiers GN=SREP2 PE=1 SV=1 - [KP02_HUMAN] 8.47 111 P13464 Ribosomal RNA processing protein 3 Do-Homo sapiers GN=SREP2 PE=1 SV=1 - [KP02_HUMAN] 8.41 112 <td>P62314</td> <td>Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMD1_HUMAN]</td> <td>9.24</td> <td>2</td>	P62314	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMD1_HUMAN]	9.24	2
P39748 Fibp endonuclease 1 OS-Homo sapiens ON-EFN1 PE-1 SF1-1 [FEN1_HUMAN] 9.21 52 P14678 Small nuclear ribonucleoprotein-associated proteins 8 and B' OS-Homo sapiens GN-SNRPB PE-1 SV2-2 [RSMB_HUMAN] 9.17 66 P17987 T-complex protein 1 subunt alpha OS-Homo sapiens GN-TCP1 PE-1 SV2-1 [TCPA_HUMAN] 8.59 9.21 P6217 60S rbosomel protein 1 SO-Homo sapiens GN-TCP1 PE-1 SV2-1 [TCPA_HUMAN] 8.63 55 P63214 Gaarine nucleotide-binding protein subunt beta-2-like 1 OS-Homo sapiens GN=GNERJL PE-1 SV3-3 [GBLP_HUMAN] 8.63 55 P03113 Serie/arginine-rick pictoring for the subunt beta-2-like 1 OS-Homo sapiens GN=GREPS F2_FLIVAN] 8.60 64 P13645 Keratin, type I cytoskeletal 10 OS-Homo sapiens GN=GREPS F257_FLIVAN] 8.60 64 P13645 Keratin, type I cytoskeletal 10 OS-Homo sapiens GN=KRP10 PE-1 SV4-1 (FB00_A_HUMAN] 8.47 21 P13645 Keratin, type I cytoskeletal 10 OS-Homo sapiens GN=KRP2 PE-1 SV4-1 (FB00_A_HUMAN] 8.47 21 P13646 Ribosomal RNA processing protein 1 homolog BOS-Homo sapiens GN=KRP1 PE-1 SV5-1 (FB00_A_HUMAN] 8.47 21 P14684 Ribosomal protein S7 OS-Homo sapiens GN=KRP5P PE-1 SV4-1 (FB00_A_HUMAN] 8.25 44	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	9.22	11
P14678 Small nuclear rbonucleoprotein-associated proteins B and B OS=Homo sapiens (N=SNRPB PE = 1 SV=2 - [RSMB_HUMAN] 9.17 P17987 T-complex protein 1 subunt alpha OS=Homo sapiens (N=PLIP PE=1 SV=2 - [RCH_HUMAN] 8.99 100 P01917 GOS rbosomal protein L8 OS=Homo sapiens (N=PLIP PE=1 SV=2 - [REL_HUMAN] 8.85 9 P0111 Ebngation factor Tu, mtochondrial OS=Homo sapiens (N=ETF43 PE=1 SV=2 - [REL_HUMAN] 8.85 9 P03244 Guanne nucleotide-binding protein subunt beta-2-like 1 OS=Homo sapiens GN=GRGNBLI PE=1 SV=3 - [GBLP_HUMAN] 8.60 6 P03101 Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRP2 PE=1 SV=4 - [SRSF2_HUMAN] 8.60 6 P03405 Keratin, type I oytoskeletal 10 OS=Homo sapiens GN=SRP2 PE=1 SV=4 - [SRSF2_HUMAN] 8.60 6 P03406 Keratin, type I oytoskeletal 10 OS=Homo sapiens GN=RRP10 PE=1 SV=5 - [KSD2_HUMAN] 8.47 2 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP10 PE=1 SV=5 - [RP18_HUMAN] 8.31 2 Q42644 Ribosomal RNA processing protein 2 OS=Homo sapiens GN=RRP10 PE=1 SV=5 - [RP18_HUMAN] 8.16 9 Q92445 Far upstream element-binding protein 2 OS=Homo sapiens GN=RRP10 PE=1 SV=5 - [RP18_HUMAN] 8.16	P39748	Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1 - [FEN1_HUMAN]	9.21	8
P17987 T-complex protein 1 subunk alpha OS=Homo sapiens CM=1CP1 PE-1 SV=1 - [TCPA_HUMAN] 8.99 10 P62917 GGS rhosomal protein L8 OS=Homo sapiens GM=TCP1 PE-1 SV=2 - [ERJ HUMAN] 8.85 5 P49411 Elongation factor 1u, mitochondrial OS=Homo sapiens GM=CME21 PE-1 SV=2 - [GELP_HUMAN] 8.83 5 P63244 Guanine mudeoltde-binding protein subunk beta-2lke 1 OS=Homo sapiens GM=CME21 PE-1 SV=3 - [GELP_HUMAN] 8.83 5 P3919 Eukaryotic hitistion factor 4-11 (DS=Homo sapiens GN=EFE43 PE-1 SV=4 - [FK42, HUMAN] 8.60 4 Q01130 Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SR5F2 PE=1 SV=4 - [SR5F2_HUMAN] 8.60 4 P13645 Keratin, type 1 cytoskeletal 10 OS=Homo sapiens GN=SR5F2 PE=1 SV=4 - [SR5F2_HUMAN] 8.60 4 P0300 Heat shock protein HSD 9-alpha OS=Homo sapiens GN=HSP02 PE=1 SV=-1 - [SM2_HUMAN] 8.47 11 Q14664 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RHSP2 PE=1 SV=-1 - [SM2_HUMAN] 8.16 9 Q9245 Far upstream element-binding protein 2 OS=Homo sapiens GN=HKSP2 PE=1 SV=-1 - [SM2_HUMAN] 8.16 9 Q12643 Methytrotonyl-CoA carboxylase subunk jamm, mitochondrial OS=Homo sapiens GN=HKSP2 PE=1 SV=-1 - [SM2_H - [HUBAN]	P14678	Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=2 - [RSMB_HUMAN]	9.17	6
P62917 60S rbosomal protein L8 OS=Horns sapiens GN=RPL8 PE=1 SV=2 [RE_JUMAN] 8.95 3 P49111 Elongation factor Tu, mtochondrial OS=Horns sapiens GN=CHFUP HE=1 SV=2 [CFTU_HUMAN] 8.85 5 P63244 Guanine nucleotide-binding protein subunt beta-2-like 1 OS=Horns sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN] 8.83 5 P03130 Serine/arginine-rich splicing factor 2 OS=Horns sapiens GN=SRPE PE=1 SV=4 - [FA3_HUMAN] 8.60 4 P13465 Keratin, type 1 cytoskeletal 10 OS=Horns sapiens GN=SRPE PE=1 SV=4 - [SR52_HUMAN] 8.65 12 P62316 Small nuclear ritionucleoprotein Sm D2 OS=Horns sapiens GN=SRPD2 PE=1 SV=4 - [SR52_HUMAN] 8.47 21 P62316 Srall nuclear ritionucleoprotein Sm D2 OS=Horns sapiens GN=RSP3 FD=1 SV=4 - [SR52_HUMAN] 8.47 21 P62814 Rbosomal protein S7 OS=Horns sapiens GN=RSP3 PE=1 SV=4 - [FUB2_HUMAN] 8.47 21 P04644 Ribosomal protein S7 OS=Horns sapiens GN=RSP3 PE=1 SV=4 - [FUB2_HUMAN] 8.25 44 P6281 40S ribosomal protein 20 CS=Horns sapiens GN=RSP3 PE=1 SV=4 - [FUB2_HUMAN] 8.16 52 Q92445 Far upstream element-binding protein 20 CS=Horns sapiens GN=RCSP PE=1 SV=4 - [FUB2_HUMAN] 8.14 10	P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	8.99	10
remail congation ractor 10, mtochondral US=Homo sapiers GN=RUFM Pt=1 SV=2 - [LF1U_FMURAN] 8.85 5 P63244 Guainine nucleotide binding proteins subunt beta-2:kle 105=Homo sapiers GN=RGREQL1 PE=1 SV=3 - [GBL2_HUMAN] 8.76 6 Q01130 Serine/arginine-rich splicing factor 2 OS=Homo sapiers GN=RSPE2 PE=1 SV=4 - [SR52_HUMAN] 8.60 4 Q01310 Serine/arginine-rich splicing factor 2 OS=Homo sapiers GN=RSPE2 PE=1 SV=4 - [SR52_HUMAN] 8.60 4 P13645 Kerath, type 1 (oxisekleta1 10 OS=Homo sapiers GN=RSPE2 PE=1 SV=4 - [SR52_HUMAN] 8.67 2 P13645 Kerath, type 1 (oxisekleta1 10 S=Homo sapiers GN=RSPE3 PE=1 SV=5 - [KS00_HUMAN] 8.47 21 P07900 Heat shock protein HSP 90-alpha OS=Homo sapiers GN=RSPE3 PE=1 SV=3 - [RP1B_HUMAN] 8.11 22 Q14684 Ribosomal RNA processing protein 1 homolg B OS=Homo sapiers GN=RSPE3 PE=1 SV=3 - [RP1B_HUMAN] 8.25 4 Q92945 Far upstream element-binding protein 2 OS=Homo sapiers GN=RENSP PE=1 SV=4 - [FUBP_LHUMAN] 8.16 92 Q926403 Methylcrotoncyl-CoA carboxylase subunit alpha, mtochondrail OS=Homo sapiers GN=RENCE PE=1 SV=3 - [MCAL_HUMAN] 8.16 92 Q12631 Transcription intermediary factor 1-beta OS=Homo sapiers GN=RTM28 PE=1 SV=4 -	P62917	605 ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]	8.95	3
Proce-minus processing processing processing software (New First Set Set Set Set Set Set Set Set Set Se	P49411	Longation ractor i u, mitochondral US=Homo Sapiens (N=1 UFM HE=1 SV=2 - [LF LU_HUMAN]	8.85	5
1.302.7 Example Construction Recur Pred In Service State Pred International Service State Pred State Pred Prime Pred Prime Pred Prime Prima Prima Prima Prime Prime Prima Primana Prime Prima Prime Prim	P03244	Data mice modecuter contains proteint subulint, betefa-zinke i u co=mouto sapients din¥ dinbeta (TFEE1 SVF3 - [GBUP_mUPPAN] Exilarante initiation factore Autili OS-Horm canaline (Charlefacta Della Charlefacta	0.83	5
Number Numer Numer Numer <td>001130</td> <td>Lower you initiate in to communicate the second sec</td> <td>8,60</td> <td>6</td>	001130	Lower you initiate in to communicate the second sec	8,60	6
P62316 Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 [SMD2_HUMAN] 8.47 P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=KRP90A1 PE=1 SV=5 · [KS90A_HUMAN] 8.47 11 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=5 · [KS90A_HUMAN] 8.47 11 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 · [RP1B_HUMAN] 8.11 12 Q92495 Far upstream element-binding protein 2 OS=Homo sapiens GN=KRSP PE=1 SV=4 · [FUBP2_HUMAN] 8.16 92 Q96RQ3 Methytcrotonoyl-CoA carboxylase subunit alpha, mtochondrial OS=Homo sapiens GN=CCC I PE=1 SV=3 · [MCAC_I HUMAN] 8.14 10 Q12363 Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM2B PE=1 SV=5 · [TF1B_HUMAN] 8.08 94 Q95492 ATD synthase subunit alpha, mtochondrial OS=Homo sapiens GN=TRIM2B PE=1 SV=5 · [TF1B_HUMAN] 8.09 96 Q13263 Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM2B PE=1 SV=1 · [ATD_HUMAN] 8.09 96 Q3384 Protein CMS51 (Fagment) OS=Homo sapiens GN=TRIM2B PE=1 SV=1 · [TRA2B_HUMAN] 8.00 2 Q147U1 Znc finger protein 846 OS=Homo sapiens GN=CMS1 PE=1 SV=1 · [CM32H_HUMAN]	P13645	Keratin, type I cytoskeletal 10 OS-Homo sapiens GN=KRT10 PE=1 SV=6 - [KIC10 HUMAN]	8.56	12
P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90A1 PE=1 SV=5 - [K590A_HUMAN] 8.47 11 Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RR1B PE=1 SV=3 - [RP1B_HUMAN] 8.31 12 P07900 Heat shock protein S7 OS=Homo sapiens GN=RR1B PE=1 SV=3 - [RP1B_HUMAN] 8.31 12 P02081 405 rbosomal protein S7 OS=Homo sapiens GN=RKPS7 PE=1 SV=1 - [RS7_HUMAN] 8.16 92 Q9245 Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN] 8.16 92 Q1263 Transcription intermediary factor baspiens GN=ECK1PSP 7E=1 SV=-5 - [TF1B_HUMAN] 8.14 10 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=ECK1PS=-1 SV=3 - [CDX1_HUMAN] 8.08 44 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=ECK1PE=1 SV=3 - [CDX1_HUMAN] 8.05 33 P06542 ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=TRA2B PE=1 SV=1 - [ATPG_HUMAN] 8.06 42 P03954 Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1 - [TRA2B_HUMAN] 8.00 2 P041474 Macrophaee midiari contrabining protein 1 OS=Homo sapiens GN=TRA2B PE=1 SV=1 - [TRA2B_HUMAN] 7.88 2	P62316	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 - [SMD2_HUMAN]	8.47	2
Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 · [RRP1B_HUMAN] 8.31 12 P62081 40S rbosomal protein 57 OS=Homo sapiens GN=RP57 PE=1 SV=1 · [RS7_HUMAN] 8.25 44 Q92945 Far upstream element-binding protein 2 OS=Homo sapiens GN=KP57 PE=1 SV=4 · [FUBP2_HUMAN] 8.16 92 Q92453 Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSP PE=1 SV=4 · [FUBP2_HUMAN] 8.14 10 Q12633 Transcription intermediary factor 1-beta OS=Homo sapiens GN=TXIN28 PE=1 SV=5 · [TIF1B_HUMAN] 8.08 44 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=TXIN28 PE=1 SV=5 · [TIF1B_HUMAN] 8.08 44 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=TXIN28 PE=1 SV=5 · [TIF1B_HUMAN] 8.08 42 P05524 The synthxes subunit gamma, mitochondrial OS=Homo sapiens GN=TXEVS1 · [CN1H_UMAN] 8.00 22 Q1384 Protein CMSS1 (Fragment) OS=Homo sapiens GN=TM28 PE=1 SV=1 · [TIR42B_HUMAN] 8.00 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=TXE8 PE=1 SV=2 · [TIR42B_HUMAN] 7.88 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=MERP2 · [ZN=2 · [ZN#46_HUMAN] 7.83 22 Q	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	8.47	11
P62081 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN] 8.25 Q92945 Far upstream element-binding protein 2 OS=Homo sapiens GN=KRRP PE=1 SV=4 - [FUBP2_HUMAN] 8.16 Q92945 Far upstream element-binding protein 2 OS=Homo sapiens GN=KRRP PE=1 SV=4 - [FUBP2_HUMAN] 8.16 Q13263 Transcription intermediary factor 1-beta OS=Homo sapiens GN=CRKI PE=1 SV=5 - [TIF1B_HUMAN] 8.14 Q13263 Transcription intermediary factor 1-beta OS=Homo sapiens GN=CRKI PE=1 SV=5 - [TIF1B_HUMAN] 8.08 Q65423 ATP synthase subunt gamma, mitochondrial OS=Homo sapiens GN=CRKI PE=1 SV=1 - [ATPG_HUMAN] 8.08 Q65424 ATP synthase subunt gamma, mitochondrial OS=Homo sapiens GN=CRKI PE=1 SV=1 - [C3384_HUMAN] 8.00 Q1384 Protein CMSS1 [Fagment) OS=Homo sapiens GN=CRKI PE=1 SV=1 - [C17R42B_HUMAN] 7.99 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=CRKI PE=1 SV=2 - [C1R426_HUMAN] 7.88 Q147U1 Zinc finger protein 1-bitory factor OS=Homo sapiens GN=CRKI PE=1 SV=2 - [RR44_HUMAN] 7.88 Q92050 KRA8 domin-containing protein 1 OS=Homo sapiens GN=RR0XI PE=2 SV=1 - [RR81_HUMAN] 7.81 Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=RD49 PE=1 SV=4 - [MHE_HUMAN] 7.81 Q9207 GOS ribo	Q14684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 - [RRP1B_HUMAN]	8.31	12
Q92945 Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN] 8.16 99 Q96RQ3 Methykrotonoyl-CoA carboxylase subunit alpha, intochondrial OS=Homo sapiens GN=MCC2 [PE=1 SV=3 - [MCCA_HUMAN] 8.14 101 Q1263 Transcription intermediary factor D-beta OS=Homo sapiens GN=MCC2 [PE=1 SV=5 - [IFLB_HUMAN] 8.14 101 Q96RQ3 Cyclin-dependent kinase 1 OS=Homo sapiens GN=HCR1 PE=1 SV=5 - [IFLB_HUMAN] 8.08 44 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=HCR1 PE=1 SV=5 - [FLB_HUMAN] 8.08 44 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=HCR1 PE=1 SV=5 - [FLB_HUMAN] 8.08 44 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=ATPSC1 PE=1 SV=1 - [ATPG_HUMAN] 8.00 36 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=HCPS1 PE=1 SV=1 - [ITR2B_HUMAN] 8.00 36 P03384 Protein CMS51 (FE=1 SV=1 - [ITR2B_HUMAN] 8.00 36 P62995 Transformer-2 protein homolog beta OS=Homo sapiens GN=IRA2B PE=1 SV=1 - [IRA2B_HUMAN] 7.88 22 P14174 Macrophage migration hibbotyn factor OS=Homo sapiens GN=HIF PE=1 SV=1 - [INE_HUMAN] 7.88 22 Q08211 <	P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	8.25	4
Op6R03 Methylcrononyl-CoA carboxylase subunit alpha, intochondrial OS=Homo sapiens GN=MCCI PE=1 SV=3 - [MCCA_HUMAN] 8.14 110 Q13263 Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRLM28 PE=1 SV=5 - [TIF1B_HUMAN] 8.04 100 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=CRLY PE=1 SV=3 - [TIF1B_HUMAN] 8.08 400 P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=CRLY PE=1 SV=3 - [TIF1B_HUMAN] 8.00 500 P03542 ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATPSCI PE=1 SV=1 - [CH7B_G HUMAN] 8.00 500 C93384 Protein CMSS1 (Fragment) OS=Homo sapiens GN=CRL28 PE=1 SV=1 - [CH7B_G HUMAN] 8.00 500 C93384 Protein CMSS1 (Fragment) OS=Homo sapiens GN=CRL28 PE=1 SV=1 - [CH7B_G HUMAN] 7.99 64 Q147/U1 Znc finger protein 846 OS=Homo sapiens GN=ZNE46 PE=1 SV=2 - [ZN846_HUMAN] 7.88 52 Q147/U1 Znc finger gargiard in hibborg factor OS=Homo sapiens GN=KRBOX1 PE=2 SV=1 - [KR8X1_HUMAN] 7.88 52 Q18201 ATP-dependent RNA helicase A OS=Homo sapiens GN=KRBOX1 PE=2 SV=1 - [KR8X1_HUMAN] 7.81 51 Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=RD2 PE_1 SV=1 - [CHX9_J HUMAN] 7.69 52 <td>Q92945</td> <td>Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN]</td> <td>8.16</td> <td>9</td>	Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN]	8.16	9
Q1252 Transcription intermediary factor 1-beta OS=Homo sepiens GN=TRIV82 PE=1 SV=5 - [TIF1B_HUMAN] 8.14 Q1 P06493 Cyclin-dependent kinase 1 OS=Homo sepiens GN=CKI PE=1 SV=5 - [CK1_HUMAN] 8.08 Q4 P06493 Cyclin-dependent kinase 1 OS=Homo sepiens GN=CKI PE=1 SV=3 - [CK1_HUMAN] 8.05 Q5 Q12524 Protein CMSS1 (Fragment) OS=Homo sepiens GN=CMSS1 PE=1 SV=1 - [C9384_HUMAN] 8.00 Q2 Q12534 Protein CMSS1 (Fragment) OS=Homo sepiens GN=CMSS1 PE=1 SV=1 - [C9384_HUMAN] 8.00 Q2 P62995 Transformer-2 protein homolog beta OS=Homo sepiens GN=ZTEV=1 - [C9384_HUMAN] 7.99 Q4 P14174 Macrophage migration inhibitory factor OS=Homo sepiens GN=ZTEV=1 - [ZN=4 - [MIF_HUMAN] 7.83 Q2 Q1417U Zinc finger protein 846 OS=Homo sepiens GN=ZNEVE - [ZN=4 - [MIF_HUMAN] 7.83 Q2 Q08211 ATP-dependent RNA helicase A OS=Homo sepiens GN=ZNEVE - [KR8XL_HUMAN] 7.81 Q3 Q08211 ATP-dependent RNA helicase A OS=Homo sepiens GN=ZNEVE - [KR8XL_HUMAN] 7.69 Q2 Q19D0 Neuresophin-1 (Fragment) OS=Homo sepiens GN=RVEVE PE=1 SV=4 - [NV=2]PLMAN] 7.69 Q2 Q19D0 Neuresophin-1 (Fragment) OS=Homo sepien	Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3 - [MCCA_HUMAN]	8.14	10
P06493 Cyclin-dependent kinase 1 OS=Homo sapiens GN=CKL PE=1 SV=3 - [CDKL_HUMAN] 8.08 44 P36542 ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATPSC1 PE=1 SV=1 - [ATPG_HUMAN] 8.05 32 O3384 Protein CMSS1 (Fragment) OS=Homo sapiens GN=CMS1 PE=1 SV=1 - [CM328_HUMAN] 8.00 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=CMS1 PE=1 SV=1 - [TRA28_HUMAN] 7.99 44 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=ZMS28 PE=1 SV=1 - [TRA28_HUMAN] 7.88 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=ZMF846 PE=1 SV=4 - [ME_HUMAN] 7.88 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=RRB0X1 PE=2 SV=1 - [KR8XL_HUMAN] 7.88 22 Q147U1 Zinc finger protein 140 OS=Homo sapiens GN=RRB0X1 PE=2 SV=1 - [KR8XL_HUMAN] 7.81 21 Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=RVB0YE PE=1 SV=4 - [ME_H_UMAN] 7.69 22 Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=RN204 PE=1 SV=4 - [ME_MUMAN] 7.69 22 Q09207 OS rbosomal protein 124 OS=Homo sapiens GN=RN204 PE=1 SV=4 - [MMAN] 7.69 22 Q19207 Neurexophlin=1 (Fragment) OS=Homo sapi	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	8.14	10
P36542 ATP synthase subunit gamme, mitochondrial OS=Homo sapiens (M=ATPSCI PE=1 SV=1 - (TRPL_JUMAN] 8.05 32 O21384 Protein CMSSI (Fragment) OS=Homo sapiens GN=CMSSI PE=1 SV=1 - (TRPL_JUMAN] 8.00 32 P62995 Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1 - (TRA2B_HUMAN] 7.99 4 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=TRA2B PE=1 SV=2 - (TRA2B_HUMAN] 7.88 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=TRA2B PE=1 SV=2 - (ZN846_HUMAN) 7.88 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=TRA2B PE=1 SV=2 - (ZN846_HUMAN) 7.88 22 Q147U1 Zinc finger protein 846 OS=Homo sapiens GN=TRA2B PE=1 SV=2 - (ZN846_HUMAN) 7.83 22 Q182U1 ATP-dependent RNA helicase A OS=Homo sapiens GN=KRBOXI PE=2 SV=1 - [KR8X1_HUMAN] 7.81 11 Q082U1 ATP-dependent RNA helicase A OS=Homo sapiens GN=RV3 = [LS3 + HUMAN] 7.69 22 Q082U1 ATP-dependent RNA helicase A OS=Homo sapiens GN=RV3 = [LS3 + -1 [VD3 PO_LUMAN] 7.69 22 Q092D7 OS ribosomal protein L34 OS=Homo sapiens GN=RV3 = [LS31 [CD3 PO_LUMAN] 7.60 24 Q192D0 Neurexophiin-1 (Fragm	P06493	Cyclin-dependent kinase 1 OS=Horro sapiens GN=CDK1 PE=1 SV=3 - [CDK1_HUMAN]	8.08	4
C9J384 Protein Unbs1 (Hrägment) US=Homo sapiens GN=CMS5 IPE=1 SVI=1 - (CJ)384_HUMAN] 8.00 22 P62995 Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SVI=1 - [TRA2B_HUMAN] 7.99 42 Q147U1 Zhn finger protein 846 OS=Homo sapiens GN=ZNP846 PE=1 SVI=2 - [ZN846_HUMAN] 7.88 22 Q147U1 Macrophage migration inhibitory factor OS=Homo sapiens GN=MIE PE=1 SVI=2 - [ZN846_HUMAN] 7.83 22 Q18104 KRAB domain-containing protein 10 S=Homo sapiens GN=KIE PE=1 SVI=2 - [KRBX1_HUMAN] 7.81 7.72 Q08211 ATTP-dependent RNA helicase A OS=Homo sapiens GN=RPI34 PE=1 SVI=3 - [RL34_HUMAN] 7.69 7.69 Q19207 60S ribosomal protein 124 OS=Homo sapiens GN=RPI34 PE=1 SVI=3 - [RL34_HUMAN] 7.69 7.69 Q19208 Neurexophin-1 (Fragment) OS=Homo sapiens GN=RVIP PE=1 SVI=3 - [RL34_HUMAN] 7.69 7.69 Q19207 60S ribosomal protein I/ OS=Homo sapiens GN=RVIP PE=1 SVI=3 - [RL34_HUMAN] 7.66 7.69 7.69 Q1214 ATTR-dependent RMID OS=Homo sapiens GN=RVIP PE=1 SVI=3 - [RL3_HUMAN] 7.66 7.60 7.60 7.60 7.60 7.66 7.60 7.60 7.60 7.60 7.60 7	P36542	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATPSCI PE=1 SV=1 - [ATPG_HUMAN]	8.05	3
reaczys Inatistumer-2 protein forming beta US=Promos appens (N-20 PE=1 SV=1 - [1R42E_PIMAN] 7.99 24 Q147011 Zinc finger protein 846 OS=Homo sapiens (N-20 PE=1 SV=2 - [1R42E_PIMAN] 7.88 22 Q147011 Zinc finger protein 846 OS=Homo sapiens (N-20 PE=1 SV=2 - [1R42E_PIMAN] 7.83 22 Q147011 Zinc finger protein 846 OS=Homo sapiens (N-20 PE=1 SV=2 - [1R84E_I_HUMAN] 7.83 22 Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=RRB0X1 PE=2 SV=1 - [1R8X1_HUMAN] 7.81 31 Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=RB0Y DE=1 SV=4 - [DKV9_HUMAN] 7.69 22 Q09207 GOS ribosomal protein 124 OS=Homo sapiens GN=RR12 H=2 SV=1 - [R12_HUMAN] 7.69 22 Q19207 Neurexophin=1 (Fragment) OS=Homo sapiens GN=RVP1 PE=4 SV=1 - [20]PDO_HUMAN] 7.69 22 Q18214 60S ribosomal protein 12 OS=Homo sapiens GN=RVP1 PE=1 SV=1 - [R12_HUMAN] 7.66 22 Q18214 60S ribosomal protein 17 OS=Homo sapiens GN=RVP2 PE=1 SV=1 - [R12_HUMAN] 7.66 22 Q18214 60S ribosomal protein 17 OS=Homo sapiens GN=RVP2 PE=1 SV=1 - [FUS_HUMAN] 7.60 24 Q182357 RNA-binding protein FUS OS=Homo sapiens GN=	C9J384	Protein LMSJ (Hragment) US=Homo sapiens GM=CMSSI PE=1 SV=1 - [C9/384_HUMAN]	8.00	2
Question Zask image procession Question Zask image procession	P02995	Indisionmenz procent nonloog bera US=homo sapiens GN= TKAZE HE=1 SV=1 - [TKAZE_HUMAN] Zho fanore norbin 946 Ore-Humon scholar CAL=ZNE46 EF=1 SV=1 - [TKAZE_HUMAN]	7.99	4
C918D0 KRA& domain-containing protein DS=Homo sapiens GN=RRI34 PE=1 SV=3 - [TeII_1OrdM] 7.81 11 Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=RRI34 PE=2 SV=1 - [KR81, HUMAN] 7.72 18 Q08201 ATP-dependent RNA helicase A OS=Homo sapiens GN=RRI34 PE=1 SV=3 - [RL34, HUMAN] 7.72 18 Q08201 ATP-dependent RNA helicase A OS=Homo sapiens GN=RRI34 PE=1 SV=3 - [RL34, HUMAN] 7.69 2 Q09200 Neurexophilm-1 (Fragment) OS=Homo sapiens GN=RRI34 PE=1 SV=3 - [RL34, HUMAN] 7.69 2 Q19200 Neurexophilm-1 (Fragment) OS=Homo sapiens GN=RRI34 PE=1 SV=3 - [RL34, HUMAN] 7.69 2 Q19200 Neurexophilm-1 (Fragment) OS=Homo sapiens GN=RRI24 PE=1 SV=3 - [RL34, HUMAN] 7.66 2 P18124 605 ribosomal protein I/ DS =Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7, HUMAN] 7.66 2 P35637 RNA-binding protein FUS OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7, HUMAN] 7.60 4	Q14/01 D14174	Laik ninge javeni oro US-TNUID Sajitels (SIR-ZINFORD FC=1 SIR-2 - [ZINFOT_TIUPHI]) Macronhane mination inhibitory factor (OC-Home canone (SIN-MIE DE-1 SI)-4, IMIE HIMANI	7.88	2
Q08211 ATP-dependent RNA helicase A OS-Homo sapiens GN=DHX0PE 1 SV=1 [INCA_IPMIN] 7.72 18 Q08211 ATP-dependent RNA helicase A OS-Homo sapiens GN=DHX0 PE=1 SV=4 - [INKV9 JHVAN] 7.72 18 Q08211 ATP-dependent RNA helicase A OS-Homo sapiens GN=RPL34 PE=1 SV=3 - [IRL34_HUMAN] 7.69 22 Q08211 ATP-dependent RNA helicase A OS-Homo sapiens GN=RPL34 PE=1 SV=3 - [IRL34_HUMAN] 7.69 22 Q19200 Neurexophin-1 (Fragmenh) OS=Homo sapiens GN=RPL34 PE=1 SV=3 - [IRL34_HUMAN] 7.69 22 Q18214 605 ribosomal protein L7 OS=Homo sapiens GN=RPL34 PE=1 SV=1 - [RL2_HUMAN] 7.66 22 Q18214 605 ribosomal protein L7 OS=Homo sapiens GN=RPL3 PE=1 SV=1 - [RL2_HUMAN] 7.66 22 Q18214 605 ribosomal protein RVS OS=Homo sapiens GN=RPL3 PE=1 SV=1 - [RL2_HUMAN] 7.60 24	C918D0	RRAD domain-containing protein 105-Lines appendix in the same treation of the same treation in the same treating in the same treation in the same treation i	7.03	2
409207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 · [RL34_HUMAN] 7.69 2 C9JPPO Neurexophin=1 (Fragment) OS=Homo sapiens GN=RPL34 PE=1 SV=3 · [RL34_HUMAN] 7.69 1 P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 · [RL2_HUMAN] 7.66 2 P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 · [RL2_HUMAN] 7.66 2 P25537 RNA-binding protein FUS OS=Homo sapiens GN=RPL7 PE=1 SV=1 · [RL2_HUMAN] 7.60 4	008211	ATD-dependent RNA helicase A OS=Horm sanjens GN=htxQ DF=1 SV=4 - [INHX] HIMANI	7.72	19
C39PD0 Neurexophilin-1 (Fragment) OS=Homo sapiens GN=NXPH1 PE=4 SV=1 - [C3)PD0_HUMAN] 7.69 11 P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RVL7 PE=1 SV=1 - [RL7_HUMAN] 7.66 22 P35637 RNA-binding protein FUS OS=Homo sapiens GN=RVL7 PE=1 SV=1 - [FUS_HUMAN] 7.60 44	P49207	605 ribosmal protein L34 OS-Homo sapiens GN-ER134 PE=1 SV=3 - (R134 HUMANI	7,69	20
P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL2_HUMAN] 7.66 2 P35637 RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN] 7.60 4	C9JPD0	Neurexophilin-1 (Fragment) OS=Homo sapiens GN=NXPH1 PE=4 SV=1 - [C9]PD0_HUMAN]	7.69	1
P35637 RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN] 7.60	P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	7.66	2
	P35637	RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN]	7.60	4

Accession	Description	5Courses as	S# DCMe
Accession	Userbito and a sector of the s	2Coverage	2# PSMS
P01077	Uniquini-curriguaring enzyme ez up cost and the server to the server to the server of	7.40	1
P35659	Protein DEN US=homo sapiens GN=UEN PE=1 SV=1 (DEN_HUMAN)	7.47	0
Q12691	Microtubule-associated protein RP/Ebitamily member 1 US=Homo sapiens un=MARKET PE=1 Sv=3 - [MARET_HUMAIN]	7.46	4
P23284	Peptidy-prolyl Cis-trans isomerase B US=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]	7.41	4
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KFNB1 PE=1 SV=2 - [IMB1_HUMAN]	7.31	10
P07477	Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1 - [TRY1_HUMAN]	7.29	17
015235	285 ribosomal protein S12, mtochondrial OS=Homo sapiens GN=MRPS12 PE=1 SV=1 - [RT12_HUMAN]	7.25	1
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 - [KHDR1_HUMAN]	7.22	9
P61927	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 - [RL37_HUMAN]	7.22	2
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	7.05	2
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	7.05	52
Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	6.99	9
P40429	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 - [RL13A_HUMAN]	6.90	4
P18754	Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [RCC1_HUMAN]	6.89	4
Q9NRW3	DNA dC->dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 - [ABC3C_HUMAN]	6.84	2
Q9NSQ0	Putative ribosomal RNA-processing protein 7 homolog B OS=Homo sapiens GN=RRP7B PE=5 SV=1 - [RRP7B_HUMAN]	6.80	1
P17039	Zinc finger protein 30 OS=Homo sapiens GN=ZNF30 PE=2 SV=5 - [ZNF30_HUMAN]	6.74	3
Q14119	Vascular endothelial zinc finger 1 OS=Homo sapiens GN=VEZF1 PE=1 SV=2 - [VEZF1_HUMAN]	6.72	e
Q5T280	Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 - [CI114_HUMAN]	6.65	3
P08621	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2 - [RU17_HUMAN]	6.64	6
P61353	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 - [RL27_HUMAN]	6.62	2
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	6.42	24
Q9NRX1	RNA-binding protein PNO1 OS=Homo sapiens GN=PNO1 PE=1 SV=1 - [PNO1_HUMAN]	6.35	2
P22234	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 - [PUR6_HUMAN]	6.35	3
J3KPG2	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1 - [J3KPG2 HUMAN]	6.25	1
Q15424	Scaffold attachment factor BI OS=Homo sapiens GN=SAFB PE=1 SV=4 - [SAFB1_HUMAN]	6.23	10
000567	Nucleolar protein 56 OS=Homo saoiens GN=NOP56 PE=1 SV=4 - [NOP56 HUMAN]	6,23	F F
086U42	Polyadenylate-binding protein 2 OS=Horno sapiens GN=PABPN1 PF=1 SV=3 - [PABP2 HLIMAN]	6.21	4
096127	The finner motein 635 (SSEHomo saniens (A)=ZNE655 PE=2 SV=1 - (ZNE65 HIIMAN)	6.21	
002804	Each might protein 025 05-1 mins soperils diversities of the 25 vers (2002) [1002] [10	6.08	
026020		6.07	
P20038	Mode the complex state is a state of the complex of the complex of the complex of the complex state of the complex of the comp	6.06	
P20040	405 Tousoniai proteini 512 05=mono septents dure (K512 KE=1 3753 - [K512 monowini)	6.06	
P20042	Eukaryout, u ansietuon minuatuon ractor z subulini z OS=nono sapienis GiveErr22 PE=1 SV=2 - [IFZD_nomAni]	5.07	
Q9BKX2	Procein peloca nomolog US=Homo saplens Giv=PELD VE=1 SV=2 - [PELD_HUMAN]	5.97	
F8W/Q3	WD repeat-containing protein 48 OS=Homo sapiens GR=WDK48 PE=1 SV=1 - [PK8W/Q3_HUMAN]	5.97	1
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 - [HPRT_HUMAN]	5.96	2
P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	5.95	12
Q6R954	Polymerase delta interacting protein 46 OS=Homo sapiens GN=PDIP46 PE=1 SV=1 - [Q6R954_HUMAN]	5.95	1
P61313	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2 - [RL15_HUMAN]	5.88	1
Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]	5.87	15
095196-3	Isoform 3 of Chondroitin sulfate proteoglycan 5 OS=Homo sapiens GN=CSPG5 - [CSPG5_HUMAN]	5.74	1
C9JGC1	Zinc finger protein neuro-d4 (Fragment) OS=Homo sapiens GN=DPF1 PE=4 SV=1 - [C9JGC1_HUMAN]	5.71	2
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]	5.56	8
Q9Y324	rRNA-processing protein FCF1 homolog OS=Homo sapiens GN=FCF1 PE=2 SV=1 - [FCF1_HUMAN]	5.56	2
P61326	Protein mago nashi homolog OS=Homo sapiens GN=MAGOH PE=1 SV=1 - [MGN_HUMAN]	5.48	1
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	5.45	3
Q8IZP2	Putative protein FAM10A4 OS=Homo sapiens GN=ST13P4 PE=5 SV=1 - [ST134_HUMAN]	5.42	2
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	5.42	4
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 - [TCPG_HUMAN]	5.32	6
P52292	Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 - [IMA1 HUMAN]	5.29	4
F8VYV2	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 - [F8V/V2 HUMAN]	5.26	1
09Y3Y2	Chromatin target of PRMT1 protein OS=Homo saniens GN=CHTOP PE=1 SV=2 - [CHTOP HUMAN]	5.24	2
060264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo saniens GN=SMARCA5 PE=1 SV-1 - [SMCA5_HIIMAN]	5,23	2
D300201	SW13/W related being and dependent signation of enotitient administry antimole 5 00-month applies are -privated size-1 5 -1 [Sindag-norman] (AC) showing an article 13 OC-Horn caniers (M-DB) 3 DE-1 S(-2, FB) 3 HIMAN]	5.25	-
A0A09714/VD	Non-second processing second separate second s	5.21	-
D702/7	Concert transmission containing proteins of the concert and the concert transmission of the concert transmission o	5.20 E 11	
064409		5.11	
Q0NAU8	Ascourtine incluing induged data CDS-FRUID Safetti GNR-ASTLETE-1 SV=7 * [ASTLETURAN]	5.10	1
C9JTW2	Nucleonii (rraginenii) uosenomo Sapiens un encle rest versa - [Usur Waz Humani)	4.96	1
P25205	Lava replication metrishing raction metris OS=MONTO Sapletts GV=MEtrometrom 97E=1.5V=3 - [mLm5_mOMAN] Passendilla Recompanya CS_Hometron and CALEPECT 10:00000000000000000000000000000000000	4.95	10
000541	rescalino normolog us=riorno sapiens (M=PES) PE=1 SV=1 - [PES_HUMAN]	4.93	e
Q9NVP1	A IP-dependent KINA neikase DDX18 OS=Horo sapiens GR=DDX18 PE=1 SV=2 - [DDX18 HUMAN]	4.93	7
P08579	U2 small nuclear ribonucleoprotein B" OS=Homo sapiens GN=SNRPB2 PE=1 SV=1 - [RU2B_HUMAN]	4.89	2
Q5C9Z4	Nucleolar MIF4G domain-containing protein 1 OS=Homo sapiens GN=NOM1 PE=1 SV=1 - [NOM1_HUMAN]	4.88	5
014602	Eukaryotic translation initiation factor 1A, Y-chromosomal OS=Homo sapiens GN=EIF1AY PE=1 SV=4 - [IF1AY_HUMAN]	4.86	2
P49959	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3 - [MRE11_HUMAN]	4.80	e
014979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3 - [HNRDL_HUMAN]	4.76	4
P82979	SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3 - [SARNP_HUMAN]	4.76	2
P12956	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 - [XRCC6_HUMAN]	4.76	e
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN]	4.68	5
P07305	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3 - [H10_HUMAN]	4.64	1
M0QZL6	Cytokine receptor-like factor 1 (Fragment) OS=Homo sapiens GN=CRLF1 PE=4 SV=1 - [MOQZL6_HUMAN]	4.62	1
075533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	4.60	5
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78 HUMAN]	4.59	6
Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 - [ILKAP HUMAN]	4.59	
075367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4 - [H2AY HUMAN]	4,57	5
O6P087	RNA nseudouridvlate synthase domain-containing protein 3 OS=Horno soniens (N=PPIISD3 PF=1 SV=3 - [RISD3 HIIMAN]	4.56	4
P30101	Protein disulfide-isomerase A3 OS=Homo saniens (Re=PDIA3 PF=1 SV=4 - (PDIA3 HIIMAN)	4.55	4
P60174	Trisenhoshate isomerase OS=Homo saniens GN=TP11PE-12V=3-TP12H_IIMAN1	4 55	3
P11177	Duringte dehydronenase F1 component sihunti beta mitochonical (S=Hom sanjens CN=PDHR DF=1 SV=3 - CDDR HI MANI	4 46	1
	- protection paragenese el component ausunicideurs de la nuclionaria do - nonto aupens dit - FDID FL-1 39-5 - [DFF_1010414]	1.70	1

Accession	Description	ΣCoverage	Σ# PSMs
H7C0N4	Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 - [H7C0N4_HUNAN]	4.44	1
Q9BYG3	MK167 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 - [MK671_HUMAN]	4.44	1
P46778	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	4.38	1
Q9Y2R4	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3 - [DDX52_HUMAN]	4.34	4
Q9Y383	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2 - [LC7L2_HUMAN]	4.34	3
Q86T24	Transcriptional regulator Kaiso 05=Homo sapiens GN=ZBTB33 PE=1 5V=2 - [KAISO_HUMAN]	4.32	6
Q99986 008170	Seme/trifeonine-protein kinase VKLI OS=homo sapiens GN=VKLI PE=1 SV=1 { [VKL_PUMPAN] Seme/amine_rich splitning factor 4 OS=homo sanjans GN=SPE4 DE=1 SV=2, [SDSE4 HIIMAN]	4.29	4
099832	Schreidigung in the spincip factor in SS-Horno spincip SR-ECTO PF=1 SV=2 - [International]	4.24	3
09UMS4	Pre-mRNA-processing factor 19 05=Homo sapiens GN=PRPF19 PE=1 SV=1 - [PRF19 HUMAN]	4.17	3
Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	4.16	14
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	4.14	6
Q15072	Zinc finger protein OZF OS=Homo sapiens GN=ZNF146 PE=1 SV=2 - [OZF_HUMAN]	4.11	1
000139	Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3 - [KIF2A_HUMAN]	4.11	6
Q5QNZ2	ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=1 - [Q5QNZ2_HUMAN]	4.10	1
P43246	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1 - [MSH2_HUMAN]	4.07	7
P35232	Promoticn US=Homo saplens GN=PHB PE=1 SV=1 - [PHB_HUMAN]	4.04	2
015347	Spicing racio uzar os kud suburit o sentino sapieris ore-uzarz re=1 sv=+ [uzarz_numin] Hich prohibity racio proteini R3 OC=Harman Sali (R3) Hick R5 (R4) Hick R5 (R4) Hick R5 (R4) Hick R5 (R4) Hick R5	4.00	2
P46109	Treger moderney group procent op Something Software (Strengthere Software) (Strengthere Software Softw	3.96	2
Q14498	RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39 HUMAN]	3.96	4
Q9NVI7	ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2 - [ATD3A_HUMAN]	3.94	5
O60832	H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3 - [DKC1_HUMAN]	3.89	3
P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 - [PSA4_HUMAN]	3.83	2
P31689	Dna) homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 - [DNJA1, HUMAN]	3.78	2
Q96T88	E3 ubiquitin-protein ligase UHRF1 OS=Hormo sapiens GN=UHRF1 PE=1 SV=1 - [UHRF1_HUMAN]	3.78	5
0/54/5	PC4 and SrKS1-interacting protein US=Homo sapens (uR=PSJP1 PE=1 SV=1 SV=1 [PSJP1, HUMAN]	3.//	6
C9JN/1	2 III. IIIgel (1/000000000000000000000000000000000000	3.77	3
P62906	Contactiant comparison of the second se	3.69	2
Q9Y3A5	Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=1 SV=4 - [SBDS_HUMAN]	3.60	1
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN]	3.53	4
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	3.50	4
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 - [RANG_HUMAN]	3.48	1
P05388	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 - [RLA0_HUMAN]	3.47	4
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	3.46	2
Q8TDN6	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens GI=BRIX1 PE=1 SV=2 - [BRX1_HUMAN]	3.40	2
P18846	Cyclic AMP-dependent transcription factor A II-1 US=homo sapiens (wi=A IF1 PE=1 SV=2 - [A IF1_HUMAN]	3.32	2
P11388	Linvopakinake protein 03-1 kill sapletis OH-LYTELT 2-2 3V-1 * [LYTELTIOPAKI]	3.27	10
Q9Y2L1	Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2 - [RRP44 HUMAN]	3.24	3
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 - [UTP18_HUMAN]	3.24	2
Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2 - [PRP31_HUMAN]	3.21	3
P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 - [RBP2_HUMAN]	3.19	15
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF182 PE=1 SV=3 - [EF1B_HUMAN]	3.11	1
Q9P016	Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1 - [THYN1_HUMAN]	3.11	1
P36873	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1 - [PP1G_HUMAN]	3.10	2
P38040	Stress-V protein, mitochononal US=homo sapiens (kii = HSYA9 YE=1 SV=2 - (GKY2)-JUMAN]	3.09	4
Q012J0	Indexive E-chreating Statistication and Statisticat	2 94	2
014204	Cytoolsaming proceeding of the second s	2.93	26
P22314	Ubiguitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1 HUMAN]	2.93	5
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	2.91	5
Q96EK4	THAP domain-containing protein 11 OS=Homo sapiens GN=THAP11 PE=1 SV=2 - [THA11_HUMAN]	2.87	2
Q5T6C4	Ataxin-7-like protein 2 OS=Homo sapiens GN=ATXN7L2 PE=4 SV=1 - [Q5T6C4_HUMAN]	2.87	1
Q53EP0-2	Isoform 2 of Fibronectin type III domain-containing protein 3B OS=Homo sapiens GN=FNDC3B - [FND3B_HUMAN]	2.86	1
P49915-2	Isoform 2 of GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS - [GUAA_HUMAN]	2.86	2
Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 - [RBM14_HUMAN]	2.84	4
091230	Nutre 2 (3) - Notific 2 (3) -	2.01	1
Q90Q00	Towication associated protein 20102-1010 and superior detailed and the Technological associated protein 20102-1010 and the Technological associated protein 20102-101000 and technological associated protein 201000 and technological associated protein 2010000 and technological ass	2.77	4
Q8N684	Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens GN=CPSF7 PE=1 SV=1 - [CPSF7 HUMAN]	2.76	2
P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	2.68	1
Q9Y5B9	FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 - [SP16H_HUMAN]	2.67	5
B7ZMI3	ITPR1 protein OS=Homo sapiens GN=ITPR1 PE=2 SV=1 - [B7ZMI3_HUMAN]	2.64	1
Q9H7B2	Ribosome production factor 2 homolog OS=Homo sapiens GN=RPF2 PE=1 SV=2 - [RPF2_HUMAN]	2.61	1
P33992	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5_HUMAN]	2.59	4
P36578	605 ribosomal protein L4 05=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	2.58	2
Q16630	Leavage and polyadenyiation specificity factor subunit 6 US=Homo sapiens GN=CPS+6 PE=1 SV=2 - [CPS+6_HUMAN]	2.54	2
075643	Inducedprotein (FN 00-100/08401616 00*1/FN FE=1.5¥=5 * [1FK_T00*W)] IS small under ribourdear ribourdear thouse that behaviore to Co-Home sensing CM-SNDND200 DE=1.5V-2 . [1IS20. H] MAM]	2.54	10
09UBX7	oo anamadaan adamadaa yaanaa ada iidadada oo ahanaa ayaanaa ada ahaa ahaa ahaa ahaa ahaa ahaa	2.48	0
043684	Mitotic checkooint protein BUB3 OS=Homo saoiens GN=BUB3 PE=1 Sv=1 - (BUB3 HUMAN1	2.44	1
Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=1 SV=2 - ISMCE1 HUMANI	2.43	2
015391	Transcription factor YY2 OS=Homo sapiens GN=YY2 PE=2 SV=1 - [TYY2_HUMAN]	2.42	2
Q9H6J7	UPF0705 protein C11orf49 OS=Homo sapiens GN=C11orf49 PE=2 SV=2 - [CK049_HUMAN]	2.42	1
P39656	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4 - [OST48_HUMAN]	2.41	2
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	2.36	3
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	2.36	6

Accession	Description	ΣCoverage	Σ# PSMs
P49711	Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1 - [CTCF_HUMAN]	2.34	3
P12268	Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 - [IMDH2_HUMAN]	2.33	1
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]	2.32	3
043929	Origin recognition complex subunit 4 OS=Homo sapiens GN=ORC4 PE=1 SV=2 - [ORC4_HUMAN]	2.29	2
Q14683	Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2 - [SMC1A_HUMAN]	2.27	4
Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2 - [TIM50_HUMAN]	2.27	2
Q14807	Kinesin-like protein KIF22 OS=Homo sapiens GN=KIF22 PE=1 SV=5 - [KIF22_HUMAN]	2.26	1
Q99615	DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7 PE=1 SV=2 - [DNJC7_HUMAN]	2.23	2
P13797	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 - [PLST_HUMAN]	2.22	2
P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LPPRC_HUMAN]	2.22	6
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	2.19	6
000442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCA PE=1 SV=1 - [RTCA_HUMAN]	2.19	1
P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	2.16	2
Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	2.14	2
Q01844	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [EWS_HUMAN]	2.13	1
Q96JP5	E3 ubiquitin-protein ligase ZFP91 OS=Homo sapiens GN=ZFP91 PE=1 SV=1 - [ZFP91_HUMAN]	2.11	2
Q9NVA2	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 - [SEP11_HUMAN]	2.10	2
P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	2.09	4
P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 - [SAHH_HUMAN]	2.08	1
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	2.08	4
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	2.07	1
Q14781	Chromobox protein homolog 2 OS=Homo sapiens GN=CBX2 PE=1 SV=2 - [CBX2_HUMAN]	2.07	1
K7ENW7	DNA (cytosine-5)-methyltransferase 1 (Fragment) OS=Homo sapiens GN=DNMT1 PE=1 SV=1 - [K7ENW7_HUMAN]	2.06	1
Q9NR56	Muscleblind-like protein 1 OS=Homo sapiens GN=MBNL1 PE=1 SV=2 - [MBNL1_HUMAN]	2.06	1
Q15637	Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4 - [SF01_HUMAN]	2.03	2
Q9H8H2	Probable ATP-dependent RNA helicase DDX31 OS=Homo sapiens GN=DDX31 PE=1 SV=2 - [DDX31_HUMAN]	2.00	2
Q8WXA9	Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens GN=SREK1 PE=1 SV=1 - [SREK1_HUMAN]	1.97	1
P56182	Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens GN=RRP1 PE=1 SV=1 - [RRP1_HUMAN]	1.95	1
075390	Cutrate synthase, mitochondral OS=Homo sapiens GN=CS PE=1 SV=2 - [CLSY_HUMAN]	1.93	2
P61619	Protein transport protein Sec61 subunit alpha isoform 1 US=Homo sapiens GN=SEC.61A1 PE=1 SV=2 - [S61A1_HUMAN]	1.89	1
Q92925	SWIJSNF-related matrix-associated actin-dependent regulator of chromatin submanify D member 2 US=Homo sapiens GN=SMARCD2 PE=1 SV=3 - [SMRD2_HUMAN]	1.88	1
Q96P11	Probable 285 rRNA (cytosme-t(s))-metrykransterase US=Homo sapiens GN=HOSUNS PE=1 SV=2 - [NSUNS_HUMAN]	1.86	2
P57740	Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1 - [NU107_HUMAN]	1.84	1
Q14839	Chromodomain-neikase-bina-pinaing protein 4 US=Horino sapiens GN=CHLP YE2 - [CHLP_HUMAIN]	1.83	0
Q08945	FACT COMPLEX SUBURIT SSKP1 US=HOMD SAPLERS GN=SSKP1 PE=1 SV=1 - [SSKP1 PL=HUMAN]	1.83	2
095831	Apoptosis-inducing factor 1, introcronoral US=Homo sapiens GN=ALIPHI PC=1 SV=1 - [ALIPMI_HUMAN]	1.79	2
P46013	Antigen KL-07 US=Homo sapiens GN=HKL07 PE=1 SY=2 - [Kto7_HUMAN] DNA bizding practice 25 Core-Marce anziene CN=DM25 ExtEnd (2014)	1.78	8
00V2T0	Nucleals complex periods 2 homes Os-Home context (1-1-33-(K0-12-)(10-14))	1.70	2
014009	Autocale complex protein 2 inditional got and in september 3 and indicate the 1 start - Trade Categoria and the second and the	1.77	4
Q14000	Cytoskeetuinessoualeu piotein 5 05-1 min sapiento dir-Cker 5 rL-1 5 v-5 - [LCker 5], ionwing	1.72	
00PV10_4	Wo repeat-containing protein ou (rr agneticity Osenonio sapieris dine workow recei sveri - (rincozz-nonekni) Trafeama - a chi alaka e acabilizzante francesa 15. Nacha euriliana ushurki Occ. Hanna canaina (rincozz-nonekni)	1.72	1
Q9DXJ9-4 D201E2	Isoformiz on realiphar-decipitalisted set 15, NACA dixilially subuliti USEEntition Section (Figure 16, 16, 16, 16, 16, 16, 16, 16, 16, 16,	1.71	2
CQUBD5	Senie dureonite procent prospitates 2A or bot explanation and prior software and software and software and a softwa	1.70	2
Q500003	Origin tectograduit complex subulints of an international source of the state of th	1.05	
015042	To initial dow proteining co-noise site of the second seco	1.65	2
D6RDY0	Tertatricoportide renear protein Q4 (Frammer) DS-Hom scalence GN=TTC0 FE=4 SV=3 - [DKEN0_HOTM]	1.65	1
015061	WD repeat-ontaining protein 43 (See Hom spinone) SOFT MD appendix TS-12 - TW/R43 (HUMAN)	1.63	2
O8NEW/8	Naryleyraminate ordidyldransferase OS=Hom sanleyr GM=CMS PET SV=2 - TMFLA HIMANI	1.61	2
012788	Transfurin beta-like notein 3 OS-Hom saniers GN-ERI 3 PE-1 SU2 - T ERI 3 HILMANI	1.61	2
043913	Origin percentition complex situations for Sections sciences (N=CRC5 FEELSV=1 - (DRC5 HIIMAN)	1.61	1
0911080	Sey comb a midleo-like protein 2.05=Homo salpetis GHOVERE159-1 [Coll 2 HillAN]	1.57	2
09H0A0	Namehylina faras gina proteini z Gomenna Ghunghini Groseni z Tarta Strat. [Gentle: Internit]	1.57	2
P49591	Scripe-tRNA linase outputsmic (Sac-Mark supers Site for the Let Stripe (Sac-Mark Stripe) (Sac-Mark Str	1.56	2
08WY05	Micronoreses compared submit DOCER 0.54-bitm safets GL/CR8 PET SV=1 - [D/CR8 HIMAN]	1.50	3
060716	Catering delta-1 OS=Homo saniers GN=CTNND1 PE=1 SV=1 - [CIND1 HUMAN]	1.55	2
043143	Putative pre-mRNA-solicing factor ATP-dependent RNA belicase DHX15 OS=Homo saniens GN=DHX15 PF=1 SV=2 - [DHX15 HI IMAN]	1.51	2
094776	Metastas-associated motein MTA2 OS-Horm saniers GN-MTA2 PE-15 V=1 - [MTA2 H][MAN]	1.50	2
013573	SWW domain-containing protein 1.05=Homo spaces (M=SWV1 PF=1.5V=1 - [SWV1 H IMAN]	1.49	2
~~~//		1.17	2

Accession	Description	ΣCoverage	Σ# PSMs
043395	U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens GN=PRPF3 PE=1 SV=2 - [PRPF3_HUMAN]	1.46	1
P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 - [TKT_HUMAN]	1.44	1
Q96T37	Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15 PE=1 SV=2 - [RBM15_HUMAN]	1.43	2
Q9UHX1	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1 - [PUF60_HUMAN]	1.43	1
Q9UPP1	Histone lysine demethylase PHF8 OS=Homo sapiens GN=PHF8 PE=1 SV=3 - [PHF8_HUMAN]	1.42	2
Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 - [SF3A1_HUMAN]	1.39	1
H7C1M2	Protein SON (Fragment) OS=Homo sapiens GN=SON PE=1 SV=1 - [H7C1M2_HUMAN]	1.38	2
P04843	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 - [RPN1_HUMAN]	1.32	2
P27816	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN]	1.30	2
Q8NE71	ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2 - [ABCF1_HUMAN]	1.30	2
Q9H307	Pinin OS=Homo sapiens GN=PNN PE=1 SV=4 - [PININ_HUMAN]	1.26	2
Q9H0D6	5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1 - [XRN2_HUMAN]	1.26	1
075400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 - [PR40A_HUMAN]	1.25	2
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 - [FAS_HUMAN]	1.15	5
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	1.15	2
000411	DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN]	1.14	2
Q9UG63	ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2 - [ABCF2_HUMAN]	1.12	2
075152	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3 - [ZC11A_HUMAN]	1.11	2
P49916	DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2 - [DNLI3_HUMAN]	1.09	2
014654	Insulin receptor substrate 4 OS=Homo sapiens GN=IRS4 PE=1 SV=1 - [IRS4_HUMAN]	1.03	1
Q63HK3	Zinc finger protein with KRAB and SCAN domains 2 OS=Homo sapiens GN=ZKSCAN2 PE=1 SV=2 - [ZKSC2_HUMAN]	1.03	1
Q8WWK9	Cytoskeleton-associated protein 2 OS=Homo sapiens GN=CKAP2 PE=1 SV=1 - [CKAP2_HUMAN]	1.02	1
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	1.01	2
Q8WTT2	Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1 SV=1 - [NOC3L_HUMAN]	1.00	1
Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	0.99	2
P55197-1	Isoform 1 of Protein AF-10 OS=Homo sapiens GN=MLLT10 - [AF10_HUMAN]	0.97	1
Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN]	0.97	2
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	0.94	2
P55198	Protein AF-17 OS=Homo sapiens GN=MLLT6 PE=1 SV=2 - [AF17_HUMAN]	0.91	2
Q12769	Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3 - [NU160_HUMAN]	0.91	1
060841	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 - [IF2P_HUMAN]	0.90	2
A1X283	SH3 and PX domain-containing protein 2B OS=Homo sapiens GN=SH3PXD2B PE=1 SV=3 - [SPD2B_HUMAN]	0.88	2
P49790	Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2 - [NU153_HUMAN]	0.88	2
Q13435	Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2 - [SF3B2_HUMAN]	0.78	2
Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205_HUMAN]	0.75	1
Q8N2Y8	Iporin OS=Homo sapiens GN=RUSC2 PE=1 SV=3 - [RUSC2_HUMAN]	0.73	1
Q8N3U4	Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2 PE=1 SV=3 - [STAG2_HUMAN]	0.73	1
014776	Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=2 - [TCRG1_HUMAN]	0.73	1
060241	Brain-specific angiogenesis inhibitor 2 OS=Homo sapiens GN=BAI2 PE=2 SV=2 - [BAI2_HUMAN]	0.69	4
015197	Ephrin type-B receptor 6 OS=Homo sapiens GN=EPHB6 PE=1 SV=4 - [EPHB6_HUMAN]	0.69	1
Q9NPP4	NLR family CARD domain-containing protein 4 OS=Homo sapiens GN=NLRC4 PE=1 SV=2 - [NLRC4_HUMAN]	0.68	1
Q9UQE7	Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 - [SMC3_HUMAN]	0.66	2
Q9BZH6	WD repeat-containing protein 11 OS=Homo sapiens GN=WDR11 PE=1 SV=1 - [WDR11_HUMAN]	0.65	1
Q8WXE0	Caskin-2 OS=Homo sapiens GN=CASKIN2 PE=1 SV=2 - [CSKI2_HUMAN]	0.58	2
Q5SW79	Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1 - [CE170_HUMAN]	0.57	2
Q8NI27	THO complex subunit 2 OS=Homo sapiens GN=THOC2 PE=1 SV=2 - [THOC2_HUMAN]	0.56	2
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]	0.55	2
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	0.54	1
Q14690	Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 - [RRP5_HUMAN]	0.53	2
P51532	Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2 - [SMCA4_HUMAN]	0.49	2
Q9HCJ0	Trinucleotide repeat-containing gene 6C protein OS=Homo sapiens GN=TNRC6C PE=1 SV=3 - [TNR6C_HUMAN]	0.47	1
Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 - [SPTN1_HUMAN]	0.44	2
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	0.34	2
Q5UIP0	Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN]	0.28	1
015149	Plectin OS=Homo sabiens GN=PLEC PE=1 SV=3 - [PLEC HUMAN]	0.15	2

## **APPENDIX-III**



Deniz Ugurlu Cimen <denizugurlu88@gmail.com>

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