# ACHIEVING SPECIFICITY IN REDOX SIGNALING AND REDOX REGULATION OF PROTEIN FUNCTION

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# Achieving Specificity in Redox Signaling and Redox Regulation of Protein Function

Specificiteit in Redox-Signaaltransductie en Redoxregulatie van Eiwitfunctie

(met een samenvatting in het Nederlands)

# Proefschrift

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# ABBREVIATIONS

ΔC	cysteine-free mutant
-CH <sub>2</sub>	methylene group
-S-S-	disulfide
-SOH	sulfenic acid
<sup>1</sup> O <sub>2</sub>	singlet oxygen
Å	ångström
ABC	ammonium bicarbonate
ΑβΡΡ	amyloid-β protein precursor
ALS	amyotrophic lateral sclerosis
ANXA2	annexin A2
APR	aggregation prone region
ASK1	apoptosis signal-regulating kinase 1
ΒΜΕ, β-ΜΕ	β-mercaptoethanol
C, Cys	cysteine
CAA	chloroacetamide
CCNE	gene encoding cyclin E
CD	circular dichroism
CDKN2A	gene encoding p16 <sup>INK4A</sup>
C-SO <sub>2</sub> H/C-	hyperoxidized cysteine (cysteine sulfinic acid and
SO <sub>3</sub> H	cysteine sulfonic acid, respectively)
CDK4	cyclin-dependent kinase 4
C.	peroxidatic cvsteine
P	I
C <sub>R</sub>	resolving cysteine
C <sub>R</sub> DAO, DAAO	resolving cysteine D-amino acid oxidase
C <sub>R</sub> DAO, DAAO DKO21	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2
DAO, DAAO DKO21 dox	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin
DAO, DAAO DKO21 dox DUOX	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase
DAO, DAAO DKO21 dox DUOX DTT	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol
DAO, DAAO DKO21 dox DUOX DTT ECAR	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate
DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase
C <sub>R</sub> DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS ER	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase endoplasmic reticulum
DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS ER ETC	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase endoplasmic reticulum electron transport chain
C <sub>R</sub> DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS ER ETC FDR	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase endoplasmic reticulum electron transport chain false discovery rate
C <sub>R</sub> DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS ER ETC FDR Fe-S cluster	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase endoplasmic reticulum electron transport chain false discovery rate iron-sulphur cluster
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C <sub>R</sub> DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS ER ETC FDR Fe-S cluster GPX Grx GR GSSG GSH	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase endoplasmic reticulum electron transport chain false discovery rate iron-sulphur cluster glutathione peroxidase glutaredoxin glutathione reductase oxidized glutathione glutathione
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C <sub>R</sub> DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS ER ETC FDR Fe-S cluster GPX Grx GR GRSG GSH H <sub>2</sub> O <sub>2</sub> HA-	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase endoplasmic reticulum electron transport chain false discovery rate iron-sulphur cluster glutathione peroxidase glutaredoxin glutathione reductase oxidized glutathione glutathione hydrogen peroxide hemagglutinin
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C <sub>R</sub> DAO, DAAO DKO21 dox DUOX DTT ECAR eNOS ER ETC FDR Fe-S cluster GPX Grx GR GSSG GSH H <sub>2</sub> O <sub>2</sub> HA- HAT1 HCO <sub>4</sub>	resolving cysteine D-amino acid oxidase double knockout cells for PRDX1 and PRDX2 doxycyclin dual oxidase dithiothreitol extracellular acidification rate endothelial nitric oxide synthase endoplasmic reticulum electron transport chain false discovery rate iron-sulphur cluster glutathione peroxidase glutaredoxin glutathione reductase oxidized glutathione hydrogen peroxide hemagglutinin histone acetyltransferase 1 peroxymonocarbonate

HO.	hydroxyl radical
HOCl	hypochlorous acid
HPS	heat-shock protein
HSQC	heteronuclear single quantum coherence
IA	iodoacetamide
iBAQ	nitensity based absolute quantification
IDR	intrinsically disordered region
IP	immunoprecipitation
iNOS	inducible nitric oxide synthase
kDa	kilodalton
LEE011	ribociclib
LFQ	label-free quantification
LMCA	last mammalian common ancestor
LVCA	last vertebrate common ancestor
М	methionine
MD	molecular dynamics
MW	molecular weight
NAD	nicotinamide adenine dinucleotide
NADH	reduced form of nicotinamide adenine dinucleotide
NADP	nicotinamide adenine dinucleotide phosphate
NADPH	reduced form of nicotinamide adenine dinucleotide
	phosphate
NMDAR	N-methyl-D-aspartate receptor
NMR	nuclear magnetic resonance
nNOS	neuronal nitric oxide synthase
NOX	NADPH oxidase
0 <sub>2</sub> .	superoxide
<sup>1</sup> O <sub>2</sub>	singlet molecular oxygen
O <sub>3</sub>	ozone
OA	okadaic acid
OCR	oxygen consumption rate
ONOO-	peroxinitrite
Orp1	yeast oxidant receptor peroxidase-1
OXPHOS	oxidative phosphorylation
PDI	protein disulfide isomerase
pK,	dissociation constant
PP2A	serine-threonine phosphatase 2A
РРР	pentose-phosphate-pathway
PRDX	peroxiredoxin
PTEN	phosphatase and tensin homologue
PTM	post-translational modification
РТР	protein tyrosine phosphatase
R.	carbon-centered radicals
RAC1	Ras-related C3 botulinum toxin substrate 1

Rb	retinoblastoma
RO.	alkoxyl radical
ROO'	peroxyl radicals
ROOH	hydroperoxide
ROS	reactive oxygen species
RT	room temperature
S, Ser	serine
SAXS	small-angle x-ray scattering
SEC	size exclusion chromatography
Sit4	serine/threonine-protein phosphatase PP1-1
SOD	superoxide dismutase
SOD1	Cu,Zn-superoxide dismutase
S-GSHylated	S-glutathionylated
S-PRDXylation	S-peroxiredoxinylation
STAT3	signal transducer and activator of transcription 3
T, Thr	threonine
Tap42	type 2a phosphatase-associated protein 42, yeast
	homolog of α4
ThT	thioflavin T
TIGAR	TP53-inducible glycolysis and apoptosis regulator
Tip41	tap42-interacting protein of 41 kDa, yeast homolo
	of TIPRL
TIPRL	TOR signaling pathway regulator-like
TNPO1	transportin 1
TOR	target of rapamycin
TR	thioredoxin reductase
TRX	thioredoxin
Tsa2	thiol-specific antioxidant protein 2
UPR	unfolded protein response
UPS	ubiquitin-proteasome system
WB	western blotting
WT	wild-type

GENERAL INTRODUCTION



ROS		Production	Radical or non-radical	Major target
Superoxide radical	0 <sub>2</sub> .	Mitochondria (ETC) and membrane (NOXs)	Radical	Fe-S clusters, NO•, lipids
Hydrogen peroxide	H <sub>2</sub> O <sub>2</sub>	Superoxide (O2 <sup>•</sup> ) dismutation, enzymatic generation	Non-radical	Thiols, highly reactive with peroxiredoxins, catalase, glutathione peroxidase
Hydroxyl radical	HO.	H <sub>2</sub> O <sub>2</sub> reduction in Fe2+-catalyzed Fenton reactions	Radical	Any macromolecule
Peroxyl radical	ROO'	Attack of HO <sup>•</sup> on methylene (-CH <sub>2</sub> ), lipid peroxidation chain reactions	Radical	Methylene groups (-CH <sub>2</sub> )
Organic hydroperoxide	ROOH	Hydrogen abstraction from lipids by peroxyl radicals (ROO <sup>•</sup> )	Non-radical	Metal ions
Alkoxyl radical	RO'	Metal-catalyzed decomposition of hydroperoxides (ROOH)	Radical	Proteins, lipids, DNA
Singlet molecular oxygen	<sup>1</sup> O <sub>2</sub>	Photoexcitation of oxygen $(O_2)$	Non-radical	Proteins, lipids, DNA
Electronically excited carbonyls	R-C=O*	Photo- or chemiexcitation of carbonyl groups (R-C=O)	Non-radical	
Ozone	0 <sub>3</sub>	Photoexcitation of oxygen (O <sub>2</sub> ) in the stratosphere, antibody-catalyzed reaction of singlet oxygen with water	Non-radical	Proteins, lipids, DNA
Hypochlorous acid	HOCI	Enzymatic generation by myeloperoxidase (MPO)	Non-radical	Proteins (cys), lipids, DNA, other ROS
Peroxymonocarbonate	HCO,	H <sub>2</sub> O <sub>2</sub> reaction with carbon dioxide	Non-radical	Cysteine, methionine

GENERAL INTRODUCTION

The human body is composed of an estimated 38 trillion cells, with extremely diverse morphologies and functions [1]. To maintain integrity, organisms need to perform many different functions, carried out and coordinated by many cell types. These tasks are extraordinarily complex and diverse, ranging from growth and development, reproduction, food digestion, movement, to defense against pathogens, detoxification and even consciousness. Specialized cells like muscle-, epithelial-, germ-, bone-, liver-, neuronal cells and lymphocytes require organization primarily based on proteins to carry out their functions. Some organismal tasks can be carried out by a single cell type, but it normally requires the combined effort of several cell types acting in a coordinated manner.

On top of these diverse intrinsic functions of cells, they are subject to constant changes in the internal and external environment. Organisms and cells are viable under a set of relatively narrow conditions. Therefore, organisms continuously employ regulatory mechanisms to maintain a steady state despite changes in the environment – also known as 'homeostasis'. To maintain homeostasis, cells harness molecular mechanisms for the sensing and transduction of signals that allows them to respond to changes and allow communication between and within cells. The failure to maintain homeostasis can result in a disruption of cellular behavior and contributes to the development of diseases including cancer, neurodegenerative disease and diabetes [2].

The reversible oxidation of protein thiols by reactive oxygen simple molecules, which raises questions on how an approspecies (ROS) underlies a fundamental signaling mechanism priate cellular response downstream of redox signaling can be called reduction-oxidation (redox) signaling. However, the achieved through the selective oxidation of cysteine residues role of ROS in cellular homeostasis is dual. At physiologiin specific proteins and not in others. cal levels, ROS (mostly in the form of  $H_2O_2$ ) act as a second messengers for redox signaling by selectively and efficiently A better understanding of redox regulation allows us to unoxidizing specific thiols on specific signaling proteins [3]. derstand the mechanisms of redox signaling, the biological Yet at excessive levels, ROS can react non-specifically with roles of oxidative regulation in cells, and how redox-regulated proteins, lipids and DNA, leading to molecular damage and pathways and processes might be linked to diseases associated cytotoxicity [4]. Our understanding of ROS has dramatically with oxidative stress. Here, we will briefly introduce cystechanged over the past decade(s). The traditional view was that ine chemistry and the two-faced nature of ROS and we will ROS production was not regulated and that ROS reacts with primarily focus on the role of physiological levels of ROS in cellular targets randomly. The damaging actions of ROS were redox signaling. recognized long before it became clear that redox signaling through the reversible oxidation of protein thiols is an important signaling mechanism. Redox-dependent signaling mechanisms as well as the cysteine residues involved are well conserved throughout evolution [3,5,6]. ROS are indisputably

# **REACTIVE OXYGEN SPECIES**

The term reactive oxygen species (ROS) describes a group of reactive molecules containing oxygen. Especially in the cell biology literature 'ROS' is often used as an umbrella term instead of specification of the exact chemical species involved. To understand how cells respond to ROS it is important to note that there are many types of ROS, with different (thiol) reactivities, differential susceptibility to scavenging by antioxidants, different steady state intracellular concentrations, and they can be strong or weak oxidants, radical or non-radical. Because of the diversity among reactive oxygen species, ROS is a term should be avoided whenever the specific species is known.

ROS production occurs mainly as a metabolic side product of oxidative phosphorylation (OXPHOS) in the mitochondrial electron transport chain (ETC) where 85-90% of O<sub>2</sub> is metabolized for ATP production. The three main types of cellular ROS (H<sub>2</sub>O<sub>2</sub> superoxide and hydroxyl radicals) are produced in the ETC when electrons escape during the four successive reduction steps of molecular oxygen (Figure 1A). In general,

the more reactive a ROS species is, the shorter its half-life and the higher its toxicity, and the lower its signaling capabilities. Among the different types of ROS (Table 1), hydrogen peroxide  $(H_2O_2)$  has been shown to act as a messenger relevant for signal transduction [3]. There is no evidence nor likelihood that any other ROS directly mediate redox signaling, as their reactivity would simply be too high to achieve target specificity rather than random oxidation [7].

There are three main species of cellular ROS: superoxide radical  $(O_{2}, \cdot)$ , hydrogen peroxide  $(H_{2}O_{2})$  and hydroxyl radical (HO<sup>•</sup>) which are produced during the four successive steps of 1-electron reduction (Figure 1A). They can further react with organic compounds, thereby forming reactive 'secondary' species. ROS can further be divided into two-electron ROS (non-radicals) and one-electron radicals (highly unstable intermediates with one or more unpaired electrons, '). Although this is by no means a complete overview, it contains basic information of selected ROS types. A more comprehensive overview can be found in references [8,9].



# Fenton reaction

 $H_2O_2 + Fe^{2+} \rightarrow HO' + HO' + Fe^{3+}$ 

### Figure 1. The chemical basis of ROS generation.

(A) ROS are produced from molecular oxygen, which undergoes 4 successive steps of 1-electron reduction. Enzymes or processes that can catalyze these reactions are indicated in blue. NOX: NADPH oxidase, ETC: electron transport chain, SOD: superoxide dismutase, ox. protein folding: oxidative protein folding, PRDX: peroxiredoxin, GPX: glutathione peroxidase. (B) H,O, is converted into the highly reactive HO<sup>•</sup> by the metal-catalyzed Fenton reactions.

### Superoxide Anion Radical (O,.)

Superoxide  $(O_2^{\bullet})$  can be produced from  $O_2$  from two main cellular sources; through leakage of electrons during mitochondrial respiration and from NADPH oxidases (NOXs) at the membrane. An estimated 1-3% of electrons escape the electron transport chain (ETC) prior to reduction of O<sub>2</sub> to water. The full conversion of O<sub>2</sub> to water involves a four-electron reduction (Figure 1A). However, O, can only react with one electron at a time a single leaking electron can thus react with  $O_2$  to form  $O_2^{\bullet}$ , which can then dismutate into  $H_2O_2[8]$ . NOXs produce high levels of  $O_{2}^{\bullet}$  at the expense of NADPH, for instance during a 'respiratory burst' [10].

 $O_2^{\bullet}$  is much less reactive than HO<sup>•</sup> and does not react with most biological molecules in solution. Its major target is iron-sulfur (Fe-S) clusters, thereby decomposing them and releasing free Fe<sup>2+</sup> [11]. It also reacts with other radicals like nitric oxide (NO<sup>•</sup>), thereby forming the tyrosine-nitrating peroxynitrite (ONOO<sup>-</sup>). O<sub>2</sub><sup>-</sup> has a relatively short lifetime (~50 ms) as it undergoes rapid spontaneous or superoxide dismutase (SOD)-catalyzed dismutation into O2 and hydrogen peroxide  $(H_2O_2)$ , which in turn may produce hydroxyl radical (HO<sup>•</sup>) [12]. As such, it is the precursor of many other types of ROS.

### Hydrogen Peroxide (H<sub>2</sub>O<sub>2</sub>)

Hydrogen peroxide  $(H_2O_2)$  can be produced from spontaneous dismutation of superoxide  $(O_2^{\bullet})$ , but also through enzycommon oxidation-derived DNA lesions in DNA. matic generation (for an overview see [13]). Enzymes that can produce cellular H<sub>2</sub>O<sub>2</sub> include superoxide dismutase (SOD), It reacts at a rate that is close to the diffusion limit, so it acts as an unspecific oxidant. Its lifetime is very short at  $\sim 10^{-9}$  s NADPH oxidase 4 (NOX4) [14] and protein-disulfide isomerases (PDIs) and ERO1 during protein folding in the ER. [12]. HO<sup>•</sup> is generated by  $H_2O_2$  reduction in Fe<sup>2+</sup>-catalyzed Fenton reactions.

 $H_2O_2$  has a relatively long lifetime of ~1 ms [12], and although it is a strong two-electron oxidant due to its high reduction Peroxyl Radical (ROO') potential, its high activation energy restricts its reactivity to a When methylene groups (-CH<sub>2</sub>) in polyunsaturated fatty few targets in cells. Direct reaction is slow with (seleno)cysteacids are attacked by HO' or ROO', a hydrogen atom will ine, methionine, glutathione and Fe-S clusters, although there be abstracted to form carbon-centered radicals (R<sup>•</sup>, on lipids are a few notable exceptions. Reactivity with cysteine is noroften called lipid radical). In turn, these react rapidly with mally  $2.9 \text{ M}^{-1} \text{ s}^{-1}$  (or ~20 M<sup>-1</sup> s<sup>-1</sup> when adjusted for thiolates) but oxygen to generate peroxyl radicals (ROO') [21]. In lipids this

in specific proteins (2-cys peroxiredoxins) this can increase up to  $1-4 \ge 10^7 \text{ M}^{-1} \text{ s}^{-1}$  [15,16]. The reactivity of cysteines partially depends on its particular pK as determined by the local protein structure and environment, thereby providing a basis for selective redox signaling (see below). Because of its long lifetime and its extreme reactivity with 2-cys peroxiredoxins (see chapter 2),  $H_2O_2$  is considered the main signaling ROS by means of reacting with cysteine thiols.

The plasma membrane allows limited diffusion of H<sub>2</sub>O<sub>2</sub> into the cell directly, and is further facilitated by aquaporins [17]. The  $H_2O_2$  gradient over the plasma membrane when  $H_2O_2$  is added extracellularly is around 650-fold, with lower concentrations on the cytosolic side [18]. The toxicity of  $H_2O_2$  at high concentrations is most likely a consequence of its reduction to the highly toxic HO<sup>•</sup>, catalyzed by Fe<sup>2+</sup> in the Fenton reaction (Figure 1B) [19]. Furthermore, H<sub>2</sub>O<sub>2</sub> can react with carbon dioxide, thereby producing the highly reactive peroxymonocarbonate  $(HCO_{1})$  [20]. H<sub>2</sub>O<sub>2</sub> levels are controlled through the coordinated actions of peroxiredoxins, catalase and glutathione peroxidase (see below).

# Hydroxyl Radical (HO<sup>•</sup>)

The Hydroxyl radical (HO<sup>•</sup>) is the most reactive ROS, and it oxidizes most biomolecules including DNA, lipids (see below), carbohydrates and proteins. As a result, it produces stable adducts such as 8-oxo-deoxyguanosine, which causes



#### Figure 2. Scavenging systems.

(A) Cellular anti-oxidant systems that control H<sub>2</sub>O<sub>2</sub> levels include several forms of superoxide dismutase (SOD, i), the peroxiredoxin system (PRDX, ii) glutathione peroxidase (GPX, iii) and peroxisomal catalase (iv). (B) Cellular disulfide reduction systems. Disulfides can be reduced by the thioredoxin system (TRX, i), glutathionylated proteins can be reduced by the glutaredoxin (GRX) system. Both use NADPH as a final electron donor. GSH: glutathione (reduced), GSSG: glutathione (oxidized), GR: glutathione reductase. TR: thioredoxin reductase

can cause a chain reaction, since the newly formed ROO' can also be created by chemiexcitations, for example through the again react with methylene groups in other lipids [22]. The encounter between two alkoxyl- or peroxyl radicals in memperoxidation of lipids causes a change in the shape and fluidity brane lipids [29]. A reaction with O<sub>2</sub> releases excited singlet of membranes, leading to permeabilization membranes. Simoxygen [30]. ilar short chain reactions can also take place in proteins [23].

Ozone  $(O_2)$  in the earth's stratosphere is known for protecting **Organic Hydroperoxide (ROOH)** the earth from damaging radiation and as an air pollutant (Lipid) peroxyl radicals (ROO') can abstract hydrogen atoms responsible for damaging the respiratory system, but it is also from nearby polyunsaturated fatty acids and sterols such as produced inside biological systems from singlet oxygen, for cholesterol, thereby forming (lipid) hydroperoxide (ROOH) example in activated neutrophils [31]. Exposure of cells to and a new carbon-centered (lipid) radical R<sup>•</sup>, which in turn can ozone can cause lipid and protein peroxidation, a disruption of cellular membranes and epithelial barrier as well as DNA trigger lipid peroxidation chain reactions. They may also further react with a metal ion to generate alkoxyl radicals (RO'). damage [32-34]. Ozone can react directly with biological molecules, generating singlet oxygen in the process [35]. On top of that, ozone in water slowly decomposes into HO<sup>•</sup> [36].

### Other ROS

Other types of ROS include alkoxyl radicals (RO<sup>•</sup>), singlet molecular oxygen (1O2), electronically excited carbonyls (R-Myeloperoxidase (MPO) is a heme protein secreted by leukocytes, which converts H<sub>2</sub>O<sub>2</sub> and Cl<sup>-</sup> into hypochlorous acid (hypochlorite, HOCl). Hypochlorous acid is highly reactive, which is why it is considered the responsible oxidant for the killing capabilities of phagocytes against pathogens [37,38]. This is also the reason HOCl is widely used as a household disinfectant (bleach). It reacts with iron via the Fenton reaction forming HO<sup>•</sup> which makes it cytotoxic. Furthermore, it can react with other ROS like O,, H2O, and OH, respectively forming OH<sup>•</sup>, <sup>1</sup>O<sub>2</sub> and ClO. HOCl can directly oxidize cysteine thiols [39].

C=O\*), ozone (O<sub>2</sub>), hypochlorous acid (HOCl) and peroxymonocarbonate (HCO<sub>4</sub>) and are briefly discussed below. There are several other types of reactive species such as reactive nitrogen species (e.g. nitrix oxide, NO' and peroxynitrite, ONOO<sup>-</sup>), but these are not discussed here. Alkoxyl radicals (RO<sup>•</sup>) are the result decomposition of hydroperoxides catalyzed by metal ions (e.g. iron or copper, such as in heme proteins) [24]. This occurs during lipid peroxidation and can theoretically cause amplification of lipid peroxidation reactions, although their cellular concentration is low [25]. They are stronger oxidants than ROO', but less H<sub>2</sub>O<sub>2</sub> can react with carbon dioxide to form peroxymonocarreactive than HO'. bonate (HCO<sub>2</sub>). The reaction is an equilibrium which lies to

Photoexcitation (such as by UV occurring in light-exposed tissues) of molecular oxygen (O<sub>2</sub>) generates singlet oxygen  $(^{1}O_{2})$  [26]. Singlet oxygen is also produced enzymatically, for instance by peroxidases, during the termination of lipid peroxidation propagation (i.e. when two peroxyl radicals react), and during reactions with ozone  $(O_2)$  [27,28].

Photoexcitation of carbonyl groups generates triplet state car-ROS can originate from many intracellular sources. The brief bonyl (R-C=O\*, where \* indicates the excited state). They can overview here will mainly discuss the sources for the primary

Α.

B.

the left. Although only ~1 % of H<sub>2</sub>O<sub>2</sub> participates in the interaction, the product, peroxymonocarbonate (HCO<sub>4</sub><sup>-</sup>), is more reactive with thiols and methionine than  $H_2O_2$  itself [40].

# **ENDOGENOUS ROS GENERATION**

# ROS species generated by reduction of oxygen (O2<sup>--</sup>), as well as $H_2O_2$ and $OH^{\bullet}$ .

# **Mitochondrial Sources of ROS**

A large part of ROS production occurs in the mitochondrial respiratory electron transport chain during oxidative phosphorylation (OXPHOS), where 85-90% of O<sub>2</sub> is metabolized. The inner mitochondrial membrane houses a series of electron transporters (complex I-IV) that shuttles electrons from NADH and FADH, to O, as the final electron acceptor. This allows proton transport into the mitochondrial intermembrane space and the resulting proton gradient drives the production of ATP using ATP synthase (complex V). Importantly, O2 ran react prematurely with electrons 'leaking' from the electron transport chain (at complexes I and III), thereby forming superoxide  $(O_2^{\cdot})$  [41]. Up to 3% of mitochondrial oxygen consumption is reduced to form superoxide (which dismutates into  $H_2O_2$  [42,43]. This rate may be affected by various factors such as the mitochondrial membrane potential, oxygen availability or electron flux though the respiratory chain [44-46].

### NADPH Oxidases (NOXs)

The membrane-bound family of NOX enzymes produce superoxide by transferring one electron from NADPH to oxygen. The catalytic subunit of the complex contains one of seven enzymes (NOX1-5, DUOX1-2), each with varying tissue distributions and activation mechanisms. NOXs (specifically NOX2) became famous for their role in the so-called respiratory burst in activated neutrophils, which produce large amounts of ROS to inactivate microorganisms [47]. Furthermore, they have been associated with redoxomes; specialized redox-active endosomes that allow compartmentalization of H<sub>2</sub>O<sub>2</sub> and localized redox signaling [48].

A wide array of extracellular signals can cause NOX activation, including cytokines, peptide growth factors, G-protein coupled receptor agonists and mechanical stretch [49]. NOX activation can be tightly controlled by the signal-mediated binding of cell-specific cofactors such as FAD and calcium

[50]. The activation of NOXs and the subsequent ROS production is crucial for signal propagation in a large number of pathways [50].

### Other Sources

Besides NOXs, there is a number of other enzymes that can generate ROS. Various types of oxidases generate ROS at specific subcellular locations (e.g. those localized to the endoplasmic reticulum (ER) and peroxisomes). For example, cytochrome P450 enzymes in the ER catalyze the heme-dependent oxidation of several metabolites but they can generate superoxide and H<sub>2</sub>O<sub>2</sub> during 'reaction uncoupling' [51]. It is now recognized that this is not merely a by-product of metabolism but rather an important redox regulatory mechanism in adrenal corticosteroid production [52]. ROS are also produced during oxidative protein folding in the ER driven by ERO1 oxidoreductases and protein disulfide isomerases (PDI), which are responsible for structural disulfide formation in proteins but also generates  $H_2O_2$  in the process [53,54]. Other ROS-producing enzymes include xanthine oxidase, nitric oxide synthase, cyclooxygenases and lipoxygenases. For a comprehensive overview see reference [13].

While not technically generating ROS de novo, superoxide dismutases (SODs) convert superoxide  $(O_2^{\bullet})$  into  $H_2O_2$  [55]. SODs are widely distributed within tissues and cells. SOD is known as an antioxidant, but although it does scavenge toxic superoxide, it converts it to another ROS species [56]. SOD

does not necessarily increase H<sub>2</sub>O<sub>2</sub> levels, since superoxide is distmutates to H<sub>2</sub>O<sub>2</sub> regardless of SOD, although SOD might change the stoichiometry between  $O_2^{\bullet}$  and  $H_2O_2$  only if the reaction prevents other reactions involving superoxide in favor of the latter [57].

ROS are also generated by exogenous factors including UV and ionizing radiation, toxins, nutrients, drugs and many more, collectively termed the 'exposome' [58,59]. The contribution of the exposome to the total cellular ROS pool is unknown due to the highly variable exposure of cells to different exposome factors.

To understand ROS biology, an important question is how much each of these ROS generating systems contribute to the total cellular pool of ROS. It was estimated that around 45% of cellular H<sub>2</sub>O<sub>2</sub> in myoblasts comes from cellular respiration, 40% from NOXs and the other 15% from other ROS sources, although this may vary strongly depending on cellular context and metabolic state [60]. Furthermore, the concentration of H<sub>2</sub>O<sub>2</sub> across cells is highly compartmentalized. It ranges from as low as 80 pM in the cytosol to 4 nM in the mitochondrial matrix and up to micromolars in the ER [61-63].

# SCAVENGING OF INTRACELLULAR H<sub>2</sub>O<sub>2</sub>

Intracellular ROS levels are under tight control. As mentioned, low levels of ROS are essential for fundamental cellular processes such as proliferation, but high levels of ROS may cause random damage. Several anti-oxidant systems are in place that can decompose ROS to constrain cellular ROS levels. Firstly, several types of SODs convert  $O_2^{\bullet}$  into  $H_2O_2$ (Figure 2A, i)[56]. In turn, H<sub>2</sub>O<sub>2</sub> levels are tightly controlled by the combined actions of peroxiredoxins (PRDXI-VI), catalase and glutathione peroxidase (GPX), which all decompose  $H_2O_2$  to water.

Glutathione peroxidase (GPX) catalyzes the reduction of H<sub>2</sub>O<sub>2</sub> and forms oxidized glutathione (GSSG), after which glutathione reductase (GR) then recycles GSSG using NADPH (Figure 2A, iii) [64].

Catalase is specifically localized to peroxisomes, where it breaks down and prevents release of H<sub>2</sub>O<sub>2</sub> generated by peroxisomal enzymes like acyl-CoA oxidase and D-amino acid oxidase (Figure 2A, iv). It may also decompose H<sub>2</sub>O<sub>2</sub> from other parts of the cell [65].

The C<sub>p</sub>-SOH is also sensitive to further oxidation (hyperoxidation; C<sub>p</sub>-SO<sub>2</sub>H), leading to the transient inactivation of peroxiredoxins mainly at higher H<sub>2</sub>O<sub>2</sub> concentrations [70].

Peroxiredoxins are more abundant than GPXs, together comprising up to 1% of total soluble protein content of cells [71]. Kinetic studies revealed that the second-order rate constants for the oxidation of the PRDX  $C_p$  is  $10^5$ - $10^6$  M<sup>-1</sup> s<sup>-1</sup>, which is up to seven orders of magnitude higher compared to cysteines described in other redox-regulated proteins [72]. Thus, peroxiredoxins are thought to scavenge more than 99% of cytosolic  $H_2O_2$  [73]. Together, this suggests that cysteine thiols in  $H_2O_2$ target proteins are generally outcompeted by peroxiredoxins for reaction with H<sub>2</sub>O<sub>2</sub>. How it is possible that H<sub>2</sub>O<sub>2</sub> oxidizes these low reactive thiols in  $H_2O_2$ -sensitive proteins in the presence of peroxiredoxins is a fundamental question in redox biology.

In addition to  $H_2O_2$  scavenging systems, cells can reduce non-structural disulfides that form between oxidized thiols in proteins. Thioredoxin (TRX) uses a thiol-disulfide exchange reaction to reduce disulfides, and TRX itself is regenerated using by thioredoxin-reductase (TR), which in turn is reduced at the expense of NADPH (**Figure 2B, i**). TRXs reduce disulfide bonds in a wide variety of proteins [74].

The glutaredoxin system utilizes the highly abundant glutathione (GSH) to resolve protein disulfide bonds, thereby oxidizing GSH to form GSSG (Figure 2B, ii). Like the thioredoxin system, the glutathione system ultimately uses NADPH as an electron donor. Increasing the cellular NADPH pool thus fuels the reducing capacity of the cell [75]. It has been proposed that the main benefit of the drastically upregulated glucose metabolism in cancer cells is not to switch to glycolysis for ATP synthesis to meet a high ATP demand in tumor cells (as speculated by Warburg). Rather, it shunts glycolytic intermediates into the pentose-phosphate-pathway (PPP) for biomass synthesis and to maintain the redox balance through the supply of NADPH [76]. Both localized production of ROS and organelle-specific anti-oxidant systems result in the compartmentalization of intracellular H2O2 levels [77,78]. As such, redox potentials (as a measure for how reducing or oxidizing an environment is) vary greatly amongst organelles (Figure 3).

# OXIDATIVE STRESS VERSUS REDOX SIGNALING

As mentioned, ROS have long been viewed as merely damaging side-products of metabolism. It was even posed that aging is the cumulative result of oxidative damage to cells and tissues [4]. While excessive levels of ROS cause random damage to macromolecules and oxidative stress, physiological levels of ROS are essential in the redox regulation of fundamental cellular processes. Prolonged disruption of redox homeostasis can therefore also be seen as oxidative stress. Examples of essential cellular processes that require oxidative modifications in order to function correctly include signal transduction at the plasma membrane [79], developmental processes such as morphogenesis and differentiation [80,81], cell proliferation, wound healing [82], muscle adaptation to exercise [83,84] and much more [82]. The exact boundary between oxidative stress and redox signaling is very vague. This is partially caused by the lack of tools for assessing endogenous levels of ROS, although sensitive ROS detection methods have recently been developed and are continuously being improved [74,85]. A good distinction between ROS as a signaling molecule versus ROS as oxidative stress has been proposed by Sies et al. [86].

# OVERVIEW OF CYSTEINE CHEMISTRY

Despite the tight control of ROS production and antioxidant systems, changes in the cellular redox state occur continuously and these changes can result in the oxidation of cysteine residues in proteins. Proteins that are oxidized by  $H_2O_2$  are sometimes described as 'ROS sensors', which function to provide an adequate cellular response to the changing cellular environment. As we will discuss below, and in **chapter 2** in this thesis, most so-called ROS sensors are likely not directly oxidized by  $H_2O_2$ . Redox signaling through the reversible oxidation of specific proteins is highly cell- and tissue-specific [87]. Hydrogen peroxide ( $H_2O_2$ ) is considered as the major ROS in reversible cysteine oxidation (see above) [13,88].

Cysteine residues are relatively low in abundance in proteins, comprising only 2.26% of amino acids where 3.28% is expected based on the relative number of codons [89,90]. Nevertheless, cysteines participating in disulfide bonds are the most evolutionary conserved amino acids, and in cases where a disulfide bond is not conserved cysteines are replaced as pairs in 99% of cases [91]. Presumably, cysteines were introduced late in evolution [92], and proteomes of more complex organisms contain more cysteines than proteomes of more primitive organisms, suggesting an ongoing increase in cysteine content [93]. This conservation and increasing number of cysteines in our proteome suggest a selective pressure that could reflect the acquisition of cysteine-oxidation based signaling functions with the evolution of complexity [3,94].



### Figure 3. The cellular redox landscape.

Approximations of  $H_2O_2$  concentrations (nM) [164], redox potentials (mV) [77,165,166] and pH [167] of subcellular compartments. Numbers vary greatly according to growth conditions and cell types [77]. Cellular mean: 10 nM [168], -160 to -260 [166,169,170]; cytosol [168,171–173]; mitochondrial matrix [77,174–180]; mitochondrial intermembrane space [178,180]; nucleus [77]; ER [63,181]; Golgi [182]; peroxisomes [104,183]; lysosomes [184]; membrane [167]; extracellular [172]. Grey/beige indicates unknown  $H_2O_2$  levels. The order of organelles from most reducing to most oxidizing is: mitochondria, nucleus, cytoplasm, lysosome, endoplasmic reticulum, and cell membrane.

The protonation state of a sulfur group is an important de-The sulfur atom makes cysteine a versatile determinant of protein structure and function, as it can adopt a variety of termining factor for protein thiol reactivity. Most oxidation oxidation states (Figure 4). This is also the molecular basis for events involve the thiolate anion as it is more nucleophilic the critical roles that cysteines play both in enzyme catalytic [96]. The thiol side chain of free cysteine has a pK of 8.3, sites and regulatory attributes of enzyme function. Reduced meaning that at physiological pH ~90% of thiols will be procysteines exist as either a thiol (-SH) or as a thiolate anion  $(-S^{-})$ tonated (-SH). However, the  $pK_1$  of specific protein thiols can when it is deprotonated. The thiolate anion is prone to oxivary considerably, ranging from as low as 2.5 to as high as 12. Thiols in redox-sensitive proteins have a low pK, such dation by H<sub>2</sub>O<sub>2</sub>, subsequently forming sulfenic acid (-SOH), sulfinic acid (-SO<sub>2</sub>H) and sulfonic acid (-SO<sub>2</sub>H) with each as 6.5 for TRX, 5.4 for PTP1B and between 5-6 for PRDXs subsequent oxidation step. Sulfinic acid can be reduced by [15,16,97,98]. The pK of a thiol is influenced by its local ensulfiredoxin1 (SRX1), although this reaction is slow [95]. vironment. Exposed thiols have a much lower pK than thiols Sulfonic acids cannot be reduced in vivo and are considered buried inside proteins on average (7.5 vs 9.5, respectively), irreversible. Sulfenic acids are short-lived and highly reactive. meaning that exposed thiols exist more often in a deproton-They readily react with other cysteine thiols to from disulfides ated state. Combined with the higher accessibility of exposed within the same (intramolecular) or another (intermolecular) thiols for  $H_2O_2$  this means they are more easily oxidized [5]. protein or with cysteines in short peptides such as glutathione For example, cysteines are stabilized in a deprotonated state (glutathionylation) (Figure 4). when located in vicinity to hydrogen bond donors, within an electropositive environment, at the N-terminus of alpha



#### Figure 4. Overview of cysteine modifications.

Cysteine sulfur groups exist in either a thiol (-SH) or as a deprotonated thiolate anion (-S) form depending on the pK and local pH. A critical initial step in redox signaling is that cysteine thiolates (-S) react with  $H_{a}O_{a}$ , thereby forming the highly reactive sulfenic acid form (-SOH). Subsequent reactions with H<sub>2</sub>O<sub>2</sub> form sulfinic (-SO<sub>2</sub>H) and sulfonic acid (-SO<sub>2</sub>H, irreversible). Sulfinic acids can be reduced anzymatically by sulfiredoxins (SRX), but sulfonic acids cannot be reduced. Sulfenic acids can react with proximal thiols and condenses into a disulfide bond (-S-S-), either intra- or intermolecularly. Disulsulfides are reduced by the thioredoxin (TRX) system or in a disulfide exchange reaction. Sulfenic acids can also form an intermolecular disulfide reaction with glutathione (GSH), a highly abundant tripeptide (Glu-Cys-Gly), a PTM that can be reduced by glutaredoxin (GRX).

helices, or when interacting with metal ions, thus enhancing their reactivity [99-101]. Another factor that influences the protonation state and reactivity of protein thiols is the local pH, which can range from 7.2 in the cytosol, nucleus and ER to 8.2 in peroxisomes and as low as 4.7 in lysosomes (Figure 3) [102–104].

As outlined above, cysteine residues are not equal in their ability to undergo redox modifications, thereby providing a basis for specificity in redox signaling. However, although an important determinant for reactivity, the ionization state is not the only determinant of reactivity since pH reactivity profiles for thiols do not simply correlate with their  $pK_{a}$  [15].

# **REACTIVITY AND** SPECIFICITY IN REDOX SIGNALING

A conceptual problem for H<sub>2</sub>O<sub>2</sub> as a second messenger is that it is unknown how it achieves the reactivity (i.e. how it reacts with low abundant targets) and specificity (i.e. reacting with specific thiols on specific proteins) required for proper signal transduction (Figure 5).

The first part of the problem is that it is unknown how  $H_2O_2$ can reach its targets in cells that are rich in antioxidant proteins whose function it is to capture ROS. In contrast to most thiol-containing proteins, the most prominent thiol peroxidases, peroxiredoxins, have rate constants for the reaction with H<sub>2</sub>O<sub>2</sub> more than six orders of magnitude higher, in the range of 10<sup>6</sup>–10<sup>8</sup> M<sup>-1</sup>s<sup>-1</sup> [105]. Peroxiredoxins are also highly abundant proteins, with concentrations up to three orders of magnitude higher than most redox-regulated proteins [71]. For this reason, they are expected to scavenge more than 99% of cellular H<sub>2</sub>O<sub>2</sub> (Figure 5A) [57].

Secondly, although H<sub>2</sub>O<sub>2</sub> is a strong oxidant, protein thiols in general have a low reactivity with H<sub>2</sub>O<sub>2</sub>. The reactivity (i.e. How it is possible that physiological levels of H<sub>2</sub>O<sub>2</sub> lead to rate constant) of  $H_2O_2$  with the cysteine thiolate anion (C-S<sup>-</sup>) is specific oxidation of these low reactive thiols in low abundant around 20 M<sup>-1</sup>s<sup>-1</sup> [105,106]. On top of this, most thiol-containproteins is a fundamental question in redox biology. Several ing proteins such as p16<sup>INK4A</sup>, are low-abundant (Figure 5B). theories have been proposed to explain reactivity and specificity of otherwise unreactive cysteines that are found to be Thirdly, it is poorly understood how H<sub>2</sub>O<sub>2</sub> causes the oxioxidized in response to redox changes. These mechanisms are visualized in Figure 6. Below, we discuss the proposed mechdation of specific redox-sensitive proteins in particular pathways in the context of virtually limitless potential targets in anisms and explore how these might help to overcome the a cell (Figure 5C). Cellular stimuli are being translated in an reactivity and specificity challenges of H<sub>2</sub>O<sub>2</sub>-based signaling.

appropriate, specific cellular response. If a general stress response is required, the source of  $H_2O_2$  might not matter. But when  $H_2O_2$  is the second messenger for a specific stimulus,



## Figure 5. The redox paradox.

redox-sensitive proteins in a pool of virtually limitless options?

this would require targeting of appropriate, specific pathways depending on the nature of the stimulus. As yet, what factors provide the necessary spatiotemporal precision for signal specificity is not entirely clear.

How is it possible that H,O, achieves the required reactivity and specificity to oxidize specific protein thiols needed for proper signal transduction? There are several challenges for H<sub>2</sub>O<sub>2</sub> to overcome: (A) Cells are rich in antioxidant proteins such as peroxiredoxins (PRDX), which have exceptional reactivity for  $H_2O_2$  and are expected to scavenge >99% of cellular  $H_2O_2$ . (B) Redox-regulated thiol proteins in general showcase a low H<sub>2</sub>O<sub>2</sub> reactivity and are low-abundant. (C) How can H<sub>2</sub>O<sub>2</sub> cause oxidation of specific

## A) Direct Oxidation

This model assumes that H<sub>2</sub>O<sub>2</sub> diffuses from its source and directly reacts with a target protein thiol to form a cysteine sulfenic acid (C-SOH) (Figure 6A). For this reaction to occur, a high reactivity of the targeted thiol and/or no competing reactions are required, like for instance for the oxidation of PRDXs by H<sub>2</sub>O<sub>2</sub> or oxidation of some thiols in purified proteins in vitro. As discussed, H2O2 normally reacts slowly with the cysteine thiol, but variations in the direct structural context of thiols in proteins causes local changes in their  $pK_{,}$  thereby affecting their protonation state. The protonation state of a sulfur group is an important determining factor for protein thiol reactivity. The  $pK_{i}$  of a cysteine can vary from 9.5 (for cysteines buried within a protein) to as low as 3.4, depending on the local environment [5,107].

Nonetheless, even while accounting for those local differences, a low p $K_{a}$  is not sufficient to explain the oxidation of some protein thiols. For example, cysteines in peroxiredoxins, glutathione peroxidases and bacterial oxyR react with  $H_2O_2$  many orders of magnitudes faster than can be explained by their  $pK_{1}$  and deprotonation state [73,108]. It was modelled that even H<sub>2</sub>O<sub>2</sub> concentrations close to a site of H<sub>2</sub>O<sub>2</sub> production may not be sufficient to directly oxidize protein thiols [109]. It was suggested that electrostatic and polar interactions of the cysteine thiol with the protein environment can not only contribute to lowering the pK but also stabilize the deprotonated state of the reaction [108]. Additionally, peroxidases like peroxiredoxins directly compete with the H2O2-mediated oxidation reaction. It is therefore assumed that in order for direct oxidation of thiols by H<sub>2</sub>O<sub>2</sub> to take place, peroxiredoxins need to be (temporarily or locally) inactivated via the socalled "floodgate mechanism" (see B).

## **B)** Floodgate Mechanism

In order to enable direct oxidation of thiols with modest reactivity, local H<sub>2</sub>O<sub>2</sub> concentrations need to increase (transiently) to a micromolar range. Although not proven, the local inactivation of antioxidant systems such as the peroxiredoxins might facilitate this increase [110]. The local inactivation of

signaling inhibitors is also observed in phosphorylation-mediated signaling, for which phosphatases need to be inactivated in order for efficient signaling to proceed [111,112]. For peroxiredoxins, inactivation can occur via two mechanisms.

- The overoxidation of the catalytic cysteine ( $C_p$ -SO<sub>2</sub>H or i) C<sub>p</sub>-SO<sub>2</sub>H) upon high levels of H<sub>2</sub>O<sub>2</sub> inactivates the catalytic activity of peroxiredoxins (Figure 6B). Of note, overoxidation of peroxiredoxin is observed at high concentrations of H<sub>2</sub>O<sub>2</sub>, meaning that H<sub>2</sub>O<sub>2</sub> levels already need to be elevated in order to facilitate a further increase. Several studies showed that H2O2 concentrations reached during signaling are not sufficient to hyperoxidize the C<sub>p</sub> of peroxiredoxins [113,114]. On the other hand, overoxidation of peroxiredoxins has been shown to reflect circadian rhythm [115,116]. Furthermore, there are selective advantages that drove the evolution of peroxiredoxin overoxidation, suggesting a purpose for reversible peroxiredoxin overoxidation [117].
- ii) Peroxiredoxins can also be inactivated by post-translational modifications (PTMs). For example, it is known that membrane receptor activation (including PDGF-R and EGF-R) activates SRC kinase, triggering the inactivating phosphorylation of PRDX1 at Y194. This inhibits PRDX1 catalytic activity and, together with local accumulation of activated NADPH oxidase (NOX) complexes in lipid rafts, this leads to a local increase of H<sub>2</sub>O<sub>2</sub> at membranes [118-120]. A similar mechanism has been shown for H2O2-activated kinases MST1 and MST2 which phosphorylate PRDX1 at T90 and T183 as well as CDK1-cyclin B which phosphorylates centrosomal PRDX1 on T90 to regulate mitotic entry [121-123]. Other PTMs that seem to play a role in regulating peroxiredoxin activity include acetylation, glutathionylation and nitrosylation but how exactly they affect local peroxide concentrations is not clear [124].

Whether local inhibition of peroxiredoxins is sufficient to locally enable direct oxidation of protein thiols is unclear. It is possible that with the inactivation of peroxiredoxins, H<sub>2</sub>O<sub>2</sub>

is merely allowed to diffuse further from its source. In other the importance of localized H<sub>2</sub>O<sub>2</sub> production -and - diffusion words, protein thiols are again facing the same challenges of in H<sub>2</sub>O<sub>2</sub>-based signaling [132]. Using this approach, it was outcompeting peroxiredoxins at this location. shown that in vascular endothelial cells, nuclear H<sub>2</sub>O<sub>2</sub> activates AMPK and causes phosphorylation of endothelial nitric oxide synthase (eNOS), while cytosolic or caveolae-derived As explained, the intrinsic reactivity of protein thiols with H<sub>2</sub>O<sub>2</sub> is generally low, and not much higher than that of other H<sub>2</sub>O<sub>2</sub> activates AMPK but does not cause eNOS phosphorbiomolecules. The floodgate model thus suggests that redox ylation [133]. Another example comes from Wnt signaling, signaling and random oxidative damage occur simultaneouswhere ROS acts in two separate pools - with seemingly oply when H<sub>2</sub>O<sub>2</sub> levels are high enough to cause overoxidation posing effects. Mitochondrial ROS resulting from the loss of of peroxiredoxins. It can thus be suggested that opening the TIGAR has an antiproliferative effect, whereas NOX-derived floodgate by overoxidation of peroxiredoxins may primarily ROS induced by the upregulation of RAC1 is pro-proliferoccur under conditions of oxidative stress or with signaling ative [134]. This suggests that the cellular response to ROS events leading to cell death. depends on the ROS source, and that these cellular responses can be independently modulated in the same cell.

### C) Localized Production of H<sub>2</sub>O<sub>2</sub>

Besides through the local inactivation of peroxiredoxins, a How much the subcellular origin of H<sub>2</sub>O<sub>2</sub> affects pathways localized build-up of  $H_2O_2$  can in principle also be achieved besides eNOS and Wnt signaling and whether this plays a at the site of H<sub>2</sub>O<sub>2</sub> production. Localized H<sub>2</sub>O<sub>2</sub> production role in different cell types is a fundamental issue for future research. Furthermore, this model does not account for difcould enable direct oxidation of protein thiols (Figure 6C). Depending on the source of  $H_2O_2$ , oxidation of protein thiols ferences in target thiol reactivity. only occurs to those that are in close proximity to that source. An example of localized H<sub>2</sub>O<sub>2</sub> production is the H<sub>2</sub>O<sub>2</sub> generat-D) Redox Relay ed by NOXs, albeit via superoxide, which are localized to spe-This concept involves the initial oxidation of a highly reactive cific membranous compartments such as lipid rafts, the nuclethiol in a 'redox sensor' which then catalyzes the oxidation of us and endosomes [125]. In C. elegans zygotes, mitochondria less favorable targets by reacting with the sulfenylated sensor relocate to the cellular cortex and locally increase H<sub>2</sub>O<sub>2</sub> levels or via disulfide exchange. The highly reactive sensor can be a to promote symmetry breaking [126]. Other sites of H<sub>2</sub>O<sub>2</sub> thiol peroxidase such as peroxiredoxin, due to its exceptional production include peroxisomes, although most H<sub>2</sub>O<sub>2</sub> genreactivity with H<sub>2</sub>O<sub>2</sub> and abundance. H<sub>2</sub>O<sub>2</sub> first reacts with erated there will be broken down by catalase [65], and oxiperoxiredoxin's peroxidatic cysteine  $(C_p)$ , and oxidized peroxdative folding in the endoplasmic reticulum (ER), for which iredoxin then forms a mixed disulfide intermediate with the the H<sub>2</sub>O<sub>2</sub> produced is most likely contained within the ER target protein (Figure 6D). Peroxiredoxin-based redox relays via recycling for oxidative folding [127–129]. Thus, cells do are recently being actively explored, and many examples have produce  $H_2O_2$  at specific sites, which remains localized due to been described [135-140]. Another important observation cellular compartmentalization as well as the highly abundant that supports the role for peroxidases in sensing and transferand reactive peroxiredoxins. Studies using sensitive genetically ring oxidative signals is that yeast cells lacking all thiol perencoded  $H_2O_2$  probes show that the  $H_2O_2$  diffusion range is oxidases are unable to orchestrate a transcriptional response to  $H_2O_2$  [141]. Furthermore, it was recently shown that  $H_2O_2$ likely limited to a few microns [130,131]. Combining these diffusion is limited by the thioredoxin system, which points probes with localized, inducible production of H2O2, for instance by targeting the H<sub>2</sub>O<sub>2</sub> generating enzyme D-amino to peroxiredoxins as an initial H<sub>2</sub>O<sub>2</sub> target since they utilize acid oxidase (DAO) to specific sites is a major tool in studying the thioredoxin system for their recycling [74].



Oxidized peroxiredoxins could in principle relay oxidizing equivalents to other thiols via two molecular mechanisms (Figure 6D). The first mechanism involves the condensation of the sulfenylated peroxidatic cysteine (C<sub>p</sub>-SOH) of peroxiredoxins directly with the cysteine thiol of a target protein. A second possible mechanism involves a disulfide exchange reaction of the disulfide linking the peroxidatic and resolving cysteine  $(C_p$ -S-S- $C_p$ ) in oxidized peroxiredoxins with a target protein thiol. The SOH-mediated mechanism in principle only needs the peroxidatic cysteine of peroxiredoxin, whereas the S-S-mediated route is dependent on both catalytic cysteines and is limited by the activity of TRX. Of note, in the S-OH-mediated mechanism, the target protein thiol is directly competing with the peroxiredoxin resolving cysteine, requiring the target thiol to be in close proximity of the C<sub>p</sub>-SOH. The existence of the SOH-mediated pathway is supported by data on the roGFP redox sensor, which is oxidized by Tsa2/PRDX2 with a mutated resolving cysteine [85].

The structure of a protein determines its biological function. Mammalian cells express five 2-cys peroxiredoxin isoforms, Newly synthesized linear polypeptide chains on ribosomes are each with their own localization, oxidation kinetics and strucfolded into 3D structures driven hydrophobic interactions, tural differences around their catalytic sites. A peroxiredoxbut also by van der Waals- and electrostatic interactions. in-based redox relay therefore explains not only the reactivi-Furthermore, the oxidizing environment of the ER and spety but could also grant selectivity in H<sub>2</sub>O<sub>2</sub>-dependent redox cialized enzymes aid the formation of disulfide bonds that signaling. ensure stabilization and assembly of native proteins that are directed for secretion of transmembrane localization. Proteins E) TRX-mediated Oxidation need to overcome energy barriers to reach their final, stable The reduction of oxidized peroxiredoxins involves the very efficient oxidation of thioredoxin (TRX) [142]. It is possible that oxidized TRX accumulates after the oxidation of peroxiredoxins, especially when the rate of TRX reduction is lower than peroxiredoxin-mediated oxidation (in which case bic residues [146].

conformation, immanently leading to the accumulation of folding intermediates [145]. Partially folded proteins are at high risk of misfolding and aggregation, due to non-native interactions through for instance the exposure of hydrophothere is also a possibility of overoxidation of peroxiredoxins, which are not a substrate for TRX), or when there is a lack of In general, oxidative modifications on proteins result in conreducing power in the form of NADPH. In this state, TRX formational changes, which could lead to changes in protein could in principle act as a thiol oxidase, thereby forming difunction [3]. These redox-induced structural changes can sulfide bonds in proteins instead of removing them (Figure thereby provide a molecular switch. Structural changes can 6E) [143,144]. However, it was suggested that TRX oxidase also trigger partial unfolding and even aggregation of proactivity does not play a major role in catalyzing thiol oxidation teins. Interestingly, a large number of proteins is predicted events in the cytosol [138]. It is poorly understood whether to contain conditionally disordered regions that are redox

TRX-oxidase activity is important for catalyzing protein oxidation in other compartments.

Importantly, none of the mechanisms described above are mutually exclusive and most likely act alongside each other, in parallel and/or at different locations. Furthermore, the redox potentials of the cytoplasm, nucleus, ER and mitochondria vary greatly [77]. Thus, each compartment responds differently to changes in the redox environment. Differential localization and oxidation and condensation kinetics of peroxiredoxin isoforms, combined with the different availability of target and/or adaptor proteins may determine which thiol oxidation mechanism can take place.

# **REDOX REGULATION OF PROTEIN STRUCTURE**

sensitive and thereby oxidation could play a key role the transition between folded and unfolded states [147]. In **chapter 4**, we show how the tumor suppressor protein p16<sup>INK4A</sup> can form  $\beta$ -amyloid-like fibrils under physiological conditions, triggered by the oxidation of a single cysteine residue and subsequent S-S-dependent homodimerization. In **chapter 5**, we discuss the intricate relationship between redox signaling and protein aggregation.

# REDOX SIGNALING IN HEALTH AND DISEASE

Under physiological conditions, ~6-10% of protein thiols are found to be reversibly oxidized [148]. Given this large number of ROS targets, it comes as no surprise that redox modifications control a diverse set of cellular functions. Many essential cellular processes require oxidative modifications in order to function correctly. There is a large interplay with other modes of signaling and PTMs which ensures intricate signaling networks [149,150]. An elaborate description of cellular roles of redox signaling is given in refs. [13,86,151].

Given the role of redox regulation in essential cellular processes, it is not surprising that a deregulation of redox homeostasis as well as random damage due to excessive ROS levels (both leading to oxidative stress) are common pathophysiological conditions [86,152]. For example, it is known that both excessive and insufficient ROS production in mice cause neuronal problems including axonal degeneration and memory deficits, which are attributed to the redox regulation of neuronal polarity, connectivity and the modulation of neuronal networks [81,153]. Furthermore, cancer cells are known to increase both ROS production as well as reducing capacity, which is thought to contribute to increased proliferation rates, rewiring of cancer cell metabolism and stress adaptation [154-156]. Because redox imbalance is closely related to cancer, treatments based both on ROS scavenging as well as ROS overproduction are being actively explored. However, redox-based therapeutic strategies have not yet yielded promising results, and finding out the underlying mechanisms for this lack of success is of great significance [156,157]. One possibility is that most redox-based therapies act on shifting the overall redox balance in cells, thus blocking or stimulating oxidation of all redox-sensitive proteins at once. But since redox signaling involves the selective oxidation of specific redox-sensitive proteins, specifically targeting redox-sensitive proteins in cancer-related pathways is likely a more effective approach. The deregulation of redox signaling is also involved in a diverse set of pathologies involving the immune system [158], the cardiovascular system [159], insulin sensitivity [160] and aging [4,161,162].

Redox signaling is at the center of cellular homeostasis, as illustrated by the diversity and widespread character of redox-related pathologies. A deeper understanding of ROS and how they control cellular processes will allow us to unravel the mechanisms of redox signaling, the biological roles of oxidative regulation in cells, and how redox-regulated pathways and processes might be linked to diseases associated with oxidative stress.

# **OUTLINE OF THIS THESIS**

Redox signaling is crucial for cells to maintain homeostasis. The goal of the research described in this thesis is to understand the molecular mechanisms that underlie redox signal propagation and how changes in the cellular redox state affect signaling pathways. This thesis is composed of seven chapters that can be divided into three themes. First of all, we study how the oxidation of proteins is achieved both efficiently and specifically. Secondly, we study several examples of how the oxidation of specific proteins can affect their function in important signaling pathways. Thirdly, we examine how redox regulation can affect protein aggregation.

How  $H_2O_2$  leads to the selective and efficient oxidation of specific thiols on specific proteins is one of the most important open questions in redox biology. In **chapter 2**, we investigate peroxiredoxin-based redox relays on a proteome-wide scale, erature on the intricate relationship between redox signaling to investigate whether this may serve as a mechanism for the and protein aggregation. specific and efficient transmission of oxidative signals. We demonstrate that all 2-cys peroxiredoxin isoforms are capable Chapter 6 describes an example of how the cellular redox state is intimately integrated with cell cycle progression [163]. of forming numerous cysteine-dependent heterodimers with We present evidence that the cell cycle regulator CDK4 and target proteins, and that each peroxiredoxin isoform displays a preference for a subset of disulfide-dependent binding partcyclin D form a temporary covalently linked complex under ners. This provides evidence that peroxiredoxins could play a oxidizing conditions. This is caused by formation of a disulrole in providing not only reactivity but also selectivity in the fide bond involving cysteine 135 in CDK4, stabilizing the transduction of peroxide signals to generate complex cellular otherwise hydrostatic non-covalent interaction between these signaling responses. proteins. Moreover, disulfide formation leads to an increased kinase activity of the CDK4-cyclin D complex. We discuss how identification of the redox sensitive C135 at the CDK4/ Chapters 3, 4 and 6 shift focus on the cysteine-dependent redox regulation of several signaling proteins. Chapter 3 decyclin D interface could provide a potential target for novel scribes the PP2A regulating protein TIPRL. We show that covalent cytostatic drugs.

**Chapters 3, 4** and 6 shift focus on the cysteine-dependenthow identification of the redox sensitive C135 at the CDK4/redox regulation of several signaling proteins. **Chapter 3** describes the PP2A regulating protein TIPRL. We show thatcyclin D interface could provide a potential target for novelTIPRL is highly sensitive to oxidation and forms three different disulfide-dependent homodimers involving cysteines C14Finally, in **chapter 7** I layout and summarize the work in thisand C87 in response to endogenous levels of  $H_2O_2$ . Preliminary data suggest a role for oxidation of TIPRL in regulatingFrom this work.phosphatase activity of PP2A-C.Finally, in chapter 7 I layout and summarize the work in this work.

**Chapter 4** describes how the tumor suppressor protein p16<sup>INK4A</sup> can form  $\beta$ -amyloid-like fibrils under physiological conditions, triggered by oxidation of the single cysteine residue and subsequent S-S-dependent homodimerization. p16<sup>INK4A</sup> amyloid formation abolishes its function as a CDK4/6 inhibitor. We use the term 'oxaggregation' to refer to the critical dependence on a reversible disulfide cross-linked dimer as a subunit for fibril formation, which highlights the role of the cellular redox state as an important regulator of fibril formation.

Excessive ROS levels can lead to random damage of proteins, including protein unfolding and aggregation, processes that have been associated with aging. On the other hand,  $H_2O_2$ acts as an essential second messenger and is important for healthy cell physiology. In **chapter 5** we discuss how these seemingly opposite effects of  $H_2O_2$  as a signaling molecule and  $H_2O_2$  as a driver of age-related protein aggregation can be united in one hypothesis. We give an overview of the lit-

- through Eukaryotic Protein Evolution. Mol Biol Evol 2011, 28, 327-334, doi:10.1093/molbev/msq194.
- 7. Forman, H.J.; Maiorino, M.; Ursini, F. Signaling Functions of Reactive Oxygen Species. Biochemistry-us 2010, 49, 835-842, doi:10.1021/
- 8. Halliwell, B.; Gutteridge, J.M.C. Free Radicals in Biology and Medicine; 2015; ISBN 9780198717478.
- 9. Hawkins, C.L.; Davies, M.J. Detection, Identification, and Quantification of Oxidative Protein Modifications. J Biol Chem 2019, 294, 19683-19708, doi:10.1074/jbc.rev119.006217.
- 10. Babior, B.M. The Respiratory Burst Oxidase. *Trends Biochem Sci* 1987, 12, 241-243, doi:10.1016/0968-0004(87)90118-6.
- 11. Hausladen, A.; Fridovich, I. Superoxide and Peroxynitrite Inactivate Aconitases, but Nitric Oxide Does Not. J Biological Chem 1994, 269, 29405-29408.
- 12. Zhang, L.; Wang, X.; Cueto, R.; Effi, C.; Zhang, Y.; Tan, H.; Qin, X.; Ji, Y.; Yang, X.; Wang, H. Biochemical Basis and Metabolic Interplay of Redox Regulation. Redox Biol 2019, 26, 101284, doi:10.1016/j. redox.2019.101284.
- 13. Sies, H.; Jones, D.P. Reactive Oxygen Species (ROS) as Pleiotropic Physiological Signalling Agents. Nat Rev Mol Cell Biology 2020, 1–21, doi:10.1038/s41580-020-0230-3.
- 14. Nisimoto, Y.; Diebold, B.A.; Cosentino-Gomes, D.; Constentino-Gomes, D.; Lambeth, J.D. Nox4: A Hydrogen Peroxide-Generating Oxygen Sensor. Biochemistry-us 2014, 53, 5111-5120, doi:10.1021/
- 15. Winterbourn, C.C.; Metodiewa, D. Reactivity of Biologically Important Thiol Compounds with Superoxide and Hydrogen Peroxide. Free Radical Bio Med 1999, 27, 322-328, doi:10.1016/s0891-5849(99)00051-9.
- Winterbourn, C.C. The High Reactivity of Peroxiredoxin 2 with H(2)O(2) Is Not Reflected in Its Reaction with Other Oxidants and Thiol Reagents. J Biol Chem 2007, 282, 11885 11892, doi:10.1074/ 30. Mano, C.M.; Prado, F.M.; Massari, J.; Ronsein, G.E.; Martinez, G.R.; jbc.m700339200.
- 17. Miller, E.W.; Dickinson, B.C.; Chang, C.J. Aquaporin-3 Mediates Hydrogen Peroxide Uptake to Regulate Downstream Intracellular Signaling. Proc National Acad Sci 2010, 107, 15681–15686, doi:10.1073/ pnas.1005776107.
- 18. Huang, B.K.; Sikes, H.D. Quantifying Intracellular Hydrogen Peroxide Perturbations in Terms of Concentration. *Redox Biol* 2014, 2, 955 962. doi:10.1016/j.redox.2014.08.001.
- 19. Imlay, J.A. PATHWAYS OF OXIDATIVE DAMAGE. Annu Rev Micro*biol* **2003**, *57*, 395–418, doi:10.1146/annurev.micro.57.030502.090938.

- 6. Wong, J.W.H.; Ho, S.Y.W.; Hogg, P.J. Disulfide Bond Acquisition 20. Dagnell, M.; Cheng, Q.; Rizvi, S.H.M.; Pace, P.E.; Boivin, B.; Winterbourn, C.C.; Arnér, E.S.J. Bicarbonate Is Essential for Protein-Tyrosine Phosphatase 1B (PTP1B) Oxidation and Cellular Signaling through EGF-Triggered Phosphorylation Cascades. J Biol Chem 2019, 294, 12330-12338, doi:10.1074/jbc.ra119.009001.
  - 21. O'Neill, P. The Chemical Basis of Radiation Biology. Int J Radiat Biology Relat Stud Phys Chem Medicine 2009, 52, 976-976, doi:10.1080/09553008714552571.
  - 22. Yin, H.; Porter, N.A. New Insights Regarding the Autoxidation of Polyunsaturated Fatty Acids. Antioxid Redox Sign 2005, 7, 170–184, doi:10.1089/ars.2005.7.170.
  - 23. Neužil, J.; Gebicki, J.M.; Stocker, R. Radical-Induced Chain Oxidation of Proteins and Its Inhibition by Chain-Breaking Antioxidants. Biochem [ 1993, 293, 601-606, doi:10.1042/bj2930601.
  - 24. Hawkins, C.L.; Davies, M.J. Generation and Propagation of Radical Reactions on Proteins. Biochimica Et Biophysica Acta Bba - Bioenergetics 2001, 1504, 196-219, doi:10.1016/s0005-2728(00)00252-8.
  - 25. Marnett, L.J.; Wilcox, A.L. The Chemistry of Lipid Alkoxyl Radicals and Their Role in Metal-Amplified Lipid Peroxidation. Biochem Soc Symp 1995, 61, 65-72, doi:10.1042/bss0610065.
  - 26. Davies, M.J. Reactive Species Formed on Proteins Exposed to Singlet Oxygen. Photochem Photobio S 2004, 3, 17-25, doi:10.1039/b307576c.
  - 27. Kanofsky, J.R.; Wright, J.; Miles-Richardson, G.E.; Tauber, A.I. Biochemical Requirements for Singlet Oxygen Production by Purified Human Myeloperoxidase. J Clin Invest 1984, 74, 1489-1495, doi:10.1172/jci111562.
  - 28. Nakano, M.; Takayama, K.; Shimizu, Y.; Tsuji, Y.; Inaba, H.; Migita, T. Spectroscopic Evidence for the Generation of Singlet Oxygen in Self-Reaction of Sec-Peroxy Radicals. JAm Chem Soc 1976, 98, 1974-1975, doi:10.1021/ja00423a060.
- 16. Peskin, A.V.; Low, F.M.; Paton, L.N.; Maghzal, G.J.; Hampton, M.B.; 29. Brash, D.E.; Goncalves, L.C.P.; Bechara, E.J.H.; Group, T.E.-S.M.W. Chemiexcitation and Its Implications for Disease. Trends Mol Med 2018, 24, 527-541, doi:10.1016/j.molmed.2018.04.004.
  - Miyamoto, S.; Cadet, J.; Sies, H.; Medeiros, M.H.G.; Bechara, E.J.H.; et al. Excited Singlet Molecular O2 (1Δg) Is Generated Enzymatically from Excited Carbonyls in the Dark. Sci Rep-uk 2014, 4, 5938, doi:10.1038/srep05938.
  - 31. Jr., P.W.; McDunn, J.E.; Wentworth, A.D.; Takeuchi, C.; Nieva, J.; Jones, T.; Bautista, C.; Ruedi, J.M.; Gutierrez, A.; Janda, K.D.; et al. Evidence for Antibody-Catalyzed Ozone Formation in Bacterial Killing and Inflammation. Science 2002, 298, 2195-2199, doi:10.1126/ science.1077642.
  - 32. Chen, C.; Arjomandi, M.; Balmes, J.; Tager, I.; Holland, N. Effects of Chronic and Acute Ozone Exposure on Lipid Peroxidation and Antioxidant Capacity in Healthy Young Adults. Environ Health Persp 2007, 115, 1732-1737, doi:10.1289/ehp.10294.

- 33. Brink, C.B.; Pretorius, A.; Niekerk, B.P.J. van; Oliver, D.W.; Venter, D.P. 48. Spencer, N.Y.; Engelhardt, J.F. The Basic Biology of Redoxosomes Studies on Cellular Resilience and Adaptation Following Acute and in Cytokine-Mediated Signal Transduction and Implications for Repetitive Exposure to Ozone in Cultured Human Epithelial (HeLa) Disease-Specific Therapies. Biochemistry-us 2014, 53, 1551-1564, Cells. Redox Rep 2013, 13, 87-100, doi:10.1179/135100008x259187. doi:10.1021/bi401719r.
- 34. Hollingsworth, J.W.; Kleeberger, S.R.; Foster, W.M. Ozone and Pul-49. Prosser, B.L.; Ward, C.W.; Lederer, W.J. X-ROS Signaling: Rapid Mechmonary Innate Immunity. Proc Am Thorac Soc 2007, 4, 240-246, ano-Chemo Transduction in Heart. Science 2011, 333, 1440-1445, doi:10.1513/pats.200701-023aw.
- 35. Kanofsky, J.R.; Sima, P. Singlet Oxygen Production from the Reac-50. Bedard, K.; Krause, K.-H. The NOX Family of ROS-Generating tions of Ozone with Biological Molecules. J Biological Chem 1991, NADPH Oxidases: Physiology and Pathophysiology. Physiol Rev 2007, 266, 9039-9042. 87, 245-313, doi:10.1152/physrev.00044.2005.
- 51. White, R.E.; Coon, M.J. Oxygen Activation by Cytochrome P-450. 36. Glaze, W.H. Reaction Products of Ozone: A Review. Environ Health Persp 1986, 69, 151-157, doi:10.1289/ehp.8669151. Annu Rev Biochem 1980, 49, 315-356, doi:10.1146/annurev. bi.49.070180.001531.
- 37. Foote, C.S.; Goyne, T.E.; Lehrer, R.I. Assessment of Chlori-52. Kil, I.S.; Lee, S.K.; Rvu, K.W.; Woo, H.A.; Hu, M.-C.; Bae, S.H.; Rhee, nation by Human Neutrophils. Nature 1983, 301, 715-716, doi:10.1038/301715a0. S.G. Feedback Control of Adrenal Steroidogenesis via H2O2-Dependent, Reversible Inactivation of Peroxiredoxin III in Mitochondria. 38. Winterbourn, C.C. Biological Reactivity and Biomarkers of the Neu-Mol Cell 2012, 46, 584–594, doi:10.1016/j.molcel.2012.05.030.
- trophil Oxidant, Hypochlorous Acid. *Toxicology* **2002**, *181*, 223–227, doi:10.1016/s0300-483x(02)00286-x.
- 53. Tu, B.P.; Weissman, J.S. The FAD- and O2-Dependent Reaction Cycle of Ero1-Mediated Oxidative Protein Folding in the Endoplasmic Retic-39. CARR, A.C.; WINTERBOURN, C.C. Oxidation of Neutrophil ulum. Mol Cell 2002, 10, 983-994, doi:10.1016/s1097-2765(02)00696-Glutathione and Protein Thiols by Myeloperoxidase-Derived Hypochlorous Acid. Biochem J 1997, 327, 275-281, doi:10.1042/bj3270275.
- 54. Tu, B.P.; Weissman, J.S. Oxidative Protein Folding in Eukaryotes. J Cell 40. Bakhmutova-Albert, E.V.; Yao, H.; Denevan, D.E.; Richardson, D.E. Biology 2004, 164, 341-346, doi:10.1083/jcb.200311055. Kinetics and Mechanism of Peroxymonocarbonate Formation. Inorg Chem 2010, 49, 11287-11296, doi:10.1021/ic1007389. 55. McCord, J.M.; Fridovich, I. Superoxide Dismutase. An Enzymic Func-
- tion for Erythrocuprein (Hemocuprein). J Biological Chem 1969, 244, 41. Balaban, R.S.; Nemoto, S.; Finkel, T. Mitochondria, Oxidants, and 6049-6055. Aging. Cell 2005, 120, 483-495, doi:10.1016/j.cell.2005.02.001.
- 56. Fukai, T.; Ushio-Fukai, M. Superoxide Dismutases: Role in Redox Sig-42. Chance, B.; Sies, H.; Boveris, A. Hydroperoxide Metabolism in Mamnaling, Vascular Function, and Diseases. Antioxid Redox Sign 2011, malian Organs. Physiol Rev 1979, 59, 527-605, doi:10.1152/phys-15, 1583-1606, doi:10.1089/ars.2011.3999. rev.1979.59.3.527.
- 57. Winterbourn, C.C. Biological Production, Detection, and Fate of 43. Bayne, A.-C.V.; Mockett, R.J.; Orr, W.C.; Sohal, R.S. Enhanced Catab-Hydrogen Peroxide. Antioxid Redox Sign 2017, 29, ars.2017.7425, olism of Mitochondrial Superoxide/Hydrogen Peroxide and Aging in doi:10.1089/ars.2017.7425. Transgenic Drosophila. Biochem J 2005, 391, 277–284, doi:10.1042/ bj20041872. 58. Niedzwiecki, M.M.; Walker, D.I.; Vermeulen, R.; Chadeau-Hyam, M.;
- Jones, D.P.; Miller, G.W. The Exposome: Molecules to Populations. 44. Mailloux, R.J.; Harper, M.-E. Mitochondrial Proticity and ROS Signal-Annu Rev Pharmacol 2018, 59, 1-21, doi:10.1146/annurev-pharming: Lessons from the Uncoupling Proteins. Trends Endocrinol Metabtox-010818-021315. olism 2012, 23, 451-458, doi:10.1016/j.tem.2012.04.004.
- 59. Yoshida, T.; Goto, S.; Kawakatsu, M.; Urata, Y.; Li, T. Mitochondrial 45. Sena, L.A.; Chandel, N.S. Physiological Roles of Mitochondrial Re-Dysfunction, a Probable Cause of Persistent Oxidative Stress after Exactive Oxygen Species. Mol Cell 2012, 48, 158 166, doi:10.1016/j. posure to Ionizing Radiation. Free Radical Res 2012, 46, 147–153, do molcel.2012.09.025. i:10.3109/10715762.2011.645207.
- 46. Anastasiou, D.; Poulogiannis, G.; Asara, J.M.; Boxer, M.B.; Jiang, J.; 60. Wong, H.-S.; Benoit, B.; Brand, M.D. Mitochondrial and Cytoso-Shen, M.; Bellinger, G.; Sasaki, A.T.; Locasale, J.W.; Auld, D.S.; et al. lic Sources of Hydrogen Peroxide in Resting C2C12 Myoblasts. Inhibition of Pyruvate Kinase M2 by Reactive Oxygen Species Con-Free Radical Bio Med 2019, 130, 140-150, doi:10.1016/j.freeradtributes to Cellular Antioxidant Responses. Science 2011, 334, 1278 biomed.2018.10.448. 1283, doi:10.1126/science.1211485.
- 47. Hampton, M.B.; Kettle, A.J.; Winterbourn, C.C. Inside the Neutrophil Phagosome: Oxidants, Myeloperoxidase, and Bacterial Killing. Blood 1998, 92, 3007-3017, doi:10.1182/blood.v92.9.3007.

- 61. Lim, J.B.; Huang, B.K.; Deen, W.M.; Sikes, H.D. Analysis of the Lifetime and Spatial Localization of Hydrogen Peroxide Generated in the Cytosol Using a Reduced Kinetic Model. *Free Radical Bio Med* **2015**, *89*, 47 53, doi:10.1016/j.freeradbiomed.2015.07.009.
- 62. Stein, K.T.; Moon, S.J.; Nguyen, A.N.; Sikes, H.D. Kinetic Modeling of H2O2 Dynamics in the Mitochondria of HeLa Cells. *Plos Comput Biol* **2020**, *16*, e1008202, doi:10.1371/journal.pcbi.1008202.
- 63. Gao, C.; Tian, Y.; Zhang, R.; Jing, J.; Zhang, X. Endoplasmic Reticulum-Directed Ratiometric Fluorescent Probe for Quantitive Detection of Basal H2O2. *Anal Chem* 2017, *89*, 12945–12950, doi:10.1021/acs. analchem.7b03809.
- 64. Toppo, S.; Flohé, L.; Ursini, F.; Vanin, S.; Maiorino, M. Catalytic Mechanisms and Specificities of Glutathione Peroxidases: Variations of a Basic Scheme. *Biochimica Et Biophysica Acta Bba - Gen Subj* 2009, *1790*, 1486–1500, doi:10.1016/j.bbagen.2009.04.007.
- Bonekamp, N.A.; Völkl, A.; Fahimi, H.D.; Schrader, M. Reactive Oxygen Species and Peroxisomes: Struggling for Balance. *Biofactors* 2009, *35*, 346–355, doi:10.1002/biof.48.
- Wood, Z.A.; Poole, L.B.; Karplus, P.A. Peroxiredoxin Evolution and the Regulation of Hydrogen Peroxide Signaling. *Science* 2003, *300*, 650 653, doi:10.1126/science.1080405.
- 67. Chae, H.Z.; Uhm, T.B.; Rhee, S.G. Dimerization of Thiol-Specific Antioxidant and the Essential Role of Cysteine 47. *Proc National Acad Sci* **1994**, *91*, 7022–7026, doi:10.1073/pnas.91.15.7022.
- Chae, H.Z.; Chung, S.J.; Rhee, S.G. Thioredoxin-Dependent Peroxide Reductase from Yeast. *J Biol Chem* 1994, *269*, 27670–27678, doi:10.1016/s0021-9258(18)47038-x.
- 69. Rhee, S.G. Overview on Peroxiredoxin. *Mol Cells* **2016**, *39*, 1 5, doi:10.14348/molcells.2016.2368.
- 70. Yang, K.-S.; Kang, S.W.; Woo, H.A.; Hwang, S.C.; Chae, H.Z.; Kim, K.; Rhee, S.G. Inactivation of Human Peroxiredoxin I during Catalysis as the Result of the Oxidation of the Catalytic Site Cysteine to Cysteine-Sulfinic Acid\*. *J Biol Chem* 2002, *277*, 38029–38036, doi:10.1074/ jbc.m206626200.
- 71. Chae, H.Z.; Kim, H.J.; Kang, S.W.; Rhee, S.G. Characterization of Three Isoforms of Mammalian Peroxiredoxin That Reduce Peroxides in the Presence of Thioredoxin. *Diabetes Res Clin Pr* **1999**, *45*, 101 112, doi:10.1016/s0168-8227(99)00037-6.
- 72. Winterbourn, C.C.; Peskin, and A.V. Kinetic Approaches to Measuring Peroxiredoxin Reactivity. *Mol Cells* **2016**, *39*, 1 5, doi:10.14348/ molcells.2016.2325.
- 73. Winterbourn, C.C.; Hampton, M.B. Thiol Chemistry and Specificity in Redox Signaling. *Free Radical Bio Med* **2008**, *45*, 549 561, doi:10.1016/j.freeradbiomed.2008.05.004.

- Mishina, N.M.; Bogdanova, Y.A.; Ermakova, Y.G.; Panova, A.S.; Kotova, D.A.; Bilan, D.S.; Steinhorn, B.; Arnér, E.S.J.; Michel, T.; Belousov, V.V. Which Antioxidant System Shapes Intracellular H2O2 Gradients? *Antioxid Redox Sign* 2019, *31*, 664–670, doi:10.1089/ars.2018.7697.
- 75. Hanschmann, E.-M.; Godoy, J.R.; Berndt, C.; Hudemann, C.; Lillig, C.H. Thioredoxins, Glutaredoxins, and Peroxiredoxins—Molecular Mechanisms and Health Significance: From Cofactors to Antioxidants to Redox Signaling. *Antioxid Redox Sign* **2013**, *19*, 1539–1605, doi:10.1089/ars.2012.4599.
- 76. Ju, H.-Q.; Lin, J.-F.; Tian, T.; Xie, D.; Xu, R.-H. NADPH Homeostasis in Cancer: Functions, Mechanisms and Therapeutic Implications. *Signal Transduct Target Ther* **2020**, *5*, 231, doi:10.1038/s41392-020-00326-0.
- 77. Go, Y.-M.; Jones, D.P. Redox Compartmentalization in Eukaryotic Cells. *Biochimica Et Biophysica Acta Bba - Gen Subj* 2008, 1780, 1273– 1290, doi:10.1016/j.bbagen.2008.01.011.
- Kaludercic, N.; Deshwal, S.; Lisa, F.D. Reactive Oxygen Species and Redox Compartmentalization. *Front Physiol* 2014, *5*, 285, doi:10.3389/ fphys.2014.00285.
- Nordzieke, D.E.; Medraño-Fernandez, I. The Plasma Membrane: A Platform for Intra- and Intercellular Redox Signaling. *Antioxidants* 2018, 7, 168, doi:10.3390/antiox7110168.
- Rampon, C.; Volovitch, M.; Joliot, A.; Vriz, S. Hydrogen Peroxide and Redox Regulation of Developments. *Antioxidants* 2018, 7, 159, doi:10.3390/antiox7110159.
- Wilson, C.; Muñoz-Palma, E.; González-Billault, C. From Birth to Death: A Role for Reactive Oxygen Species in Neuronal Development. *Semin Cell Dev Biol* 2018, *80*, 43–49, doi:10.1016/j. semcdb.2017.09.012.
- 82. Niethammer, P.; Grabher, C.; Look, A.T.; Mitchison, T.J. A Tissue-Scale Gradient of Hydrogen Peroxide Mediates Rapid Wound Detection in Zebrafish. *Nature* 2009, 459, 996–999, doi:10.1038/nature08119.
- Trinity, J.D.; Broxterman, R.M.; Richardson, R.S. Regulation of Exercise Blood Flow: Role of Free Radicals. *Free Radical Bio Med* 2016, 98, 90–102, doi:10.1016/j.freeradbiomed.2016.01.017.
- 84. Jackson, M.J.; Stretton, C.; McArdle, A. Hydrogen Peroxide as a Signal for Skeletal Muscle Adaptations to Exercise: What Do Concentrations Tell Us about Potential Mechanisms? *Redox Biol* 2020, *35*, 101484, doi:10.1016/j.redox.2020.101484.
- Morgan, B.; Laer, K.V.; Owusu, T.N.E.; Ezeriņa, D.; Pastor-Flores, D.; Amponsah, P.S.; Tursch, A.; Dick, T.P. Real-Time Monitoring of Basal H2O2 Levels with Peroxiredoxin-Based Probes. *Nat Chem Biol* 2016, *12*, 437 443, doi:10.1038/nchembio.2067.
- Sies, H.; Berndt, C.; Jones, D.P. Oxidative Stress. *Annu Rev Biochem* 2017, *86*, 715–748, doi:10.1146/annurev-biochem-061516-045037.

- 87. Xiao, H.; Jedrychowski, M.P.; Schweppe, D.K.; Huttlin, E.L.; Yu, Q.; Heppner, D.E.; Li, J.; Long, J.; Mills, E.L.; Szpyt, J.; et al. A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. Cell 2020, doi:10.1016/j.cell.2020.02.012.
   101. Kortemme, T.; Creighton, T.E. Ionisation of Cysteine Residues at the Termini of Model α-Helical Peptides. Relevance to Unusual Thiol PKa-Values in Proteins of the Thioredoxin Family. J Mol Biol 1995, 253, 799–812, doi:10.1006/jmbi.1995.0592.
- 88. D'Autréaux, B.; Toledano, M.B. ROS as Signalling Molecules: Mechanisms That Generate Specificity in ROS Homeostasis. *Nat Rev Mol Cell Bio* 2007, *8*, 813–824, doi:10.1038/nrm2256.
   89. Miseta, A.; Csutora, P. Relationship Between the Occurrence of Cyste-
- Miseta, A.; Csutora, P. Relationship Between the Occurrence of Cysteine in Proteins and the Complexity of Organisms. *Mol Biol Evol* 2000, *17*, 1232–1239, doi:10.1093/oxfordjournals.molbev.a026406.
- 90. Brooks, D.J.; Fresco, J.R. Increased Frequency of Cysteine, Tyrosine, and Phenylalanine Residues Since the Last Universal Ancestor\*. *Mol Cell Proteomics* 2002, *1*, 125–131, doi:10.1074/mcp.m100001-mcp200.
- Thornton, J.M. Disulphide Bridges in Globular Proteins. J Mol Biol 1981, 151, 261–287, doi:10.1016/0022-2836(81)90515-5.
- Wong, J.T.-F. A Co-Evolution Theory of the Genetic Code. *Proc Nation*al Acad Sci **1975**, 72, 1909–1912, doi:10.1073/pnas.72.5.1909.
- 93. Jordan, I.K.; Kondrashov, F.A.; Adzhubei, I.A.; Wolf, Y.I.; Koonin, E.V.; Kondrashov, A.S.; Sunyaev, S. A Universal Trend of Amino Acid Gain and Loss in Protein Evolution. *Nature* 2005, 433, 633–638, doi:10.1038/nature03306.
- 94. Jones, D.P. Redox Sensing: Orthogonal Control in Cell Cycle and Apoptosis Signalling. *J Intern Med* **2010**, *268*, 432–448, doi:10.1111/j.1365-2796.2010.02268.x.
- 95. Chang, T.-S.; Jeong, W.; Woo, H.A.; Lee, S.M.; Park, S.; Rhee, S.G. Characterization of Mammalian Sulfiredoxin and Its Reactivation of Hyperoxidized Peroxiredoxin through Reduction of Cysteine Sulfinic Acid in the Active Site to Cysteine\*. *J Biol Chem* 2004, 279, 50994– 51001, doi:10.1074/jbc.m409482200.
- Poole, L.B.; Karplus, P.A.; Claiborne, A. Protein Sulfenic Acids in Redox Signaling. *Pharmacol Toxicol* 2004, 44, 325–347, doi:10.1146/ annurev.pharmtox.44.101802.121735.
- 97. Goldman, R.; Stoyanovsky, D.A.; Day, B.W.; Kagan, V.E. Reduction of Phenoxyl Radicals by Thioredoxin Results in Selective Oxidation of Its SH-Groups to Disulfides. An Antioxidant Function of Thioredoxin. *Biochemistry-us* 1995, 34, 4765–4772, doi:10.1021/bi00014a034.
- 98. Denu, J.M.; Tanner, K.G. Specific and Reversible Inactivation of Protein Tyrosine Phosphatases by Hydrogen Peroxide: Evidence for a Sulfenic Acid Intermediate and Implications for Redox Regulation †. *Biochemistry-us* **1998**, *37*, 5633–5642, doi:10.1021/bi973035t.
- 99. Kiley, P.J.; Beinert, H. The Role of Fe–S Proteins in Sensing and Regulation in Bacteria. *Curr Opin Microbiol* 2003, 6, 181–185, doi:10.1016/s1369-5274(03)00039-0.
- 100. Roos, G.; Foloppe, N.; Messens, J. Understanding the PKa of Redox Cysteines: The Key Role of Hydrogen Bonding. *Antioxid Redox Sign* 2013, 18, 94 127, doi:10.1089/ars.2012.4521.

- 103. Casey, J.R.; Grinstein, S.; Orlowski, J. Sensors and Regulators of Intracellular PH. *Nat Rev Mol Cell Bio* **2010**, *11*, 50–61, doi:10.1038/ nrm2820.
- 104. Dansen, T.B.; Wirtz, K.W.A.; Wanders, R.J.A.; Pap, E.H.W. Peroxisomes in Human Fibroblasts Have a Basic PH. *Nat Cell Biol* 2000, 2, 51–53, doi:10.1038/71375.
- 105. Winterbourn, C.C. The Biological Chemistry of Hydrogen Peroxide. *Methods Enzymol* 2013, *528*, 3–25, doi:10.1016/b978-0-12-405881-1.00001-x.
- 106. Marinho, H.S.; Real, C.; Cyrne, L.; Soares, H.; Antunes, F. Hydrogen Peroxide Sensing, Signaling and Regulation of Transcription Factors. *Redox Biol* **2014**, *2*, 535 562, doi:10.1016/j.redox.2014.02.006.
- 107. Grauschopf, U.; Winther, J.R.; Korber, P.; Zander, T.; Dallinger, P.; Bardwell, J.C.A. Why Is DsbA Such an Oxidizing Disulfide Catalyst? *Cell* **1995**, *83*, 947–955, doi:10.1016/0092-8674(95)90210-4.
- 108. Ferrer-Sueta, G.; Manta, B.; Botti, H.; Radi, R.; Trujillo, M.; Denicola, A. Factors Affecting Protein Thiol Reactivity and Specificity in Peroxide Reduction. *Chem Res Toxicol* **2011**, *24*, 434 450, doi:10.1021/ tx100413v.
- 109. Travasso, R.D.M.; Aidos, F.S. dos; Bayani, A.; Abranches, P.; Salvador, A. Localized Redox Relays as a Privileged Mode of Cytoplasmic Hydrogen Peroxide Signaling. *Redox Biol* **2017**, *12*, 233 245, doi:10.1016/j. redox.2017.01.003.
- Rhee, S.G.; Woo, H.A. Multiple Functions of Peroxiredoxins: Peroxidases, Sensors and Regulators of the Intracellular Messenger H<sub>2</sub>O<sub>2</sub>, and Protein Chaperones. *Antioxid Redox Sign* **2011**, *15*, 781 794, doi:10.1089/ars.2010.3393.
- 111. Bauman, A.L.; Scott, J.D. Kinase- and Phosphatase-Anchoring Proteins: Harnessing the Dynamic Duo. *Nat Cell Biol* 2002, *4*, E203– E206, doi:10.1038/ncb0802-e203.
- 112. Cordeiro, M.H.; Smith, R.J.; Saurin, A.T. A Fine Balancing Act: A Delicate Kinase-Phosphatase Equilibrium That Protects against Chromosomal Instability and Cancer. *Int J Biochem Cell Biology* **2018**, *96*, 148–156, doi:10.1016/j.biocel.2017.10.017.
- 113. Jarvis, R.M.; Hughes, S.M.; Ledgerwood, E.C. Peroxiredoxin 1 Functions as a Signal Peroxidase to Receive, Transduce, and Transmit Peroxide Signals in Mammalian Cells. *Free Radical Bio Med* **2012**, *53*, 1522 1530, doi:10.1016/j.freeradbiomed.2012.08.001.

- 114. Truong, T.H.; Carroll, K.S. Redox Regulation of Epidermal Growth Factor Receptor Signaling through Cysteine Oxidation. Biochemistry-us 2012, 51, 9954-9965, doi:10.1021/bi301441e.
- 115. Edgar, R.S.; Green, E.W.; Zhao, Y.; Ooijen, G. van; Olmedo, M.; Qin, X.; Xu, Y.; Pan, M.; Valekunja, U.K.; Feeney, K.A.; et al. Peroxiredoxins Are Conserved Markers of Circadian Rhythms. *Nature* **2012**, *485*, 459-464, doi:10.1038/nature11088.
- 116. Cho, C.-S.; Yoon, H.J.; Kim, J.Y.; Woo, H.A.; Rhee, S.G. Circadian Rhythm of Hyperoxidized Peroxiredoxin II Is Determined by Hemoglobin Autoxidation and the 20S Proteasome in Red Blood Cells. Proc National Acad Sci 2014, 111, 12043-12048, doi:10.1073/
- 117. Veal, E.A.; Underwood, Z.E.; Tomalin, L.E.; Morgan, B.A.; Pillay, C.S. Hyperoxidation of Peroxiredoxins: Gain or Loss of Function? Antioxid Redox Sign 2017, 28, ars.2017.7214, doi:10.1089/ars.2017.7214.
- 118. Woo, H.A.; Yim, S.H.; Shin, D.H.; Kang, D.; Yu, D.-Y.; Rhee, S.G. Inactivation of Peroxiredoxin I by Phosphorylation Allows Localized H(2)O(2) Accumulation for Cell Signaling. Cell 2010, 140, 517 528, doi:10.1016/j.cell.2010.01.009.
- 119. Rhee, S.G.; Woo, H.A.; Kil, I.S.; Kil, I.S.; Bae, S.H. Peroxiredoxin Functions as a Peroxidase and a Regulator and Sensor of Local Peroxides. J Biol Chem 2012, 287, 4403 4410, doi:10.1074/jbc.r111.283432.
- 120. Panday, A.; Sahoo, M.K.; Osorio, D.; Batra, S. NADPH Oxidases: An Overview from Structure to Innate Immunity-Associated Pathologies. Cell Mol Immunol 2015, 12, 5–23, doi:10.1038/cmi.2014.89.
- 121. Rawat, S.J.; Creasy, C.L.; Peterson, J.R.; Chernoff, J. The Tumor Suppressor Mst1 Promotes Changes in the Cellular Redox State by Phosphorylation and Inactivation of Peroxiredoxin-1 Protein\*. *J Biol Chem* 2013, 288, 8762-8771, doi:10.1074/jbc.m112.414524.
- 122. Lim, J.M.; Lee, K.S.; Woo, H.A.; Kang, D.; Rhee, S.G. Control of the Pericentrosomal H2O2 Level by Peroxiredoxin I Is Critical for Mitotic Progression. J Cell Biology 2015, 210, 23 33, doi:10.1083/ jcb.201412068.
- 123. Chang, T.-S.; Jeong, W.; Choi, S.Y.; Yu, S.; Kang, S.W.; Rhee, S.G. Regulation of Peroxiredoxin I Activity by Cdc2-Mediated Phosphorylation. J Biol Chem 2002, 277, 25370 25376, doi:10.1074/jbc. m110432200.
- 124. Rhee, S.G.; Woo, H.A. Multiple Functions of 2-Cvs Peroxiredoxins, I and II, and Their Regulations via Post-Translational Modifications. Free Radical Bio Med 2020, 152, 107-115, doi:10.1016/j.freeradbiomed.2020.02.028.
- 125. Ushio-Fukai, M. Compartmentalization of Redox Signaling Through NADPH Oxidase-Derived ROS. Antioxid Redox Sign 2009, 11, 1289-1299, doi:10.1089/ars.2008.2333.
- 126. Henau, S.D.; Pagès-Gallego, M.; Pannekoek, W.-J.; Dansen, T.B. Mitochondria-Derived H2O2 Promotes Symmetry Breaking of the C. Elegans Zygote. Dev Cell 2020, 53, 263-271.e6, doi:10.1016/j. devcel.2020.03.008.

- 127. Hansen, H.G.; Schmidt, J.D.; Søltoft, C.L.; Ramming, T.; Geertz-Hansen, H.M.; Christensen, B.; Sørensen, E.S.; Juncker, A.S.; Appenzeller-Herzog, C.; Ellgaard, L. Hyperactivity of the Ero1a Oxidase Elicits Endoplasmic Reticulum Stress but No Broad Antioxidant Response. J Biol Chem 2012, 287, 39513-39523, doi:10.1074/jbc.m112.405050.
- 128. Tavender, T.J.; Springate, J.J.; Bulleid, N.J. Recycling of Peroxiredoxin IV Provides a Novel Pathway for Disulphide Formation in the Endoplasmic Reticulum. Embo J 2010, 29, 4185-4197, doi:10.1038/ emboj.2010.273.
- 129. Ramming, T.; Hansen, H.G.; Nagata, K.; Ellgaard, L.; Appenzeller-Herzog, C. GPx8 Peroxidase Prevents Leakage of H2O2 from the Endoplasmic Reticulum. Free Radical Bio Med 2014, 70, 106-116, doi:10.1016/j.freeradbiomed.2014.01.018.
- 130. Mishina, N.M.; Tyurin-Kuzmin, P.A.; Markvicheva, K.N.; Vorotnikov, A.V.; Tkachuk, V.A.; Laketa, V.; Schultz, C.; Lukyanov, S.; Belousov, V.V. Does Cellular Hydrogen Peroxide Diffuse or Act Locally? Antioxid Redox Sign 2011, 14, 1-7, doi:10.1089/ars.2010.3539.
- 131. Pak, V.V.; Ezeriņa, D.; Lyublinskaya, O.G.; Pedre, B.; Tyurin-Kuzmin, P.A.; Mishina, N.M.; Thauvin, M.; Young, D.; Wahni, K.; Gache, S.A.M.; et al. Ultrasensitive Genetically Encoded Indicator for Hydrogen Peroxide Identifies Roles for the Oxidant in Cell Migration and Mitochondrial Function. Cell Metab 2020, 31, 642-653.e6, doi:10.1016/j. cmet.2020.02.003.
- 132. Matlashov, M.E.; Belousov, V.V.; Enikolopov, G. How Much H2O2 Is Produced by Recombinant D-Amino Acid Oxidase in Mammalian Cells? Antioxid Redox Sign 2014, 20, 1039-1044, doi:10.1089/ ars.2013.5618.
- 133. Saravi, S.S.S.; Eroglu, E.; Waldeck-Weiermair, M.; Sorrentino, A.; Steinhorn, B.; Belousov, V.; Michel, T. Differential Endothelial Signaling Responses Elicited by Chemogenetic H2O2 Synthesis. Redox Biol 2020, 36, 101605, doi:10.1016/j.redox.2020.101605.
- 134. Cheung, E.C.; Lee, P.; Ceteci, F.; Nixon, C.; Blyth, K.; Sansom, O.J.; Vousden, K.H. Opposing Effects of TIGAR- and RAC1-Derived ROS on Wnt-Driven Proliferation in the Mouse Intestine. Gene Dev 2016, *30*, 52 63, doi:10.1101/gad.271130.115.
- 135. Delaunay, A.; Pflieger, D.; Barrault, M.-B.; Vinh, J.; Toledano, M.B. A Thiol Peroxidase Is an H2O2 Receptor and Redox-Transducer in Gene Activation. Cell 2002, 111, 471-481, doi:10.1016/s0092-8674(02)01048-6.
- 136. Veal, E.A.; Findlay, V.J.; Day, A.M.; Bozonet, S.M.; Evans, J.M.; Quinn, J.; Morgan, B.A. A 2-Cys Peroxiredoxin Regulates Peroxide-Induced Oxidation and Activation of a Stress-Activated MAP Kinase. Mol Cell 2004, 15, 129 139, doi:10.1016/j.molcel.2004.06.021.
- 137. Sobotta, M.C.; Liou, W.; cker, S.S. ouml; Talwar, D.; Oehler, M.; Ruppert, T.; Scharf, A.N.D.; Dick, T.P. Peroxiredoxin-2 and STAT3 Form a Redox Relay for H2O2 Signaling. Nat Chem Biol 2014, 11, 1 8, doi:10.1038/nchembio.1695.

- 138. Stöcker, S.; Maurer, M.; Ruppert, T.; Dick, T.P. A Role for 2-Cys Perox-151. Hornsveld, M.; Dansen, T.B. The Hallmarks of Cancer from a Redox iredoxins in Facilitating Cytosolic Protein Thiol Oxidation. Nat Chem Perspective. Antioxid Redox Sign 2016, 25, 300 325, doi:10.1089/ Biol 2017, 14, doi:10.1038/nchembio.2536. ars.2015.6580.
- 139. Brandstaedter, C.; Delahunty, C.; Schipper, S.; Rahlfs, S.; Yates, J.R.; 152. Milkovic, L.; Gasparovic, A.C.; Cindric, M.; Mouthuy, P.-A.; Zarkov-Becker, K. The Interactome of 2-Cys Peroxiredoxins in Plasmodium ic, N. Short Overview of ROS as Cell Function Regulators and Their Falciparum. Sci Rep-uk 2019, 9, 13542, doi:10.1038/s41598-019-49841-Implications in Therapy Concepts. Cells 2019, 8, 793, doi:10.3390/ cells8080793.
- 140. Barata, A.G.; Dick, T.P. A Role for Peroxiredoxins in H2O2- and ME-153. Oswald, M.C.W.; Garnham, N.; Sweeney, S.T.; Landgraf, M. Regula-KK-Dependent Activation of the P38 Signaling Pathway. Redox Biol tion of Neuronal Development and Function by ROS. Febs Lett 2018, 2020, 28, 101340, doi:10.1016/j.redox.2019.101340. *592*, 679–691, doi:10.1002/1873-3468.12972.
- 141. Fomenko, D.E.; Koc, A.; Agisheva, N.; Jacobsen, M.; Kaya, A.; Ma-154. Kalyanaraman, B.; Cheng, G.; Hardy, M.; Ouari, O.; Bennett, B.; linouski, M.; Rutherford, J.C.; Siu, K.-L.; Jin, D.-Y.; Winge, D.R.; et al. Zielonka, J. Teaching the Basics of Reactive Oxygen Species and Their Thiol Peroxidases Mediate Specific Genome-Wide Regulation of Gene Relevance to Cancer Biology: Mitochondrial Reactive Oxygen Species Expression in Response to Hydrogen Peroxide. Proc National Acad Sci Detection, Redox Signaling, and Targeted Therapies. Redox Biol 2018, 2011, 108, 2729 2734, doi:10.1073/pnas.1010721108. 15, 347-362, doi:10.1016/j.redox.2017.12.012.
- 142. Netto, L.E.S.; Antunes, and F. The Roles of Peroxiredoxin and Thiore-155. Parascandolo, A.; Laukkanen, M.O. Carcinogenesis and Reactive doxin in Hydrogen Peroxide Sensing and in Signal Transduction. *Mol* Oxygen Species Signaling: Interaction of the NADPH Oxidase Cells 2016, 39, 65 71, doi:10.14348/molcells.2016.2349. NOX1-5 and Superoxide Dismutase 1-3 Signal Transduction Pathways. Antioxid Redox Sign 2019, 30, 443-486, doi:10.1089/ 143. Stewart, E.J.; Åslund, F.; Beckwith, J. Disulfide Bond Formation in the ars.2017.7268.
- Escherichia Coli Cytoplasm: An in Vivo Role Reversal for the Thioredoxins. Embo J 1998, 17, 5543-5550, doi:10.1093/emboj/17.19.5543.
- 144. García-Santamarina, S.; Boronat, S.; Calvo, I.A.; Rodríguez-Gabriel, M.; Ayté, J.; Molina, H.; Hidalgo, E. Is Oxidized Thioredoxin a Major Trigger for Cysteine Oxidation? Clues from a Redox Proteomics Approach. Antioxid Redox Sign 2013, 18, 1549-1556, doi:10.1089/ ars.2012.5037.
- 145. Brockwell, D.J.; Radford, S.E. Intermediates: Ubiquitous Species on Folding Energy Landscapes? Curr Opin Struc Biol 2007, 17, 30-37, doi:10.1016/j.sbi.2007.01.003.
- 146. Weids, A.J.; Ibstedt, S.; Tamás, M.J.; Grant, C.M. Distinct Stress Conditions Result in Aggregation of Proteins with Similar Properties. Sci Rep-uk 2016, 6, srep24554, doi:10.1038/srep24554.
- 147. Erdős, G.; Mészáros, B.; Reichmann, D.; Dosztányi, Z. Large-Scale 160. Watson, J.D. Type 2 Diabetes as a Redox Disease. Lancet 2014, 383, Analysis of Redox-Sensitive Conditionally Disordered Protein Re-841-843, doi:10.1016/s0140-6736(13)62365-x. gions Reveals Their Widespread Nature and Key Roles in High-Level 161. Bazopoulou, D.; Knoefler, D.; Zheng, Y.; Ulrich, K.; Oleson, B.J.; Xie, Eukaryotic Processes. Proteomics 2019, 19, 1800070, doi:10.1002/ L.; Kim, M.; Kaufmann, A.; Lee, Y.-T.; Dou, Y.; et al. Developmental pmic.201800070. ROS Individualizes Organismal Stress Resistance and Lifespan. Nature 148. Hansen, R.E.; Roth, D.; Winther, J.R. Quantifying the Global Cellular 2019, 576, 301-305, doi:10.1038/s41586-019-1814-v.
- Thiol-Disulfide Status. Proc National Acad Sci 2009, 106, 422 427, doi:10.1073/pnas.0812149106.
- 149. Forrester, S.J.; Kikuchi, D.S.; Hernandes, M.S.; Xu, Q.; Griendling, K.K. Reactive Oxygen Species in Metabolic and Inflammatory Signaling. Circ Res 2018, 122, 877–902, doi:10.1161/circresaha.117.311401.
- 150. Chen, P.-H.; Chi, J.-T.; Boyce, M. Functional Crosstalk among Oxidative Stress and O-GlcNAc Signaling Pathways. *Glycobiology* **2018**, *28*, 556-564, doi:10.1093/glycob/cwy027.

- 156. DeBerardinis, R.J.; Chandel, N.S. Fundamentals of Cancer Metabolism. Sci Adv 2016, 2, e1600200, doi:10.1126/sciadv.1600200.
- 157. Kim, J.; Kim, J.; Bae, J.-S. ROS Homeostasis and Metabolism: A Critical Liaison for Cancer Therapy. Exp Mol Medicine 2016, 48, e269e269, doi:10.1038/emm.2016.119.
- 158. Nathan, C.; Cunningham-Bussel, A. Beyond Oxidative Stress: An Immunologist's Guide to Reactive Oxygen Species. Nat Rev Immunol **2013**, *13*, 349–361, doi:10.1038/nri3423.
- 159. Incalza, M.A.; D'Oria, R.; Natalicchio, A.; Perrini, S.; Laviola, L.; Giorgino, F. Oxidative Stress and Reactive Oxygen Species in Endothelial Dysfunction Associated with Cardiovascular and Metabolic Diseases. Vasc Pharmacol 2018, 100, 1-19, doi:10.1016/j.vph.2017.05.005.

- 162. Golubev, A.; Hanson, A.D.; Gladyshev, V.N. A Tale of Two Concepts: Harmonizing the Free Radical and Antagonistic Pleiotropy Theories of Aging. Antioxid Redox Sign 2018, 29, 1003-1017, doi:10.1089/ ars.2017.7105.
- 163. Burhans, W.C.; Heintz, N.H. The Cell Cycle Is a Redox Cycle: Linking Phase-Specific Targets to Cell Fate. Free Radical Bio Med 2009, 47, 1282 1293, doi:10.1016/j.freeradbiomed.2009.05.026.
- 164. Sies, H. Oxidative Eustress: On Constant Alert for Redox Homeostasis. Redox Biol 2021, 101867, doi:10.1016/j.redox.2021.101867.

- 165. Meng, J.; Lv, Z.; Zhang, Y.; Wang, Y.; Qiao, X.; Sun, C.; Chen, Y.; Guo, M.; Han, W.; Ye, A.; et al. Precision Redox: The Key for Antioxidant Pharmacology. Antioxid Redox Sign 2021, 34, 1069–1082, doi:10.1089/ ars.2020.8212.
- *Exp Ther* **2012**, *342*, 608–618, doi:10.1124/jpet.112.192120.
- 167. Hansen, J.M.; Go, Y.-M.; Jones, D.P. Nuclear and Mitochondrial Compartmentation of Oxidative Stress and Redox Signaling. Annu Rev Pharmacol 2006, 46, 215-234, doi:10.1146/annurev.pharmtox.46.120604.141122.
- 168. Lyublinskaya, O.; Antunes, F. Measuring Intracellular Concentration of Hydrogen Peroxide with the Use of Genetically Encoded H2O2 Biosensor HyPer. Redox Biol 2019, 24, 101200, doi:10.1016/j. redox.2019.101200.
- 169. Nkabyo, Y.S.; Ziegler, T.R.; Gu, L.H.; Watson, W.H.; Jones, D.P. Glutathione and Thioredoxin Redox during Differentiation in Human Colon Epithelial (Caco-2) Cells. Am J Physiol-gastr L 2002, 283, G1352-G1359, doi:10.1152/ajpgi.00183.2002.
- 170. Schafer, F.Q.; Buettner, G.R. Redox Environment of the Cell as Viewed through the Redox State of the Glutathione Disulfide/Glutathione Couple. Free Radical Bio Med 2001, 30, 1191-1212, doi:10.1016/ s0891-5849(01)00480-4.
- 171. Morgan, B.; Ezeriņa, D.; Amoako, T.N.E.; Riemer, J.; Seedorf, M.; Dick, T.P. Multiple Glutathione Disulfide Removal Pathways Mediate Cytosolic Redox Homeostasis. Nat Chem Biol 2013, 9, 119-125, doi:10.1038/nchembio.1142.
- 172. Jones, D.P.; Mody, V.C.; Carlson, J.L.; Lynn, M.J.; Sternberg, P. Redox Analysis of Human Plasma Allows Separation of Pro-Oxidant Events of Aging from Decline in Antioxidant Defenses. Free Radical Bio Med **2002**, *33*, 1290–1300, doi:10.1016/s0891-5849(02)01040-7.
- 173. Lim, J.B.; Langford, T.F.; Huang, B.K.; Deen, W.M.; Sikes, H.D. A Reaction-Diffusion Model of Cytosolic Hydrogen Peroxide. Free Radical Bio Med 2016, 90, 85-90, doi:10.1016/j.freeradbiomed.2015.11.005.
- 174. Rebrin, I.; Sohal, R.S. Comparison of Thiol Redox State of Mitochondria and Homogenates of Various Tissues between Two Strains of Mice with Different Longevities. Exp Gerontol 2004, 39, 1513–1519, doi:10.1016/j.exger.2004.08.014.
- 175. Shen, D.; Dalton, T.P.; Nebert, D.W.; Shertzer, H.G. Glutathione Redox State Regulates Mitochondrial Reactive OxygenProduction\*. J Biol Chem 2005, 280, 25305–25312, doi:10.1074/jbc.m500095200.
- 176. Hu, J.; Dong, L.; Outten, C.E. The Redox Environment in the Mitochondrial Intermembrane Space Is Maintained Separately from the Cytosol and Matrix \* *J Biol Chem* 2008, 283, 29126–29134, doi:10.1074/
- 177. Matsuyama, S.; Llopis, J.; Deveraux, Q.L.; Tsien, R.Y.; Reed, J.C. Changes in Intramitochondrial and Cytosolic PH: Early Events That Modulate Caspase Activation during Apoptosis. Nat Cell Biol 2000, 2, 318-325, doi:10.1038/35014006.

- 178. Porcelli, A.M.; Ghelli, A.; Zanna, C.; Pinton, P.; Rizzuto, R.; Rugolo, M. PH Difference across the Outer Mitochondrial Membrane Measured with a Green Fluorescent Protein Mutant. Biochem Bioph Res Co 2005, 326, 799-804, doi:10.1016/j.bbrc.2004.11.105.
- 166. Naviaux, R.K. Oxidative Shielding or Oxidative Stress? J Pharmacol 179. Abad, M.F.C.; Benedetto, G.D.; Magalhães, P.J.; Filippin, L.; Pozzan, T. Mitochondrial PH Monitored by a New Engineered Green Fluorescent Protein Mutant\*. J Biol Chem 2004, 279, 11521-11529, doi:10.1074/ jbc.m306766200.
  - 180. Poburko, D.; Santo-Domingo, J.; Demaurex, N. Dynamic Regulation of the Mitochondrial Proton Gradient during Cytosolic Calcium Elevations\*. J Biological Chem 2011, 286, 11672-11684, doi:10.1074/jbc.
  - 181. Hwang, C.; Sinskey, A.J.; Lodish, H.F. Oxidized Redox State of Glutathione in the Endoplasmic Reticulum. Science 1992, 257, 1496–1502, doi:10.1126/science.1523409.
  - 182. Navas, P.; Sun, I.; Crane, F.L.; Morré, D.M.; Morré, D.J. Monoascorbate Free Radical-Dependent Oxidation-Reduction Reactions of Liver Golgi Apparatus Membranes. J Bioenerg Biomembr 2010, 42, 181–187, doi:10.1007/s10863-010-9272-0.
  - 183. Yano, T.; Oku, M.; Akeyama, N.; Itoyama, A.; Yurimoto, H.; Kuge, S.; Fujiki, Y.; Sakai, Y. A Novel Fluorescent Sensor Protein for Visualization of Redox States in the Cytoplasm and in Peroxisomes  $\nabla$  †. *Mol* Cell Biol 2010, 30, 3758-3766, doi:10.1128/mcb.00121-10.
  - 184. Gille, L.; Nohl, H. The Existence of a Lysosomal Redox Chain and the Role of Ubiquinone. Arch Biochem Biophys 2000, 375, 347-354, doi:10.1006/abbi.1999.1649.



THE HUMAN 2-CYS PEROXIREDOXINS FORM WIDESPREAD, CYSTEINE-DEPENDENT- AND ISOFORM-SPECIFIC PROTEIN-PROTEIN INTERACTIONS

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# INTRODUCTION

In order to adapt to a changing environment, cells continuously translate extracellular cues into appropriate cellular in S. pombe [9]. In mammalian cells, the ASK1 kinase and STAT3 transcription factor are oxidized by PRDX1 and responses through cascades of protein-protein interactions and post-translational modifications known as signal trans-PRDX2, respectively [10,11], and ER-localized PRDX4 is duction. A recently discovered form of signal transduction known to induce disulfide formation through the oxidation termed redox signaling, uses hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) as a of protein disulfide isomerase (PDI) [12]. second messenger, and proceeds through the reversible oxidation of specific cysteine thiols in proteins (for a review, see ref. Others have shown a more widespread role for peroxiredoxins [1]). To function as a reliable second messenger, H<sub>2</sub>O<sub>2</sub> should in H<sub>2</sub>O<sub>2</sub>-induced thiol oxidation [13,14] . In this so-called be able to discriminate which cysteines it needs to oxidize peroxiredoxin-based relay model, the extremely reactive perspecifically in order to trigger the proper signaling cascade. oxidatic cysteine of peroxiredoxins first reacts with H<sub>2</sub>O<sub>2</sub> Although numerous H<sub>2</sub>O<sub>2</sub>-regulated proteins and processes and subsequently the oxidized peroxiredoxin catalyzes the have been discovered, it is unclear how exactly redox signaloxidation of low reactivity thiols in redox-regulated proteins ing achieves the required reactivity and specificity, which are (see Figure 1A). This mechanism could explain how so many intrinsically unreactive protein thiols can be found to be refundamental requirements for coherent cellular signaling. versibly oxidized in response to H2O2-dependent redox signaling, despite the presence of a highly abundant and reactive  $H_2O_2$  is considered the major reactive oxygen species (ROS)  $H_2O_2$  scavenging system.

for signaling because of its relative stability compared to other cellular reactive oxygen species (ROS, i.e., O<sub>2</sub><sup>--</sup> and OH) [2]. However, this relative stability also means that H<sub>2</sub>O<sub>2</sub> reacts Although the peroxiredoxin-based relay model may explain poorly with most cysteine thiols, with rate constants ranging how the reactivity of H<sub>2</sub>O<sub>2</sub> with protein thiols is overcome, from 20 to 200 M<sup>-1</sup>s<sup>-1</sup> [3-5]. Additionally, dedicated H<sub>2</sub>O<sub>2</sub> it does not as yet explain how the selectivity in H<sub>2</sub>O<sub>2</sub>-depenscavengers like peroxiredoxins (PRDXs) are estimated to dent redox signaling is achieved. In order to produce relevant eliminate >99% of cellular  $H_2O_2$  [6], because their catalytic biological signals, selective substrate targeting is required to cysteines react with many orders of magnitude faster with achieve proper signaling outputs. In redox signaling, this H<sub>2</sub>O<sub>2</sub> than other thiols in cysteine side chains in proteins, would mean that in the presence of numerous potential subincluding those found to be redox regulated. Peroxiredoxins strates, specific subsets of redox-regulated proteins should be oxidized dependent on, for instance, the subcellular localizaare highly abundant and ubiquitous proteins, with isoforms localized to cytoplasm, mitochondria, ER and other cellular tion or the local concentration of H<sub>2</sub>O<sub>2</sub>. Mammalian cells compartments [7]. The poor reactivity of thiols with H<sub>2</sub>O<sub>2</sub> express five 2-cys peroxiredoxin isoforms, each with their combined with the effective elimination of H<sub>2</sub>O<sub>2</sub> by peroxown localization, oxidation kinetics and structural differiredoxins seems to challenge the idea that reactivity and selecences around their catalytic sites. We therefore hypothesized tivity in redox signaling can be achieved by a simple molecule that reactivity and selectivity in redox signaling could also be like H<sub>2</sub>O<sub>2</sub>. provided by the different 2-cys peroxiredoxins.

Peroxiredoxins do not only scavenge H<sub>2</sub>O<sub>2</sub>; in fact, oxidized According to this line of reasoning, peroxiredoxins would 2-cys peroxiredoxins have also been shown to act as peroxibe expected to participate in temporary covalent complexes dases and facilitate H2O2-dependent protein oxidation via diwith isoform-specific subsets of target proteins, mediated by

**THE HUMAN 2-CYS PEROXIREDOXINS FORM** WIDESPREAD, CYSTEINE-**DEPENDENT- AND ISOFORM-SPECIFIC PROTEIN-PROTEIN INTERACTIONS** 

# ABSTRACT

Redox signaling is controlled by the reversible oxidation of cysteine thiols, a post-translational modification triggered by  $H_2O_2$ 

sulfide exchange reactions. For example, in S. cerevisiae, Tsa1 and Orp1 peroxidases relay towards the Yap1 transcription factor [8] and a similar mechanism was identified for Sty1 in



#### Figure 1. Peroxiredoxins form many H2O2- and cysteine-dependent interactions.

(A) Scheme depicting the canonical oxidation/reduction cycle of 2-cys peroxiredoxins and the possibilities for forming covalent reaction intermediates with target proteins (1 and 2). NADPH; nicotinamide adenine dinucleotide phosphate, TRX; thioredoxin, TRX-R; thioredoxin reductase, PRDX; peroxiredoxin. (B) HEK293T cells expressing Flag-tagged peroxiredoxin isoforms were treated for 2 min with H<sub>2</sub>O<sub>2</sub> and analyzed by immunoblotting. H<sub>2</sub>O<sub>2</sub> concentrations were 100 µM for PRDX1, 3, 4 and 5, and 25 µM for PRDX2. Non-reducing SDS-PAGE and immunoblotting shows overall H<sub>2</sub>O<sub>2</sub>-induced protein interactions for each PRDX isoform, reflected by the formation of PRDX-S-S-X conjugates. Immuno-precipitated Flag-peroxiredoxin isoforms also form PRDX-S-S-X conjugates in a cysteine-dependent manner. (C) All immunoblots shown in this figure are from the same gel and membrane with different exposure for each isoform, representative of multiple experiments ( $n \ge 3$ ). IP: immunoprecipitation; WB: Western blotting; input: cleared cell lysate as used for immunoprecipitation, reduced sample.

disulfides that form between their catalytic cysteine and a cysteine in these target proteins (see Figure 1A). To test this hypothesis, we used a systematic mass-spectrometry-based approach to identify cysteine-dependent interactors of the five human 2-cys peroxiredoxins. Indeed, our results suggest that all five human 2-cys peroxiredoxins are capable of forming disulfide-dependent heterodimers with a large set of proteins, and that each peroxiredoxin isoform displays a preference for a subset of disulfide-dependent binding partners. We explore what isoform-specific properties underlie these observations

and we provide evidence that peroxiredoxin-based redox relays can proceed via two distinct molecular mechanisms. These findings support the idea that peroxiredoxins could play a role in providing not only reactivity but also selectivity in the transduction of peroxide signals to generate complex cellular signaling responses.

# RESULTS

# All Five Human 2-cys Peroxiredoxins Have Many H,O,- And Cysteine-Dependent Interactors

As described above, peroxiredoxin-catalyzed cysteine oxcan be isolated by immunoprecipitation. idation proceeds through the (transient) formation of a disulfide bond between peroxiredoxins and target proteins, as A Proteome-Wide Screen Identifies the Interactome of Human 2-cys Peroxiredoxins has been shown for PRDX1 and PRDX2 [13]. If all human Having confirmed the ability of all five 2-cys peroxiredoxins 2-cys peroxiredoxins are involved in redox relay signaling, disulfide-dependent heterodimers (i.e., PRDX-S-S-X) would to form intermolecular disulfide-dependent complexes, we be expected to be formed upon oxidation of PRDX1-5. wondered about the scale of the interactome and the identities These disulfide-dependent heterodimers would show up as of the disulfide-dependent interacting proteins. To answer PRDX-containing high-molecular weight bands upon septhese questions, we performed an unbiased, quantitative aration on non-reducing SDS-PAGE followed by Western mass-spectrometry-based screen to identify cysteine-depenblotting. Indeed, a number of high-molecular weight bands dent interactors for each PRDX isoform. A workflow for this containing PRDX1-5 can be detected upon a 2-min pulse of screen is shown in Figure 2A. In short, cells expressing Flag-H<sub>2</sub>O<sub>2</sub> (Figure 1B). These Flag-PRDX1-5-containing comtagged PRDX were exposed to a short pulse of H<sub>2</sub>O<sub>2</sub> followed plexes are indeed sensitive to reduction, confirming the presby cell lysis. To prevent post-lysis oxidation and reduction, ence of disulfides. For PRDX1, 3, 4 and 5 we used 100  $\mu$ M free thiols are quenched before and after lysis using N-ethylmaleimide (NEM) and iodoacetamide (IA), respectively.  $H_2O_2$ , since that concentration showed many interaction partners in another study investigating PRDX binding partners in Flag-PRDX1-5 were pulled-down along with their interactors this cell type [13]. PRDX2 shows substantial hyperoxidation and subsequently exposed to a stringent high-salt wash to diminish non-covalent interactors. We then identified the interat 100  $\mu$ M H<sub>2</sub>O<sub>2</sub> and we therefore used 25  $\mu$ M H<sub>2</sub>O<sub>2</sub> for the experiments using PRDX2 (Figure S1). acting proteins using quantitative tandem mass spectrometry (MS/MS) followed by strict filtering and data analysis.

The covalent, disulfide-dependent heterodimeric complexes of Flag-PRDX1-5 and their interaction partners could be **Figures 2B–F** display scatter plots of the mean log<sub>2</sub> intensities isolated by immunoprecipitation (Figure 1C). Mutation of of the interacting proteins identified for PRDX1-5 wild-type the catalytic cysteines ( $C_p$  and  $C_p$ ) to serine (PRDX  $C_{pp}$ S) (WT) and corresponding PRDX-C<sub>DD</sub>S mutants from three abolished the formation of the majority H<sub>2</sub>O<sub>2</sub>-induced dibiological replicates. Marginal line graphs of the data distrisulfide-dependent binding partners for all PRDX isoforms bution visualize data points that are hidden by overcrowding. (Figure 1C), indicating that the catalytic cysteines in all 2-cys Proteins interacting with both WT and mutant peroxiredoxin peroxiredoxins form disulfide-dependent complexes with appear on a diagonal, while proteins interacting with only several other proteins upon oxidation. The PRDX1-5 con-WT will have no intensity in the corresponding  $C_{pp}$  S mutant taining complexes migrate different distances than the disuland are thus visible off the diagonal. This data indicates that fide dependent homodimers (for PRDX 1-4). Note that for all five isoforms interact with a large number of proteins, and PRDX4 and PRDX5 a band runs at about twice their MW that many of those interactions are dependent on the perox-(Figure 1B), which is also present in the  $C_{\mu\nu}S$  mutant; hence iredoxin catalytic cysteines. For most peroxiredoxin isoforms, this cannot be the oxidized peroxiredoxin homodimer. For but especially PRDX1, PRDX2 and PRDX3, the number of PRDX5 this is not unexpected since this is the only a-typical proteins that bind exclusively to wild-type is higher than to

2-cys PRDX and forms an intramolecular rather than intermolecular disulfide upon oxidation by H<sub>2</sub>O<sub>2</sub>. In summary, these results show that the five 2-cys PRDX isoforms form many H2O2-induced, disulfide-dependent interactions that



### Figure 2. A proteome-wide screen to identify the interactome of human 2-cys peroxiredoxins.

(A) Schematic representation of our workflow. Cells expressing Flag-PRDX isoforms (either wild-type or mutant) were treated with H<sub>2</sub>O<sub>2</sub> and alkylated with NEM and IA prior to and during lysis, respectively. H,O, concentrations were 100 μM for PRDX1, 3, 4 and 5 and 25 μM for PRDX2. Flag-peroxiredoxins and their interacting proteins were pulled down using immobilized anti-Flag-M2 and subsequently exposed to a stringent high-salt wash and binding partners were measured by mass spectrometry. After stringent filtering we inferred protein differential abundance by probabilistic dropout modeling. PRDX; peroxiredoxin, WT; wild-type, CP; peroxidatic cysteine; CR; resolving cysteine, IP; immunoprecipitation, MS/MS; tandem mass spectrometry. (B-F) Marginal scatter plots for peroxiredoxins 1–5, depicting the mean log, LFQ intensity for both wild-type and C<sub>no</sub>S mutant peroxiredoxin. Colored proteins are identified with a p-value <0.05, and the distribution of these proteins are also visualized in the marginal density plots. Proteins interacting with both WT and mutant peroxiredoxin appear on a diagonal, while proteins that bind only WT or the C<sub>100</sub>S mutant appear along the horizontal or vertical axis, respectively, and can be found at the edges of the marginal plots. (G) Scatter plot of log, fold change between wild-type and C<sub>up</sub>S-peroxiredoxin isoforms. Horizontal lines are positioned at log, fold change of 1 and –1 (i.e., a 2-fold change). Colored proteins are identified with a p-value <0.05. (H) Number of cysteine-dependent interaction partners per peroxiredoxin isoform identified with p-value <0.05 and log, fold change >1 in our screen. (I) Bar chart representing the percentage of interactors per PRDX that are previously identified as redox-sensitive in a large-scale mass-spectrometry-based screen. The reference proteome contains 75071 human UniProt entries with "reference proteome" as keyword.

the corresponding mutant (visualized in the marginal plots of Figures 2B-F and Figure S2), suggesting that their interaction is cysteine-dependent. PRDX4 and PRDX5 seem to have a lower number of cysteine-dependent binders than the other isoforms. As yet we do not have a biological explanation for what the  $C_{pp}$  S-specific interactors would represent.

A major challenge that is inherent to mass spectrometry data of the sample. To determine a suitable cutoff for our data, analysis, especially in proteome-wide protein-protein interacwe randomized the data-labels a hundred times between WT tion studies like these, is that not all proteins are identified or and  $C_{pp}$  S data and recalculated the log<sub>2</sub> fold change. With the quantified in each biological replicate and sample, therefore randomized data, we calculate that with a log, fold change the data contains many missing values (an average of 34% threshold of >0.401, 5% of the randomized data is within per sample) [15]. It is well known that many of these missing the 95th quantile (i.e., an FDR of 5%,); on the other hand, values are non-random and that their absence correlates with 25.2% of the non-randomized data are included using the a low overall intensity. If the hypothesis that proteins bind to same threshold. In order to increase confidence, we used a PRDX in a largely disulfide-dependent manner holds true, more stringent cutoff of log, fold change >1 (FDR of 0.02%, missing values are actually expected to occur more often in Figure S3). Therefore, proteins are considered to be signifithe PRDX-C<sub>pp</sub>S mutant pull-downs. Thus, non-random cantly enriched when detected with at least twice the abunmissing data could hold important information in this exdance (i.e.,  $\log_2$  fold change >1) as compared to the average periment. In our analysis done for Figure 2B-F we simply expression of a protein around the limit of detection of the ignored the missing values. Although this approach produces experiment, and a *p*-value <0.05. A total of 1233 proteins a general picture of the data, for a detailed analysis it is not pass these criteria as catalytic cysteine-dependent binders of optimal. Several MS data analysis approaches replace missing peroxiredoxins (Figure 2G and Supplementary Table S1). values with a reasonable value (imputation). However, im-Collectively, the results from our screen indicate that a large puting non-random missing values can overestimate peptide number of proteins form disulfide-dependent heterodimers abundances and obscure available information, meaning that with the five 2-cys peroxiredoxin isoforms. imputed values will be considered with the same confidence as measured values. This will lead to biased results, skewing We set out to characterize the isoform-specific interaction data in a sample-dependent manner. For these reasons, we partners of peroxiredoxins in more detail. Specifically, we reanalyzed our data using a method called proDA (inference asked what proportion has previously been identified in a of protein differential abundance by probabilistic dropout large-scale mass-spectrometry-based screen for redox-sensianalysis). This method aims to combine the sigmoidal droptive proteins [17]. Of the proteins identified in our screen, out curve for missing values with the information from the 80.5% contained cysteines that have previously been reported observed values without direct value imputation. This allows as sensitive to oxidative modification, compared to 13% in for a more robust analysis that combines both the information the reference proteome (Figure 2I). We also observed this from measured and missing values [16]. enrichment for redox-sensitive proteins for each individual PRDX isoform.

Cysteine-dependent interactors for each PRDX are visualized by plotting the fold change in intensity for each interactor Peroxiredoxin Isoforms Interact With a Specific Set of Target Proteins pulled down with either WT,  $C_{PR}$ S or both, on a log<sub>2</sub> scale. In the proDA analysis, a large log, fold change means that The subcellular localization of the five 2-cys PRDX isoforms, the protein was detected with high abundance in the WT as well as their reaction kinetics, are not identical, and we peroxiredoxin pulldown and with no or low abundance in therefore predicted that this could be reflected in their cysteine-dependent interactomes. We therefore next asked what  $C_{np}S$  peroxiredoxin. Specifically, the difference between means (log, fold change) is calculated based on the distributhe extent of overlap is between cysteine-dependent binding tion of measured values and, when values are missing, the partners of different PRDX isoforms. A quantitative analysis distribution of these is based on the average detection limit of the intersections between the interactomes is shown in a

matrix layout using an Upset plot (Figure 3A). Figure 3B presents the overlap in a more traditional color-coded Venn diagram. Interestingly, in this comparison we found that each peroxiredoxin isoform has a largely differential set of cysteine-dependent binding partners. This suggests that each of the peroxiredoxins catalyze the oxidation of a specific set of substrates.

Next, we investigated whether the subcellular localization of isoform-specific cysteine-dependent binding partners corresponds with the known localization of peroxiredoxin isoforms. To do so, we used SubCellBarCode [18], a resource that documents the subcellular localization of proteins in multiple cell lines. Indeed, most peroxiredoxin-binding proteins are overrepresented in the compartment where the peroxiredoxin isoform they interact with is reportedly localized (Figure 3C). For example, mitochondrial PRDX3, ER-localized PRDX4 and nuclear PRDX5 show an enrichment of proteins in the mitochondrial, secretory and nuclear compartments, respectively. The analysis is thus in line with the hypothesis that isoform-specific preferred localization could, at least to some extent, explain the PRDX-specificity of binding partners. A note of caution is due here since the generalizability to other cell lines is uncertain; additionally, not all databases report the same predominant localization for the peroxiredoxins [19-21]. This may vary depending on the cell state, tissue type, cell cycle and post-translational modifications (for an overview, see [22]).

PRDX1 and PRDX2 share 90% sequence similarity (Figure 3D) and have the same reported subcellular localization (cytoplasm), but we found approximately one third of PRDX2 interactors to overlap with PRDX1 interaction partners, suggesting that localization is apparently not the sole determinant of PRDX isoform-specific disulfide-dependent binding. Differences in the molecular interface surrounding the cysteines of the binding partners that bind the catalytic cysteine of the peroxiredoxin isoforms could be the underlying mechanism behind this specific binding. For instance, it is known that deprotonation of the cysteine thiol at physiological pH is governed by the local environment, and the thiolate is more readily oxidized [23]. Recently, it was suggested that positively charged amino acid side chains (arginine, lysine, histidine) and the N-terminus can stabilize the thiolate of a proximal cysteine [17]. We therefore investigated whether the local environment around the cysteines of peroxiredoxin isoform-specific interactors is enriched for certain amino acids that can potentially alter the reactivity of a proximal cysteine. A challenge here is that our screen does not report on which specific cysteine of a binding partner is involved in the interaction with the PRDX, and we therefore analyzed all cysteines present in the binding partner, which would likely dilute any specific motifs. To investigate the presence of characteristic molecular environments, we extracted the eight amino acids flanking all cysteine residues of cysteine-dependent interactors for each peroxiredoxin isoform. Subsequently, we examined the amino acids surrounding each cysteine and calculated the fold change in the presence of each amino acid in one peroxiredoxin compared to all other isoforms. The amino acid enrichment or depletion in possible binding sites of specific peroxiredoxin isoforms is shown in Figure 3E-I. In general, these calculations suggest that the local amino acid composition of interactors of a specific peroxiredoxin looks different from that of the interactors of the other peroxiredoxin isoforms. Note that this analysis is based purely on the primary sequence of the binding partners, and that a 3D structure and pinpointing which cysteine actually forms the interaction would likely reveal a clearer picture of differences in the molecular interface, but we consider that beyond the scope of this study.

The analysis of peroxiredoxin interactors described above is based on the comparison of cysteine-dependent binders to each peroxiredoxin isoform. It is possible, however, that proteins bind to one peroxiredoxin isoform in a cysteine-dependent manner, but independent of cysteines to another peroxiredoxin isoform. To analyze the peroxiredoxin-specificity for cysteine-dependent interactors with a different approach, we re-analyzed our dataset in order to identify isoform-specific interactors. For each peroxiredoxin, we fit a new probabilistic



(A) UpSet plot and (B) Venn diagram to visualize cysteine-dependent target protein set intersections per peroxiredoxin isoform in a matrix layout. A color gradient from light (no overlap) to dark (high overlap) indicates the amount of overlap in the Venn diagram. (C) Localization of the top isoform-specific cysteine-dependent binders (>10-fold better binding to WT as compared to CprS) using the SubCellBarcode resource. Missing values are colored grey. (D) Sequence similarity for peroxiredoxins 1-5 calculated using the pairwise alignment tool EMBOSS needle. (E-I) Bar charts representing fold enrichment of the local amino acid composition around each cysteine in isoform-specific, cysteine-dependent peroxiredoxin interactors compared to the interactors of all other peroxiredoxin isoforms. Eight amino acids were extracted centered around each cysteine, with sequences shuffled 100 times as a control. \* p < 0.05; \*\* p < 0.01; \*\*\* p < 0.001. (J) Scatter plot of log, fold change comparing each peroxiredoxin isoform to all other isoforms. Horizontal lines are positioned at log, fold change of 1 and -1 (i.e., a 2-fold change). Colored proteins are identified with Benjamini–Hochberg adjusted p < 0.05. (K) Similar to (J) but filtered for cysteine-dependent binders as analyzed in Figure 2G. (L) UpSet plot and (M) Venn diagram visualizing peroxiredoxin isoform-specific target protein set intersections in a matrix layout. A color gradient from light (no overlap) to dark (high overlap) indicates the amount of overlap in the Venn diagram.

dropout model using proDA, now testing which proteins are enriched in each peroxiredoxin isoform compared to the other isoforms irrespective of cysteine-dependency. Isoform-dependent interactors for each peroxiredoxin are visualized by plotting the log, fold change in abundance comparing PRDX1-5 (i.e., the difference between the analyzed peroxiredoxin and all other isoforms on a log, scale). Proteins that were enriched in pulldowns for one peroxiredoxin isoform (WT) but not in the other isoforms (with a log ratio of >1) are considered peroxiredoxin-specific binders. These data show a large number of proteins that bind to peroxiredoxins in an isoform-specific manner, irrespective of whether this is cysteine-dependent (Figure 3J). Again, we see that all PRDX isoforms have a large set of peroxiredoxin-specific interactors, which accords with our earlier observations, suggesting that each peroxiredoxin isoform has a largely differential set of cysteine-dependent binding partners (Figure 3A,B). Overlaying this analysis with the results obtained for cysteine-dependency in Figure 2G results in Figure 3K, which shows preferential binding partners for each PRDX isoform that do not bind to the  $C_{DP}$  S mutant of that isoform. This is shown in the Upset plot and Venn diagram in Figure 3L and M, respectively.

Although we use a stringent wash buffer (containing 1 M NaCl) after the immunopurification of PRDX1-5 to enrich for disulfide-dependent covalent interactions, a large number of proteins were found to interact with the PRDX C<sub>pp</sub>S mutants (Supplemental Figure S4, light bars). The peroxiredoxin specificity of our data including both cysteine-dependent as well as -independent binders reassures that the observed interactions are not an artefact of post-lysis binding to all PRDXs or the anti-Flag coated beads in which case they would be expected to largely overlap. When we look at the top 100 proteins with the lowest *p*-values and allow them to cluster per peroxiredoxin isoform, we also observe different patterns of interacting proteins for the five PRDX isoforms (Supplemental Figure S5).

These results support the idea that all five peroxiredoxin isoforms bind a specific set of cysteine-dependent interactors, which could suggest that PRDX isoforms each control the oxidation of a different subset of the proteome through which redox relay signaling. The cysteine-dependent binding partners of peroxiredoxins contain a large fraction of proteins that have been reported as redox-sensitive. The localization of peroxiredoxin interactors, together with apparent differences in the local environment of interactor cysteines, could potentially explain isoform specificity.

# The Peroxidatic Cysteine is Sufficient to Form Cysteine-Dependent, Peroxiredoxin-Specific Interactions

Oxidized peroxiredoxins could in principle relay oxidizing equivalents to other thiols via two molecular mechanisms. The first mechanism involves the condensation of sulfenylated peroxidatic cysteine (C<sub>p</sub>-SOH) of peroxiredoxins directly with the cysteine thiol of a target protein (Figure 1A, 1). A second possible mechanism involves a disulfide exchange reaction of the disulfide between the peroxidatic and resolving cysteine (Cp- $S-S-C_p$ ) in oxidized peroxiredoxins with a target protein thiol (Figure 1A, 2). The SOH-mediated mechanism in principle only needs the peroxidatic cysteine of peroxiredoxin, whereas the S-S-mediated route is dependent on both catalytic cysteines.

To test which of these mechanisms is involved in the formation of S-S-dependent PRDX-target heterodimers, we performed not the  $C_p$ -S-S- $C_p$  dependent mechanism. another mass-spectrometry-based screen similar to the one described above, but now comparing  $C_p S$  mutants to the catalytic Peroxiredoxin C<sub>p</sub>S mutants of all five isoforms can still pardead mutants ( $C_{PR}$ S) of each peroxired oxin isoform. The  $C_{R}$ S ticipate in disulfide-dependent interactions with many pro-



Figure 4. The peroxidatic cysteine is sufficient to form cysteine-dependent, peroxiredoxin-specific interactions. (A) Scatter plot of the log<sub>2</sub> fold change in binding of proteins to each of the  $C_{\rm p}$ S-mutant peroxired oxin isoforms compared to the  $C_{\rm pp}$ S-mutant of the same peroxiredoxin isoform. Horizontal lines are positioned at log, fold change of 1 and -1 (i.e., a 2-fold change). Colored proteins are identified with a *p*-value <0.05. (B) Number of peroxidatic cysteine  $C_p$ -dependent interaction partners per peroxired oxin isoform identified with *p*-value <0.05 and log, fold change >1 in our screen. (C) Bar chart representing the percentage of peroxidatic cysteine  $C_{y}$ -dependent binders that are also identified as cysteine-dependent binders in wild-type peroxiredoxin (Figure 2). (D) UpSet plot and (E) Venn diagram that visualize peroxidatic cysteine C<sub>v</sub>-dependent target protein set intersections per peroxiredoxin isoform in a matrix layout. A color gradient from white (no overlap) to blue (high overlap) indicates the amount of overlap in the Venn diagram.

mutant could in theory still relay through the (C<sub>p</sub>-SOH) but

teins: a total of 1032 cysteine-dependent binding partners (compared to 1145 for wild-type) was identified (Figure 4A,B and Supplemental Table S3). This strongly suggests that many peroxiredoxin binding partners are capable of binding through the C<sub>p</sub>-SOH-mediated mechanism. We then analyzed how many of the cysteine-dependent binders of PRDX-C<sub>p</sub>S are also identified as WT cysteine-dependent binders. We found that of the proteins identified to form cysteine-dependent interactions with PRDX-C<sub>p</sub>S, over 60% for PRDX1, PRDX3 and PRDX5 and approximately half for PRDX2 and 4, also do so using WT peroxiredoxins as bait (Figure 4C). When comparing peroxidatic cysteine-dependent binding partners for the five peroxiredoxin isoforms we again found that each has a largely different set of target proteins (Figure 4D,E). This confirms our conclusion regarding the peroxiredoxin-isoform-specific binding partners that we based on the mass-spectrometry screen comparing wild-type peroxiredoxins.

Thus, for many cysteine-dependent interactors of the peroxiredoxins, the peroxidatic cysteine suffices to mediate the interaction in the absence of the resolving catalytic cysteine. This does not mean however that the interaction cannot be established starting from C<sub>p</sub>-S-S-C<sub>p</sub> under normal conditions.

# Peroxiredoxins Bind Target Proteins Via Two Distinct Mechanisms

We observed that cysteine-dependent heterodimerization of peroxiredoxins with many target proteins also occurs in mutants lacking the resolving cysteine. However, this might not apply to all identified interactors, and in principle, a C<sub>p</sub>-S-S-C<sub>p</sub> could be required for a subset of the cysteine-dependent PRDX binding partners. We questioned whether, for each PRDX, all binding partners follow the C<sub>p</sub>-SOH-mediated mechanism, or whether some might use the C<sub>p</sub>-S-S-C<sub>p</sub>-mediated route. We compared cysteine-dependent binders of wild-type peroxiredoxins to cysteine-dependent binders of the C<sub>p</sub>S mutant (Figure 5A and Table S4). Proteins that do not bind the resolving cysteine mutant  $C_p S$ , but that do bind

the wild-type peroxired oxin, likely depend on the  $C_p$ -S-S- $C_p$ -mediated relay mechanism. We found that the majority of cysteine-dependent interactors of the WT and C<sub>n</sub>S mutant datasets overlap. However, a number of proteins are exclusively found to interact with the WT peroxiredoxins and hence depend on a C<sub>p</sub>-S-S-C<sub>p</sub> mediated relay. We also identified a small number of interactors that are only pulled down with the C<sub>p</sub>S mutant, but not with the WT peroxiredoxin.

Next, we compared the extent of  $C_p$ -S-S- $C_p$ - and  $C_p$ -SOH-mediated binding between peroxiredoxin isoforms. As shown in Figure 5B, there are large differences in the distribution of the relay mechanisms between isoforms. The percentage of C<sub>p</sub>-S- $S-C_{R}$ -mediated binders ranges from 21% to 16% for PRDX2 and PRDX3, respectively, while PRDX1 and PRDX4 have 44% and 58% C<sub>p</sub>-S-S-C<sub>p</sub> interactors. Interestingly, as much as 73% of PRDX5 interactors follow the  $C_p$ -S-S- $C_p$ -mechanism. It is not unlikely that the absence of the resolving cysteine may actually stabilize or facilitate disulfide formation with cysteines in other proteins.

A possible explanation as to why disulfides with binding partners are formed preferably starting from either C<sub>p</sub>-SOH or  $C_p$ -S-S- $C_p$  might lie in the amino acid region surrounding the cysteine in an interacting protein. Since C<sub>p</sub>-SOH and C<sub>p</sub>-S-S- $C_p$  are structurally distinct, the local environment of an interacting cysteine could determine whether an interaction is favorable. We investigated whether the local environments of cysteines in interactors that preferentially bind to C<sub>p</sub>-SOH or  $C_p$ -S-S- $C_p$  can be distinguished. Interactors of all PRDX isoforms were separated into two groups based on their preference for either  $C_p$ -SOH or  $C_p$ -S-S- $C_p$ -mediated interaction. For both groups, we extracted the eight amino acids flanking all cysteine residues. Using the motif-x algorithm [24], we analyzed potential motifs in each group of interactors, using the other group as a background. While both C<sub>p</sub>-SOH and C<sub>p</sub>-S-S-C<sub>p</sub>-mediated interactors are enriched in the CxxC motif, a well-known motif in redox proteins (Tables S5 and **S6**), differences in enriched motifs found in  $C_p$ -SOH and  $C_p$ -S-S-C<sub>p</sub>-mediated interactors could be found (Figure 5C,D);

for example, the YCE motifs enriched in C<sub>p</sub>-SOH-mediated interactors as compared to C<sub>p</sub>-S-S-C<sub>p</sub>-mediated interactors. Peroxiredoxin-catalyzed oxidation has been suggested to answer the question as to how thiols with low intrinsic reactivity can be oxidized by low levels of  $H_2O_2$  despite the presence of abundant and highly reactive peroxidases. Here we show that all isoforms are capable of forming numerous cysteine-dependent heterodimers. Our in-depth mass-spectrometry and complementary bioinformatics approach provides, first of all, a resource of potential 2-cys peroxiredoxin-catalyzed cysteine oxidation substrates. Many of the proteins that we identified as cysteine-dependent peroxiredoxin binders were indeed identified previously to contain redox sensitive cysteines [17]. This overlap could point at a major role for peroxiredoxins in cysteine oxidation in other proteins. It is

This supports the idea that proteins might preferentially form interactions with peroxired xin  $C_p$ -SOH or  $C_p$ -S-S- $C_p$  based on their local amino acid composition. Based on these observations, we conclude that oxidized peroxiredoxins bind their interaction partners starting from the --SOH- or -S-S-state, and that a subset of interactors can only bind PRDX in the S-S state. A possible explanation for this might be found in amino acid motifs surrounding cysteine residues in the interaction partners. S-S vs. -SOH dependent relay could point to an additional level of specificity in peroxiredoxin-based interaction that may have implications for cellular redox regulation.



А.

C

	motif	score	fold increase
1	YCE	309.4	00
2	.IC.K	12.9	3.4
3	YCK	11.4	4.4
4	V.CY.	11.4	5.8
5	CI.P.	11.4	4.2
6	RAC	10.3	2.7
7	C.V.N	8.4	2.7
8	.RCT	8.4	3.8
9	ACA.	8.1	2.1
10	QEC	7.9	2.5

Figure 5. Peroxiredoxins interact via two distinct mechanisms. (A) Analysis comparing cysteine-dependent interactors of wild-type and C<sub>v</sub>S-mutant peroxiredoxins showing the log, fold peroxiredoxins (D) with sequences shuffled 100 times as a control.

# DISCUSSION

-SOH -S-S-

#### D.

motif	score	fold increase	
Top 10 amino acid mo	tifs in C <sub>P</sub> -S-S	-C <sub>R</sub> -mediated interac	tors

1	.CF	6.5	2.5	
2	CCG	6.4	1.9	
3	R.CL.	5.9	1.9	
4	CP.C.	5.9	2.5	
5	EQC	5.7	2.5	
6	T.C.V	5.2	2.3	
7	ECK.	4.7	2.1	
8	.CC.E	4.6	2.3	
9	LCQ	4.6	1.9	
10	PTC	4.5	2.5	

change in binding of proteins to wild-type compared to the C<sub>p</sub>S-mutant peroxiredoxin isoforms. Horizontal lines are positioned at log, fold change of 1 and -1 (i.e., a 2-fold change). Colored proteins are identified as cysteine-dependent binders in the analyses presented in Figure 2 and 4. (B) Bar chart representing the percentage of C<sub>v</sub>-S-S-C<sub>v</sub>-mediated and C<sub>v</sub>-SOH cysteine-dependent interactors per peroxiredoxin isoform. Proteins interacting with the C<sub>10</sub>S-mutant only are not included in this analysis. Local amino acid motifs around each cysteine of C<sub>0</sub>-SOH cysteine-dependent interactors (C) and C<sub>0</sub>-S-S-C<sub>0</sub>-mediated interactors of

not clear what follows after peroxiredoxin-dependent cysteine oxidation, but one could think of three possible scenarios following intermolecular disulfide formation between peroxiredoxin and a target protein. 1) The intermolecular disulfide could be rapidly resolved by disulfide exchange to the resolving cysteine of the peroxiredoxin, forming the canonical  $C_p$ -S-S- $C_p$  and leaving the target reduced. 2) The intermolecular disulfide could be resolved by disulfide exchange to another cysteine in the binding protein (or protein complex), forming an intra- or intermolecular disulfide in that protein and leaving peroxiredoxin reduced. 3) The intermolecular disulfide dependent complex of peroxiredoxin and its target could represent a novel type of post-translational modification on cysteine, that for instance alters the function of the target, that we would like to coin S-peroxiredoxinylation (S-PRDXylation). Others have shown that many of the PRDX1 and PRDX2-dependent binders were also identified in a TRX-trap pull down, confirming that proteins binding to peroxiredoxin in a cysteine-dependent manner indeed become oxidized [13]. This observation probably does not exclude S-PRDXylation. Widespread S-PRDXylation could also be in accordance with the identification of many oxidation-sensitive cysteines in redox proteomics studies, as these would not distinguish S-PRDXylation from other intra- or intermolecular disulfides [25]. Besides a role as a post-translational modification impacting the function of specific proteins, widespread peroxiredoxinylation could in principle also serve as a redox buffer.

Our data furthermore provides evidence that the peroxiredoxin-dependent redox relay model could also explain how selectivity in redox signaling can be achieved. Selectivity stems from the observation that each peroxiredoxin isoform interacts with a largely specific subset of proteins. This could in part depend on isoform-specific subcellular localization, but the relatively low overlap in binders for PRDX1 and PRDX2, which share the same subcellular localization and a high sequence similarity, suggests that this is not the only determinant for binding of a protein to a specific peroxiredoxin isoform. Analysis of local structural differences surrounding the region around the cysteine of the binding protein could also contribute to selective binding of proteins to the different PRDXs. A second layer of specificity is suggested by the observation that peroxiredoxin-mediated relays can proceed through two distinct molecular mechanisms, starting from either  $C_p$ -SOH or  $C_p$ -S-S- $C_p$ , and that peroxired xin isoforms and targets display varying preferences for these mechanisms. Each PRDX has different kinetics for C<sub>p</sub>-SOH and C<sub>p</sub>-S-S-C<sub>n</sub> formation and reduction, and these kinetics could dictate which cysteines in target proteins can be oxidized under specific conditions. For instance, at low levels of peroxide, PRDX2 would be the first to form C<sub>p</sub>-SOH, whereas only under conditions where TRX activity is limiting oxidized peroxiredoxin in the  $C_{p}$ -S-S- $C_{R}$  form would it be sufficiently abundant to oxidize another set of targets. Interestingly, when we look at isoform-specific differences in the frequency of C<sub>p</sub>-SOH and  $C_p$ -S-S- $C_p$ -mediated interactors, we find that there are large differences in the distribution of the relay mechanisms between isoforms.

A fair number of proteins seems to bind peroxiredoxins independent of its catalytic cysteines (Figure 3L, grey dots), despite high-salt washing. The peroxiredoxin isoform dependent specificity irrespective of cysteine-dependency suggests that these interactions are probably not artefacts of the used method. This leaves the possibility that some of these proteins could function as adaptor proteins to facilitate peroxiredoxin-dependent relays to cysteine-dependent binding proteins. Although this would need to be explored, adaptor proteins have been shown to be involved in peroxidase-dependent redox relays. For instance, Orp1-dependent Yap1 oxidation is dependent on the presence of the adapter protein Ybp1, shielding oxidized Orp1 from reduction [26,27]. Similarly, the PRDX2-STAT3 redox relay depends on association with the membrane-associated scaffold protein ANXA2 [28]. We indeed also identify ANXA2 as a PRDX2-specific and cysteine-dependent interactor in our screen (Table S2). It is conceivable that many more peroxiredoxin-based redox relays may proceed via the formation of ternary complexes with scaffold proteins. This would not only increase the chances that a peroxiredoxin finds a target, but would also add another iredoxins under basal conditions, be it cysteine dependent or level of specificity, coming from the interaction of specific not. Future work will be needed to carefully validate each properoxiredoxin isoforms with specific scaffolds for the relay tein found as a cysteine-dependent peroxiredoxin interactor. of oxidation to subsets of target proteins.

It is not unthinkable that differences in the level of overex-Taken together, our observations regarding widespread cystepression of the Flag-tagged PRDX1-5 or their mutants may ine-dependent binding of proteins to the 2-cys peroxiredoxins lead to variation in the number of proteins pulled down. In provides a model that could explain both the reactivity and general, the  $C_{pp}$ S mutants of each PRDX1–5 isoform had selectivity of the extensive cysteine oxidation observed in revery similar expression and IP efficiency as compared to their sponse to low amounts of  $H_2O_2$ . wildtype isoform counterparts (see for instance Figure 1C, reducing IP and input), suggesting that whether an interactor is identified as a cysteine-dependent binder is not much affect-Conclusions ed by variable expression levels. The levels of overexpression of In conclusion, our findings suggest that all five human 2-cys peroxiredoxins can form disulfide-dependent heterodimers Flag-PRDX1-5 compared to each are somewhat variable, and with a large set of proteins, and that each peroxiredoxin isofor his reason MS/MS data was log<sub>2</sub>-transformed followed by form displays a preference for a subset of disulfide-dependent quantile normalization to simultaneously correct for overall binding partners. We highlight the isoform-specific characprotein content and IP efficiency in an attempt to lower the teristics that might justify this preference. Furthermore, we chance that differences in expression levels affect our analysis.

propose that peroxiredoxin-based redox relays can progress order to generate appropriate signaling responses.

via one of two molecular mechanisms starting from either The analysis of the chemical environment of cysteines oxidized  $C_p$ -SOH or  $C_p$ -S-S- $C_p$ . These findings provide a framework through peroxiredoxin dependent relays would greatly benefit for peroxiredoxin biology and implicate a widespread role for from knowing which cysteine in a binding partner is being oxperoxiredoxins in selectively transducing peroxide signals in idized. Here we have analyzed all cysteines in the interactors which obviously dilutes any specific pattern. Combining peroxiredoxin-interactome screens as described here with redox Limitations of this study proteomics or ways to keep the disulfide between peroxiredoxin The cut-offs used in the analysis of our mass-spectrometry and its targets intact and suitable for analysis by MS/MS in screen are quite stringent, and whether proteins bind only in a future studies could be a way to achieve this. It is difficult to cysteine-dependent manner or to only a certain peroxiredoxin unambiguously exclude that proteins no longer bind to the isoform may not be as unambiguous. Furthermore, to keep used peroxiredoxin mutants due to structural changes other than loss of the cysteine thiol. For the resolving cysteine muthe number of mass-spectrometry samples manageable the analysis was performed at a single timepoint following a single tants at least, a recent study shows that the cysteine to serine concentration of  $H_2O_2$  treatment. It is not unthinkable that mutation has only a limited effect on the rate of oxidation of proteins found to interact specifically to one peroxiredoxin the peroxidatic cysteine in PRDX2 [29]. Characterization of isoform in this study will in fact interact with others when the functional consequences of specific peroxiredoxin-based inanalyzed at other timepoints or H<sub>2</sub>O<sub>2</sub> concentrations. The use teractions is outside the scope of this study. However, it would of the  $H_2O_2$  treated  $C_{np}S$  mutants as a control rather than also be interesting to investigate the mechanisms and fate of these including untreated samples for WT PRDX1-5 (for the same complexes in more detail. Additionally, further work is needed reason of keeping the number of mass-spectrometry samples to link the mechanisms of peroxiredoxin specificity to biologmanageable) may obscure whether proteins also bind peroxical cues that determine downstream signaling.

# MATERIALS AND METHODS

# Cell lines and culturing

HEK293T were cultured in bicarbonate-buffered DMEM, supplemented with 10% FBS (Bodinco BDC-40506-C05), 2 mM L-glutamine (Lonza, BE17-605E) and 100 U/mL penicillin-streptomycin (Lonza, DE17-602E) and kept at 37 °C and under a 6% CO<sup>2</sup> atmosphere. Transfections of HEK293T cells were carried out using PEI (Sigma-Aldrich, P3640) or FugeneHD reagent (Promega, E2311) following the manufacturer's instructions. After two days, cells were harvested for further analysis.

# **Plasmids and Reagents**

Human PRDX1-5 with att recombination sites were cloned from cDNA using the following primers: PRDX1\_att F-5'-GGGGACAAGTTTGTACAAAAAGCAGGCT-TAATGTCTTCAGGAAATGCTAAAATTGGGC-3', PRDX1 att R-5'-GGGGACCACTTTGTACAAGAAAGCT-G G G T C C T A C T T C T G C T T G G A G A A A -TATTCTTTGCT-3', PRDX2\_att\_F-5'-GG-G G A C A A G T T T G T A C A A A A A A G C A G -G C T T A A T G G C C T C C G G T A A C G C - 3', PRDX2\_att\_R5GGGGACCACTTTGTACAAGAAAGCTGGGTTCTA ATTGTGTTTGGAGAAATATTCCTTGCTGT-3', PRDX3 att F-5'-GGGGACAAGTTTGTACAAAAAG-CAGGCTTAATGGCGGCTGCTGTAGG-3', PRDX3 att\_R-5'-GGGGACCACTTTGTACAAGAAAGCTGG-GTTCTACTGATTTACCTTCTGAAAGTACTCTTTGGAAG3, PRDX4 att F-5'-GGGGGACAAGTTTGTA-CAAAAAGCAGGCTTAATGGAGGCGCTG-CCG-3', PRDX4 att R-5'-GGGGGACCACTTTG-TACAAGAAAGCTGGGTTTTTCAGTTTATC-GAAATACTTCAGCTTTCCAG-3', PRDX5\_att\_F-5'-GGGGACAAGTTTGTACAAAAAG-CAGGCTTAATGGGACTAGCTGGCGTG-3', PRDX5 att\_R-5'-GGGGACCACTTTGTACAAGAAAGCTG-GGTTTCAGAGCTGTGAGATGATATTGGGTG-3'. Using Gateway technology (Invitrogen) entry clones were generated. The peroxidatic and resolving cysteine

mutants of PRDX1-5 were created by site-directed mutagenesis PCR using the following primers: PRDX1\_ C52S F-5'-CTTTGTGTCCCCCACGGAG-3', PRDX1 C52S.\_R-5'-CTCCGTGGGGGGACACAAAG-3', PRDX1\_C173S\_F-5'-GGGAAGTGTCCCCAGCTGG-3', PRDX1 C173S. R-5'-CCAGCTGGGGGACACTTCCC-3', PRDX2\_C51S\_F-5'-TCACTTTTGTGTCTCCCAC-CGAGATCATCGCG-3', PRDX2\_C51S.\_R-5'-CGCGAT-GATCTCGGTGGGAGACACAAAAGTGA-3', PRDX2 C172S\_F-5'-CATGGGGAAGTTTCTCCCGCTGGCT-3', PRDX2\_C172S.\_R-5'-AGCCAGCGGGAGAAACTTC-CCCATG-3', PRDX3 C108S F-5'-TCACCTTTGT-GTCTCCTACAGAAATTGTTGCT-3', PRDX3\_C108S.\_R-5'-AGCAACAATTTCTGTAGGAG-ACACAAAGGTGA-3', PRDX3 C229S F-5'-ACACATG-GAGAAGTCTCTCCAGCGAACTGGACA-3', PRDX3\_ C229S. R5TGTCCAGTTCGCTGGAGAGACTTCTCCATGTGT3, PRDX4\_C124S\_F-5'-ATTTCACATTTGTGTCTC-CAACTGAAATTATCGCTTTTGG-3', PRDX4 C 1 2 4 S . R - 5 ' - C C A A A A G C G A T A -ATTTCAGTTGGAGACACAAATGTGAAAT-3', PRDX4\_C245S\_F-5'-GGAGAAGTCTCCCCT-GCTGGCTGGAA-3', PRDX4 C245S. R-5'-TTC-CAGCCAGCAGGGGAGACTTCTCC-3', PRDX5\_C47S\_F-5'-TTCACCCCTGGATCTTCCAAG-ACACACCTG-3', PRDX5 C47S. R-5'-CAGGTGT-GTCTTGGAAGATCCAGGGGTGAA-3', PRDX5 C151S\_F-5'-CAGGCCTCACCTCCAGCCTGGCA-3', PRDX5\_C151S.\_R-5'-TGCCAGGCTGGAGGTGAGG-CCTG-3'. Gateway technology (Life Technologies) was used to create N-terminally tagged Flag-HIS-PRDX1-3 and 5, and C-terminally tagged PRDX4-Flag-HIS constructs (backbone pCDNA3). Furthermore, 30% H<sub>2</sub>O<sub>2</sub> (Sigma 31642) was freshly diluted to a stock of 10 or 100 mM in H<sub>2</sub>O for every experiment. Unless stated otherwise, H2O2 treatments were 25 µM (PRDX2) and 100 µM (other isoforms) for 2 min.

# **Co-immunoprecipitation experiments and Western** blotting

For the identification of cysteine-dependent interactors the After treatment with  $H_2O_2$ , cells were scraped in 100 mM lysate of  $4 \times 20$  cm dishes were used for each pulldown on N-ethylmaleimide (NEM, Sigma E3876) in PBS for 5 min 75 µL of Flag-M2 beads similar to the immunoprecipitation at 37 °C to trap free thiols in their in vivo redox state during experiments described above. All immunoprecipitations were sample preparation and collected by centrifugation at 1200 performed using three biological replicates. After washing, rpm for 3 min. Cells were lysed using a buffer containing 50 beads were resuspended with 8 M urea in 1 M ammonium mM Tris-HCl pH 7.5, 1% TX100, 1.5 mM MgCl<sub>2</sub>, 5 mM bicarbonate (ABC), reduced and alkylated in 10 mM TCEP EDTA, 100 mM NaCl, NaF, Leupeptin and Aprotinin. and 40 mM chloroacetamide (CAA) for 30 min at RT. After Furthermore, 100 mM iodoacetamide was added to the lysis fourfold dilution with 1 M ABC, proteins were digested overbuffer to prevent post-lysis cysteine oxidation and to inacnight on-bead with 250 ng Trypsin/LysC (Promega V5071) tivate disulfide reducing enzymes. After centrifugation at per sample at 37 °C. Samples were cleaned up with in-house-14,000 rpm for 10 min, 5% of the supernatant was kept as made C18 stagetips. input and the remaining supernatant was used for immunoprecipitation with anti-Flag-M2 affinity gel (Sigma A222). Mass Spectrometry After a 2 h incubation, immunoprecipitates were washed 4 Mass spectrometry was performed as previously described

# Antibodies

times with lysis buffer containing 1 M NaCl and samples [30]. Peptides were separated on a 30-cm pico-tip column (75 were boiled for 5 min in sample buffer with or without the  $\mu$ m ID, New Objective) and were packed in-house with 3  $\mu$ m reducing agent β-mercaptoethanol. Samples were separated on aquapur gold C-18 material (Dr. Maisch) using a 140-min graa 10% polyacrylamide gel and transferred to immobilon-FL dient (7-80% ACN 0.1% FA), delivered by an easy-nLC 1000 membranes before staining. (LC120, Thermo Scientific), and electro-sprayed directly into an Orbitrap Fusion Tribrid Mass Spectrometer (Thermo Scientific). Raw files were analyzed with MaxQuant software The following antibodies were used in this study: anti-Flag version 1.5.2.8 with oxidation of methionine, alkylation with antibody and anti-Flag-M2 beads (Sigma F3165 and A222, N-ethylmaleimide and carbamidomethylation set as variable respectively), monoclonal anti-HA antibody (12CA5) was modifications. The human protein database of UniProt was searched with both the peptide as well as the protein false prepared using hybridoma cell lines, anti-tubulin (Merck Millipore CP06), anti-peroxiredoxin-SO<sub>3</sub> (Abcam ab16830), discovery rate set to 1%. The mass spectrometry proteomics anti-peroxiredoxin 1 (Abcam ab15571), anti-peroxiredoxin 2 data were uploaded into the ProteomeXchange Consortium (Abcam ab15572), anti-peroxiredoxin 3 (Abcam ab73349), via the PRIDE [31] partner repository with the dataset identifier PXD024114. Downstream analysis was done using R anti-peroxiredoxin 4 (Abcam ab59542) and anti-peroxiredoxin 5 (Abcam ab16944). Detection of 2 fluorescent secondary version 4.0.2. antibodies was done simultaneously using the LI-COR Biosciences Odyssey Infrared Imaging System or the Amersham Data Filtering and proDA Modeling Typhoon NIR Plus Biomolecular Imager (GE Healthcare), The code used was uploaded to GitHub at https://github. detection of HRP-coupled secondary antibodies was percom/loesoe/peroxiredoxin. In short, LFQ data from the formed using the FUJIFILM Luminescent Image Analyzer MaxQuant proteinGroups file and corresponding protein LAS-3000. information was used. Proteins were filtered for reverse hits and standard contaminants. Next, we selected proteins that were identified with three or more unique peptides and were

# Mass Spectrometry Sample Preparation

measured in at least one sample in two or more replicates. Data was log<sub>2</sub>-transformed and normalized using quantile normalization to simultaneously correct for overall protein content and immunoprecipitation (IP) efficiency. ProDA model fitting was performed using the number of proteins in the data as the number of subsamples. To test for differential protein abundance, a proDa model was fit to compare WT against mutant for each peroxiredoxin.

## Threshold cutoff calculation

To determine the cutoff for out data, we fitted a proDA model for wild-type and mutant peroxiredoxin, without considering the isoform. Next, we repeated this 100 times, but instead with randomized labels. The difference at which 5% of the randomized data was included was determined as the cutoff.

### **Known Redox-Sensitive Proteins**

A reference proteome containing 75,071 human entries from Uniprot tagged with the keyword reference proteome was downloaded from https://www.uniprot.org/help/reference\_proteome. Proteins that were previously identified in a screen for redox-sensitive proteins in human cell lines (293T and HCT116) were taken from [17].

### Upset plot and Venn diagrams

To visualize the isoform-specific set of intersections we used the UpsetR package [32]. Venn diagrams were created using the Venn version 1.9 package and colored manually.

## **Localization Analysis**

We analyzed the localization of isoform-specific interactors using the neighborhood/compartment predictions data for A431 cells from https://www.subcellbarcode.org [18]. Peroxiredoxin interactors with the highest fold change (>10-fold) were matched with their neighborhood data and their fold enrichment were calculated compared to the cell line data. Main localization of peroxiredoxin isoforms from this tool are as follows: PRDX1 PRDX2 and PRDX5, cytosol; PRDX3, mitochondria; PRDX4, unclassified.

#### Sequence Similarity

PRDX sequences were loaded as a FASTA file. Pairwise alignment was calculated using EMBOSS needle (https://www. ebi.ac.uk/Tools/psa/emboss\_needl, accessed on 2 July 2016), which uses the Needleman-Wunsch global alignment algorithm to find the optimum global alignment. Similarity (the percentage of matches between the two aligned sequences) was plotted for each peroxiredoxin isoform pair.

### AA composition and motifs

The sequences for PRDX isoform-specific interactors were retrieved from Uniprot (https://www.uniprot.org/uploadlists, accessed on 2 January 2021). Sequences were loaded using the Biostrings package, sequences were shuffled 100 times as a background using the universalmotif package. Motifs were extracted of 9 amino acids centered around each cysteine. The amino acid composition was calculated for the isoform-specific sequences, the shuffled background and total protein using the alphabetFrequency function. Fold enrichment and Benjamini-Hochberg adjusted *p*-values were calculated per peroxiredoxin isoform using the amino acid composition of all other isoforms as a control. Motifs were analyzed using motif-x (rmotifx package) using the shuffled sequences as a background [24].





# Figure S1. Immunoprecipitated Flag-PRDX Western blots. HEK293T cells expressing Flag-tagged peroxiredoxin isoforms were treated for 2 min with H2O2 and analyzed by immunoblotting cipitation; WB: Western blotting; input: cleared cell lysate as used for immunoprecipitation, reduced sample.



#### Figure S2

Ridge plot showing the density distribution centered around 0 of the mean log ratio of wild-type and C<sub>nn</sub>S-peroxiredoxin, corresponding to Figures 2B-F (ignoring the missing values). Most PRDX isoforms show a higher density peak corresponding to WT-specific interactors (mean log ratio>0) than the peak for C<sub>np</sub>S-specific interactors (mean log ratio <0), indicating that most of the interactors are indeed cysteine-dependent binders and not false positives.

# SUPPLEMENTARY FIGURES AND LEGENDS



dimer monomer dimer monomer PRDX-SO, Flag-PRDX1



under parallel reducing and non-reducing conditions. H2O2 concentrations were as indicated. The concentrations of H2O2 applied were optimized for each PRDX isoform to yield considerable disulfide-dependent homodimerization without inducing detectable hyperoxidation (PRDX-SO3). Immunoblots shown in this figure are representative of multiple experiments ( $n \ge 3$ ). IP: immunopre-



mean log ratio (WT/CeeS)



### Figure S3. Log<sup>2</sup> fold change distribution of data presented in Figure 2G (blue curve).

Data was randomized a hundred times between wild-type and CPRS mutant peroxiredoxin data and the log2 fold change was recalculated (grey curve). With the randomized data, we calculate that at a  $\log_2$  fold change threshold of >0.401, 5% of the randomized data is included (left dashed line). A more stringent cutoff of 1 includes 0.02% of randomized data (FDR; right dashed line).



### Figure S4

Bar chart depicting the number cysteine-dependent binders (as defined in Figures 2 and 4) in the set of PRDX isoform-specific binders as depicted in Figure 3J. Dark colored bars indicate proteins interacting with WT PRDXs; light bars indicate proteins interacting with PRDX  $C_{pR}S$  mutants.



### Figure S5

Heatmaps of the top 100 (based on adjusted p-value) peroxiredoxin isoform-specific binders, specified for each isoform relative to the other 4 isoforms. Heatmaps were created using the pheatmap package in R, with row scaling and Ward D2 correlation clustering.

# SUPPLEMENTARY TABLES

For an online version of the tables, please follow <u>https://doi.</u> <u>org/10.3390/antiox10040627#suppl\_id</u>, or see the final pages of this file (pdf only)

Table S1: Cysteine-dependent interactors (wild-type).

 Table S2: Isoform-specific cysteine-dependent interactors.

Table S3: Peroxidatic cysteine-dependent interactors (C<sub>R</sub>S).

**Table S4**: All cysteine-dependent interactors (wild-type and  $C_{R}S$ ).

Table S5: Amino acid motifs in  $C_p$ -SOH-mediated interactors.

**Table S6**: Amino acid motifs in  $C_p$ -S-S- $C_p$ -mediated interactors.

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# SUPPLEMENTARY TABLES

### Table S1: cysteine-dependent interactors (wild-type)

uniprot ID	gene	protein	log ratio	p-value
PRDX1 cysteine-depen	dent interactors		Ť	
P15924	DSP	Desmoplakin	4,9	< 0.001
Q15149	PLEC	Plectin	4,8	< 0.001
Q15185	PTGES3	Prostaglandin E synthase 3	4,8	< 0.001
P08559	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	4,5	< 0.001
P62273	RPS29	40S ribosomal protein S29	4,4	< 0.001
A0A024R4E5	HDLBP	High density lipoprotein binding protein	4,4	< 0.001
Q9Y2V2	CARHSP1	Calcium-regulated heat-stable protein 1	4,4	< 0.001
P55084	HADHB	Trifunctional enzyme subunit beta, mitochondrial	4,4	< 0.001
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	4,3	< 0.001
P24666	ACP1	Low molecular weight phosphotyrosine protein phosphatase	4,3	< 0.001
Q9GZT3	SLIRP	SRA stem-loop-interacting RNA-binding protein, mitochondrial	4,1	< 0.001
Q15654	TRIP6	Thyroid receptor-interacting protein 6	4	< 0.001
E7EX90	DCTN1	Dynactin subunit 1	4	< 0.001
Q01081	U2AF1	Splicing factor U2AF 35 kDa subunit	4	0,001
Q9BY32	ITPA	Inosine triphosphate pyrophosphatase	3,9	< 0.001
Q14008	CKAP5	Cytoskeleton-associated protein 5	3,8	< 0.001
Q9P2J5	LARS1	LeucinetRNA ligase, cytoplasmic	3,8	< 0.001
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	3,8	< 0.001
Q16513	PKN2	Serine/threonine-protein kinase N2	3,7	< 0.001
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	3,7	< 0.001
A0A087WZ13	RAVER1	Ribonucleoprotein PTB-binding 1	3,7	< 0.001
P39023	RPL3	60S ribosomal protein L3	3,7	< 0.001
P13667	PDIA4	Protein disulfide-isomerase A4	3,6	< 0.001
P61011	SRP54	Signal recognition particle 54 kDa protein	3,6	< 0.001
C9JZR2	CTNND1	Catenin delta-1	3,6	< 0.001
Q53H12	AGK	Acylglycerol kinase, mitochondrial	3,6	< 0.001
P46940	IQGAP1	Ras GTPase-activating-like protein IQGAP1	3,5	< 0.001
E3W994	CLASP2	CLIP-associating protein 2	3,5	< 0.001
P62316	SNRPD2	Small nuclear ribonucleoprotein Sm D2	3,5	< 0.001
P53621	COPA	Coatomer subunit alpha	3,5	< 0.001
Q99615	DNAJC7	DnaJ homolog subfamily C member 7	3,5	< 0.001
P62829	RPL23	60S ribosomal protein L23	3,5	< 0.001
Q9UQE7	SMC3	Structural maintenance of chromosomes protein 3	3,4	< 0.001
Q9H0C8	ILKAP	Integrin-linked kinase-associated serine/threonine phosphatase 2C	3,4	< 0.001
Q14684	RRP1B	Ribosomal RNA processing protein 1 homolog B	3,4	< 0.001
Q7Z6Z7	HUWE1	E3 ubiquitin-protein ligase HUWE1	3,4	< 0.001
P31689	DNAJA1	DnaJ homolog subfamily A member 1	3,4	< 0.001
Q7L2E3	DHX30	ATP-dependent RNA helicase DHX30	3,3	< 0.001
E7EVH7	E7EVH7	Kinesin light chain	3,3	< 0.001
Q14204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	3,3	< 0.001
Q9ULV4	CORO1C	Coronin-1C	3,3	< 0.001
P63165	SUMO1	Small ubiquitin-related modifier 1	3,3	< 0.001
P49790	NUP153	Nuclear pore complex protein Nup153	3,3	< 0.001
P15170	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	3,3	< 0.001
P23258	TUBG1	Tubulin gamma-1 chain	3,3	0,001
Q92879	CELF1	CUGBP Elav-like family member 1	3,2	< 0.001
Q14683	SMC1A	Structural maintenance of chromosomes protein 1A	3,2	< 0.001
P55809	OXCT1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	3,2	< 0.001
075531	BANF1	Barrier-to-autointegration factor	3,2	0,001
O14964	HGS	Hepatocyte growth factor-regulated tyrosine kinase substrate	3,2	0,001
Q9NY93	DDX56	Probable ATP-dependent RNA helicase DDX56	3,2	0,001
O94760	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	3,2	0,002
Q08211	DHX9	ATP-dependent RNA helicase A	3,2	0,03
Q9C0C2	TNKS1BP1	182 kDa tankyrase-1-binding protein	3,1	< 0.001
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	3,1	< 0.001
H3BPE1	MACF1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	3,1	< 0.001
Q9BQG0	MYBBP1A	Myb-binding protein 1A	3,1	< 0.001
Q7Z406	MYH14	Myosin-14	3,1	< 0.001
P22307	SCP2	Non-specific lipid-transfer protein	3,1	< 0.001
P62266	RPS23	40S ribosomal protein S23	3,1	< 0.001
Q5SW79	CEP170	Centrosomal protein of 170 kDa	3,1	< 0.001
Q6P1L8	MRPL14	39S ribosomal protein L14, mitochondrial	3,1	< 0.001
P55735	SEC13	Protein SEC13 homolog	3,1	0,001
P21964	COMT	Catechol O-methyltransferase	3,1	0,001
Q99460	PSMD1	26S proteasome non-ATPase regulatory subunit 1	3,1	0,001

P11387	TOP1	DNA topoisomerase 1	3,1	0,002
Q5JTH9	RRP12	RRP12-like protein	3	< 0.001
Q96I25	RBM17	Splicing factor 45	3	< 0.001
E7ESP9	NEFM	160 kDa neurofilament protein	3	< 0.001
P62851	RPS25	40S ribosomal protein S25	3	< 0.001
013561	DCTN2	Dynactin subunit 2	3	< 0.001
O9UHI6	DDX20	Probable ATP-dependent R NA helicase DDX20	3	< 0.001
O9UNE7	STUB1	F3 ubiquitin-protein ligase CHIP	3	<0.001
00(12)	DTDN11	Turceine protein phoenhatese per recentor tupe 11	3	<0.001
Q06124	FIFNII	Tyrosine-protein phosphatase non-receptor type 11	3	<0.001
P19525	EIFZAK2	Interferon-induced, double-stranded KINA-activated protein kinase	3	0,001
Q96KB5	PBK	Lymphokine-activated killer 1-cell-originated protein kinase	3	0,004
Q9HD26	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein	3	0,005
A0A0A0MRT6	ABI1	Abl interactor 1	2,9	< 0.001
Q8N9T8	KRI1	Protein KRI1 homolog	2,9	< 0.001
Q8N1F7	NUP93	Nuclear pore complex protein Nup93	2,9	< 0.001
E9PD53	SMC4	Structural maintenance of chromosomes protein	2,9	< 0.001
P46060	RANGAP1	Ran GTPase-activating protein 1	2,9	< 0.001
Q99961	SH3GL1	Endophilin-A2	2,9	< 0.001
Q96N67	DOCK7	Dedicator of cytokinesis protein 7	2,9	< 0.001
O94979	SEC31A	Protein transport protein Sec31A	2,9	< 0.001
09H2G2	SLK	STE20-like serine/threonine-protein kinase	2.9	< 0.001
09H0B6	KLC2	Kinesin light chain 2	2.9	<0.001
0911654	MAD3K7	Mitogen activated protein kinase kinase kinase	2.9	<0.001
D1/17/	MIT JK/	Manage activated protein kinase kinase	2,9	0.001
P141/4	MIF	Macrophage migration inhibitory ractor	2,9	0,001
P2//08	CAD	CAD protein Includes: Glutamine-dependent carbamoyl-phosphate synthase	2,9	0,004
P68133	ACTA1	Actin, alpha skeletal muscle	2,9	0,015
Q7L1Q6	BZW1	Basic leucine zipper and W2 domain-containing protein 1	2,8	<0.001
I3L2Z5	MAZ	Myc-associated zinc finger protein	2,8	< 0.001
Q5JRX3	PITRM1	Presequence protease, mitochondrial	2,8	< 0.001
O43837	IDH3B	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	2,8	< 0.001
P63272	SUPT4H1	Transcription elongation factor SPT4	2,8	< 0.001
P57740	NUP107	Nuclear pore complex protein Nup107	2,8	< 0.001
P08708	RPS17	40S ribosomal protein S17	2,8	< 0.001
Q9UG63	ABCF2	ATP-binding cassette sub-family F member 2	2,8	< 0.001
P48444	ARCN1	Coatomer subunit delta	2.8	< 0.001
P41252	LARS1	IsoleucinetRNA ligase, cytoplasmic	28	< 0.001
P36915	GNI 1	Guanine nucleotide binding protein-like 1	2.8	<0.001
O9UHB6	LIMA1	LIM domain and actin binding protein 1	2,0	<0.001
AGA 1W2DDV5	SMN2	Survival motor pouron protein	2,0	0.001
AUATW2PKV5	5MIN2		2,8	0,001
Q9BV44	THUMPD3	1 HUMP domain-containing protein 3	2,8	0,002
075874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	2,8	0,002
O95801	TTC4	Tetratricopeptide repeat protein 4	2,8	0,004
P43897	TSFM	Elongation factor Ts, mitochondrial	2,8	0,004
Q13813	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	2,8	0,005
Q5VYK3	ECPAS	Proteasome adapter and scaffold protein ECM29	2,8	0,005
Q9NR30	DDX21	Nucleolar RNA helicase 2	2,8	0,009
Q02241	KIF23	Kinesin-like protein KIF23	2,7	< 0.001
P61163	ACTR1A	Alpha-centractin	2,7	< 0.001
Q8WVM8	SCFD1	Sec1 family domain-containing protein 1	2,7	< 0.001
P20042	EIF2S2	Eukarvotic translation initiation factor 2 subunit 2	2.7	< 0.001
P83731	R PL 24	60S ribosomal protein L.24	27	< 0.001
A0A2R8YDO9	SUCLA2	SuccinateCoA ligase [ADP-forming] subunit beta mitochondrial	2.7	<0.001
D25/59	NUID214	Nuclear para complex protein Nup216	2,7	<0.001
09/11/9	INUF214		2,7	<0.001
Q86 V48	LUZPI		2,/	<0.001
060493	SNX3	Sorting nexin-3	2,/	0,001
Q15717	ELAVL1	ELAV-like protein 1	2,7	0,003
P23919	DTYMK	Thymidylate kinase	2,7	0,003
P46013	MKI67	Proliferation marker protein Ki-67	2,7	0,003
Q92974	ARHGEF2	Rho guanine nucleotide exchange factor 2	2,7	0,003
Q15075	EEA1	Early endosome antigen 1	2,7	0,007
P06132	UROD	Uroporphyrinogen decarboxylase	2,7	0,012
Q14152	EIF3A	Eukaryotic translation initiation factor 3 subunit A	2,6	< 0.001
O6P2E9	EDC4	Enhancer of mRNA-decapping protein 4	2,6	< 0.001
075369	FLNB	Filamin-B	26	< 0.001
096R P9	GFM1	Flongation factor G mitochondrial	2,0	<0.001
X/01(1)	DDI IM7	DD7 and LIM domain protain 7	2,0	<0.001
OONID 12	PDLIM/	FDL and LIM domain protein /	2,6	<0.001
Q9NR12	00.072	D CI :	2.4	< 0.001
Q9NR12 A0A3B3IRP5	CDC73	Parafibromin	2,6	
Q9NR12 A0A3B3IRP5 P78344	CDC73 EIF4G2	Parafibromin Eukaryotic translation initiation factor 4 gamma 2	2,6	< 0.001
Q9NR12 A0A3B3IRP5 P78344 F8WB06	CDC73 EIF4G2 ATXN2	Parafibromin Eukaryotic translation initiation factor 4 gamma 2 Ataxin-2	2,6 2,6 2,6	<0.001 <0.001
Q9NR12 A0A3B3IRP5 P78344 F8WB06 P49207	CDC73 EIF4G2 ATXN2 RPL34	Parafibromin Eukaryotic translation initiation factor 4 gamma 2 Ataxin-2 60S ribosomal protein L34	2,6 2,6 2,6 2,6	<0.001 <0.001 <0.001
Q9NR12 A0A3B3IRP5 P78344 F8WB06 P49207 P48634	CDC73 EIF4G2 ATXN2 RPL34 PRRC2A	Parafibromin Eukaryotic translation initiation factor 4 gamma 2 Ataxin-2 60S ribosomal protein L34 Protein PRRC2A	2,6 2,6 2,6 2,6 2,6 2,6	<0.001 <0.001 <0.001 <0.001
Q9NR12 A0A3B3IRP5 P78344 F8WB06 P49207 P48634 P42704	CDC73 EIF4G2 ATXN2 RPL34 PRRC2A LRPPRC	Parafibromin Eukaryotic translation initiation factor 4 gamma 2 Ataxin-2 60S ribosomal protein L34 Protein PRRC2A Leucine-rich PPR motif-containing protein, mitochondrial	2,6 2,6 2,6 2,6 2,6 2,6 2,6	<0.001 <0.001 <0.001 <0.001 0,001
Q9NR12 A0A3B3IRP5 P78344 F8WB06 P49207 P48634 P42704 P42704 P33991	CDC73 EIF4G2 ATXN2 RPL34 PRRC2A LRPPRC MCM4	Parafibromin Eukaryotic translation initiation factor 4 gamma 2 Ataxin-2 60S ribosomal protein L34 Protein PRRC2A Leucine-rich PPR motif-containing protein, mitochondrial DNA replication licensing factor MCM4	2,6 2,6 2,6 2,6 2,6 2,6 2,6 2,6 2,6	<0.001 <0.001 <0.001 <0.001 0,001 0,001

E7ETK0	R PS24	40S ribosomal protein \$24	2.6	0.003
060762	DPM1	Dalichal-phoenbare mannasyltransferase subunit 1	2,6	0.003
D29144	TDD2	Trinantidul nantidasa 2	2,0	0.003
P27694	R PA 1	Replication protein A 70 kDa DNA-binding subunit	2,0	0.003
092(15	LADD/D	Le related protein 6 P	2,6	0,003
Q92615	CVC1		2,6	0,004
P1380/	GISI	Giveogen [starch] synthase, muscle	2,6	0,004
P51452	DUSP3	Dual specificity protein phosphatase 3	2,6	0,004
Q6P587	FAHD1	Acylpyruvase FAHD1, mitochondrial	2,6	0,005
O76021	RSL1D1	Ribosomal L1 domain-containing protein 1	2,6	0,008
Q9H840	GEMIN7	Gem-associated protein 7	2,6	0,01
O00425	IGF2BP3	Insulin-like growth factor 2 mRNA-binding protein 3	2,5	< 0.001
F8W8I6	TIA1	Nucleolysin TIA-1 isoform p40	2,5	< 0.001
A0A087WTZ5	UBXN1	UBX domain-containing protein 1	2,5	< 0.001
P04637	TP53	Cellular tumor antigen p53	2,5	< 0.001
P61160	ACTR2	Actin-related protein 2	2,5	< 0.001
Q9UHV9	PFDN2	Prefoldin subunit 2	2,5	< 0.001
Q8IWZ3	ANKHD1	Ankyrin repeat and KH domain-containing protein 1	2,5	< 0.001
P00568	AK1	Adenylate kinase isoenzyme 1	2,5	< 0.001
A0A087WVM4	MTHFD1L	Formyltetrahydrofolate synthetase	2,5	< 0.001
M0R0F0	RPS5	40S ribosomal protein S5	2,5	< 0.001
Q15042	R A B3GAP1	Rab3 GTPase-activating protein catalytic subunit	2.5	< 0.001
P61081	UBE2M	NFDD8-conjugating enzyme Ubc12	2.5	<0.001
A0A0U1RRM6	FNAH	Protein enabled homolog	2,5	<0.001
D1((15	ATD2A2	Samon learning (and an learning maticulum calaium ATDess 2	2,5	<0.001
P16615	ATP2A2	Sarcopiasmic/endopiasmic reticulum calcium A I Pase 2	2,5	<0.001
P2/824	CANA	Cainexin	2,5	0,001
P/8316	NOP14	Nucleolar protein 14	2,5	0,002
P52788	SMS	Spermine synthase	2,5	0,003
P37108	SRP14	Signal recognition particle 14 kDa protein	2,5	0,003
Q6IAA8	LAMTOR1	Ragulator complex protein LAMTOR1	2,5	0,004
P08243	ASNS	Asparagine synthetase [glutamine-hydrolyzing]	2,5	0,005
A0A087X1A5	STAU1	Double-stranded RNA-binding protein Staufen homolog 1	2,5	0,005
Q8WUH6	TMEM263	Transmembrane protein 263	2,5	0,005
Q8TCG1	CIP2A	Protein CIP2A	2,5	0,006
Q9Y5Y2	NUBP2	Cytosolic Fe-S cluster assembly factor NUBP2	2,5	0,007
Q86U42	PABPN1	Polyadenylate-binding protein 2	2,5	0,007
015446	POLR1G	DNA-directed RNA polymerase I subunit RPA34	2,5	0,008
O8TAT6	NPLOC4	Nuclear protein localization protein 4 homolog	2,5	0.008
P07196	NEFL	Neurofilament light polypeptide	2.5	0.008
09Y5K6	CD2AP	CD2-associated protein	2.5	0.008
D19105	MVI 124	Myocin regulatory light chain 12 A	2,5	0.012
F17103	MILIZA NUDISS	Myosin regulatory light chain 12A	2,5	0,012
00(101	TUOCI		2,5	0,012
Q96J01	THUC3	THO complex subunit 3	2,5	0,015
Q14690	PDCD11	Protein RRP5 homolog	2,5	0,015
P61758	V BP1	Prefoldin subunit 3	2,5	0,015
P47897	QARS1	GlutaminetRNA ligase	2,4	< 0.001
095782	AP2A1	AP-2 complex subunit alpha-1	2,4	< 0.001
Q02252	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	2,4	< 0.001
Q14157	UBAP2L	Ubiquitin-associated protein 2-like	2,4	< 0.001
B1AK87	CAPZB	F-actin-capping protein subunit beta	2,4	< 0.001
Q14151	SAFB2	Scaffold attachment factor B2	2,4	< 0.001
B7Z7F3	RANBP3	Ran-binding protein 3	2,4	0,001
P19623	SRM	Spermidine synthase	2,4	0,001
Q9H9A6	LRRC40	Leucine-rich repeat-containing protein 40	2,4	0,001
Q96PK6	RBM14	RNA-binding protein 14	2,4	0,001
P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	2,4	0,002
P39748	FEN1	Flap endonuclease 1	2,4	0.003
P49841	GSK3B	Glycogen synthase kinase-3 beta	2.4	0.006
071UI9	H2AZ2	Histone H2 A V	2.4	0.006
A0A0C4DGX4	CUI 1	Cullin.1	2,1	0.007
ESH4E2	MYO1C	Unconventional myosin Ic	2,4	0.007
1 01 0L2	CTNNP1	Crearlie have 1	2,4	0,007
AUA2K81804	CINNBI	Catenin beta-1	2,4	0,008
Q07021	CLOBB	r robable LKNA pseudouridine syntnase 1	2,4	0,008
<u>Q0/021</u>	CIQBP	Comprement component I Q subcomponent-binding protein, mitochondrial	2,4	0,008
Q16698	DECK1	2,4-dienoyi-CoA reductase, mitochondrial	2,4	0,009
P40939	HADHA	I ritunctional enzyme subunit alpha, mitochondrial	2,4	0,009
O14497	ARID1A	AT-rich interactive domain-containing protein 1A	2,4	0,01
G3V1C3	API5	Apoptosis inhibitor 5	2,4	0,011
O95373	IPO7	Importin-7	2,4	0,011
A0A3B3ISG5	IDE	Insulin-degrading enzyme	2,4	0,012
Q16204	CCDC6	Coiled-coil domain-containing protein 6	2,4	0,024
Q8N1G4	LRRC47	Leucine-rich repeat-containing protein 47	2,3	< 0.001
O15160	POLR1C	DNA-directed RNA polymerases I and III subunit RPAC1	2,3	< 0.001
Q99543	DNAJC2	DnaJ homolog subfamily C member 2	2,3	< 0.001

P19367	HK1	Hexokinase-1	2,3	< 0.001
Q07666	KHDRBS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	2,3	< 0.001
Q9BSH4	TACO1	Translational activator of cytochrome c oxidase 1	2,3	< 0.001
Q5TDH0	DDI2	Protein DDI1 homolog 2	2,3	< 0.001
B5MCF9	PES1	Pescadillo homolog	2,3	< 0.001
P46776	RPL27A	60S ribosomal protein L27a	2,3	< 0.001
075569	PRKRA	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	2.3	< 0.001
P13861	PRKAR2A	c A MP-dependent protein kinase type II-alpha regulatory subunit	2,3	<0.001
0(V7WI	CICVE2	CB B10 interacting CVE matrix 2	2,5	<0.001
042447	DDUU	Dentified method in terror in the	2,5	<0.001
04344/	PPIH	Peptidyi-prolyl cis-trans isomerase H	2,3	0,001
P43686	PSMC4	265 proteasome regulatory subunit 6B	2,3	0,001
Q16352	INA	Alpha-internexin	2,3	0,001
Q96D71	REPS1	RalBP1-associated Eps domain-containing protein 1	2,3	0,002
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	2,3	0,002
Q99959	PKP2	Plakophilin-2	2,3	0,002
O00399	DCTN6	Dynactin subunit 6	2,3	0,002
Q9Y3I0	RTCB	RNA-splicing ligase RtcB homolog	2,3	0,002
Q9Y2L1	DIS3	Exosome complex exonuclease RRP44	2,3	0,004
075592	MYCBP2	E3 ubiquitin-protein ligase MYCBP2	2,3	0,004
P09110	ACAA1	3-ketoacyl-CoA thiolase, peroxisomal	2,3	0,008
P38432	COIL	Coilin	23	0.008
095747	OXSR 1	Serine/threonine-protein kinase OSR 1	2,3	0.008
OSHVIR	R A BI 3	R ab like protein 3	2,3	0,009
D22/2/	LIND NDA 2D1	I have been in a second s	2,5	0,007
P22626	HINKINPA2DI		2,5	0,01
P62318	SNRPD3	Small nuclear ribonucleoprotein Sm D3	2,3	0,011
Q9BXP5	SRRI	Serrate KNA effector molecule homolog	2,3	0,011
P50570	DNM2	Dynamin-2	2,3	0,013
Q9BQ39	DDX50	ATP-dependent RNA helicase DDX50	2,3	0,014
O43143	DHX15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	2,3	0,019
Q13573	SNW1	SNW domain-containing protein 1	2,3	0,039
Q5JTZ9	AARS2	AlaninetRNA ligase, mitochondrial	2,2	< 0.001
P27144	AK4	Adenylate kinase 4, mitochondrial	2,2	< 0.001
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	2,2	< 0.001
Q13509	TUBB3	Tubulin beta-3 chain	2,2	< 0.001
P54578	USP14	Ubiquitin carboxyl-terminal hydrolase 14	2,2	< 0.001
013136	PPFIA1	Liprin-alpha-1	2.2	< 0.001
P30520	ADSS2	Adenvlosuccinate synthetase isozyme 2	2,2	<0.001
099/97	DARK7	Parkingon disease protein 7	2,2	<0.001
D27802	TACLN2	Targaradia 2	2,2	<0.001
P3/802	TAGLINZ	Transgein-2	2,2	<0.001
Q/IRC2	LARP4	La-related protein 4	2,2	<0.001
P30153	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	2,2	<0.001
P51114	FXR1	Fragile X mental retardation syndrome-related protein 1	2,2	< 0.001
D6RBD7	EEF1E1	Eukaryotic translation elongation factor 1 epsilon-1	2,2	< 0.001
P08754	GNAI3	Guanine nucleotide-binding protein G(i) subunit alpha	2,2	0,001
Q02543	RPL18A	60S ribosomal protein L18a	2,2	0,001
Q9Y6Y8	SEC23IP	SEC23-interacting protein	2,2	0,001
P28838	LAP3	Cytosol aminopeptidase	2,2	0,001
Q9NSK0	KLC4	Kinesin light chain 4	2,2	0,001
M0OXL5	FBL	rRNA 2'-O-methyltransferase fibrillarin	2,2	0,002
P35268	RPL22	60S ribosomal protein L22	2,2	0,002
008123	NSUN2	R NA cytosine C(5)-methyltransferase NSUN2	2.2	0.002
013/6/	ROCK1	R ha accordiated protein kinase 1	2,2	0.004
LIOVDUR	DDDcC		2,2	0.01
002072	TNDO	Serine/Infeohine-protein phosphatase	2,2	0,01
Q92973	INPOI	Transportin-1	2,2	0,012
Q15084	PDIA6	Protein disulhde-isomerase A6	2,2	0,012
Q15750	TAB1	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	2,2	0,012
O43660	PLRG1	Pleiotropic regulator 1	2,2	0,013
Q01813	PFKP	ATP-dependent 6-phosphofructokinase, platelet type	2,2	0,015
Q9BUQ8	DDX23	Probable ATP-dependent RNA helicase DDX23	2,2	0,016
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	2,2	0,019
P82921	MRPS21	28S ribosomal protein S21, mitochondrial	2,2	0,02
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	2,2	0,024
P31323	PRKAR2B	cAMP-dependent protein kinase type II-beta regulatory subunit	2,2	0,05
O52LI0	FAM98B	Protein FAM98B	2 1	<0.001
A0A1C7CVY9	DPYSI 2	Dihydronyrimidinase-related protein 2	2,1	<0.001
01/2/7	OTTN	See substrate contraction	2,1	<0.001
V1424/	CIIN	JIL TO LEAST AND A STATE OF TAXABLE STAT	2,1	<0.001
P50502	\$113	Hsc/U-interacting protein	2,1	< 0.001
P55795	HNRNPH2	Heterogeneous nuclear ribonucleoprotein H2	2,1	< 0.001
Q8WXF1	PSPC1	Paraspeckle component 1	2,1	< 0.001
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	2,1	< 0.001
Q9BQ69	MACROD1	ADP-ribose glycohydrolase MACROD1	2,1	< 0.001
B4DDF4	CNN2	Calponin	2,1	0,001
	GTF3C5	General transcription factor 3C polypeptide 5	2.1	0,001
Q5T7U1			-,-	

P46459	NSF	Vesicle-fusing ATPase	2.1	0.001
07(002	CLP V2	Clusterodovie 2	2,1	0,001
404040MP M9	NOLCI	Nucleolar and soiled body phosphonrotein 1	2,1	0,001
AUAUAUMICM19	ADIA		2,1	0,003
P00519	ABLI	Tyrosine-protein kinase ABLI	2,1	0,003
P49959	MRE11	Double-strand break repair protein MRE11	2,1	0,004
P51570	GALK1	Galactokinase	2,1	0,004
P46777	RPL5	60S ribosomal protein L5	2,1	0,005
P11388	TOP2A	DNA topoisomerase 2-alpha	2,1	0,009
P62906	RPL10A	60S ribosomal protein L10a	2,1	0,012
Q9NXH9	TRMT1	tRNA	2,1	0,012
Q9BXJ9	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	2,1	0,017
B4DLN1	B4DLN1	cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier	2,1	0,017
O9BT25	HAUS8	HAUS augmin-like complex subunit 8	2,1	0,018
014654	IR S4	Insulin recentor substrate 4	2.1	0.021
042707	ACTN		2,1	0,021
D18021	ACTIN4	Alpha-acthin-4	2,1	0,026
P18031	PIPNI	Tyrosine-protein phosphatase non-receptor type 1	2,1	0,02/
A0A3B3IUD2	MSTO1	Protein misato homolog 1	2,1	0,036
Q53H96	PYCR3	Pyrroline-5-carboxylate reductase 3	2,1	0,042
P19022	CDH2	Cadherin-2	2,1	0,043
Q8WWK9	CKAP2	Cytoskeleton-associated protein 2	2	< 0.001
Q9NZI8	IGF2BP1	Insulin-like growth factor 2 mRNA-binding protein 1	2	< 0.001
P25490	YY1	Transcriptional repressor protein YY1	2	< 0.001
P25325	MPST	3-mercaptopyruvate sulfurtransferase	2	< 0.001
096464	LRRC59	Jancing rich reneat containing protein 59	2	<0.001
QUINT	AUCTEI		2	0.001
Q8WYP5	AHCIFI	Protein ELYS	2	<0.001
X1W128	RPL10	60S ribosomal protein L10	2	< 0.001
E7EPN9	PRRC2C	Protein PRRC2C	2	< 0.001
P13804	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial	2	< 0.001
E7EVA0	MAP4	Microtubule-associated protein	2	< 0.001
P26640	VARS1	ValinetRNA ligase	2	< 0.001
P62280	RPS11	40S ribosomal protein S11	2	< 0.001
P31942	HNR NPH3	Heterogeneous nuclear ribonucleoprotein H3	2	< 0.001
01/126	DSG2	Demoglein 2	2	<0.001
Q14126	D302	Desinogieni-2	2	0.001
Q9H613	RPAP3	KNA polymerase II-associated protein 3	2	0,001
P46063	RECQL	A I P-dependent DNA helicase Q1	2	0,001
Q9UGI8	TES	Testin	2	0,001
A0A0G2JNZ2	SCRIB	Protein scribble homolog	2	0,001
P24534	EEF1B2	Elongation factor 1-beta	2	0,001
Q86UK7	ZNF598	E3 ubiquitin-protein ligase ZNF598	2	0,001
P62258	YWHAE	14-3-3 protein epsilon	2	0,001
075152	ZC3H11A	Zinc finger CCCH domain-containing protein 11A	2.	0.002
015305	PMM2	Dhoenhomannomutaes 2	2	0.002
01)30)	DNIAAE		2	0,002
Q86156	DINAAF5	Dynein assembly ractor 5, axonemai	2	0,002
P55265	ADAR	Double-stranded KNA-specific adenosine deaminase	2	0,002
J3QR09	RPL19	Ribosomal protein L19	2	0,002
Q99569	PKP4	Plakophilin-4	2	0,003
Q14258	TRIM25	E3 ubiquitin/ISG15 ligase TRIM25	2	0,004
A5YKK6	CNOT1	CCR4-NOT transcription complex subunit 1	2	0,008
J3KTA4	DDX5	DEAD box protein 5	2	0,01
Q9GZS1	POLR1E	DNA-directed RNA polymerase I subunit RPA49	2	0,012
P35579	MYH9	Myosin-9	2	0.018
014744	PR MT5	Protein arginine N-methyltransferase 5	2	0.018
	VAR S2	Turacine + B NA ligase mitachandrial	2	0.019
Q)1224	LIQOV2	TyrosinetKINA ligase, introctional fai	2	0,017
Q86V38	NDDG	Protein Hook nomolog 5	2	0,02
Q90GV2	NDRG3	Protein NDRG3	2	0,02
F5GWT4	WNK1	Non-specific serine/threonine protein kinase	2	0,02
D6R938	CAMK2D	Calcium/calmodulin-dependent protein kinase	2	0,021
Q16822	PCK2	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	2	0,021
Q9GZL7	WDR12	Ribosome biogenesis protein WDR12	2	0,023
Q8NCA5	FAM98A	Protein FAM98A	2	0,024
O92665	MRPS31	28S ribosomal protein S31, mitochondrial	2	0,025
A0A0A6YYL4	CORO7-PAM16	Coronin	2	0.025
013625	TP53BP2	Apoptosis-stimulating of p53 protein 2	2	0.026
09(401	EED MT2	Formitin family homeles 2	-	0.029
QJ6ACI	TERMIZ		2	0,028
Q15031	LARS2	Probable leucinetKNA ligase, mitochondrial	2	0,029
Q9BTY7	HGH1	Protein HGH1 homolog	2	0,032
Q5UIP0	RIF1	Telomere-associated protein RIF1	2	0,032
Q96DH6	MSI2	RNA-binding protein Musashi homolog 2	2	0,036
Q9HAV4	XPO5	Exportin-5	2	0,037
Q9BYG3	NIFK	MKI67 FHA domain-interacting nucleolar phosphoprotein	2	0,039
P15880	RPS2	40S ribosomal protein S2	1.9	< 0.001
P52948	NUP98	Nuclear pore complex protein Nup98-Nup96	1.9	< 0.001
404087WVW/	P DI 17	60\$ ribosomal protein I 17	-,-	<0.001
1101100/ W A1010	121 1.1/	ooo noosonaa protein E1/	1,/	~0.001

O43159	RRP8	Ribosomal RNA-processing protein 8	1,9	< 0.001
Q9Y2Z0	SUGT1	Protein SGT1 homolog	1,9	< 0.001
P43246	MSH2	DNA mismatch repair protein Msh2	1,9	< 0.001
Q16527	CSRP2	Cysteine and glycine-rich protein 2	1,9	< 0.001
P46939	UTRN	Utrophin	1,9	< 0.001
Q9BV20	MRI1	Methylthioribose-1-phosphate isomerase	1,9	< 0.001
Q7RTV0	PHF5A	PHD finger-like domain-containing protein 5A	1,9	< 0.001
Q8ND83	SLAIN1	SLAIN motif-containing protein 1	1,9	< 0.001
Q96MU7	YTHDC1	YTH domain-containing protein 1	1,9	0,001
P18615	NELFE	Negative elongation factor E	1,9	0,001
P52701	MSH6	DNA mismatch repair protein Msh6	1,9	0,001
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	1,9	0,001
O60684	KPNA6	Importin subunit alpha-7	1,9	0,002
Q8NCW5	NAXE	NAD(P)H-hydrate epimerase	1,9	0,003
Q9H0H5	RACGAP1	Rac GTPase-activating protein 1	1,9	0,005
A0A087X0K9	TJP1	Tight junction protein ZO-1	1,9	0,005
P50995	ANXA11	Annexin A11	1,9	0,005
Q9BYN8	MRPS26	28S ribosomal protein S26, mitochondrial	1,9	0,007
075436	VPS26A	Vacuolar protein sorting-associated protein 26A	1,9	0,007
Q12849	GRSF1	G-rich sequence factor 1	1,9	0,01
O14974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	1,9	0,011
Q9BVP2	GNL3	Guanine nucleotide-binding protein-like 3	1,9	0,011
Q9BQ67	GRWD1	Glutamate-rich WD repeat-containing protein 1	1,9	0,012
Q13144	EIF2B5	Translation initiation factor eIF-2B subunit epsilon	1,9	0,019
Q86WJ1	CHD1L	Chromodomain-helicase-DNA-binding protein 1-like	1,9	0,02
O60701	UGDH	UDP-glucose 6-dehydrogenase	1,9	0,022
Q9BR76	CORO1B	Coronin-1B	1,9	0,025
A0A087WY71	AP2M1	AP-2 complex subunit mu	1,9	0,028
Q9ULT8	HECTD1	E3 ubiquitin-protein ligase HECTD1	1,9	0,029
P50542	PEX5	Peroxisomal targeting signal 1 receptor	1,9	0,029
Q5TFE4	NT5DC1	5'-nucleotidase domain-containing protein 1	1,9	0,03
O00487	PSMD14	26S proteasome non-ATPase regulatory subunit 14	1,9	0,03
Q8WX93	PALLD	Palladin	1,9	0,031
Q13618	CUL3	Cullin-3	1,9	0,031
015020	SPTBN2	Spectrin beta chain, non-erythrocytic 2	1,9	0,032
000267	SUP15H	Transcription elongation factor SP15	1,9	0,033
Q9BVJ6	UTP14A	U3 small nucleolar RNA-associated protein 14 homolog A	1,9	0,034
095/85	WIZ	Protein Wiz	1,9	0,035
Q/LOY3	TRMTIOC	tKNA methyltransterase 10 homolog C	1,9	0,036
Q96FV9	THOCI	AD 2 A L A K L L A	1,9	0,038
01461/	AP3DI ZNIF(20	AP-3 complex subunit delta-1	1,9	0,038
Q14966	ZINF638		1,9	0,038
Q12948	ORICUI	Cluterrine rich metrin 1	1,9	0,04
Q2IAL8	DVNU B B1	Gutamine-rich protein 1	1,7	0,04
Q7NP9/	CTRD1	C terrial his dia matrix 1	1,9	0,041
Q13363	CIBPI ENIR NIR200	C-terminal-binding protein 1	1,9	0,048
D/02/9	CCT2	T complex protein 1 subunit comme	1,7	<0.001
P47368	LIRADO	I-complex protein I subunit gamma	1,8	<0.001
Q516F2 Q105(7	A D1P1	A D 1 complex subunit here 1	1,8	<0.001
D550(0	CSE1I	Exportin 2	1,0	<0.001
075792	R NASEH2A	R ibonuclease H2 subunit A	1,0	<0.001
097/90	TI N1	Talip 1	1,0	<0.001
D30084	FCHS1	Fraul CoA hydratese mitochondrial	1,8	<0.001
4041B0CWF2	STYRD1	Syntaxin hinding protein 1	1,0	<0.001
ADAIDUGWI2	MVOC	Unconvertional protein 1	1,0	<0.001
OCVN16	HSDI 2	Hudrovysteroid debydrogenose like protein 2	1,8	<0.001
016658	FSCN1	Faccin	1,0	<0.001
D/6778	P DI 21	60\$ ribocomal protein I 21	1,0	<0.001
013/51	FKRD5	Deptidul prolul cis trans icomerase EKBD5	1,8	<0.001
OSWIIM4	PDCD4IP	Programmed cell death 6 interacting protein	1,0	<0.001
4041W2DD75	TCFA1	Transcription elongation factor A protein 1	1,0	<0.001
095239	KIE4 A	Chromosome associated kinesin KIE4A	1,8	0.001
V/DI92	CUL /P	Cullin (P. isoform CP.A. s	1,0	0,001
O9BR X2	DEI O	Protein pelota homolog	1,0	0.001
043390	HNRNDR	Heterogeneous nuclear ribonucleoprotein P	1,0	0.001
01/1/4	TTTL 12	Tubulin, tyrocine ligase like protein 12	1,0	0.001
D41313	P DI 15	400 ribosomal protein 1 15	1,0	0.001
P12004	DCNA	Draliferating call pucker antigen	1,8	0.001
112004 U7C5E4	VD N1	5' 2' avarihannalaren 1	1,8	0.001
012195	CRV2	Channah an martain hannahar 2	1,8	0,001
Q13185	UBX3	Unromodox protein nomolog 5	1,8	0,001
00522(	WDK6	w D repeat-containing protein 6	1,8	0,001
095336	PGLS	6-phosphogluconolactonase	1,8	0,001

OONI7P2	EA M120A	Constitution acception for DDA P, common like protein 1	1.9	0.002
Q/NZB2	TAMIZUA	Constitutive coactivator of PTAK-gamma-nke protein 1	1,0	0,002
Q9BUF5	TUBB6	Tubulin beta-6 chain	1,8	0,002
P26373	RPL13	60S ribosomal protein L13	1,8	0,002
Q08752	PPID	Peptidyl-prolyl cis-trans isomerase D	1,8	0,002
Q9UPN7	PPP6R1	Serine/threonine-protein phosphatase 6 regulatory subunit 1	1,8	0,003
F8W0I6	NAP1L1	Nucleosome assembly protein 1-like 1	1.8	0.003
D2/2/8	LI2 A E2		1.9	0.003
F 20300	02AF2	Splitting factor 02AP 65 kDa subulint	1,0	0,003
Q9P0K7	RAI14	Ankycorbin	1,8	0,004
P52272	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	1,8	0,004
Q9UHB9	SRP68	Signal recognition particle subunit SR P68	1,8	0,005
O95861	BPNT1	3'(2'),5'-bisphosphate nucleotidase 1	1,8	0,005
013595	TRA2A	Transformer-2 protein homolog alpha	1.8	0.005
D12277	CKB	Creating kinges B type	1.8	0.006
0.001/000	DIDIOUT		1,0	0,000
Q916G9	DYNCILII	Cytoplasmic dynein I light intermediate chain I	1,8	0,006
Q9BSJ8	ESYT1	Extended synaptotagmin-1	1,8	0,006
P53597	SUCLG1	SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	1,8	0,006
O75131	CPNE3	Copine-3	1,8	0,006
P55010	EIF5	Eukarvotic translation initiation factor 5	1.8	0.006
D52732	KIE11	Kinesia like protein KIE11	1.8	0.007
015001	NGADDA		1,0	0,007
Q15021	NCAPD2	Condensin complex subunit 1	1,8	0,009
Q14161	GIT2	ARF GTPase-activating protein GIT2	1,8	0,009
Q8IY81	FTSJ3	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3	1,8	0,014
Q92616	GCN1	eIF-2-alpha kinase activator GCN1	1,8	0,015
095347	SMC2	Structural maintenance of chromosomes protein 2.	1.8	0.022
D25205	MCM2	DNA subjection lieuwing fester MCM2	1.9	0.026
F23203	MCM3	Divertepication neersing factor memory	1,0	0,028
P53582	METAPI	Methionine aminopeptidase 1	1,8	0,02/
P30154	PPP2R1B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	1,8	0,032
Q92878	RAD50	DNA repair protein RAD50	1,8	0,032
P54920	NAPA	Alpha-soluble NSF attachment protein	1,8	0,034
O92797	SYMPK	Symplekin	1.8	0,035
005048	CSTE1	Cleavage stimulation factor subunit 1	1.8	0.035
0(0822	DVC1	U/ACA -ik-and-anathin actor subunit 1	1,0	0,035
060832	DKCI	H/ACA hoonucleoprotein complex subunit DKC1	1,8	0,036
Q06210	GFPT1	Glutaminefructose-6-phosphate aminotransferase [isomerizing] 1	1,8	0,036
Q53EL6	PDCD4	Programmed cell death protein 4	1,8	0,043
Q9UQN3	CHMP2B	Charged multivesicular body protein 2b	1,8	0,043
E9PKP7	UBTF	Nucleolar transcription factor 1	1.8	0,046
P17252	PRKCA	Protein kinase Calnha type	1.8	0.049
117292 A0A087WIVEE	WTA1	Observations of a prior of the form of the form of the the	1,0	:0.001
AUAU8/ W 155	VIAI	Chromosome 6 open reading frame 55, isoform CKA_D	1,/	<0.001
Q9UPQ9	TNRC6B	I rinucleotide repeat-containing gene 6B protein	1,7	< 0.001
P49321	NASP	Nuclear autoantigenic sperm protein	1,7	< 0.001
Q8TD19	NEK9	Serine/threonine-protein kinase Nek9	1,7	< 0.001
Q86YP4	GATAD2A	Transcriptional repressor p66-alpha	1,7	< 0.001
09H7F9	C8orf33	UPF0488 protein C8orf33	17	< 0.001
D25221	CTNNA1		1.7	<0.001
F 33221	CINNAI	Catenin alpha-1	1,/	<0.001
Q9UQ80	PA2G4	Proliferation-associated protein 2G4	1,7	<0.001
Q7Z4H3	HDDC2	5'-deoxynucleotidase HDDC2	1,7	< 0.001
P60228	EIF3E	Eukaryotic translation initiation factor 3 subunit E	1,7	0,001
Q15003	NCAPH	Condensin complex subunit 2	1,7	0,001
P62333	PSMC6	26S proteasome regulatory subunit 10B	17	0.001
09V549	VTHDE2	200 proteusome regulator y subunit 102	137	0,001
Q/1)/1/	11111112	VTH domain containing family protein 2	17	0.001
P60660	) (VI (	YTH domain-containing family protein 2	1,7	0,001
	MYL6	YTH domain-containing family protein 2 Myosin light polypeptide 6	1,7 1,7	0,001 0,001
Q15785	MYL6 TOMM34	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34	1,7 1,7 1,7	0,001 0,001 0,001
Q15785 Q8N163	MYL6 TOMM34 CCAR2	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2	1,7 1,7 1,7 1,7	0,001 0,001 0,001 0,002
Q15785 Q8N163 C9JRJ5	MYL6 TOMM34 CCAR2 LIMD1	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1	1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,001 0,002 0,002
Q15785 Q8N163 C9JRJ5 Q96GD0	MYL6 TOMM34 CCAR2 LIMD1 PDXP	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase	1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,001 0,002 0,002 0,002
Q15785 Q8N163 C9JRJ5 Q96GD0 P33176	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesina, heavy chain	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,001 0,002 0,002 0,003 0,004
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           D25240	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Burli with Grang Courborning	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004
Q15785 Q8N163 C9JRJ5 Q96GD0 P33176 P35249	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004
Q15785 Q8N163 C9JRJ5 Q96GD0 P33176 P35249 Q9NYJ8	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004
Q15785 Q8N163 C9JRJ5 Q96GD0 P33176 P35249 Q9NYJ8 Q96F86	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004
Q15785 Q8N163 C9JRJ5 Q96GD0 P33176 P35249 Q9NYJ8 Q96F86 O60783	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006
Q15785 Q8N163 C9JRJ5 Q96GD0 P33176 P35249 Q9NYJ8 Q90YJ8 Q96F86 O60783 P56192	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           O9NK45	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial Methionine-rRNA ligase, cytoplasmic Sialie acid surthase	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9N455           Q9N455	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Dentidel proble is trans incomparse NIM A interacting 6	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,007
Q15785 Q8N163 C9JRJ5 Q96GD0 P33176 P35249 Q9NYJ8 Q96F86 O60783 P56192 Q9NR45 Q9Y237 Q90237	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 OUTCO	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,007 0,007
Q15785           Q8N163           C3JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NR45           Q9Y237           Q00610	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialie acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,007 0,007
Q15785           Q8N163           C9JRJ5           Q%6GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NK45           Q92377           Q00610           P62249	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC RPS16	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial Methionine-rtRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,007 0,007 0,007
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NŁ45           Q9Y237           Q00610           P62249           Q1KMD3	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC RPS16 HNRNPUL2	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007
Q15785           Q8N163           C3JRJ5           Q96GD0           P33176           P35249           Q96F86           O60783           P56192           Q9NR45           Q90010           P62249           QUKMD3           Q13283	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC RPS16 HNRNPUL2 G3BP1	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2 Ras GTPase-activating protein-binding protein 1	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,001
Q15785           Q8N163           C3JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NR45           Q9Y237           Q00610           P62249           Q1XBX3           P25685	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC RPS16 HNRNPUL2 G3BP1 DNAIB1	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2 Ras GTPase-activating protein-binding protein 1 Dnal homolog subfamily B member 1	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,001 0,007 0,003
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NR45           Q92377           Q00610           P62249           Q1KMD3           Q13283           P25685           O9H3111	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC CLTC RPS16 HNRNPUL2 G3BP1 DNAJB1 UNC45A	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2 Ras GTPase-activating protein-binding protein 1 Dnal homolog subfamily B member 1 Protein une 45 homolog A	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,007 0,
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NX45           Q9Y237           Q00610           P62249           Q1KMD3           Q13283           P25685           Q9H3U1           Q152%	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC RPS16 HNRNPUL2 G3BP1 DNAJB1 UNC45A	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2 Ras GTPase-activating protein-binding protein 1 Dnal homolog subfamily B member 1 Protein unc-45 homolog A	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,
Q15785           Q8N163           C3JRJ5           Q96GD0           P33176           P35249           Q90F86           O60783           P56192           Q9NR45           Q9K45           Q0KMD3           Q13283           P25685           Q9H3U1           O15226	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC RPS16 HNRNPUL2 G3BP1 DNAJB1 UNC45A NKRF	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial MethioninetRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2 Ras GTPase-activating protein-binding protein 1 Dnal homolog subfamily B member 1 Protein unc-45 homolog A NF-kappa-B-repressing factor	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,001 0,013 0,015 0,018
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NK45           Q9Y237           Q00610           P62249           QIKMD3           Q13283           P25685           Q9H3U1           O15226           P35659	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC RPS16 HNRNPUL2 G3BP1 DNAJB1 UNC45A NKRF DEK	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial Methionine-tRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2 Ras GTPase-activating protein-binding protein 1 DnaJ homolog subfamily B member 1 Protein unc-45 homolog A NF-kappa-B-repressing factor Protein DEK	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,013 0,015 0,018 0,018
Q15785           Q8N163           C9JRJ5           Q96GD0           P33176           P35249           Q9NYJ8           Q96F86           O60783           P56192           Q9NK45           Q9VX45           Q92437           Q00610           P62249           Q1KMD3           Q13283           P25685           Q9H3U1           O15226           P35659           Q8WTT2	MYL6 TOMM34 CCAR2 LIMD1 PDXP KIF5B RFC4 TAB2 EDC3 MRPS14 MARS1 NANS PIN4 CLTC CLTC RPS16 HNRNPUL2 G3BP1 DNAJB1 UNC45A NKRF DEK NOC3L	YTH domain-containing family protein 2 Myosin light polypeptide 6 Mitochondrial import receptor subunit TOM34 Cell cycle and apoptosis regulator protein 2 LIM domain-containing protein 1 Pyridoxal phosphate phosphatase Kinesin-1 heavy chain Replication factor C subunit 4 TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 Enhancer of mRNA-decapping protein 3 28S ribosomal protein S14, mitochondrial Methionine-rRNA ligase, cytoplasmic Sialic acid synthase Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 Clathrin heavy chain 1 40S ribosomal protein S16 Heterogeneous nuclear ribonucleoprotein U-like protein 2 Ras GTPase-activating protein-binding protein 1 Dnal homolog subfamily B member 1 Protein unc-45 homolog A NF-kappa-B-repressing factor Protein DEK Nucleolar complex protein 3 homolog	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,001 0,001 0,002 0,002 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,007 0,013 0,013 0,018 0,018 0,027

Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	1,7	0,032
O9H814	PHAX	Phosphorylated adapter RNA export protein	1,7	0,034
096646	DUS3I	rRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	17	0.037
Fabbau	HK2	Hevolvinose	1,7	0.04
OR (VD(	CAND1	Cullin according NEDD® dissociated protein 1	1,7	0.042
Q86 V P6	DUV20	ATD 1 - DNAL 1: DNX20	1,7	0,042
Q/Z4/8	DHX29	The full state of the second s	1,7	0,043
Q4KMP/	I BCIDIOB	I BCI domain family member 10B	1,7	0,044
P29558	RBMS1	RNA-binding motif, single-stranded-interacting protein 1	1,7	0,044
Q9H845	ACAD9	Complex I assembly factor ACAD9, mitochondrial	1,7	0,045
Q9HCD5	NCOA5	Nuclear receptor coactivator 5	1,7	0,048
P78347	GTF2I	General transcription factor II-I	1,7	0,049
Q5JSZ5	PRRC2B	Protein PRRC2B	1,6	< 0.001
P61158	ACTR3	Actin-related protein 3	1,6	< 0.001
Q9NSD9	FARSB	PhenylalaninetRNA ligase beta subunit	1,6	< 0.001
Q00796	SORD	Sorbitol dehydrogenase	1,6	< 0.001
Q14974	KPNB1	Importin subunit beta-1	1,6	< 0.001
P30566	ADSL	Adenvlosuccinate lyase	1,6	0,001
P38117	ETFB	Electron transfer flavoprotein subunit beta	1.6	0.001
K7FIL1	AP1M1	AP-1 complex subunit mu-1	16	0.001
D/2166	TMPO	Lamina accoriated polynentide 2 icoform alpha	1,0	0.001
015271	FIE2D	Eularization translation initiation factor 2 subunit D	1,0	0,001
D155/1	LIF3D MCM7	DNA surface in a factor MCN/7	1,6	0,001
P 33773	MCM/	COLUMN TECHNING TACTOR MCM/	1,6	0,001
P46//9	RPL28	605 ribosomal protein L28	1,6	0,002
O43264	ZW10	Centromere/kinetochore protein zw10 homolog	1,6	0,002
O00170	AIP	AH receptor-interacting protein	1,6	0,002
Q9ULX3	NOB1	RNA-binding protein NOB1	1,6	0,002
A0A0G2JH68	DIAPH1	Protein diaphanous homolog 1	1,6	0,002
M0R3C3	TECR	Very-long-chain enoyl-CoA reductase	1,6	0,002
Q9BW92	TARS2	ThreoninetRNA ligase, mitochondrial	1,6	0,003
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	1,6	0,004
Q15637	SF1	Splicing factor 1	1,6	0,004
P52294	KPNA1	Importin subunit alpha-5	1,6	0,004
O15424	SAFB	Scaffold attachment factor B1	1.6	0.005
A6NDG6	PGP	Glycerol-3-phosphate phosphatase	16	0.005
P60174	TPI1	Triosenhosphate isomerase	1,6	0.006
B4F1N1	AR MC6	Armadillo repeat containing protein 6	1,0	0.006
015/17	CNN2	Colorania 2	1,0	0,000
0011120	TR MT112	Calponin-3	1,6	0,008
Q90130	I KM I II2	Multirunctional methyltransferase subunit 1 KM112-like protein	1,6	0,008
Q91450	HBSIL	HBSI-like protein	1,6	0,009
P43490	NAMPI	Nicotinamide phosphoribosyltransferase	1,6	0,009
Q9BZE4	GTPBP4	Nucleolar GTP-binding protein 1	1,6	0,01
A0A087X2D5	MRPL45	39S ribosomal protein L45, mitochondrial	1,6	0,011
Q9H2P0	ADNP	Activity-dependent neuroprotector homeobox protein	1,6	0,011
Q13247	SRSF6	Serine/arginine-rich splicing factor 6	1,6	0,015
O00571	DDX3X	ATP-dependent RNA helicase DDX3X	1,6	0,015
Q9NW13	RBM28	RNA-binding protein 28	1,6	0,015
Q15813	TBCE	Tubulin-specific chaperone E	1,6	0,015
P19338	NCL	Nucleolin	1,6	0,017
O00231	PSMD11	26S proteasome non-ATPase regulatory subunit 11	1.6	0,018
O8NB90	SPATA5	ATPase family protein 2 homolog	1.6	0.021
F8W8R 3	POLD2	DNA polymerase delta subunit 2	1.6	0.024
043719	HTATSF1	HIV Tat-specific factor 1	1,6	0.026
09BV77	POL DIP3	Dolumerase delta interactino protein 3	1,6	0.027
Q)DI//	TOLUD	T-II interacting protein 5	1,6	0,02/
Q7110E2	DULLIF		1,6	0,044
0/5150	KNF40	E3 ubiquitin-protein ligase BKE1B	1,6	0,045
Q81WB7	WDFY1	WD repeat and FYVE domain-containing protein 1	1,6	0,046
P22102	GART	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase	1,5	< 0.001
Q15233	NONO	Non-POU domain-containing octamer-binding protein	1,5	< 0.001
Q14669	TRIP12	E3 ubiquitin-protein ligase TRIP12	1,5	< 0.001
P31948	STIP1	Stress-induced-phosphoprotein 1	1,5	< 0.001
P48643	CCT5	T-complex protein 1 subunit epsilon	1,5	< 0.001
P29692	EEF1D	Elongation factor 1-delta	1,5	< 0.001
Q02790	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	1,5	0,001
P61586	RHOA	Transforming protein RhoA	1,5	0,001
O43237	DYNC1LI2	Cytoplasmic dynein 1 light intermediate chain 2	1.5	0,001
P07814	EPR S1	Bifunctional glutamate/prolinetRNA ligase	1.5	0.001
095816	BAG2	BAG family molecular chaperone regulator 2	1,5	0.001
ONDIC	DCD1 A	mP.NA decomplex common 14	1,2	0,001
QUINPI6	DCPIA A CDCCD 1	Takan sanataina UBX Januta fan CUUT	1,5	0,002
Q9BZE9	ASPSCR1	1etner containing UBX domain for GLU14	1,5	0,003
P63241	EIF5A	Eukaryotic translation initiation factor 5A-1	1,5	0,004
P41240	CSK	Tyrosine-protein kinase CSK	1,5	0,005
Q8IWX8	CHERP	Calcium homeostasis endoplasmic reticulum protein	1,5	0,006
O75534	CSDE1	Cold shock domain-containing protein E1	1,5	0,006

095573	ACSL3	Long-chain-fatty-acidCoA ligase 3	1.5	0.006
013428	TCOF1	Treacle protein	15	0.006
D78371	CCT2	T complex protein 1 subunit bata	15	0.006
09NYZ3	GTSF1	G2 and Sphase-expressed protein 1	1,5	0.007
QUIVIC	EVOC	G2 and 5 phase-expressed protein 1	1,5	0,009
Q01110	LINDNDC	Execuse complex component a	1,5	0,009
D4D108	EXOSC2	Freerogeneous nuclear fibonucleoproteins C1/C2	1,5	0,009
QINQIS	EXUSC3	Exosome complex component RRP40	1,5	0,01
P50213	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	1,5	0,014
Q9UQ35	SRRM2	Serine/arginine repetitive matrix protein 2	1,5	0,016
O43395	PRPF3	U4/U6 small nuclear ribonucleoprotein Prp3	1,5	0,018
Q02878	RPL6	60S ribosomal protein L6	1,5	0,018
O00273	DFFA	DNA fragmentation factor subunit alpha	1,5	0,019
P63010	AP2B1	AP-2 complex subunit beta	1,5	0,023
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	1,5	0,023
Q9H2U1	DHX36	ATP-dependent DNA/RNA helicase DHX36	1,5	0,024
O43252	PAPSS1	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	1,5	0,028
P48507	GCLM	Glutamatecysteine ligase regulatory subunit	1.5	0.032
09HC35	FMI 4	Echinoderm microtubule-associated protein-like 4	1.4	<0.001
D(2)(33	CNBP	Cellular nucleic acid binding protain	1,4	<0.001
02000 000000	CINDI	Central nuclei acid-binding protein	1,4	<0.001
Qainux/	SPARI	Spartin	1,4	<0.001
P25786	PSMA1	Proteasome subunit alpha type-1	1,4	< 0.001
P40227	CC16A	I-complex protein 1 subunit zeta	1,4	<0.001
Q5JXI8	FHL1	Four and a half LIM domains protein 1	1,4	< 0.001
Q86TB9	PATL1	Protein PAT1 homolog 1	1,4	< 0.001
O94826	TOMM70	Mitochondrial import receptor subunit TOM70	1,4	0,001
Q99613	EIF3C	Eukaryotic translation initiation factor 3 subunit C	1,4	0,001
Q9UJU6	DBNL	Drebrin-like protein	1,4	0,001
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	1,4	0,002
Q9UNY4	TTF2	Transcription termination factor 2	1,4	0,002
P33240	CSTF2	Cleavage stimulation factor subunit 2	1.4	0.002
F9POV9	DCUN1D5	DCN1-like protein	1.4	0.003
D/2696	R BM34	R NA binding protein 3/	1,4	0.004
00111101	CHOP DC1	Custoine and histiding rich domain containing protein 1	1,4	0.004
	CHURDEI	Cysteine and nistidine-rich domain-containing protein 1	1,4	0,004
A0A3B3IR12	CTPS1	CTP synthase	1,4	0,005
Q14C86	GAPVD1	G I Pase-activating protein and V PS9 domain-containing protein 1	1,4	0,005
P62244	RPS15A	40S ribosomal protein S15a	1,4	0,006
Q12904	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	1,4	0,007
Q9NTI5	PDS5B	Sister chromatid cohesion protein PDS5 homolog B	1,4	0,008
Q9NSV4	DIAPH3	Protein diaphanous homolog 3	1,4	0,008
P49588	AARS1	AlaninetRNA ligase, cytoplasmic	1,4	0,009
P46783	RPS10	40S ribosomal protein S10	1,4	0,009
A0A140T9R1	FLOT1	Flotillin	1,4	0,011
Q9UKM9	RALY	RNA-binding protein Raly	1,4	0,014
P51572	BCAP31	B-cell receptor-associated protein 31	1,4	0.015
043290	SART1	U4/U6 U5 tri-snR NP-associated protein 1	1.4	0.015
09/906	DR DE4	Dra mRNA processing factor 6	1,1	0.017
O9P2P 2	A NIVEV1	P abaptroin S	1,4	0.019
Q)F2K3	AGOTZ	Rabankyim-5	1,4	0,017
000154	ACOT/	Cytosolic acyl coenzyme A thioester hydrolase	1,4	0,02/
P27540	ARNT	Aryl hydrocarbon receptor nuclear translocator	1,4	0,028
P52597	HNRNPF	Heterogeneous nuclear ribonucleoprotein F	1,4	0,028
O95453	PARN	Poly(A)-specific ribonuclease PARN	1,4	0,03
C9J4Z3	RPL37A	60S ribosomal protein L37a	1,4	0,032
Q9UKD2	MRTO4	mRNA turnover protein 4 homolog	1,4	0,033
P18583	SON	Protein SON	1,4	0,035
Q92667	AKAP1	A-kinase anchor protein 1, mitochondrial	1,4	0,042
O14980	XPO1	Exportin-1	1,4	0,049
P62913	RPL11	60S ribosomal protein L11	1,3	< 0.001
O13045	FLII	Protein flightless-1 homolog	1.3	< 0.001
O9BTE6	A A R SD1	AlapyLtR NA editing protein Aarsd1	13	<0.001
E6T100	PDF12	2' 5' nhoenhodiaetaraca 12	1,3	0.001
071 PC(	KDM2R	Luciae analia danahalar 20	1,5	0,001
Q/LBC6	KDM3D	Lysine-specific demethylase 3B	1,5	0,001
r 50991	CC14	1-complex protein 1 subunit delta	1,5	0,001
Q15365	PCBPI	Poly(rC)-binding protein 1	1,3	0,001
Q2TAM5	RELA	RELA protein	1,3	0,002
Q14677	CLINT1	Clathrin interactor 1	1,3	0,002
P57772	EEFSEC	Selenocysteine-specific elongation factor	1,3	0,003
Q5QJE6	DNTTIP2	Deoxynucleotidyltransferase terminal-interacting protein 2	1,3	0,004
Q8IWS0	PHF6	PHD finger protein 6	1,3	0,004
P09525	ANXA4	Annexin A4	1,3	0,005
Q01469	FABP5	Fatty acid-binding protein 5	1,3	0,008
P62753	RPS6	40S ribosomal protein S6	1.3	0.009
O9Y3S2	ZNF330	Zinc finger protein 330	1.3	0,011
	and the second sec		/-	.,
O9UNM6	PSMD13	26S proteasome non-ATPase regulatory subunit 13	1.3	0.012

Q8IZ83	ALDH16A1	Aldehyde dehydrogenase family 16 member A1	1,3	0,012
A0A1B0GV47	KIF21A	Kinesin-like protein KIF21A	1,3	0,012
C9JP00	MBNL1	Muscleblind-like protein 1	1,3	0,013
P62241	RPS8	40S ribosomal protein S8	1,3	0,013
P34897	SHMT2	Serine hydroxymethyltransferase, mitochondrial	1,3	0,013
A0A2R8Y880	RBBP6	E3 ubiquitin-protein ligase RBBP6	1,3	0,014
P49736	MCM2	DNA replication licensing factor MCM2	1,3	0,018
H0Y5D5	CIZ1	Cip1-interacting zinc finger protein	1,3	0,019
Q9NWH9	SLTM	SAFB-like transcription modulator	1,3	0,019
Q13838	DDX39B	Spliceosome RNA helicase DDX 39B	1,3	0,019
Q8WWQ0	PHIP	PH-interacting protein	1,3	0,021
Q9UKF6	CPSF3	Cleavage and polyadenylation specificity factor subunit 3	1,3	0,022
Q99426	TBCB	Tubulin-folding cofactor B	1,3	0,022
Q13148	TARDBP	TAR DNA-binding protein 43	1,3	0,022
P35250	RFC2	Replication factor C subunit 2	1,3	0,022
P51153	RAB13	Ras-related protein Rab-13	1,3	0,023
O94927	HAUS5	HAUS augmin-like complex subunit 5	1,3	0,023
P11177	PDHB	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	1,3	0,032
P11172	UMPS	Uridine 5'-monophosphate synthase	1,3	0,033
075717	WDHD1	WD repeat and HMG-box DNA-binding protein 1	1,3	0,034
P09543	CNP	2',3'-cyclic-nucleotide 3'-phosphodiesterase	1,3	0,034
F2Z2T2	XPA	DNA repair protein-complementing XP-A cells	1,3	0,036
Q16543	CDC37	Hsp90 co-chaperone Cdc37	1,3	0,039
Q9BWF3	RBM4	RNA-binding protein 4	1,3	0,043
Q15154	PCM1	Pericentriolar material 1 protein	1,3	0,045
P13797	PLS3	Plastin-3	1,2	< 0.001
Q9UHD8	SEPTIN9	Septin-9	1,2	0,001
P10606	COX5B	Cytochrome c oxidase subunit 5B, mitochondrial	1,2	0,003
Q92597	NDRG1	Protein NDRG1	1,2	0,004
Q13347	EIF3I	Eukaryotic translation initiation factor 3 subunit I	1,2	0,004
P36578	RPL4	60S ribosomal protein L4	1,2	0,004
A0A0C4DGA6	HLTF	Helicase-like transcription factor	1,2	0,005
Q9UMS4	PRPF19	Pre-mRNA-processing factor 19	1,2	0,007
P62701	RPS4X	40S ribosomal protein S4, X isoform	1,2	0,008
Q6PKG0	LARP1	La-related protein 1	1,2	0,008
P23246	SFPQ	Splicing factor, proline- and glutamine-rich	1,2	0,009
Q5BKZ1	ZNF326	DBIRD complex subunit ZNF326	1,2	0,012
060884	DNAJA2	DnaJ homolog subtamily A member 2	1,2	0,012
Q8WVJ2	NUDCD2	NudC domain-containing protein 2	1,2	0,013
P55884	EIF3B D DC10	Eukaryotic translation initiation factor 3 subunit B	1,2	0,018
075822	RP518 DEMD10	405 ribosomai protein 518	1,2	0,022
0/5832	PSMD10	265 proteasome non-A 1 Pase regulatory subunit 10	1,2	0,023
G5EA36	DC2/	Cell division cycle 2/, isoform CKA_c	1,2	0,02/
P4075/	TDOUG	Nie de dei lierent incompletent tradicio de la completent de	1,2	0,038
D1/8//	LIND NDI	Listen on a sub-sub-sub-sub-sub-sub-sub-sub-sub-sub-	1,2	0,039
012/25	SE2P2	Splising faster 2B suburit 2	1,2	0,045
D17087	TCD1	T complex protein 1 subunit alpha	1,2	0,047
P1/78/	DLD	Dihududian dahudu ana ang ang ang ang ang ang ang ang ang	1,1	0,003
P07622	DLD	2(S protocomo regulatory subunit 8	1,1	0,003
096036	DVCR 2	Durroline 5 carboxylate reductore 2	1,1	0,004
0150/7	SETDIA	Histone Jusine N methyltransferace SETD1 A	1,1	0,007
01/8/7	I ASD1	LIM and \$H3 domain protain 1	1,1	0,009
P49327	FASN	Fatty acid synthese	1,1	0,009
015555	MADRE2	Microtubule associated protein P D/FB family member 2	1,1	0,009
A0A 2R 8Y855	SMARCE1	SWI/SNF-related matrix-associated actin-denendent regulator of chromatin subfamily F member 1	1,1	0.015
015294	OGT	UDP.N-acetylalucosaminepentide N-acetylalucosaminyltransferase 110 kDa subunit	1,1	0.017
015126	PMVK	Phosphomevalonate kinase	11	0.02
098581	SNX9	Sorting nevin.9	1,1	0.021
P45974	USP5	Ubiquitin carboxyl-terminal hydrolase 5	1.1	0.023
O9UPT5	EXOC7	Fxocvst complex component 7	11	0.023
P54136	R A R S1	ArgininetRNA ligase, cytoplasmic	1.1	0.024
032MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	1.1	0.026
09H0D6	XRN2	5'-3' exoribonuclease 2	1.1	0.027
P53618	COPB1	Coatomer subunit beta	1,1	0,028
P35580	MYH10	Myosin-10	1.1	0,03
O9NVH2	INTS7	Integrator complex subunit 7	1.1	0,03
013907	IDI1	Isopentenyl-diphosphate Delta-isomerase 1	1.1	0,031
O9BSD7	NTPCR	Cancer-related nucleoside-triphosphatase	1.1	0,033
095232	LUC7L3	Luc7-like protein 3	1 1	0.033
09UN86	G3BP2	Ras GTPase-activating protein-binding protein 2	1 1	0,038
O9UIC3	HOOK1	Protein Hook homolog 1	1.1	0,042
P56545	CTBP2	C-terminal-binding protein 2	1 1	0,043
- /0/1/	01012	C community protein 2	1,1	0,015

LOLOD OVER	770.00	77.1 ·		2.2//
AUA2R8Y5F1	18C2	Iuberin	1,1	0,044
Q15008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	1,1	0,045
Q7Z417	NUFIP2	Nuclear fragile X mental retardation-interacting protein 2	1	0,001
Q8ND24	RNF214	RING finger protein 214	1	0,008
P53396	ACLY	ATP-citrate synthase	1	0,008
013155	AIMP2	A minoacyl tR NA synthese complex-interacting multifunctional protein 2	1	0.009
D38919	FIE4 A 3	Fukarvatic initiation factor 4 A III	1	0.01
00110127	VDC ( A		1	0,01
Q9UN3/	VPS4A	Vacuolar protein sorting-associated protein 4A	1	0,015
P26639	TARS1	ThreoninetRNA ligase 1, cytoplasmic	1	0,02
Q9Y613	FHOD1	FH1/FH2 domain-containing protein 1	1	0,028
P18858	LIG1	DNA ligase 1	1	0,032
P49591	SAR S1	SerinerRNA ligase. cytoplasmic	1	0.035
P62917	R PI 8	60\$ ribosomal protein I 8	1	0.037
	1	oos noosoniai protein 20	1	0,007
PKDX2 cysteine-depend	dent interactors			
Q9BQA1	WDR77	Methylosome protein 50	7,2	< 0.001
Q9NQX3	GPHN	Gephyrin [Includes: Molybdopterin adenylyltransferase	6,4	< 0.001
E7EVA0	MAP4	Microtubule-associated protein	6,1	< 0.001
O14744	PRMT5	Protein arginine N-methyltransferase 5	6	< 0.001
09C0C2	TNKS1BP1	182 kDa tankyrase-1-binding protein	5.8	< 0.001
D07355	ANY A 2	A provin A 2	5,0	<0.001
T 07 333	ON DI		5,6	0.001
E9PGZI	CALDI	Caldesmon	5,3	<0.001
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	5,2	< 0.001
Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	4,6	< 0.001
O60664	PLIN3	Perilipin-3	4,4	< 0.001
O9UHV9	PFDN2	Prefoldin subunit 2	4.4	< 0.001
08NC51	SEP BD1	Plasminogen activator inhibitor 1 P NA hinding protein	/ /	<0.001
Qalvest	VOTDA			0.001
Q9NXV2	KCTD5	B I B/POZ domain-containing protein KC I DS	4,4	0,033
Q14247	CTTN	Src substrate cortactin	4	< 0.001
O96007	MOCS2	Molybdopterin synthase catalytic subunit	4	0,014
Q9Y266	NUDC	Nuclear migration protein nudC	3,8	< 0.001
O5T6F2	UBAP2	Ubiquitin-associated protein 2	3.7	< 0.001
O9NPH2	ISYNA1	Inositol-3-phosphate synthese 1	3.6	0.001
0000002	TVINC	Commentarilia	3,0	-0.001
QINUQ3	I ALNG	Gamma-taxilin	3,5	<0.001
Q9Y570	PPME1	Protein phosphatase methylesterase 1	3,5	< 0.001
P11802	CDK4	Cyclin-dependent kinase 4	3,5	< 0.001
Q13541	EIF4EBP1	Eukaryotic translation initiation factor 4E-binding protein 1	3,5	0,001
Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	3,5	0,001
O9UI W0	TPX2	Targeting protein for Xklp?	3.5	0.002
01/0/5		Aurora binora A	2.4	:0.001
014965	AUKKA	Autora kinase A	5,4	<0.001
P10599	TXN	Thioredoxin	3,4	< 0.001
Q5SW79	CEP170	Centrosomal protein of 170 kDa	3,4	< 0.001
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	3,3	< 0.001
P61758	VBP1	Prefoldin subunit 3	3,3	0,001
O32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	3.2	< 0.001
	ENIZEDD	Vatasamina 2 kinasa	2.1	<0.001
Q/11A64	MADAD	Ketosaninie-5-kinase	5,1	<0.001
P46821	MAPIB	Microtubule-associated protein 1B	3,1	<0.001
P35520	CBS	Cystathionine beta-synthase	3,1	< 0.001
Q9P2B4	CTTNBP2NL	CTTNBP2 N-terminal-like protein	3,1	0,001
Q16204	CCDC6	Coiled-coil domain-containing protein 6	3,1	0,004
A6NGP5	IPT2	Jupiter microtubule-associated homolog 2	3	< 0.001
D52888	THOP1	Thimet oligonentidase	3	<0.001
012/20	TCOL			.0.001
Q13428	ICOFI	I reacle protein	3	<0.001
Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	3	0,001
P26599	PTBP1	Polypyrimidine tract-binding protein 1	2,9	< 0.001
P40222	TXLNA	Alpha-taxilin	2,9	0,002
Q13542	EIF4EBP2	Eukaryotic translation initiation factor 4E-binding protein 2	2,9	0,024
E7EPN9	PRRC2C	Protein PRRC2C	2.8	< 0.001
404087W/TM1	POPO1	Roundshout homolog 1	2.8	0.002
AUAU8/ WIMI	ROBOI		2,0	0,002
Q96F45	ZNF503	Zinc finger protein 503	2,8	0,003
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	2,8	0,005
Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	2,7	0,003
Q8IWB7	WDFY1	WD repeat and FYVE domain-containing protein 1	2,7	0,004
O95104	SCAF4	SR-related and CTD-associated factor 4	2.7	0,005
P52907	CAP741	F-actin-capping protein subunit alpha 1	2 (	<0.001
0011772	DOTDD	CTD 1 1 1 1	2,0	0.001
<u>Q9H773</u>	DCTPP1	aC 1 P pyropnosphatase 1	2,6	0,001
Q9H2U2	PPA2	Inorganic pyrophosphatase 2, mitochondrial	2,6	0,002
B7Z7F3	RANBP3	Ran-binding protein 3	2,6	0,004
E7EV99	ADD1	Alpha-adducin	2,6	0,005
P30740	SERPINB1	Leukocyte elastase inhibitor	2,6	0,005
A0A0A0MR N5	OGER	Opioid growth factor receptor	2.6	0.005
D/0/24	DDDC24	Denote DD DC2A	2,0	-0.001
148634	PKKCZA	CDD (CLL)	2,5	<0.001
060547	GMDS	GDP-mannose 4,6 dehydratase	2,5	0,005
F5H8D7	XRCC1	DNA repair protein XRCC1	2,5	0,006

P85037	FOXK1	Forkhead box protein K1	2,5	0,013
O75223	GGCT	Gamma-glutamylcyclotransferase	2,5	0,02
Q9BRP1	PDCD2L	Programmed cell death protein 2-like	2,4	0,005
Q8N3X1	FNBP4	Formin-binding protein 4	2,4	0,006
P12955	PEPD	Xaa-Pro dipeptidase	2,4	0,021
Q8N6M0	OTUD6B	Deubiquitinase OTUD6B	2,4	0,022
015511	ARPC5	Actin-related protein 2/3 complex subunit 5	2,4	0,043
Q06124	PTPN11	Tyrosine-protein phosphatase non-receptor type 11	2,3	< 0.001
Q12948	FOXC1	Forkhead box protein C1	2,3	0,002
O00629	KPNA4	Importin subunit alpha-3	2,3	0,01
O43809	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	2,3	0,011
Q9H0S4	DDX47	Probable ATP-dependent RNA helicase DDX47	2,3	0,017
Q96EA4	SPDL1	Protein Spindly	2,3	0,033
A0A1B0GW38	CBL	E3 ubiquitin-protein ligase CBL	2,2	< 0.001
H0YNW5	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase	2,2	< 0.001
Q16576	R.BBP7	Histone-binding protein RBBP7	2,2	< 0.001
Q86V48	LUZP1	Leucine zipper protein 1	2,2	< 0.001
P35237	SERPINB6	Serpin B6	2,2	< 0.001
P48507	GCLM	Glutamatecysteine ligase regulatory subunit	2,2	0,002
Q9P258	RCC2	Protein RCC2	2,2	0,002
Q8TAQ2	SMARCC2	SWI/SNF complex subunit SMARCC2	2,2	0,008
O43143	DHX15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	2,2	0,008
Q96IZ0	PAWR	PRKC apoptosis WT1 regulator protein	2,2	0,015
P49903	SEPHS1	Selenide, water dikinase 1	2,2	0,028
Q6FI81	CIAPIN1	Anamorsin	2,2	0,033
Q8N806	UBR7	Putative E3 ubiquitin-protein ligase UBR7	2,2	0,035
Q6PKG0	LARP1	La-related protein 1	2,1	< 0.001
J3KN29	PSMD9	26S proteasome non-ATPase regulatory subunit 9	2,1	0,001
Q96K76	USP47	Ubiquitin carboxyl-terminal hydrolase 47	2,1	0,014
O60826	CCDC22	Coiled-coil domain-containing protein 22	2,1	0,019
Q99598	TSNAX	Translin-associated protein X	2,1	0,026
Q9NVP1	DDX18	ATP-dependent RNA helicase DDX18	2,1	0,029
Q8WVC2	RPS21	40S ribosomal protein S21	2,1	0,029
000566	MPHOSPH10	U3 small nucleolar ribonucleoprotein protein MPP10	2,1	0,035
C9J019	ZC3HC1	Nuclear-interacting partner of ALK	2	<0.001
Q9Y3F4	SIRAP	Serine-threonine kinase receptor-associated protein	2	<0.001
Q93034	CULS	Cullin-5	2	0,001
AUAV 11	UBA6	C biquitin-like modifier-activating enzyme 6	2	0,003
P54646	PKKAAZ	5 -AMP-activated protein kinase catalytic subunit alpha-2	2	0,006
Q6IQ49	SDE2	Transport and Calai graphication protoin 1 homolog	2	0,018
	A V A DOI	A kiness and bog protoin 2 like	2	0.026
4/D180	VIPC2	Killer call location like recenter subfamily C member 2	2	0,028
09H3K6	BOLA2	Rol A like protein 2	2	<0.001
050PM7	DSME1	Dontrike protein 2	1,9	<0.001
096E86	FDC3	Enhancer of mR NA decomping protein 3	1,9	0.002
015417	CNN3	Calponin-3	1,9	0.002
P10301	RRAS	R as-related protein R-R as	1,9	0.017
D1917/	DI CC1	1 phoenhatidulinosital / 5 bienhoenhate phoenhadiesterase gamma 1	1,9	0.025
09UL15	BAG5	BAG family molecular chaperone regulator 5	1,9	0.028
O8WYA6	CTNNBL1	Beta-catenin-like protein 1	19	0.038
05T4K5	CRTC2	CR FB-regulated transcription coactivator 2	19	0.04
P82921	MR PS21	28S ribosomal protein \$21 mitochondrial	1,9	0.04
B1AK87	CAPZB	F-actin-capping protein subunit beta	1.8	<0.001
P53985	SLC16A1	Monocarboxylate transporter 1	1.8	< 0.001
O9H3S7	PTPN23	Tyrosine-protein phosphatase non-receptor type 23	1.8	0.03
O9BT25	HAUS8	HAUS augmin-like complex subunit 8	1,8	0.039
P49458	SRP9	Signal recognition particle 9 kDa protein	1.8	0,048
B4DDF4	CNN2	Calponin	1.7	0.008
I300Z9	PNPO	Pyridoxal 5'-phosphate synthase	1.7	0,016
013547	HDAC1	Histone deacetylase 1	1.7	0,017
O92783	STAM	Signal transducing adapter molecule 1	1.7	0,04
Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	1,7	0,04
Q9NXF7	DCAF16	DDB1- and CUL4-associated factor 16	1,7	0,041
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	1,6	0,001
Q9UNF1	MAGED2	Melanoma-associated antigen D2	1,6	0,001
O00273	DFFA	DNA fragmentation factor subunit alpha	1,6	0,002
Q9UHD1	CHORDC1	Cysteine and histidine-rich domain-containing protein 1	1,6	0,002
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	1,6	0,004
O14929	HAT1	Histone acetyltransferase type B catalytic subunit	1.6	0,008
P49790	NUP153	Nuclear pore complex protein Nup153	1.6	0,01
P63167	DYNLL1	Dynein light chain 1, cytoplasmic	1,6	0,031
O9UOE7	SMC3	Structural maintenance of chromosomes protein 3	1.6	0,035
× - × "			1,0	-,>
Q14240	EIF4A2	Eukaryotic initiation factor 4A-II	1,6	0,048
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E9PGT1	TSN	Component 3 of promoter of RISC	1,6	0,048
P45985	MAP2K4	Dual specificity mitogen-activated protein kinase kinase 4	1.5	< 0.001
P22314	UBA1	Ubionitin-like modifier-activating enzyme 1	15	0.015
001112	ATDOULL		1,5	0,011
Q90112	AIPGVIH	V-type proton A I Pase subunit H	1,4	0,001
Q9BTE6	AARSD1	Alanyl-tRNA editing protein Aarsd1	1,4	0,001
P42771	CDKN2A	Cyclin-dependent kinase inhibitor 2A	1,4	0,001
O15365	PCBP1	Poly(rC)-binding protein 1	1.4	0,001
007666	KHDR BS1	KH domain containing RNA binding signal transduction associated protein 1	1.4	0.017
00/000	KIID(D)	KT doman containing, RTVP-billing, signa transduction-associated protein T	1,4	0,017
Q90N3/	VPS4A	Vacuolar protein sorting-associated protein 4A	1,4	0,018
O14974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	1,4	0,041
Q96D09	GPRASP2	G-protein coupled receptor-associated sorting protein 2	1,3	0,005
P51452	DUSP3	Dual specificity protein phosphatase 3	1.3	0,006
O8WWK9	CKAD2	Curoskalston according to protein 2	1.3	0.009
Qowwk)	CKAF2		1,5	0,007
A0MZ66	SHTN1	Shootin-1	1,3	0,024
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	1,3	0,025
Q92667	AKAP1	A-kinase anchor protein 1, mitochondrial	1,3	0,034
075663	TIPRL	TIP41-like protein	1.3	0.036
09NV73	CTSF1	C2 and share expressed protein 1	1.3	0.043
Q/N125	GIJLI		1,5	0,045
G3XAG1	ZNF512	Zinc finger protein 512	1,3	0,05
P13797	PLS3	Plastin-3	1,2	0,001
Q92945	KHSRP	Far upstream element-binding protein 2	1,2	0,003
O9H7E9	C8orf33	UPF0488 protein C8orf33	1.2	0,008
09(4)(4)	DDLIMS	DDZ and LIM domain protein 5	1.2	0.01
Q/011C4	PDLINI)		1,2	0,01
E9PLA9	CAPRIN1	Caprin-1	1,2	0,014
O95816	BAG2	BAG family molecular chaperone regulator 2	1,2	0,03
Q7Z6Z7	HUWE1	E3 ubiquitin-protein ligase HUWE1	1,2	0,038
092598	HSPH1	Heat shock protein 105 kDa	11	0.007
Q2NIKX9	FRCCA	DNA analian protein PDCC ( like	1.1	0.01/
QZINKAO	ERCCOL	Diversion repair protein ERCC-o-like	1,1	0,014
Q86YP4	GATAD2A	Iranscriptional repressor p66-alpha	1,1	0,017
Q68EM7	ARHGAP17	Rho GTPase-activating protein 17	1,1	0,021
O00170	AIP	AH receptor-interacting protein	1,1	0,031
092769	HDAC2	Histone deacetylase 2	1.1	0.044
Q9(D/7	ACAD2	Aref CAD with CTDays ANK speak and DL domain containing protein 2	1	0.007
Q/0F4/	AGAF3	All-GAP with GTPace, AIX repeat and PTP domain-containing protein 5	1	0,007
Q13200	PSMD2	265 proteasome non-A I Pase regulatory subunit 2	1	0,009
O60343	TBC1D4	TBC1 domain family member 4	1	0,018
P49321	NASP	Nuclear autoantigenic sperm protein	1	0,019
1 1/001	141101	rucical autoantigenie sperin protein	*	
PRDX3 cysteine-depend	ent interactors	Nuclear autoantigente sperin protein		
PRDX3 cysteine-depend	ent interactors	Sering/thranning protein protein	- 6 6	<0.001
PRDX3 cysteine-depend F8VYE8	ent interactors PPP1CC PD12	Serine/threonine-protein phosphatase	4,4	<0.001
PRDX3 cysteine-depend F8VYE8 P05386	ent interactors PPP1CC RPLP1	Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1	4,4 4,3	<0.001 <0.001
PRDX3 cysteine-depend F8VYE8 P05386 Q8N5K1	ent interactors PPP1CC RPLP1 CISD2	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2	4,4 4,3 4,1	<0.001 <0.001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766	PPP1CC RPLP1 CISD2 ADH5	Serine/threonine-protein protein 605 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3	4,4 4,3 4,1 4	<0.001 <0.001 <0.001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148	PPPICC RPLP1 CISD2 ADH5 RAB5C	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C	4,4 4,3 4,1 4 3,9	<0.001 <0.001 <0.001 <0.001 0.001
PRDX3 cysteine-depend F8VYE8 P05386 Q8N5K1 P11766 P51148 Q71 2H7	PPPICC PPPICC RPLP1 CISD2 ADH5 RAB5C FIF3M	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukarsotic translation initiation factor 3 subunit M	4,4 4,3 4,1 4 3,9 3,7	<0.001 <0.001 <0.001 <0.001 0,001 <0.001
PRDX3 cysteine-depend F8VYE8 P05386 Q8N5K1 P11766 P51148 Q7L2H7 Pacta2	ent interactors PPPICC RPLP1 CISD2 ADH5 RABSC EIF3M UBOD	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M	4,4 4,3 4,1 4 3,9 3,7 2,7	<0.001 <0.001 <0.001 <0.001 0,001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132	ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase	4,4 4,3 4,1 4 3,9 3,7 3,7 3,7	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001
PRDX3 cysteine-depend F8VYE8 P05386 Q8N5K1 P11766 P51148 Q7L2H7 P06132 P40616	ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1	4,4 4,3 4,1 4 3,9 3,7 3,7 3,6	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084	ent interactors PPP1CC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6	4,4 4,3 4,1 4,3 3,9 3,7 3,7 3,6 3,6 3,6	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           O6DK11	ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1	4,4 4,3 4,1 4 3,9 3,7 3,7 3,6 3,6 3,6 3,6	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           O07820	Ania ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-SC Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced medoid leukemic cell differentiation protein McL1	4,4 4,3 4,1 4 3,9 3,7 3,7 3,6 3,6 3,6 3,6	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 <0.001 0,001 0,001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           OctBeo	ent interactors PPP1CC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF22	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1	4,4 4,3 4,1 4 3,9 3,7 3,6 3,6 3,6 3,6 3,6 3,5 2,4	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 <0.001 <0.001 <0.001 0,001 0,001 0,001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P406132           P40616           Q15084           Q6DK11           Q07820           Q61BS0	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2	4,4           4,3           4,1           4           3,9           3,7           3,7           3,6           3,6           3,6           3,6           3,6           3,6           3,5           3,4	<0.001 <0.001 <0.001 <0.001 <0.001 0,001 <0.001 <0.001 <0.001 0,001 0,001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2	ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase	4,4 4,3 4,1 4 3,9 3,7 3,7 3,6 3,6 3,6 3,6 3,6 3,5 3,4 3,4	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 0,001 0,001 <0.001 <0.001 <0.001 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022	ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2	Serine/threonine-protein protein Gerine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2	4,4 4,3 4,1 4 3,9 3,7 3,7 3,6 3,6 3,6 3,6 3,5 3,4 3,4 3,4 3,4	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 <0.001 0,001 0,001 <0.001 0,001 <0.001 0,001 <0.001 0,003
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021	ent interactors PPP1CC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CCDH2 CLQBP	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial	4,4 4,3 4,1 4 3,9 3,7 3,6 3,6 3,6 3,6 3,6 3,6 3,6 3,6 3,4 3,4 3,4 3,3	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 0,001 <0.001 0,003 <0.001
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P10725	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 C1QBP ANXA2	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,3         3,3	<0.001 <0.001 <0.001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 0,001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.00
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07055           P20041	Anisi ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CDH2 CIQBP ANXA2 PD DV/	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Deravised zin 6	4,4 4,3 4,1 4 3,9 3,7 3,7 3,6 3,6 3,6 3,6 3,6 3,6 3,5 3,4 3,4 3,4 3,3 3,3 2,2	<ul> <li>&lt;0.001</li> </ul>
PRDX3 cysteine-depend F8VYE8 P05386 Q8N5K1 P1766 P51148 Q7L2H7 P06132 P40616 Q15084 Q6DK11 Q07820 Q6IBS0 H3BTA2 P19022 Q07021 P07355 P30041	Philod ent interactors PPP1CC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CCDH2 C1QBP ANXA2 PRDX6 COH2	Serine/threonine-protein protein 605 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 605 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxitedoxin-6	4,4 4,3 4,1 4 3,9 3,7 3,6 3,6 3,6 3,6 3,6 3,6 3,6 3,5 3,4 3,4 3,4 3,3 3,3 3,3	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.00
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CIQBP ANXA2 PRDX6 PCMT1	Serine/threonine-protein protein 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,3         3,3         3,3         3,3         3,3	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 <0.001 <0.001 0,001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 0,002
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P107021           P07355           P30041           P22061           Q9NS69	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 COH2 CQBP ANXA2 PRDX6 PCMT1 TOMM22	Serine/threonine-protein protein Ges acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,8         3,3         3,3         3,3         3,3         3,2	<ul> <li>&lt;0.001</li> <li>&lt;0.001</li></ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174	Anixa PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CDH2 CDH2 CDH2 CDH2 CDH2 RNXA2 PRDX6 PCMT1 TOMM22 MIF	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor	4,4           4,3           4,1           4           3,9           3,7           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,4           3,3           3,3           3,3           3,3           3,2           3,2	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> </ul>
PRDX3 cysteine-depend F8VYE8 P05386 Q8N5K1 P11766 P51148 Q7L2H7 P06132 P40616 Q15084 Q6DK11 Q07820 Q6IBS0 H3BTA2 P19022 Q07021 P19022 Q07021 P19022 P07355 P30041 P22061 Q2NS69 P14174 OSSZR4	PPPICC ent interactors PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CCDH2 CIQBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDRKH	Serine/threonine-protein protein Serine/threonine-protein phosphatase 605 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 605 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor	4,4 4,3 4,1 4 3,9 3,7 3,6 3,6 3,6 3,6 3,6 3,6 3,6 3,6 3,6 3,5 3,4 3,4 3,3 3,3 3,3 3,3 3,3 3,2 3,2 3,2	<0.001 <0.001 <0.001 <0.001 0,001 <0.001 <0.001 <0.001 0,001 <0.001 0,001 <0.001 0,003 <0.001 0,003 <0.001 0,003 <0.001 0,002 0,001 0,002 0,007
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q15874           Q15844	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CIQBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDCKH TBCC	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,6         3,7         3,6         3,6         3,4         3,3         3,3         3,3         3,2         3,2	<0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0.001 <0
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P109021           Q07021           P07355           P30041           P22061           Q9NS69           P14174           Q5SZR4           Q15814           A0A2B SVELV5	PMIAD         ent interactors         PPPICC         RPLP1         CISD2         ADH5         RAB5C         EIF3M         UROD         ARL1         PDIA6         RPL7L1         MCL1         TWF2         PPP4C         CDH2         C1QBP         ANXA2         PRDX6         PCMT1         TOMM22         MIF         TDRKH         TBCC	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,8         3,3         3,3         3,3         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.007</li> <li>&lt;0.013</li> <li>&lt;0.02</li> </ul>
PRDX3 cysteine-depend F8VYE8 P05386 Q8N5K1 P11766 P51148 Q7L2H7 P06132 P40616 Q15084 Q6DK11 Q07820 Q6IBS0 H3BTA2 P19022 Q07021 P07355 P30041 P22061 Q9NS69 P14174 Q5SZR4 Q15814 A0A2R8YFH5	PPP1CC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 C1QBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDRKH TBCC SEC23B	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23	4,4         4,3         4,1         4         3,7         3,6         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,3         3,3         3,3         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.007</li> <li>&lt;0.013</li> <li>&lt;0.042</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           Q5SZR4           Q15814           A0A2R8YFH5           Q9NWV4	PPPICC PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CCDH2 C1QBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDRKH TBCC SEC23B CZIB	Serine/threonine-protein protein Serine/threonine-protein phosphatase 605 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 605 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein	4,4         4,3         4,1         4         3,7         3,6         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,6         3,7         3,6         3,4         3,3         3,3         3,2         3,2         3,2         3,1	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.002</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           Q15814           A042R8YFH5           Q9NWV4           Q86WA6	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CIQBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDRKH TBCC SEC23B CZIB BPHL	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,3         3,3         3,3         3,2         3,1	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.002</li> <li>&lt;0.003</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07020           Q6IBS0           H3BTA2           P19022           Q07021           P02061           Q2NS69           P14174           Q5SZR4           Q15814           A0A2R8YFH5           Q86WA6           P51809	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CDH2 CDH2 CDH2 CQBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDRKH TBCC SEC23B CZIB BPHL VAMP7	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein -L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7	4,4           4,3           4,1           4           3,9           3,7           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,6           3,4           3,3           3,3           3,3           3,2           3,2           3,2           3,2           3,2           3,2           3,2           3,2           3,2           3,2           3,2           3,2           3,2           3,1           3,1	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q5SZR4           Q15814           A0A2R8YFH5           Q9NWV4           Q86WA6           P51809           O9ULX3	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CIQBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDRKH TBCC SEC23B CZIB BPHL VAMP7 NOB1	Serine/threonine-protein protein Serine/threonine-protein phosphatase 605 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 605 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase	4,4         4,3         4,1         4         3,9         3,7         3,6         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,3         3,3         3,2         3,2         3,2         3,1         3,1         3	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.001</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P1766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q61BS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q158K4           Q158K4           Q058ZR4           Q15814           A0A2R8YFH5           Q9NWV4           Q86WA6           P51809           Q9ULX3           Q9VSV2	PPPICC RPLP1 CISD2 ADH5 RAB5C EIF3M UROD ARL1 PDIA6 RPL7L1 MCL1 TWF2 PPP4C CDH2 CCDH2 CCDH2 CQBP ANXA2 PRDX6 PCMT1 TOMM22 MIF TDRKH TBCC SEC23B CZIB BPHL VAMP7 NUIBP2	Serine/threonine-protein protein Serine/threonine-protein phosphatase 608 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 608 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Curtoxolic E & Schutzer accemptib factor MIBP2	4,4         4,3         4,1         4         3,7         3,6         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,3         3,3         3,3         3,2         3,2         3,1         3,1         3	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.0042</li> <li>&lt;0.003</li> <li>&lt;0.0046</li> <li>&lt;0.001</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P17766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P10022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           Q15814           A0A2R8YFH5           Q9NVV4           Q86WA6           P51809           Q9ULX3           Q9YSV2	NIMA           PNPICC           RPLP1           CISD2           ADH5           RAB5C           EIF3M           UROD           ARL1           PDIA6           RPL7L1           MCL1           TWF2           PPP4C           CDH2           C1QBP           ANXA2           PRDX6           PCMT1           TOMM22           MIF           TDRKH           TBCC           SEC23B           CZIB           BPHL           VAMP7           NOB1           NURP2	Serine/threonine-protein protein Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Cytosolic Fe-S cluster assembly factor NUBP2	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,3         3,3         3,3         3,2         3,1         3,1         3,1         3         2	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           Q5SZR4           Q15814           A0A2R8YFH5           Q9NWV4           Q86WA6           P51809           Q9ULX3           Q9Y5Y2           Q5SY16	NUMPPPICCRPLP1CISD2ADH5RAB5CEIF3MURODARL1PDIA6RPL7L1MCL1TWF2PPP4CCDH2C1QBPANXA2PRDX6PCMT1TOMM22MIFTDRKHTBCCSEC23BCZIBBPHLVAMP7NOB1NUBP2NOL9	Serine/threonine-protein protein Serine/threonine-protein phosphatase 605 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 605 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zine binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Cytosolic Fe-S cluster assembly factor NUBP2 Polynucleotide 5'-hydroxyl-kinase NOL9	4,4         4,3         4,1         4         3,9         3,7         3,6         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,3         3,3         3,3         3,2         3,2         3,2         3,2         3,2         3,1         3,1         3         3         3	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P1766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           QSSZR4           Q15814           A0A2R8YFH5           Q9NWV4           Q86WA6           P51809           Q9ULX3           Q92S90	NUMPPPICCRPLP1CISD2ADH5RAB5CEIF3MURODARL1PDIA6RPL7L1MCL1TWF2PPP4CCDH2CIQBPANXA2PRDX6PCMT1TOMM22MIFTBCCSEC23BCZIBBPHLVAMP7NOB1NUBP2NNL92GLMN	Serine/threonine-protein phosphatase         60S acidic ribosomal protein P1         CDGSH iron-sulfur domain-containing protein 2         Alcohol dehydrogenase class-3         Ras-related protein Rab-5C         Eukaryotic translation initiation factor 3 subunit M         Uroporphyrinogen decarboxylase         ADP-ribosylation factor-like protein 1         Protein disulfide-isomerase A6         60S ribosomal protein L7-like 1         Induced myeloid leukemia cell differentiation protein Mcl-1         Twinfilin-2         Serine/threonine-protein phosphatase         Cadherin-2         Complement component 1 Q subcomponent-binding protein, mitochondrial         Annexin A2         Perostiredoxin-6         Protein-L-isoaspartate(D-aspartate) O-methyltransferase         Mitochondrial import receptor subunit TOM22 homolog         Macrophage migration inhibitory factor         Tuduin-specific chaperone C         Protein transport protein SEC23         CXXXC motif containing zinc binding protein         Valacyclovir hydrolase         Vesicle-associated membrane protein 7         RNA-binding protein NOB1         Cytosolic Fe-S cluster assembly factor NUBP2         Polynucleotide 5'-hydroxyl-kinase NOL9         Glomulin	4,4         4,3         4,1         4         3,9         3,7         3,6         3,7         3,6         3,7         3,6         3,7         3,6         3,7         3,6         3,7         3,6         3,6         3,4         3,3         3,3         3,3         3,2         3,2         3,2         3,1         3,1         3         3         3	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P11766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q61BS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q15874           Q15814           A0A2R8YFH5           Q9WVV4           Q86WA6           P51809           Q9ULX3           Q9Y5Y2           Q358Y16           Q2990           Q26EA4	NUMPPPICCRPLP1CISD2ADH5RAB5CEIF3MURODARL1PDIA6RPL7L1MCL1TWF2PPP4CCDH2CIQBPANXA2PRDX6PCMT1TOMM22MIFTBCCSEC23BCZIBBPHLVAMP7NOB1NUL9GLMNSPDL1	Serine/threonine-protein phosphatase 60S acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein C7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate)O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Cytosolic F-5 cluster assembly factor NUBP2 Polynucleotide 5'-hydroxyl-kinase NOL9	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,3         3,3         3,3         3,3         3,2         3,1         3,1         3         3         3         3         3         3         3         3         3         3         3         3         3         3         3         3          3          3          4          4          5          5          5          5          5          5	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.0042</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.0042</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P1766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           Q5SZR4           Q15814           A0A2R8YFH5           Q9WWV4           Q86WA6           P51809           Q9ULX3           Q9Y5Y2           Q5SY16           Q926EA4           Q5W32	NumPPPICCRPLP1CISD2ADH5RAB5CEIF3MURODARL1PDIA6RPL7L1MCL1TWF2PPP4CCDH2C1QBPANXA2PRDX6PCMT1TORKHTBCCSEC23BCZIBBPHLVAMP7NOB1NUBP2NOL9GLMNSPDL1BROX	Serine/threonine-protein phothatase 608 acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 608 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein-L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Cytosolic Fe-S cluster assembly factor NUBP2 Polynucleotide 5'-hydroxyl-kinase NOL9 Glomulin Protein Spindly BRO1 domain-containing protein BROX	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,4         3,3         3,3         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,2         3,1         3,1         3         3         3         3         3         3         3         3          3         4         4         4         5         5         5         5         5         5         5 <tb< td=""><td><ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.0042</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.009</li> </ul></td></tb<>	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.0042</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.009</li> </ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P1766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           Q5SZR4           Q15814           A0A2R8YFH5           Q9NWV4           Q86WA6           P51809           Q9VLX3           Q9Y5Y2           Q35SY16           Q22990           Q6EA4           Q5VW32	NUMPPPICCRPLP1CISD2ADH5RAB5CEIF3MURODARL1PDIA6RPL7L1MCL1TWF2PPP4CCDH2C1QBPANXA2PRDX6PCMT1TORKHTBCCSEC23BCZIBBPHLVAMP7NOB1NUBP2NOL9GLMNSPDL1BROX	Serine/threonine-protein phoseni Alcohol dehydrogenase class-3 Alcohol dehydrogenase class-3 Reas-related protein R45-C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-riboxylation factor-like protein 1 Protein disulfide-isomerase A6 605 ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein L-isoaspartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chapterone C Protein transport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Cytosolic Fe-5 cluster assembly factor NUBP2 Polynucleotic 5'-hydroxyl-kinase NOL9 Glomulin Protein Spindly BROI domain-containing protein BROX	4,4         4,3         4,1         4         3,9         3,7         3,6         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,4         3,3         3,3         3,2         3,2         3,2         3,1         3,1         3	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.007</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li></ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P1766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q6IBS0           H3BTA2           P19022           Q07021           P07355           P30041           P22061           Q9NS69           P14174           QSSZR4           Q15184           A0A2R8YFH5           Q9NWV4           Q86WA6           P51809           Q9ULX3           Q9Y5Y2           Q5SY16           Q32990           Q946EA4           Q5VW32           G5EA06	NUMPPPICCRPLP1CISD2ADH5RAB5CEIF3MURODARL1PDIA6RPL7L1MCL1TWF2PPP4CCDH2CIQBPANXA2PRDX6PCMT1TORKHTBCCSEC23BCZIBBPHLVAMP7NOB1NUBP2NOL9GLMNSPDL1BROXMRPS27	Serine/threonine-protein phoseni Serine/threonine-protein phoseni Alcohol dehydrogenase class-3 Res-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 605 ribosomal protein L7-like 1 Induced myeloid leukenia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein L-sioaspartate(D-aspartate)O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein transport protein SEC23 CXX motif containing zinc binding protein Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Cytosolic Fe-Schuster assembly factor NUBP2 Polynucleotide 5 <sup>1</sup> -hydroxyl-kinase NOL9 BRO1 domain-containing protein BROX 285 ribosomal protein SZ7, mitochondrial	4,4         4,3         4,1         4         3,7         3,6         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,6         3,7         3,6         3,3         3,3         3,3         3,2         3,2         3,2         3,1         3 <td><ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.0042</li> <li>&lt;0.003</li> <li>&lt;0.006</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.004</li> <li>&lt;0.005</li> <li>&lt;0.005</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.004</li> <li>&lt;0.005</li> <li>&lt;0.005</li></ul></td>	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.0042</li> <li>&lt;0.003</li> <li>&lt;0.006</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.004</li> <li>&lt;0.005</li> <li>&lt;0.005</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.003</li> <li>&lt;0.004</li> <li>&lt;0.004</li> <li>&lt;0.005</li> <li>&lt;0.005</li></ul>
PRDX3 cysteine-depend           F8VYE8           P05386           Q8N5K1           P1766           P51148           Q7L2H7           P06132           P40616           Q15084           Q6DK11           Q07820           Q61BS0           H3BTA2           P19022           Q07021           P007355           P30041           P22061           Q9NS69           P14174           Q15814           A0A2R8YFH5           Q9WWV4           Q86WA6           P51809           Q9ULX3           Q95SY16           Q9290           Q96EA4           Q5VW32           G5EA06           Q92785	NUMPPPICCRPLP1CISD2ADH5RAB5CEIF3MURODARL1PDIA6RPL7L1MCL1TWF2PPP4CCDH2CIQBPANXA2PRDX6PCMT1TOMM22MIFTBCCSEC23BCZIBBPHLVAMP7NOB1NUBP2NOL9GLMNSPDL1BROXMRPS27DPF2	Serine/threonine-protein phosena Serine/threonine-protein phosena GOS acidic ribosomal protein P1 CDGSH iron-sulfur domain-containing protein 2 Alcohol dehydrogenase class-3 Ras-related protein Rab-5C Eukaryotic translation initiation factor 3 subunit M Uroporphyrinogen decarboxylase ADP-ribosylation factor-like protein 1 Protein disulfide-isomerase A6 60S ribosomal protein L7-like 1 Induced myeloid leukemia cell differentiation protein Mcl-1 Twinfilin-2 Serine/threonine-protein phosphatase Cadherin-2 Complement component 1 Q subcomponent-binding protein, mitochondrial Annexin A2 Peroxiredoxin-6 Protein disopartate(D-aspartate) O-methyltransferase Mitochondrial import receptor subunit TOM22 homolog Macrophage migration inhibitory factor Tudor and KH domain containing, isoform CRA_a Tubulin-specific chaperone C Protein Fusport protein SEC23 CXXC motif containing zinc binding protein Valacyclovir hydrolase Vesicle-associated membrane protein 7 RNA-binding protein NOB1 Cytosolic Fe-S cluster assembly factor NUBP2 Polynucleotide 5'-hydroxyl-kinase NOL9 Glomulin Protein Spindly BRO1 domain-containing protein BROX 288 ribossomal protein S27, mitochondrial Zinc finger protein ubi-d4	4,4         4,3         4,1         4         3,9         3,7         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,6         3,7         3,6         3,7         3,3         3,3         3,3         3,2         3,2         3,1         3,1         3,1         3,3         3 </td <td><ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.004</li> </ul></td>	<ul> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.001</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.002</li> <li>&lt;0.003</li> <li>&lt;0.004</li> </ul>

Q9BSJ8	ESYT1	Extended synaptotagmin-1	2,8	< 0.001
O43809	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	2,8	0,003
B3KUS5	USP30	Ubiquitin carboxyl-terminal hydrolase	2,8	0,007
H3BRY6	INTS14	Integrator complex subunit 14	2.8	0.029
AGNDU8	C5orf51	LIDE0600 protein CSorf51	2,0	0.034
D(110(	D A D14	P a selate deservaire D als 16	2,0	-0.001
P61106	RADI4	Ras-related protein Rab-14	2,7	<0.001
P/8346	KPP30	Kibonuclease P protein subunit p30	2,/	0,001
Q9Y4B6	DCAF1	DDB1- and CUL4-associated factor 1	2,7	0,002
Q9UKK9	NUDT5	ADP-sugar pyrophosphatase	2,7	0,002
Q9NYK5	MRPL39	39S ribosomal protein L39, mitochondrial	2,7	0,004
F8W038	C17orf49	Chromosome 17 open reading frame 49	2,7	0,007
O66PI3	ARL6IP4	ADP-rihosylation factor-like protein 6-interacting protein 4	2.7	0.007
Q51R 11	SR SE10	Serine/arginine rich splicing factor 10	2,7	0.036
077/2/	31(3110		2,7	0,000
Q/Z434	MAVS	Mitochondrial antiviral-signaling protein	2,6	<0.001
Q9Y3D0	CIAO2B	Cytosolic iron-sulfur assembly component 2B	2,6	0,005
P57076	CFAP298	Cilia- and flagella-associated protein 298	2,6	0,007
Q9NZ45	CISD1	CDGSH iron-sulfur domain-containing protein 1	2,6	0,029
Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	2,5	0,006
O9NP61	ARFGAP3	ADP-ribosylation factor GTPase-activating protein 3	2.5	0.006
O9BTE1	DCTNS	Dynactin cubunit 5	2.5	0.012
QUBIEI	DCINS		2,5	0,012
Q92804	IAF15	I A I A-binding protein-associated factor 2N	2,5	0,017
Q9HD26	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein	2,5	0,018
C9JAW5	C9JAW5	HIG1 domain-containing protein	2,5	0,018
M0R026	ILVBL	2-hydroxyacyl-CoA lyase 2	2,4	0,002
B4DI81	NDUF\$1	NADH-ubiguinone oxidoreductase 75 kDa subunit, mitochondrial	2.4	0,003
015291	R BBP5	Retinoblastoma binding protein 5	2.4	0.004
0011/22	NCAT		2,4	0,004
Q81V52	MCAI	Malonyi-CoA-acyi carrier protein transacylase, mitochondrial	2,4	0,004
D6RA00	ENOPH1	Enolase-phosphatase E1	2,4	0,004
A0A087WU06	TUBGCP3	Gamma-tubulin complex component	2,4	0,009
Q16698	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	2,4	0,009
F5H008	VPS33B	Vacuolar protein sorting-associated protein 33B	2,4	0,013
O9H9P8	L2HGDH	L-2-bydroxyglutarate debydrogenase, mitochondrial	2.4	0.017
40404034829	MEE	2 2 hjulokýghtulate delýdloghtub, hitochohdrad	2,1	0.027
DIOSOO	1/11/1		2,4	0,027
P10599	TXN	Thioredoxin	2,3	0,002
Q16718	NDUFA5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	2,3	0,003
Q9P287	BCCIP	BRCA2 and CDKN1A-interacting protein	2,3	0,004
Q9NP97	DYNLRB1	Dynein light chain roadblock-type 1	2,3	0,009
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	2.3	0.012
014161	GIT2	ARE GTPase-activating protein GIT2	23	0.013
075144	UID1D	Hereinaria interesti a sectoria 1 seleted associa	2,5	0.016
0/5146	HIPIK	Fluntingtin-interacting protein 1-related protein	2,5	0,016
P00492	HPKII	Hypoxanthine-guanine phosphoribosyltransferase	2,3	0,016
Q8N6M0	OTUD6B	Deubiquitinase OTUD6B	2,3	0,018
Q8WVC2	RPS21	40S ribosomal protein S21	2,3	0,022
P18669	PGAM1	Phosphoglycerate mutase 1	2,3	0,04
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	2,2	0,001
O8N6T3	AR EGAP1	A DP-ribosylation factor GTPase-activating protein 1	2.2	0.003
Q0R0C3	DDU2	2 /2 aming 2 ambaumpronul)histiding superhass suburit 2	2,2	0,009
Q9BQC3	DPHZ	2-(5-amino-3-carboxypropyi)nistidine syntnase subunit 2	2,2	0,009
Q961U4	ABHD14B	Protein ABHD14B	2,2	0,022
095295	SNAPIN	SNARE-associated protein Snapin	2,2	0,023
Q8N6R0	EEF1AKNMT	eEF1A lysine and N-terminal methyltransferase	2,2	0,025
Q9BYN0	SRXN1	Sulfiredoxin-1	2,2	0,044
P11802	CDK4	Cyclin-dependent kinase 4	2,1	0,001
A0A0A0MTB8	WDR 36	WD repeat-containing protein 36	2.1	0.01
V(D M00	EBC1	FI KS /D sh ( interesting /C A ST formily member 1	2,1	0,01
AGRMUU	EKCI	ELK5/ Rab6-interacting/CK51 ramity member 1	2,1	0,016
P30740	SERPINB1	Leukocyte elastase inhibitor	2,1	0,017
Q13509	TUBB3	Tubulin beta-3 chain	2,1	0,017
H3BV80	RNPS1	RNA-binding protein with serine-rich domain 1	2,1	0,022
Q5T749	KPRP	Keratinocyte proline-rich protein	2,1	0,034
092667	AKAP1	A-kinase anchor protein 1. mitochondrial	2	0.003
O8NBU5	ATAD1	ATPase family A A A domain-containing protein 1	2	0.011
096479	p pr	Ribulase phoenbate 3 enimerana	2	0.015
Q/6/17	RFE CONTE	Ribulose-phosphate 3-epimerase	2	0,015
Q9UQR0	SCML2	Sex comb on midleg-like protein 2	2	0,018
Q9UHD2	TBK1	Serine/threonine-protein kinase TBK1	2	0,02
Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	2	0,022
O43815	STRN	Striatin	2	0,025
Q9BZX2	UCK2	Uridine-cytidine kinase 2	2.	0,029
<		Dolichyl-dinhosphooligosaccharide, protein glycogyltransforms sylwait 1	1 0	0.002
P04843	R DVI1	A ORDANY TATALANDAR DEPONDALA HALIOCTOLOLOLU PLYCONVETADSPETASE SUDUDIE 1	1,7	0,002
P04843	CNIP2			0.007
P04843 P62879	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	1,9	0,007
P04843 P62879 Q2M2I8	RPN1 GNB2 AAK1	Guanine nucleotide-binding protein G(1)/G(S)/G(T) subunit beta-2 AP2-associated protein kinase 1	1,9 1,9	0,007 0,02
P04843 P62879 Q2M2I8 O75600	GNB2 AAK1 GCAT	Guanine nucleotide-binding protein G(1)/G(S)/G(T) subunit beta-2 AP2-associated protein kinase 1 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	1,9 1,9 1,9	0,007 0,02 0,038
P04843 P62879 Q2M2I8 O75600 Q96S44	RPN1 GNB2 AAK1 GCAT TP53RK	Guaine nucleotides binding protein G(I)/G(S)/G(T) subunit beta-2 AP2-associated protein kinase 1 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial EKC/KEOPS complex subunit TP53RK	1,9 1,9 1,9 1,9 1,8	0,007 0,02 0,038 0,033
P04843 P62879 Q2M2I8 O75600 Q96S44 O15269	RPN1 GNB2 AAK1 GCAT TP53RK SPTLC1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 AP2-associated protein kinase 1 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial EKC/KEOPS complex subunit TP53RK Serine palmitovltransferase 1	1,9 1,9 1,9 1,8 1,7	0,007 0,02 0,038 0,033 0,009
P04843 P62879 Q2M2I8 O75600 Q96S44 O15269 O36BW9	RPN1 GNB2 AAK1 GCAT TP53RK SPTLC1 TAMM41	Guanne nucleotide-binding protein G(1)/G(S)/G(T) subunit beta-2 AP2-associated protein kinase 1 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial EKC/KEOPS complex subunit TP53RK Serine palmitoyltransferase 1 Phoephendiate outdolltransferace mitoches deich	1,9 1,9 1,9 1,8 1,7	0,007 0,02 0,038 0,033 0,009 0,027

Q96A49	SYAP1	Synapse-associated protein 1	1.7	0.033
043237	DYNC1L12	Cytoplasmic dynein 1 light intermediate chain 2	1.7	0.036
09HB71	CACYBP	Calcyclin.binding protein	17	0.041
Q9H974	OTRT2	Ouenine tR NA-ribosyltransferase accessory subunit 2	17	0.048
404040MR09	DTDN9	Turocine protein phocphatace non-recentor tune 9	1.7	0.05
D(2979	P D\$274	Ubiquitie 405 sibocomel protein \$27a	1,/	0,004
P627/7	AUD1	Ubiquitin-403 Fibosomai protein 52/a	1,6	0,004
Q916/9	AUPI		1,6	0,034
E9PJN0	ACOIS	Acyl-coenzyme A thioesterase 8	1,6	0,044
P35268	RPL22	605 ribosomal protein L22	1,6	0,045
Q8TDH9	BLOC185	Biogenesis of lysosome-related organelles complex 1 subunit 5	1,5	0,004
B7WPG3	HNRNPLL	Heterogeneous nuclear ribonucleoprotein L-like	1,5	0,007
O14828	SCAMP3	Secretory carrier-associated membrane protein 3	1,5	0,034
Q9H0E2	TOLLIP	Toll-interacting protein	1,5	0,037
Q14318	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8	1,4	0,009
P27824	CANX	Calnexin	1,4	0,011
P18031	PTPN1	Tyrosine-protein phosphatase non-receptor type 1	1,4	0,026
Q9UL15	BAG5	BAG family molecular chaperone regulator 5	1,4	0,041
Q9UBE0	SAE1	SUMO-activating enzyme subunit 1	1,4	0,043
Q6PKG0	LARP1	La-related protein 1	1,3	0,009
P21964	COMT	Catechol O-methyltransferase	1,3	0,011
P62081	R PS7	40S ribosomal protein S7	1.3	0.017
P35520	CBS	Cystathionine beta-synthase	13	0.026
060784	TOM1	Target of Muh protein 1	1.2	0.005
050DM7	DSME1	Destancement in hibitate DI21 suburit	1,2	0,005
QSQPM/	PSMFI		1,2	0,011
P50454	SERPINHI	Serpin H1	1,2	0,013
QSIDHO	DDI2	Protein DD11 homolog 2	1,2	0,014
P31040	SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	1,2	0,016
K7ERF1	EIF3K	Eukaryotic translation initiation factor 3 subunit K	1,2	0,024
Q9UJS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	1,2	0,035
Q9H0U4	RAB1B	Ras-related protein Rab-1B	1,2	0,048
P35237	SERPINB6	Serpin B6	1,1	0,006
P62873	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	1,1	0,007
Q9GZS3	WDR61	WD repeat-containing protein 61	1,1	0,012
G3V279	ERH	Enhancer of rudimentary homolog	1,1	0,022
P08240	SRPRA	Signal recognition particle receptor subunit alpha	1,1	0,023
Q14697	GANAB	Neutral alpha-glucosidase AB	1,1	0,026
H7BXI1	ESYT2	Extended synaptotagmin-2	1.1	0,047
P22695	UOCRC2	Cvtochrome b-c1 complex subunit 2, mitochondrial	1	0,024
PR DX4 cysteine-depend	ent interactors			
I 31 1P8	SI C 25A 11	Mitochondrial 2-ovodutarate/malate carrier protein	3.9	<0.001
09B\$26	5EC25111	Endonlasmic reticulum resident protein 44	3.8	0.002
Q7D520	TVNDCS	Thiordovin domain containing protein 5	3,0	<0.001
Q814D37	TANDC3	Energia for the horizon of the second s	3,/	<0.001
Q96ACI	FERM12		3,4	<0.001
Q912KS	MKP51/	285 ribosomai protein 51/, mitocnondriai	<b>5</b> /	0.002
F5H6E2	NUNCHO		3,2	0,002
	MYO1C	Unconventional myosin-Ic	2,8	0,003
Q9BSJ8	MYO1C ESYT1	Unconventional myosin-Ic Extended synaptotagmin-1	2,8 2,7	0,003 0,002
Q9BSJ8 A0A0B4J1Z1	MYO1C ESYT1 SRSF7	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7	2,8 2,7 2,7	0,002 0,003 0,002 0,007
Q9BSJ8 A0A0B4J1Z1 Q66K74	MYO1C ESYT1 SRSF7 MAP1S	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S	2,8 2,7 2,7 2,7 2,4	0,003 0,002 0,007 0,008
Q9BSJ8 A0A0B4J1Z1 Q66K74 Q12797	MYOIC ESYT1 SRSF7 MAP1S ASPH	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase	2,8 2,7 2,7 2,7 2,4 2,3	0,003 0,002 0,007 0,008 0,002
Q9BSJ8 A0A0B4J1Z1 Q66K74 Q12797 D6RA00	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1	2,8 2,7 2,7 2,7 2,4 2,3 2,3	0,003 0,002 0,007 0,008 0,002 0,008
Q9BSJ8         A0A0B4J1Z1           Q66K74         Q12797           D6RA00         P30154	MYO1C ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3	0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012
Q9BSJ8         A0A0B4J1Z1           Q66K74         Q12797           D6RA00         P30154           P09110         P09110	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal	2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,004
Q9BSJ8         A0A0B4J1Z1           Q66K74         Q12797           D6RA00         P30154           P09110         P30041	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6	2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2 2,2	0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012
Q9BSJ8         Q9BSJ8           A0A0B4J1Z1         Q66K74           Q12797         D6RA00           P30154         P09110           P30041         Q92783	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1	2,8 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2 2,2 2,2 2,2	0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,004 0,012 0,015
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2	2,2 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2 2,2	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012 0,015 0,026
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12 SLC3A2	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain	2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2 2,2	0,002 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012 0,004 0,012 0,015 0,026 0,008
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70	2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2 2,2	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012 0,004 0,015 0,005 0,008 0,005 0,008 0,002 0,003 0,002 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,004 0,002 0,005 0,002 0,002 0,004 0,005 0,005 0,005 0,002 0,
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012 0,015 0,026 0,002 0,022
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12 SLC3A2 WDR70 NDUFS1 MTOR	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR	3,2           2,8           2,7           2,7           2,7           2,7           2,7           2,7           2,7           2,7           2,7           2,7           2,7           2,7           2,3           2,3           2,2           2,2           2,2           2,2           2,2           2,1           2           2           2	0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,004 0,012 0,015 0,026 0,008 0,029 0,029 0,022 0,031
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q1584	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PDIA6	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6	2,8 2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2 2,2	0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,012 0,012 0,015 0,026 0,008 0,029 0,022 0,031 0,029
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q03034	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUILS	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5	2,2 2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2 2,1 2 1,9 1,8	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012 0,015 0,026 0,008 0,029 0,022 0,031 0,029 0,021
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZ86           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P2234	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoriheculemionimidatole nucline-protemioneric double curved and subunity in the subunity in the subunity in the subunity in the subary in the subunity	2,8 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2 2 1,9 1,8 17	0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,004 0,015 0,026 0,008 0,029 0,022 0,031 0,029 0,021 0,029 0,041 0,003
QBSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P22234           P62249	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS RPS16	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	2,2 2,7 2,7 2,7 2,4 2,3 2,3 2,3 2,3 2,2 2,2 2,2 2,2 2,2 2,2	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012 0,004 0,015 0,026 0,008 0,029 0,022 0,031 0,029 0,003 0,002 0,004 0,002 0,002 0,004 0,002 0,004 0,002 0,002 0,004 0,002 0,004 0,002 0,002 0,004 0,002 0,002 0,004 0,002 0,002 0,004 0,002 0,004 0,002 0,002 0,004 0,002 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,004 0,002 0,004 0,
Q9B\$J8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZ\$6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P22234           P62249           Q14739	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS RPSI6 LBP	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein SIB	3,2           2,8           2,7           2,7           2,7           2,4           2,3           2,3           2,2           2,2           2,2           2,2           2,2           2,2           2,2           2,2           2,2           2,1           2,1           2,1           2,1           2,1           2,1           1,9           1,8           1,7           1,7           1,7	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,004 0,012 0,015 0,026 0,008 0,029 0,022 0,008 0,029 0,022 0,031 0,029 0,041 0,003 0,006 0,001
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P22234           P62249           Q14739	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12 SLC3A2 WDR70 NDUFS1 MTOR PD1A6 CUL5 PAICS RPS16 LBR BDL16	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein S16 Delta(14)-sterol reductase LBR	3,8       2,8       2,7       2,7       2,7       2,7       2,7       2,7       2,7       2,7       2,7       2,3       2,3       2,2       2,2       2,2       2,1       2,1       2,1       2,1       1,9       1,8       1,7       1,7       1,7	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,004 0,012 0,015 0,026 0,008 0,029 0,029 0,022 0,031 0,022 0,031 0,022 0,031 0,002 0,003 0,002 0,003 0,002 0,004 0,002 0,004 0,005 0,005 0,007 0,008 0,007 0,008 0,007 0,008 0,002 0,002 0,004 0,002 0,002 0,002 0,004 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,003 0,002 0,000000
QBSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q23034           P22234           P62249           Q14739           P62206           C02K2	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12 SLC3A2 WDR70 NDUFS1 MTOR PD1A6 CUL5 PD1A6 CUL5 PDIA6 CUL5 RP516 LBR RPL10A	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein S16 Delta(14)-sterol reductase LBR 60S ribosomal protein L10a	3,8       2,8       2,7       2,7       2,7       2,7       2,7       2,7       2,7       2,7       2,7       2,3       2,3       2,2       2,2       2,2       2,1       2,2       2,1       2,1       2,1       1,9       1,8       1,7       1,7       1,7       1,7       1,7	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,012 0,012 0,015 0,026 0,008 0,029 0,029 0,022 0,031 0,029 0,031 0,003 0,003 0,003 0,004 0,003 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,004 0,002 0,007 0,008 0,002 0,002 0,000000
QBSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P22234           P62249           Q14739           P62906           C299K3	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS RPS16 LBR RPS10 RPS10 RPSA NDS7	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein S16 Delta(14)-sterol reductase LBR 60S ribosomal protein SA	3,2         2,8         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,3         2,3         2,2         2,2         2,2         2,1         2,1         2,1         2,1         2,1         2,1         2,1         2,1         1,9         1,8         1,7         1,7         1,7         1,7         1,7         1,7         1,6	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,012 0,012 0,015 0,026 0,004 0,029 0,022 0,031 0,002 0,003 0,0029 0,004 0,003 0,006 0,001 0,004 0,004 0,004
QBSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZ86           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P22234           P62249           Q14739           P62906           C9J9K3           Q9UHV9	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS RP516 LBR RP516 LBR RPL10A RPSA PFDN2	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein SI6 Delta(14)-sterol reductase LBR 60S ribosomal protein SA Prefoldin subunit 2 Treventing 2	3,2         2,8         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,3         2,3         2,2         2,2         2,1         2,2         2,1         2,1         2,2         2,1         2,1         2,2         2,1         2,1         2,2         2,1         2,1         2,1         2,1         2,1         1,9         1,8         1,7         1,7         1,7         1,6         1,6	0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,014 0,015 0,026 0,008 0,029 0,029 0,022 0,031 0,029 0,029 0,0041 0,003 0,006 0,001 0,004 0,004 0,004 0,005
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P62206           C9J9K3           Q9UHV9           O43809	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS RPS16 LBR RPS16 LBR RPL10A RPSA PFDN2 NUDT21	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein L10a 40S ribosomal protein L10a	3,2         2,8         2,7         2,7         2,7         2,4         2,3         2,3         2,2         2,2         2,2         2,2         2,2         2,2         2,2         2,2         2,2         2,1         2,1         2,1         2,1         2,1         2,1         2,1         1,9         1,8         1,7         1,7         1,7         1,6         1,6         1,6         1,6         1,6	0,003 0,003 0,002 0,007 0,008 0,002 0,008 0,012 0,012 0,014 0,015 0,026 0,008 0,029 0,022 0,008 0,029 0,022 0,031 0,029 0,041 0,003 0,004 0,006 0,004 0,004 0,005 0,013
Q9B\$J8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZ\$6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P22234           P62249           Q14739           P62906           C59J9K3           Q9UHV9           Q43809           Q96K76	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS RPS16 LBR RPS16 LBR RPL10A RPSA PFDN2 NUDT21 USP47	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein SI6 Delta(14)-sterol reductase LBR 60S ribosomal protein SA Prefoldin subunit 2 Cleavage and polyadenylation specificity factor subunit 5 Ubiquitin carboxyl-terminal hydrolase 47	3,8         2,8         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,3         2,3         2,2         2,2         2,2         2,2         2,1         2,1         2,1         2,1         2,1         2         1,9         1,8         1,7         1,7         1,6         1,6         1,5	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,004 0,012 0,004 0,012 0,004 0,029 0,029 0,029 0,022 0,031 0,029 0,022 0,031 0,029 0,041 0,003 0,006 0,01 0,006 0,001 0,004 0,005 0,001 0,005 0,002
Q9BSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P330041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P62249           Q14739           P62206           C9J9K3           Q9UHV9           Q43809           Q96K76           Q55W79	MYOIC ESYT1 SRSF7 MAPIS ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MS12 SLC3A2 WDR70 NDUFS1 MTOR PDIA6 CUL5 PAICS RP516 LBR RP516 LBR RP516 LBR RP516 LBR RP516 UL5 PAICS RP516 UL5 PAICS RP516 LBR RP516 CUL5 PAICS RP516 PAICS RP516 PAICS RP516 PAICS RP516 PAICS RP516 PAICS RP517 PAICS RP516 PAICS RP516 PAICS RP517 PAICS RP517 PAICS RP517 PAICS RP517 PAICS PAIC	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musash homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein I0a 60S ribosomal protein SA Prefoldin subunit 2 Cleavage and polyadenylation specificity factor subunit 5 Ubiquitin carboxyl-terminal hydrolase 47 Centrosomal protein of 170 kDa	3,8         2,8         2,7         2,7         2,7         2,4         2,3         2,3         2,2         2,2         2,2         2,2         2,2         2,1         2,1         2,2         2,1         2,1         2,1         2,1         1,9         1,8         1,7         1,7         1,7         1,6         1,6         1,5	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,012 0,012 0,012 0,015 0,026 0,008 0,029 0,029 0,029 0,022 0,031 0,002 0,004 0,003 0,002 0,004 0,004 0,004 0,005 0,013 0,002 0,006
Q3B5J8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q23034           P62234           P62249           Q14739           P62906           C9J9K3           Q94HV9           O43809           Q96K76           Q5SW79           P22307	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SLC3A2 WDR70 NDUFS1 MTOR PD1A6 CUL5 PAICS RPS16 LBR RPS16 LBR RPS16 LBR RPS16 UBS RPS16 UBS RPS16 UBS RPS16 UBS RPS16 UBS RPS16 UBS RPS16 UBS RPS16 UBS RPS16 CUL5 PAICS RPS16 CUL5 PAICS RPS16 CUL5 PAICS RPS16 CUL5 PAICS RPS16 CUL5 PAICS RPS16 CUE5 PAICS RPS16 PAICS RPS16 PAICS RPS16 PAICS RPS16 PAICS RPS16 PAICS RPS16 PAICS RPS16 PAICS RPS16 PAICS RPS16 PAICS PAIC	Unconventional myosin-Ic Extended synaptotagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein S16 Delta(14)-sterol reductase LBR 60S ribosomal protein SA Prefoldin subunit 2 Cleavage and polyadenylation specificity factor subunit 5 Ubiquitin carboxyl-terminal hydrolase 47 Centrosomal protein of 170 kDa	3,8         2,8         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,3         2,3         2,2         2,2         2,2         2,1         2,2         2,1         2,1         2,2         2,1         2,1         2,2         2,1         2,2         2,1         2,1         2,2         2,1         2,1         2,1         2,2         2,1         2,1         2,2         1,9         1,8         1,7         1,7         1,6         1,6         1,5         1,5         1,5	0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,002 0,008 0,012 0,012 0,015 0,026 0,008 0,029 0,029 0,029 0,022 0,002 0,002 0,001 0,002 0,004 0,003 0,004 0,004 0,005 0,005 0,0005 0,0006 0,006 0,006
QBSJ8           A0A0B4J1Z1           Q66K74           Q12797           D6RA00           P30154           P09110           P30041           Q92783           Q96DH6           F5GZS6           Q9NW82           B4DJ81           P42345           Q15084           Q93034           P22234           P62249           Q14739           P62906           C395K3           Q94HV9           O43809           Q965K76           Q58W79           P22307           P49411	MYOIC ESYT1 SRSF7 MAP1S ASPH ENOPH1 PPP2R1B ACAA1 PRDX6 STAM MSI2 SIC3A2 WDR70 NDUFS1 MTOR PD1A6 CUL5 PAICS RP516 LBR RP516 LBR RP516 LBR RP516 LBR RP516 CUL5 PAICS CU15 PAICS	Unconventional myosin-Ic Extended synaptor tagmin-1 Serine/arginine-rich-splicing factor 7 Microtubule-associated protein 1S Aspartyl/asparaginyl beta-hydroxylase Enolase-phosphatase E1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform 3-ketoacyl-CoA thiolase, peroxisomal Peroxiredoxin-6 Signal transducing adapter molecule 1 RNA-binding protein Musashi homolog 2 4F2 cell-surface antigen heavy chain WD repeat-containing protein 70 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial Serine/threonine-protein kinase mTOR Protein disulfide-isomerase A6 Cullin-5 Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase 40S ribosomal protein S16 Delta(14)-sterol reductase LBR 60S ribosomal protein SA Prefoldin subunit 2 Cleavage and polyadenylation specificity factor subunit 5 Ubiquitin carboxyl-terminal hydrolase 47 Centrosomal protein of 170 kDa	3,8         2,8         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,7         2,3         2,3         2,2         2,2         2,2         2,1         2,1         2,1         2,1         2,1         2,1         2,1         2,2         2,2         2,1         2,1         2,2         2,2         2,1         2,1         2,2         2,2         2,1         2,1         2,1         2,1         1,7         1,7         1,7         1,6         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1	0,002 0,003 0,002 0,007 0,008 0,002 0,008 0,002 0,008 0,012 0,012 0,012 0,012 0,015 0,026 0,004 0,029 0,029 0,022 0,021 0,002 0,004 0,003 0,006 0,001 0,005 0,006 0,006 0,006 0,006 0,001

E9PGZ1	CALD1	Caldesmon	1,5	0,045
Q14697	GANAB	Neutral alpha-glucosidase AB	1,4	0,004
P60174	TPI1	Triosephosphate isomerase	1,4	0,011
Q9UQR0	SCML2	Sex comb on midleg-like protein 2	1,4	0,017
Q16513	PKN2	Serine/threonine-protein kinase N2	1,4	0,019
P10599	TXN	Thioredoxin	1,4	0,041
O14974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	1,4	0,043
Q14152	EIF3A	Eukaryotic translation initiation factor 3 subunit A	1,4	0,046
Q86UP2	KTN1	Kinectin	1,3	0,006
Q9Y4B6	DCAF1	DDB1- and CUL4-associated factor 1	1,3	0,017
O96199	SUCLG2	SuccinateCoA ligase [GDP-forming] subunit beta, mitochondrial	1,3	0,033
013257	MAD2L1	Mitoric spindle assembly checkpoint protein MAD2A	1.3	0.038
O9P2I5	LARS1	LeucinetRNA ligase, cytoplasmic	1,3	0,049
P06576	ATP5F1B	ATP synthase subunit beta mitochondrial	1.2	0.002
P06733	FNO1	Alpha-enolase	1.2	0.006
O9BTZ2	DHR S4	Debydrogenase/reductase SDR family member 4	1,2	0.011
P34897	SHMT2	Serine hydroxymethyltransferase mitochondrial	1,2	0.015
P05388	R PI PO	60\$ acidic ribosomal protein P0	1.2	0.016
P26599	PT'RP1	Polynyrimidine tract-binding protein 1	1,2	0.017
D18858	LIGI	DNA ligase 1	1.2	0.02
P10030	D DI 25 A	ON riberry languin 1.25	1,2	0,02
0011CD5	NCOAS	Subsomal protein L55a	1,2	0,024
016272	FIETH	Nuclear receptor coactivator 5	1,2	0,03/
0153/2	EIF3H	Eukaryotic translation initiation factor 3 subunit H		0,024
A0A087WY71	AP2M1	AP-2 complex subunit mu	1,1	0,024
Q12904	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	1,1	0,036
Q96C36	PYCR2	Pyrroline-5-carboxylate reductase 2	1	0,012
Q13347	EIF3I	Eukaryotic translation initiation factor 3 subunit I	1	0,017
P34949	MPI	Mannose-6-phosphate isomerase	1	0,022
P13489	RNH1	Ribonuclease inhibitor	1	0,036
P15880	RPS2	40S ribosomal protein S2	1	0,04
PRDX5 cysteine-dep	endent interactors			
P36551	CPOX	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	5,2	< 0.001
Q96A49	SYAP1	Synapse-associated protein 1	4,6	< 0.001
Q15388	TOMM20	Mitochondrial import receptor subunit TOM20 homolog	4	0,001
A0A0C4DGQ6	RPRD1A	Regulation of nuclear pre-mRNA domain-containing protein 1A	3,2	< 0.001
Q9H2P9	DPH5	Diphthine methyl ester synthase	3,2	0,003
P26599	PTBP1	Polypyrimidine tract-binding protein 1	3	< 0.001
Q9GZU8	PSME3IP1	PSME3-interacting protein	3	0,002
Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	3	0,006
P78371	CCT2	T-complex protein 1 subunit beta	2,9	< 0.001
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	2,9	< 0.001
Q53GQ0	HSD17B12	Very-long-chain 3-oxoacyl-CoA reductase	2,9	0,002
E9PGT1	TSN	Component 3 of promoter of RISC	2,8	< 0.001
P63167	DYNLL1	Dynein light chain 1, cytoplasmic	2,8	0,007
O95801	TTC4	Tetratricopeptide repeat protein 4	2,7	0,005
O6DKK2	TTC19	Tetratricopeptide repeat protein 19. mitochondrial	2.7	0.008
O2TAM5	RELA	R EL A protein	2.6	0.004
099598	TSNAX	Translin-associated protein X	2.5	<0.001
Q5T760	SR SE11	Serine/arginine-rich-splicing factor 11	2.5	0.006
060664	PI IN3	Derilinin-3	2,5	0.006
016698	DECR1	2 4 dienard Co A reductase mitochandrial	2,5	0.007
010713	PMPCA	Mitachandrial processing paptidase subunit alpha	2,5	0.008
01(822	DCV2	Dhoenhoon olaveuwata cashowikinaga [CTD] mitochon drial	2,5	0,008
Q10022 P777E2	P A NIPD2	Phosphoenolpyruvate carboxykinase [GTF], intochondriai	2,5	<0.001
D/Z/13	NUDC	Nuclear minuting protein 5	2,4	0.002
Q91266	CLYON		2,4	0,002
Q92990	GLMN	Glomulin	2,4	0,01
Q8N6M0	OTUD6B	Deubiquitinase OTUD6B	2,4	0,014
P8503/	FOXKI	Forkhead box protein K1	2,4	0,019
Q6PID6	11C33	Tetratricopeptide repeat protein 33	2,4	0,02
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	2,3	<0.001
P43304	GPD2	Glycerol-3-phosphate dehydrogenase, mitochondrial	2,3	0,001
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	2,3	0,001
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	2,3	0,009
H7C128	BRD8	Bromodomain-containing protein 8	2,2	0,001
A0A0B4J1Z1	SRSF7	Serine/arginine-rich-splicing factor 7	2,2	0,029
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	2,2	0,036
Q9HB71	CACYBP	Calcyclin-binding protein	2,1	< 0.001
Q8N3X1	FNBP4	Formin-binding protein 4	2,1	< 0.001
Q14C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	2,1	< 0.001
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	2,1	0,001
Q05655	PRKCD	Protein kinase C delta type	2,1	0,001
O00483	NDUFA4	Cytochrome c oxidase subunit NDUFA4	2,1	0,016
Q15750	TAB1	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	2,1	0,022
-		01		

09H2U1	DHX36	ATP-dependent DNA/RNA belicase DHX36	2.1	0.024
A0A024R442	A0A024R442	NTT dependent DTTT, for the incluse DTTTGO Ntr A0A024R 442   A0A024R 442 HUMAN Aspartyl aminopentidase isoform CRA h OS-Homo sapiens	2.1	0.032
1101102-11(112	110110241(142	OX=9606 GN=DNPEP PE=1 SV=1:>splO9ULA0 DNPEP_HUMAN Aspartyl aminopeptidase OS=Homo	2,1	0,052
		sapiens OX=9606 GN=DNPEP PE=1 SV=1:>tr/E7ETB3/E7ETB3 HUMAN Aspartyl aminopeptidase, iso		
P40222	TXLNA	Alpha-taxilin	2	0.001
P43686	PSMC4	26S protessome regulatory subunit 6B	2	0.003
0011772	DCTDD1	205 processione regulatory subunit ob	2	0,005
Q90775	UCUI		2	0,005
Q9B11/	HGHI	Protein HGH1 homolog	2	0,007
P12955	PEPD	Xaa-Pro dipeptidase	2	0,025
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	1,9	0,001
Q9BSJ8	ESYT1	Extended synaptotagmin-1	1,9	0,002
P07355	ANXA2	Annexin A2	1,9	0,007
P30041	PRDX6	Peroxiredoxin-6	1,9	0,015
Q9H0E2	TOLLIP	Toll-interacting protein	1,9	0,016
Q9P2N5	RBM27	RNA-binding protein 27	1,9	0,028
O5IR A6	MIA3	Transport and Golgi organization protein 1 homolog	1.9	0.03
O6WK74	R A B11FIP1	Rahl1 family interacting protein 1	1.9	0.034
015(45	TP ID12	Rabitrania) interacting protein 1	1,9	0.027
Q15645	1 KIP15	Pachytene checkpoint protein 2 nomolog	1,9	0,03/
E9PJN0	ACOIS	Acyl-coenzyme A thioesterase 8	1,8	< 0.001
Q8NC51	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	1,8	0,001
F5GZS6	SLC3A2	4F2 cell-surface antigen heavy chain	1,8	0,005
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	1,8	0,012
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	1,8	0,016
Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	1,8	0,016
E9PGZ1	CALD1	Caldesmon	1,8	0,019
O9BW92	TAR S2	ThreoninetRNA ligase. mitochondrial	1.8	0.019
015061	WDR43	WD repeat-containing protein 43	1.8	0.033
Q15001	A D L (ID4	ADD site substanting protein 45	1,0	0,035
Q66PJ5	ARL61P4	ADP-fibosylation ractor-like protein 6-interacting protein 4	1,8	0,034
Q04446	GBEI	1,4-aipna-glucan-branching enzyme	1,8	0,045
A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6	1,7	0,005
Q9UL15	BAG5	BAG family molecular chaperone regulator 5	1,7	0,005
O43815	STRN	Striatin	1,7	0,008
E7EV99	ADD1	Alpha-adducin	1,7	0,019
Q9BQA1	WDR77	Methylosome protein 50	1,7	0,036
O9NOX3	GPHN	Gephyrin [Includes: Molybdopterin adenylyltransferase	1.7	0.036
P14174	MIF	Macrophage migration inhibitory factor	1.7	0.045
D31689	DNAIA1	Daal homolog subfamily A member 1	1.6	<0.001
	DDME1	Brasin nh cup secondarily it includes 1	1,0	0.000
Q915/0	PPMEI	Protein phosphatase methylesterase 1	1,6	0,009
014929	HAII	Histone acetyltransferase type B catalytic subunit	1,6	0,009
O00165	HAX1	HCLS1-associated protein X-1	1,6	0,013
F8W1A4	AK2	Adenylate kinase 2, mitochondrial	1,6	0,026
Q9NT62	ATG3	Ubiquitin-like-conjugating enzyme ATG3	1,6	0,029
Q9NQP4	PFDN4	Prefoldin subunit 4	1,6	0,049
Q9BQ69	MACROD1	ADP-ribose glycohydrolase MACROD1	1,6	0,05
Q15276	RABEP1	Rab GTPase-binding effector protein 1	1,5	0,003
C919K3	R PSA	40S ribosomal protein SA	1.5	0.004
09BSD7	NTPCR	Cancer-related nucleoside-trinhosphatase	15	0.006
002952	AKAD12	A kingse anchor protein 12	1,5	0.015
Q02752	DIOV1	Series (herenies metric bieses P IO)	1,5	0,015
Q96K32	RIOKI		1,5	0,016
Q9C0C2	INKSIBPI	182 kDa tankyrase-1-binding protein	1,5	0,039
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	1,4	0,001
Q16531	DDB1	DNA damage-binding protein 1	1,4	0,003
P05386	RPLP1	60S acidic ribosomal protein P1	1,4	0,004
Q96IZ0	PAWR	PRKC apoptosis WT1 regulator protein	1,4	0,008
Q9NZL9	MAT2B	Methionine adenosyltransferase 2 subunit beta	1,4	0,015
Q8NBU5	ATAD1	ATPase family AAA domain-containing protein 1	1,4	0,016
P52888	THOP1	Thimet oligopeptidase	1,4	0,027
012931	TR AP1	Heat shock protein 75 kDa, mitochondrial	1.3	0.003
032M74	I R R FIP1	Leucine-rich reneat flightless-interacting protein 1	13	0.01
D15990	P DS2	40S sibacamal protoin \$2	1,5	0.012
P15880	CDV2	403 ribosomai protein 52	1,5	0,012
Q13185	CBA3	Chromobox protein homolog 5	1,3	0,012
Q96RL1	UIMC1	BRCA1-A complex subunit RAP80	1,3	0,014
H7BZM7	ZPR1	Zinc finger protein ZPR1	1,2	0,003
P51665	PSMD7	26S proteasome non-ATPase regulatory subunit 7	1,2	0,006
Q9Y3F4	STRAP	Serine-threonine kinase receptor-associated protein	1,2	0,006
Q9UNM6	PSMD13	26S proteasome non-ATPase regulatory subunit 13	1,2	0,01
P04843	RPN1	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 1	1,2	0,036
P46821	MAP1B	Microtubule-associated protein 1B	1.2	0,047
F9PLA9	CAPR IN1	Caprin-1	11	0.002
404087WUT	FIESR	Suprim 2 Fukarvoric translation initiation factor SB	11	0.008
D020570	LIFJD		1,1	0,000
r225/0	LDAK	INADITI:adrenodoxin oxidoreductase, mitochondrial	1,1	0,008
Q9U112	ATP6V1H	V-type proton A I Pase subunit H	1,1	0,014
Q5T6F2	UBAP2	Ubiquitin-associated protein 2	1,1	0,015

E7EVA0	MAP4	Microtubule-associated protein	1,1	0,022
C9J4Z3	RPL37A	60S ribosomal protein L37a	1,1	0,041
P62195	PSMC5	26S proteasome regulatory subunit 8	1	0,005
P25398	RPS12	40S ribosomal protein S12	1	0,016
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	1	0,036
P62333	PSMC6	26S proteasome regulatory subunit 10B	1	0,037
O14579	COPE	Coatomer subunit epsilon	1	0,038

Table \$2: isoform-specific cysteine-dependent interactors

gene	uniprot ID	protein	fold change	adj. p-value	against
PRDX1 -specific in	nteractors				
A0A075B6R9	IGKV2D-24	Probable non-functional immunoglobulin kappa variable 2D-24	2,9	0,001	PRDX2
F8W9F9	WNK2	Non-specific serine/threonine protein kinase	2,5	0,001	PRDX2
Q06830	PRDX1	Peroxiredoxin-1	2,4	0	PRDX2
O60566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	2,4	0,001	PRDX2
G3V3B9	GSTZ1	Maleylacetoacetate isomerase	2,4	0,001	PRDX2
Q6NZY4	ZCCHC8	Zinc finger CCHC domain-containing protein 8	2,4	0,008	PRDX2
P30044	PRDX5	Peroxiredoxin-5, mitochondrial	2,3	0,028	PRDX2
O95218	ZRANB2	Zinc finger Ran-binding domain-containing protein 2	2,2	0,003	PRDX2
P19387	POLR2C	DNA-directed RNA polymerase II subunit RPB3	2,2	0,004	PRDX2
O9Y3B7	MRPL11	39S ribosomal protein L11, mitochondrial	2,1	0	PRDX2
A0A 3B3ITI4	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	2.1	0.004	PR DX2
000399	DCTN6	Dynactin subunit 6	2,1	0.006	PR DX2
09¥3D9	MR PS23	28\$ ribosomal protein \$23 mitochondrial	2,1	0.017	PR DX2
404087¥1B1	IKBKG	NE kappa B essential modulator	2,1	0.009	PR DY2
D14625	CCNR1	C2/mitotic excite such B1	2	0,007	DP DV2
0(UWE0	LDCAMI	G2/Infibite-specific cyclin-D1	2	0,01	PRDX2
Q60 WE0	EDCo	ES ubiquitili-protein ligase EKSAM1	1.0	0,011	PRDA2
01(252)	EP58	All la income in	1,9	0,007	PRDA2
Q16352	INA	Alpha-Internexin	1,8	0	PRDX2
P0/196	NEFL TR	Neurofilament light polypeptide	1,8	0,001	PRDX2
Q12933	I RAF2	1 NF receptor-associated factor 2	1,8	0,013	PRDX2
Q13418	ILK	Integrin-linked protein kinase	1,8	0,018	PRDX2
Q96DA6	DNAJC19	Mitochondrial import inner membrane translocase subunit TIM14	1,8	0,019	PRDX2
Q99956	DUSP9	Dual specificity protein phosphatase 9	1,8	0,024	PRDX2
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	1,7	0	PRDX2
Q9H0H5	RACGAP1	Rac GTPase-activating protein 1	1,7	0	PRDX2
Q8WVC0	LEO1	RNA polymerase-associated protein LEO1	1,7	0,026	PRDX2
Q9C026	TRIM9	E3 ubiquitin-protein ligase TRIM9	1,7	0,029	PRDX2
075616	ERAL1	GTPase Era, mitochondrial	1,7	0,036	PRDX2
Q15398	DLGAP5	Disks large-associated protein 5	1,6	0,001	PRDX2
Q9ULX3	NOB1	RNA-binding protein NOB1	1,6	0,002	PRDX2
Q9BR76	CORO1B	Coronin-1B	1,6	0,012	PRDX2
Q9BW83	IFT27	Intraflagellar transport protein 27 homolog	1,6	0,024	PRDX2
Q6R327	RICTOR	Rapamycin-insensitive companion of mTOR	1,6	0,027	PRDX2
Q96B36	AKT1S1	Proline-rich AKT1 substrate 1	1,6	0,031	PRDX2
H3BPJ9	NDUFB10	Complex I-PDSW	1,6	0,032	PRDX2
P09497	CLTB	Clathrin light chain B	1,6	0,04	PRDX2
Q92974	ARHGEF2	Rho guanine nucleotide exchange factor 2	1,5	0	PRDX2
A0A0G2JNZ2	SCRIB	Protein scribble homolog	1,5	0,001	PRDX2
Q04837	SSBP1	Single-stranded DNA-binding protein, mitochondrial	1,5	0,001	PRDX2
Q96RT1	ERBIN	Erbin	1,5	0,003	PRDX2
Q6FI81	CIAPIN1	Anamorsin	1,5	0,013	PRDX2
Q13573	SNW1	SNW domain-containing protein 1	1,5	0,02	PRDX2
Q99447	PCYT2	Ethanolamine-phosphate cytidylyltransferase	1,5	0,028	PRDX2
F5H345	HMBS	Hvdroxymethylbilane synthase	1,5	0,038	PRDX2
013015	MLLT11	Protein A F1a	1.5	0.049	PR DX2
O9Y5M8	SR PR B	Signal recognition particle receptor subunit beta	1.4	0	PR DX2
A0A087WW06	TTC28	Tetratricopentide repeat protein 28	1.4	0	PR DX2
086¥56	DNA A F5	Dynein assembly factor 5 avonemal	1.4	0.004	PR DX2
Q80190	EFF1AKNMT	eFF1A lysine and N-terminal methyltransferase	1,1	0.05	PR DX2
OSND24	D NE214	PINC forget protein 21/	1,7	0,05	DP DV2
D39019	P D\$19	40\$ ribosomal protein \$19	1,3	0	DR DY2
 	VDC4A	Vacualar protein sorting associated protein 4 A	1,3	0.002	DP DV2
0911102	V F34A	vacuorar protein sorting-associated protein 4A	1,3	0,002	PRDA2
404.00778/11/20	HUUKI		1,3	0,005	PKDA2
AUAU8/WUK2	HNKNPDL	Heterogeneous nuclear ribonucleoprotein D-like	1,3	0,006	PKDX2
Q13625	1 P53BP2	Apoptosis-stimulating of p53 protein 2	1,3	0,006	PRDX2
091352	ZNF330	Zinc finger protein 330	1,3	0,016	PKDX2
Q99569	PKP4	Plakophilin-4	1,3	0,019	PRDX2
Q5VVQ6	YOD1	Ubiquitin thioesterase OTU1	1,3	0,045	PRDX2

Colling         Dial Researce         Dial Researce         Dial Researce         Dial Researce           SPREME         ATXNI         Aminia         1.2         0.001         PRDX2           SPREME         ATXNI         Aminia         1.2         0.004         PRDX2           SPREME         ATXNI         Aminia         1.2         0.004         PRDX2           SPREME         ATXNI         Aminia         1.3         0.005         PRDX2           SPREME         ATXNI         Aminia         1.3         0.005         PRDX2           SPREME         ATXNI         Margin Sectore         1.3         0.015         PRDX2           SPREME         ATXNI         Margin Sectore         0.015         PRDX2           SPREME         Type Sectore         1.1         0.015         PRDX2           SPREME         Type Sectore	O/MCS5	AMOT	A	1.2	0.040	DD DV2
C3B/5         LIM0         LIM0         PR02           PSP8/6         LIM2         Attria 2         0.005         PR02           ADMOUNDAM         MYNN         Ensemmention probate         1.2         0.005         PR02           LONDAUGAMA         MYNN         Ensemmention probate         1.2         0.005         PR022           Q2290         GLAN         Gonralia         1.4         0.005         PR022           Q21753         K         Prace field         1.3         0.025         PR022           Q2154         MAPSYC         Mongenetization field income finance fi	Q4VCS5	AMOI	Angiomotin	1,3	0,049	PKDX2
FitVB06         ATXN2         Attain 2         0.04         PEXX2           95998         FMC2         AS processor: spin quary subseth 7         1.2         0.044         PEXX2           A000MMRM8         MTON         Conserved metric large state         1.2         0.041         PEXX2           A000MMRM8         MADE         Conserved protein bias kinnse         1.2         0.041         PEXX2           QUVG4         MADE         Made grammed and grammed: Gegic complex whem 1         1.2         0.043         PEXX2           QUVG4         MADE         Conserved algement: Gegic complex whem 1         1.2         0.041         PEXX2           QUVG4         MADE         Associaa         Associaa         1.3         0.041         PEXX2           QUVG4         ASC33         Asteriza 3         1.1         0         PEXX2         QUVG4         PEXX2	C9JRJ5	LIMD1	LIM domain-containing protein 1	1,2	0,001	PRDX2
P3999         PMC2         285 postanore equilary ubair 7         1.3         0.001         PRD2           MAMMAMAS         More of Locomatical graphs in 6         1.3         0.005         PRD2           PC38-4         XRN1         55' cardiomachan         1.3         0.005         PRD2           QPL04         GLMN         General dupments of degraphs subara1         1.3         0.015         PRD2           QPL05         MAPSIN         Magenesin fand guards fands and in a 1         1.2         0.014         PRD2           QPL05         MASC3         Actional guard antice graphs subara1         1.2         0.014         PRD2           QPL05         MASC3         Actional guard antice graph subara1         1.2         0.014         PRD2           QPL05         MASC3         Actional guard antice graph subara1         1.3         0.01         PRD2           QPL05         MASC4         Mayrin 3         1.3         0.01         PRD2           QPL05         PMAC2         PRD2         1.3         0.01         PRD2           QPL05         PMAC2         PRD2         1.3         0.01         PRD2           QPL05         PMAC2         PMAC2         PRD2         QPL05         QPL05 <td< td=""><td>F8WB06</td><td>ATXN2</td><td>Ataxin-2</td><td>1,2</td><td>0,003</td><td>PRDX2</td></td<>	F8WB06	ATXN2	Ataxin-2	1,2	0,003	PRDX2
AddMAMMAMMYGEUnconnantand mynin-61-20.005PEDD2Q29294GLMNClasulia1.20.005PEDD2Q292951GLMNClasulia1.20.013PEDD2Q292951MAPINCMergers sertured promits hana kinase kinase1.20.013PEDD2Q19173IKPaciefs Kell1.30.025PEDD2Q19174COCIConsertured digments Generic sequences1.30.031PEDD2Q20565MAPINSMergers sertured digments Generic sequences1.30.031PEDD2Q20576ANDAAchigruis1.00.01PEDD2Q20576ANDAAchigruis1.00.01PEDD2Q20576ANDAAchigruis1.10.01PEDD2Q20576ANDAAchigruis1.10.01PEDD2Q20576ANDAAchigruis1.10.01PEDD2Q20576ANDAAchigruis1.10.01PEDD2Q20576ANDAAchigruis1.10.01PEDD2Q20576ANDAAchigruis1.10.01PEDD2Q20576NUPUNNuclear proceensing high genoticentice1.10.01PEDD2Q20576NUPUNNuclear proceensing high genoticentice1.10.01PEDD2Q20576NUPUNNuclear proceensing high genoticentice1.10.01PEDD2Q20576NUPUNNuclear proceensing high genoticentice1.10.01PEDD2Q	P35998	PSMC2	26S proteasome regulatory subunit 7	1,2	0,004	PRDX2
JHC554         KR1N         6-3 <sup>+</sup> enrobunchenz         1.2         0.005         PRDX2           Q29595         GLAN         Glownhn         1.2         0.005         PRDX2           Q29575         MA2PX         Micopa activitation protein kinase kinase kinase         1.2         0.003         PRDX2           Q29576         MA2PX         Micopa activitation signal consignation i consigna obtainiti 3         1.2         0.003         PRDX2           Q29426         MAPX3         Micopa activitation signal consignation i consigna obtainiti 3         1.2         0.013         PRDX2           Q29426         MAX3         Advertiniti 3         1.2         0.01         PRDX2           Q29556         MAX4         Protoconsignation signal consignation i consignation signal consigna consignation signal consigna consignation signal consig	A0A0A0MRM8	MYO6	Unconventional myosin-6	1,2	0,004	PRDX2
QP2990         GLAM         Gaunala         L2         Q.005         MARENY         Microgen activate print insize kinase insize         L2         Q.013         FRXZ           Q.012.0         IK         Protein Red	H7C5E4	XRN1	5'-3' exoribonuclease 1	1,2	0,005	PRDX2
OPUC44         MAPP         Magaesentrad pench Kase kunse kunse         1.2         0.033         PRDX2           QNFT VP         COG1         Conserved digometric Gagic amplica whenis 1         1.2         0.035         PRDX2           QNFT VP         COG1         Conserved digometric Gagic amplica whenis 1         1.2         0.035         PRDX2           QNFTX         Accienting ingual conservation 20-1         1.2         0.041         PRDX2           QNFTX         Anky NA         Advino 3         1.1         0         PRDX2           QUE55         ANK3         Advino 3         1.1         0.01         PRDX2           QUE56         MAK         Advino 3         1.1         0.002         PRDX2           QUE56         MAK         Processore whening protein 3         1.1         0.001         PRDX2           QUE56         MAK         Processore whening protein 3         1.1         0.001         PRDX2           QUE56         MAK         Processore whening protein 3         1.1         0.017         PRDX2           QUE56         MAK         Processore whening protein 3         1.1         0.017         PRDX2           QUE56         MAK         Processore whenin in 1         0.016         PRDX2 <td>Q92990</td> <td>GLMN</td> <td>Glomulin</td> <td>1.2</td> <td>0.006</td> <td>PRDX2</td>	Q92990	GLMN	Glomulin	1.2	0.006	PRDX2
OLD 3         BC         Perms Ref.         1.2         0.93         PRUX2           QPWTW CGG1         Conserved slopmert, Gaja congle submari 1         1.2         0.93         PRUX2           QPS66         MKPS1         285 rhossmal presins S1, microheshini 1         1.2         0.93         PRUX2           QPS66         MKS7         The interimiting stand conserved longer should 3         1.2         0.94         PRUX2           QPS66         MKS1         Adverting stand conserved longer should a light type.5         1.1         0         PRUX2           QS555         MKS1         Protesserve submit alget type.5         1.1         0.01         PRUX2           QS554         PMKY         Propager-submit (n genesis happer)         1.1         0.01         PRUX2           QS554         PMKY         Propager-submit (n genesis happer)         1.1         0.015         PRUX2           QV1546         GB42         Demospheric break straining presin happer)         1.1         0.015         PRUX2           QV1546         GB42         Demospheric break straining presin happer)         1.1         0.015         PRUX2           QV1546         GF44         SAFB         Sofid attrainment factor B1         1.1         0.015         PRUX2 <t< td=""><td>09UG54</td><td>MAD3K7</td><td>Mitogen activated protein kinase kinase kinase</td><td>1.2</td><td>0.013</td><td>DR DY2</td></t<>	09UG54	MAD3K7	Mitogen activated protein kinase kinase kinase	1.2	0.013	DR DY2
QUITY         LO         CO	012122	IV IV	Dentrin Ded	1,2	0.022	DR DV2
QPM M         CD61         Conserve displantic segment is submit 1         1.2         0.035         PRDX2           QPM M         ABCC1         Accorning space longing and tongenese submit 3         1.2         0.015         PRDX2           QPM M         ABCC1         Accorning space longing and tongenese submit 3         1.2         0.011         PRDX2           QPM M         ABC1         Accorning space longing and tongenese submit 3         1.4         0.0         PRDX2           QPM M         PRDX4         Processes and space submit 3 plant ryse5         1.1         0.001         PRDX2           QPM M         PRDX2         1.1         0.001         PRDX2         1.1         0.001         PRDX2           QPM M         Processes closure submit a space-balancy constraints grance-balancy constraints granconstraints grance-balancy constraints granconstrain	Q13123	IK		1,2	0,025	PRDAZ
Q2465         MIR-31         28 bitsonal protein 331, mischondrial         1.1         0.013         PRDX2           QANGCI         ACC, A. A. Arbrains grand complex bubint 1         1.2         0.014         PRDX2           Q2555         ANKS         A. Arbrains grand consigned to Alber type 5         1.1         0         PRDX1           Q2554         DNAK         A. Arbrain W. Sharins         1.1         0.01         PRDX2           Q2554         DNAK         A. Arbrain W. Sharins         1.1         0.01         PRDX2           Q2554         DNAK         A. Arbrain W. Sharins         1.1         0.01         PRDX2           Q2554         DNAK         Dody Insolid gubtainly C. Cambrain grants-halle grants-halle gubtainly G. Gambard         1.1         0.015         PRDX2           Q2554         DNAK         Does consolid consolid gubtainly G. Gambard         1.1         0.015         PRDX2           Q1126         DSG2         Decomplete-2         1.1         0.015         PRDX2           Q1136         DSG2         Decomplete-2         1.1         0.017         PRDX2           Q11361         DSG2         Decomplete-2         1.1         0.017         PRDX2           Q114161         Heroprosona machar those relegorosona m	Q8W1W3	COGI	Conserved oligomeric Golgi complex subunit 1	1,2	0,025	PRDX2
QMNCo         Acteriang signal coinsegrent 1 complex medunit3         1.2         0.014         PRDX2           QMPSX6         TPIP         Tright junction powerint 20-1         1.2         0.014         PRDX2           QMPSX6         MNKA         Ankyrins3         1.1         0         PRDX2           QMPSX6         WNNPP         ATAsas WNNP         1.1         0.001         PRDX2           QMPSX6         WNNPP         ATAsas WNNP         1.1         0.001         PRDX2           QMPSX6         GMP2         1.1         0.011         PRDX2           QMPSX6         GMP2         Ata CTP2a-acterizing person-binding posinia         1.1         0.015         PRDX2           QMPSX6         DMP3A         DMP3A         PRDX2         PRDX2         PRDX2           QMPS0         NUSPO         Nusleer posic complex toxinome differencing         1.1         0.017         PRDX2           QMP3A         IBSG         Descodaria         1.1         0.017         PRDX2           QMP3A         Histing acting toxinome differencing         1.1         0.017         PRDX2           QMP3A         Histing acting toxinome differencing         1.1         0.017         PRDX2           QMP3A         Histing	Q92665	MRPS31	28S ribosomal protein S31, mitochondrial	1,2	0,033	PRDX2
ADMPCNNCP         TJP1         Tight incodes groots ADO-1         1.1         0.0+1         PRDX2           Q2555         ANKS         Ankyrin 3.         1.1         0.0         PRDX2           Q28656         PSMA5         Processone substring hypes 5.         1.1         0.001         PRDX2           Q28553         WANTP         Probab models gatisfing for simple of the simple processon proceson processon proceson pro	Q8N3C0	ASCC3	Activating signal cointegrator 1 complex subunit 3	1,2	0,034	PRDX2
Q1295         ANK3         Ankyrn-3         1.1         0         PR022           Q2865         WRNPI         ATbac WRNPI         1.1         0.001         PR022           Q2855         WRNPI         ATbac WRNPI         1.1         0.001         PR022           Q29543         DNAJC2         Dual formolog ubrandy (member 2         1.1         0.011         PR022           Q29543         DNAJC2         Dual formolog ubrandy (member 2         1.1         0.015         PR022           Q1126         DSG2         Demogéner 2         1.1         0.015         PR022           Q1126         DSG2         Demogéner 2         1.1         0.017         PR023           Q1124         SAFB         Scafied attachment facts B         1.1         0.017         PR023           Q1124         SAFB         Scafied attachment facts B         1.1         0.029         PR023           Q1124         SAFB         Scafied attachment facts B         1.1         0.029         PR023           Q1124         SAFB         Scafied attachment facts B         1.1         0.049         PR023           Q1124         AFB         Scafied attachment facts B         1.1         0.049         PR023	A0A087X0K9	TJP1	Tight junction protein ZO-1	1,2	0,041	PRDX2
P3866P685.Portane whan right rge 5.1.10.0PRX2Q8575.PKNVPhophoneralours kinas1.40.002PRX02Q8176.PKNVPhophoneralours kinas1.40.01PKN22Q8178.0DNAJ(C2Durb londing adding from frage1.40.01PKN22Q8178.0DNAJ(C2Durb londing adding from frage1.40.01PKN22Q8178.0DSAG2Donesder person hype frage1.40.01PKN22Q9174.0DSAG2Donesder person hype frage1.40.07PKN22QNS74SAFBSanding trachinera factor B1.40.02PKN22QNS74SAFBSanding trachinera factor B1.40.02PKN22QNS75CSNC3Donesse compocert RPN41.40.02PKN22QNS74GAFBSanding trachinera factor B1.40.02PKN22QNS74GAFBNacleor COmpocert RPN41.40.02PKN22QNS74GAFBNacleor COmpocert RPN41.40.02PKN22QNS74GAFBNacleor COmpocert RPN41.40.03PKN22QNS74GAFBNacleor COmpocert RPN41.40.03PKN22QNS74GAFBNacleor COmpocert RPN41.40.04PKN22QNS74GAFBNacleor COmpocert RPN41.40.04PKN22QNS74GAFBNacleor COmpocert RPN41.40.04PKN22QNS74GAFBNacleor COmpocert RPN41.4 </td <td>Q12955</td> <td>ANK3</td> <td>Ankyrin-3</td> <td>1,1</td> <td>0</td> <td>PRDX2</td>	Q12955	ANK3	Ankyrin-3	1,1	0	PRDX2
Q8655         WR.NPI         ATPa WENTPI         1.1         0.001         PRDX2           Q9336         PMVK         Phosphoens/constrainstance         1.1         0.011         PRDX2           Q99439         DNA(C2         Drail homolog subfamily framming protein-banding protein 2         1.1         0.011         PRDX2           P577a0         NUP107         Nuclear port complex protein Nup107         1.1         0.015         PRDX2           Q11362         DSG2         Demosphic 2         1.1         0.017         PRDX2           Q15141         SATB         Scrifdel arten-hock 70 MD protein 10         1.1         0.026         PRDX2           QNV175         EXOG3         Exome complex comporant RP4P0         1.1         0.026         PRDX2           Q91241         HITEROSPICIAL Interpretentartering protein and art monic-legoregroterin A         1.1         0.038         PRDX2           Q01356         PTP1A1         Laproporting complex motein 1         1.1         0.048         PRDX2           Q01316         PTP1A1         Laproporting complex motein and art monic-legorestimatein and	P28066	PSMA5	Proteasome subunit alpha type-5	1,1	0	PRDX2
Q1516         PMVK         Prophenors/burk fixase.         1.1         0.002         PRIX2           Q959A3         DNA(C2         Dnaj honolog public provine honding provine 2         1.1         0.013         PRIX2           Q91M8         G3892         Ra GTIssa activating provine honding provine 2         1.1         0.015         PRIX2           Q91M16         DSS2         Demopsite 2         1.1         0.015         PRIX2           Q1M126         DSS2         Demopsite 2         1.1         0.017         PRIX2           Q1M215         EXOSC3         Exosore complex composer R1P40         1.1         0.029         PRIX2           Q1M215         EXOSC3         Exosore complex composer R1P40         1.1         0.029         PRIX2           Q0M215         Mackodar GTTShoning protein 1         1.4         0.029         PRIX2           Q0175         Mackodar GTTShoning protein 1         1.4         0.031         PRIX2           Q0184         PMIA1         Liptro-lipha         1.4         0.049         PRIX2           Q1184         ANACCI         Anghase promoting complex solutini 1         1.4         0.049         PRIX2           Q1354         PMIA1         Liptro-lipha         Lipha         0.049	096855	WRNIP1	ATPase WR NIP1	1.1	0.001	PRDX2
XOP543         DNA1c2         Dual hemologuskamity G muslew 2         11         0.01         PRDX2           QVDN86         G3B72         R.o GTIses extinuing protein 2         11         0.01         PRDX2           QVDN86         G3B72         R.o GTIses extinuing protein 2         11         0.015         PRDX2           QVDN86         DSG2         Demogle protein Napt         11         0.017         PRDX2           QVA154         SAFB         Safford AVA2 protein 1B         11         0.017         PRDX2           QVA244         SAFB         Safford attachment for DB         11         0.017         PRDX2           QVA075         Extonscc. Ongettor RAP40         11         0.029         PRDX2           QV0075         AIP         Nackolar GTP-binding protein 1         11         0.031         PRDX2           QV2255         DPF2         Zine forger protein is did 4         11         0.044         PRDX2           QV1314         AAAPCL         Anaphase promoting complex submit 1         11         0.054         PRDX2           QV2255         DPF2         Zine forger protein sub 44         11         0.054         PRDX2           QV2344         RAACKL         Rasocial growtin kinasa 1         11	015126	PMVK	Phosphomevalonate kinase	11	0.002	PR DX2
Q2P35         DPACA2         Doubling under durating protein handing protein 2         11         0.01         PRDX1           P5760         NUP107         Nuclear port complex protein Napt07         14         0.015         PRDX2           P57760         NUP107         Nuclear port complex protein B         14         0.015         PRDX2           P0DAV9         HSNL1B         Heat book 70 kD protein B         14         0.017         PRDX2           QN0215         EXX0C3         Examon complex component R 4P 40         14         0.029         PRDX3           QN0215         EXX0C3         Examon complex component R 4P 40         14         0.029         PRDX3           QN0215         EXX0C3         Examon complex component R 4P 40         14         0.029         PRDX3           QN0215         EXX0C3         Examon complex component R 4P 40         14         0.029         PRDX3           QN0215         EXX0C3         Examon complex component R 4P 40         14         0.029         PRDX3           QN124         At ANAPC1         Anaphase promoting complex subant 1         14         0.494         PRDX2           QN134         FRDX4         Anaphase promoting complex subant 1         14         0.494         PRDX2	0995.42	DNAIC2	Drathandar when in Commerce 2	1,1	0,002	DR DV2
QPUN8         CBM2         Rate 1 prise critical protein hunding protein 2         1.1         0.013         PRDX2           QP1426         DSC2         Desnogetin 2         1.1         0.015         PRDX2           QPUN79         HSDn1B         1.1         0.015         PRDX2           QPUN74         HSDn1B         1.1         0.017         PRDX2           QPN0T5         Exconce complex omporter RAP0         1.1         0.027         PRDX2           QPN0T5         Exconce complex comporter RAP0         1.1         0.028         PRDX2           QPN0T5         HNNPM         Heterogene comporter RAP0         1.1         0.03         PRDX2           QPN0T5         AIP         AII receptor interacting protein n         1.1         0.048         PRDX2           QP134         GTPBPA         Nuclear GTPC resins tabs 4         1.1         0.048         PRDX2           QP144         ANAPCI         Anaphase-prometring somplex subants 1         1.1         0.048         PRDX2           Q2484         ROCKI         Rob sex-scintarg protein insare 1         1.1         0.048         PRDX2           Q3454         ROCKI         Rob sex-scintarg protein insare 1         1.0         0.058         PRDX2	Q77545	DNAJC2	Dhaj homolog subranny C member 2	1,1	0,011	PRDAZ
P37740         NUP107         Nuclear pore complex protein Nup107         1.1         0.015         PRDX2           Q1H26         DSG2         Dexnoglin-2         1.1         0.017         PRDX2           Q1N126         DSG2         Dexnoglin-2         1.1         0.017         PRDX2           QNQT5         EXOSC3         Exosome complex component R.R140         1.1         0.022         PRDX2           QPNQT5         EXOSC3         Exosome complex component R.R140         1.1         0.022         PRDX2           Q00170         AIP         AH receptor-interacting protein         1.1         0.032         PRDX2           Q91314         Nacelear CTP Inhinding protein         1.1         0.042         PRDX2           Q9214A         ANAPCI         Angulax protein divida         1.1         0.048         PRDX2           Q9238         DP12         Zinc finger protein divida         1.1         0.048         PRDX2           Q92484         AKOCK         Rebuscating protein divida         1.1         0.048         PRDX2           Q92485         ARDEFI         Protein divida         1.1         0.048         PRDX2           Q94540         NGLY         Protein divida         1.1         0.048	Q90 N86	G3BP2	Ras G I Pase-activating protein-binding protein 2	1,1	0,013	PRDX2
QH126         DSC2         Demoglen-3         1.1         0.017         PRDX2           QDMVP         HSPA1B         Heatsbock 70kDa protein B         1.1         0.017         PRDX2           QI5424         SAFB         Saf6d strachment factors B         1.1         0.017         PRDX2           QVRQTS         EXX0SC3         Exxosme complex component RFP40         1.1         0.022         PRDX2           PS227         HNRNPM         Henrogeneous nuclear thomacleoprotein M         1.1         0.032         PRDX2           Q98264         GTBP44         Nacleadar GTP-Hinding protein 1         1.1         0.043         PRDX2           Q91316         PPR17         Zinc finger protein ubi-d4         1.1         0.048         PRDX2           Q1344         ANCKI         Rube-associaded postin kinase 1         1.1         0.048         PRDX2           Q13451         KBP5         Protein-Vick-Associaded postin kinase 1         1.0         0.055         PRDX2           Q13451         KBP5         Protein-Vick-Associaded postin kinase indep rotein 8         1.1         0.068         PRDX2           Q13451         KBP5         Protein-Vick-Associaded postin kinase indep rotein 1         1         0.069         PRDX2           Q13454	P57740	NUP107	Nuclear pore complex protein Nup107	1,1	0,015	PRDX2
PDDMVP         INFA1B         Hertochec.70 kDp protein 18         1.1         0.017         PRDX2           QSV241         SAFB         Sarafid attractionmer factor B1         1.1         0.026         PRDX2           QNV075         EXOSC3         Exosome complex component R.RP40         1.1         0.022         PRDX2           QONTO         AIP         AI receptor-interacting protein         1.1         0.022         PRDX2           QUBL54         GTTBPH         Nuclesker TP-Heinding protein         1.1         0.032         PRDX2           QUBL54         GTTBPH         Nuclesker TP-Heinding protein function         1.1         0.048         PRDX2           QUBL54         ANAPCI         Anaphase promoting complex suburit 1         1.1         0.048         PRDX2           QUB154         AXAPS         Akames ranker protein function         1.1         0.048         PRDX2           QUB354         HOCK1         Reprode/protein functions         PRDX2         PRDX2         PRDX2           QUB354         HOCK1         Reprode/protein functions         PRDX2         PRDX2         PRDX2           QUB354         RACDS3         1         0.055         PRDX2           QUB354         RACDS3         1         0.066	Q14126	DSG2	Desmoglein-2	1,1	0,015	PRDX2
Qi542         SAFB         Safdid attachment factor B1         1.1         0.017         PRDX2           QNQTS         EXX0SC3         Rooms: complex rubhandsoprotein M.         1.1         0.029         PRDX2           PS222         HNRNPM         Hercosponces nuclear ithonucleoprotein M.         1.1         0.029         PRDX2           QB262         GTBP4         Naleolar GTP binding protein 1         1.1         0.031         PRDX2           QB275         DPF2         Zinc fingg protein ingen protein inde-4         1.1         0.044         PRDX2           Q2755         DPF2         Zinc fingg protein inde-4         1.1         0.044         PRDX2           Q3136         AKAP8         Akinase androp rotein 8         1.1         0.044         PRDX2           Q45151         KBPS         Peptdo-10x-lock-seqbosantinylaparaging anitias         1.1         0.046         PRDX2           Q1451         KBPS         Peptdo-10x-lock-seqbosantinylaparaging anitias         1.1         0.046         PRDX2           Q1451         KBPS         Peptdo-10x-lock-seqbosantinylaparaging anitias         1.1         0.048         PRDX2           Q1451         KBPS         Peptdo-10x-lock-seqbosantinylaparaging anitias         1.1         0.049         PRDX2	P0DMV9	HSPA1B	Heat shock 70 kDa protein 1B	1,1	0,017	PRDX2
QPNQT5LNSC3Encome complex complex RRP401.10.02PRDX2P32272HNR NMHeresponens macher ribonatolesporetin M1.10.02PRDX2Q98ZF4GTPBY4Nuclear GTP binding protein1.10.03PRDX2Q98ZF4GTPBY4Nuclear GTP binding protein1.10.042PRDX2Q98ZF4GTPBY4Nuclear GTP binding protein1.10.043PRDX2Q2735DPF2Zine finger protein sin-11.10.048PRDX2Q13464ROCK1Ro associated protein kinas 11.10.048PRDX2Q46V0NGL1Puptids-N()-(N-sery)-betz glacoannin/)paparagine amdase1.10.068PRDX2Q3454RKBFPuptids-N()-(N-sery)-betz glacoannin/)paparagine amdase1.40.068PRDX2Q3454RKBFPuptids-N()-(N-sery)-betz glacoannin/)paparagine amdase1.40.068PRDX2Q3454RKBFPuptids-N()-(N-sery)-betz glacoannin/)paparagine amdase1.40.068PRDX2Q3454RANBRRan-percin CTPTas-activating protein1.40.061PRDX2Q91356BOLA2BoLA11protein Hock borndog31.40.002PRDX3Q91364PRDX1Percointeloain 5, ninechandrial3.10.002PRDX3Q90364PRDX2Proteinteloain 5, ninechandrial3.10.002PRDX3Q9044PRDX5Proteinteloain 5, ninechandrial2.70PRDX3Q90574KAB1FIPKab11 fuml-interescritug protein 1<	Q15424	SAFB	Scaffold attachment factor B1	1,1	0,017	PRDX2
P3227         HNR NTM         Herrogeneon under roboux/coprosein M         1.1         0.029         PRDX2           000170         AIP         All recrogeneon under roboux/coprosein 1         1.1         0.029         PRDX2           Q01316         PFF1A1         Liprin-alpha-1         1.1         0.032         PRDX2           Q21316         PFF1A1         Liprin-alpha-1         1.1         0.042         PRDX2           Q22385         DFF2         Zinc finger protein wid-4         1.1         0.048         PRDX2           Q31346         ROCKI         Rob associated protein finance 1         1.1         0.048         PRDX2           Q48433         KARP8         Akinase ancher protein silo anomyling-program undere         1.1         0.048         PRDX2           Q48431         RABP1         Ranogencific GTPse-activating protein         1         0.006         PRDX2           Q48438         HOOK3         Protein Hock bronleg 3         1         0.014         PRDX2           Q48458         HOOK3         Protein Hock bronleg 3         1         0.014         PRDX2           Q48458         HOOK3         Protein Hock bronleg 3         1         0.014         PRDX2           Q4915K6         BOLA12         BoL A	O9NOT5	EXOSC3	Exosome complex component RRP40	1,1	0,026	PRDX2
Autom         Interpretation         Interpretation         Interpretation         Interpretation         Interpretation           QPBZE4         GTPBP4         Nucleolar GTP binding protein         1.1         0.03         PRDX2           QPBZE4         GTPBP4         Nucleolar GTP binding protein         1.1         0.043         PRDX2           QPBL74         ANAPC1         Anaphase-protein dis-14         1.1         0.044         PRDX2           Q2735         DPF2         Zine finger protein dis-64         1.1         0.048         PRDX2           Q3434         ROCK1         Rho associated protein kinase 1         1.1         0.048         PRDX2           Q941V0         NGIY1         Peptide/N(i)(N-aceryl-betre/glacoaminyl)aparagine amidase         1.1         0.045         PRDX2           Q94353         AKABE7         RANBPI         Ran-specific GTPasa-activating protein         1         0.0046         PRDX2           Q94575         RANBPI         Ran-specific GTPasa-activating protein         1         0.018         PRDX2           Q94586         BOLA2         BolA-like protein 2         1         0.018         PRDX3           Q90530         PRDX1         Perosiredonin-1         3.1         0         PRDX3	P52272	HNR NPM	Heterogeneous nuclear ribonucleoprotein M	11	0.029	PR DX2
Optimization         All         Optimization of the protein         1.1         0.00.2         PRDX2           QB3EE4         GTTBPH All         Liptin sights-1         1.1         0.014         PRDX2           QB3E5         PPF1A1         Liptin sights-1         1.1         0.044         PRDX2           Q2235         DPF2         Zincfinger protein bul-d4         1.1         0.044         PRDX2           Q2235         AKAP8         Akinase anchor protein Kinase 1         1.1         0.048         PRDX2           Q3364         ROCKI         Rho-scalard protein Kinase 1         1.1         0.048         PRDX2           Q4849         NG1/1         Peptidyl-problectrage incoming/happraging andiase         1.1         0.048         PRDX2           Q4849         RANBP1         Ras-specific GTPase activating protein         1         0.006         PRDX2           Q4848         HOOX3         Protein Hook homolog 3         1         0.014         PRDX2           Q4958         HOOX3         Protein Hook homolog 3         1         0.014         PRDX2           Q49588         HOOX3         Protein Hook homolog 3         1         0.014         PRDX2           Q49548         HOOX4         Protein Hook homolog 3 <td>000170</td> <td>AID</td> <td>All recentor interacting protain</td> <td>1,1</td> <td>0.029</td> <td>DP DY2</td>	000170	AID	All recentor interacting protain	1,1	0.029	DP DY2
QPB24         G17B94         Nucleastr G1 Primaling protein 1         1.1         0.03         PRDX2           QPH1A4         ANAPC1         Anaphase-promoting complex subunit 1         1.1         0.045         PRDX2           QPH34         ROCK1         Rho-associated protein kinase 1         1.1         0.045         PRDX2           Q13464         ROCK1         Rho-associated protein kinase 1         1.1         0.045         PRDX2           Q94104         NGK11         Peptide-N(4)(N-assrt)-beta glucosaminy)aparagine amidase         1.1         0.055         PRDX2           Q94100         NGK11         Peptide-N(4)(N-assrt)-beta glucosaminy)aparagine amidase         1.1         0.066         PRDX2           Q94383         AKAPB         Rhoshbenolog 3         1         0.016         PRDX2           Q94384         RANBP1         Ran-specific GTPase activating protein         1         0.018         PRDX2           Q94385         PROX1         Prosite/Achebohoolg 3         1         0.014         PRDX2           Q91386         BOLA2         BolA-like protein 2         1         0.018         PRDX2           Q914366         BOLA2         Pablabit protein (assite activating protein 1         2,7         0         PRDX3	000170	AIF CTDDD/	N l l CTD1: l:	1,1	0,027	PR DY2
Q13136         PPTA1         Liprin-alpha-1         1,1         0,032         PRDS2           Q21738         DF2         Zinc finger protein ubi-44         1,1         0,044         PRDS2           Q22738         DF2         Zinc finger protein ubi-44         1,1         0,048         PRDS2           Q43844         ROCKI         Rho-associated protein finansa 1.         1,1         0,048         PRDS2           Q43823         AKAP8         A-kinase ancher protein finansa 1.         0,050         PRDS2           Q43843         RAMP5         Leptide/N(4)-(K-acerty-bets glucosaming/laparagine anidase         1,1         0,068         PRDS2           Q23848         ARIGEF1         Rho guanine nucleotide exchange factor 1         1         0,006         PRDS2           Q48V38         HOOK3         Protein Hook homolog 3         1         0,014         PRDS2           Q913164         BOLA2         Calherin-2         1         0,034         PRDS2           Q90430         PRDX1         Perosiredoxin-5, mitochondrial         3,1         0.002         PRDS3           Q9044         PRDX1         Perosiredoxin-5, mitochondrial         3,1         0.002         PRDS3           Q6WX24         RAB1HFP1         Rabi-1 family-inte	Q9BZE4	GTPBP4	Nucleolar G I P-binding protein 1	1,1	0,03	PKDX2
QPH1A4         ANAPC1         Anaphase-promoting complex subanti 1         1,1         0,044         PRDN2           Q22785         DPF2         Zinc finger protein in kinase 1         1,1         0,048         PRDN2           Q13464         ROCK1         Rho-associated protein kinase 1         1,1         0,048         PRDN2           Q64V0         NGLY1         Peptidel-Net/et/Natertyl-betrag incomaning/laparagine amiduse         1,1         0,055         PRDN2           Q13451         FKBP5         Peptidel-probl (ist trans isomerase FKBP5         1         0,006         PRDN2           Q28488         ARABEP1         Ran-specific GTPas-activating protein         1         0,018         PRDN2           Q86V58         BOLA2         BolA-like protein 2         1         0,018         PRDN2           Q96305         PRDN31         Proxitrodoxin-5         3,1         0         PRDN3           Q96434         PRDN35         Peroxitrodoxin-5         3,1         0,002         PRDN3           P19022         CDH2         Calaberin2         1         0,018         PRDN3           P19034         PRDN35         Peroxitrodoxin-5, minochondrial         3,1         0,002         PRDN3           P19044         PRDN35	Q13136	PPFIA1	Liprin-alpha-1	1,1	0,032	PRDX2
Q2278         DP12         Zinc finger protein ubi-di         1.1         0.048         PRDX2           Q13646         ROCK1         Rho associated protein finase 1         1.1         0.048         PRDX2           Q04170         NGLY1         Peptide-N(4)(N-sceryl-beta-gluconaminyl)aparagine amidase         1.1         0.065         PRDX2           Q04170         NGLY1         Peptide-N(4)(N-sceryl-beta-gluconaminyl)aparagine amidase         1.1         0.065         PRDX2           Q04384         RANBP1         Rn-specific GTPas-acciatizing protein         1         0.066         PRDX2           Q34387         RANBP1         Rn-specific GTPas-acciatizing protein         1         0.018         PRDX2           Q48478         ROLA         Bol-Alke protein 2         1         0.018         PRDX2           Q48430         PRDX1         Perosiridoxin-5, mitochondrial         3.1         0         PRDX3           Q68430         PRDX1         Perosiridoxin-5, mitochondrial         3.1         0.002         PRDX3           Q68430         PRDX1         No-specific serice/Arrinomic protein fixase         2.7         0         PRDX3           Q68430         PRDX1         No-specific serice/Arrinomic protein fixase         2.4         0.002         PRDX3	Q9H1A4	ANAPC1	Anaphase-promoting complex subunit 1	1,1	0,044	PRDX2
Q13464         ROCK1         Rho-associated protein kinase 1         1.1         0.048         PRDX2           Q64503         AKADB         Akinase anchor protein B         1.1         0.055         PRDX2           Q61V0         NGLY1         Peptide/Prob/16 strans isomerase FKBP3         1         0.065         PRDX2           Q13451         FKBP3         Peptide/Prob/16 strans isomerase FKBP3         1         0.066         PRDX2           Q43483         AARHGEFI         Rhog annie nucleedite schwang factor 1         1         0.068         PRDX2           Q48VS8         HOOK3         Protein Hook homolog 3         1         0.014         PRDX2           Q9H3K6         BOLA2         BolA/like protein 2         1         0.034         PRDX2           Q9H3K6         PRDX1         Prostriedoxin-1         3.1         0         PRDX3           P19022         CDH2         Cadherin-2         1         0.034         PRDX3           P30044         PRDX5         Perostriedoxin-1         3.1         0.002         PRDX3           P30404         PRDX5         Perostriedoxin-1         3.1         0.002         PRDX3           SWB79         WKK2         Nons-specific strinc/threenine protein fixase         2.	Q92785	DPF2	Zinc finger protein ubi-d4	1,1	0,045	PRDX2
Q43823         AKAP8         A-kinase anchor protein 8         1.1         0.048         PRDX2           Q961V0         NGLY1         Peptide-N(4)-(N-acer)-beta-glucosaninyl)aspragine amidase         1.1         0.065         PRDX2           Q13451         FKBP5         Peptide/h(4)-(N-acer)-beta-glucosaninyl)aspragine amidase         1.1         0.066         PRDX2           Q2288         ARHOEF1         Rho guanne nucleotide exchange factor 1         1         0.068         PRDX2           Q86578         HOOK3         Protein Hook homolog 3         1         0.014         PRDX2           Q913K6         BOLA2         BolA-like protein 2         1         0.018         PRDX2           Q06530         PRDX1         Perositedoxin 1         3.1         0         PRDX3           Q66540         PRDX1         Perositedoxin 5, mitochondrial         3.1         0.02         PRDX3           Q66547         PRDX1         Perositedoxin 5, mitochondrial         2.7         0         PRDX3           Q66547         PRDX1         Pachobale non-functorial immunoglobulin kapa variable 2D-24         2.7         0         PRDX3           Q674787         WK2         Non-specific sertine/threonine protein ingase 42.5         0.02         PRDX3	Q13464	ROCK1	Rho-associated protein kinase 1	1,1	0,048	PRDX2
Op61V0         NGLY1         Peptide/Net/CN-accrybeta-glucesaming/japaragine amidase         I.1         0.05         PRDX2           Q13451         FKBP5         Peptidyl-polyl cistrans isomerase FKBP5         1         0.006         PRDX2           Q2858         ARHGEFI         Rhog nuine nucleotide exchange fictor 1         1         0.008         PRDX2           Q84578         HAOK3         Protein Hook homolog 3         1         0.014         PRDX2           Q9H3K6         BOLA2         BolA-like protein 2         1         0.018         PRDX2           Q9H3K6         PRDX1         Perositedoxin-1         3,1         0.02         PRDX3           Q66300         PRDX1         Perositedoxin-1         3,1         0.02         PRDX3           Q60434         PRDX5         Prostitedoxin-5, nitochondrial         3,1         0,002         PRDX3           Q60435         Prostitedoxin-1         3,1         0,002         PRDX3           Q60437         PRDX5         Prostitedoxin-1         2,7         0         PRDX3           Q60447         RABH1PPI         Rub1Findinyl-interacting protein linase         2,7         0.002         PRDX3           Q6W526         Probable non-functional immunoglobulinkappa variable 2D-24	O43823	AKAP8	A-kinase anchor protein 8	1,1	0,048	PRDX2
Q13451         FKBP5         Peptidyl-prolyl cis-trans isomerase FKBP5         1         0.005         PRDX2           Q2288         ARHGEFI         Rho guanite machentide exchange fractor 1         1         0.006         PRDX2           Q3481         RANBPI         Ran-specific GTBase-activating protein         1         0.014         PRDX2           Q86V58         HOOK3         Protein Hook homolog 3         1         0.014         PRDX2           Q913K6         BOLA2         BolAkile protein 2         1         0.018         PRDX2           Q0650         PRDX1         Perostriedosin-1         3,1         0         PRDX3           S0044         PRDX5         Prostriedosin-1         2,7         0         PRDX3           SWFP9         WNK2         Non-specific serine/threonine protein linase         2,7         0         PRDX3           SWF9P9         WNK2         Non-specific serine/threonine protein linase         2,6         0         PRDX3           SWF9P9         GKYZD-24         Probable non-functional immunoglobulin kppa variable 2D-24         2,7         0.002         PRDX3           GYJ8P         GST21         Maleylacetoactrate isomerase         2,6         0         PRDX3           P14174         MEF </td <td>O96IV0</td> <td>NGLY1</td> <td>Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase</td> <td>1.1</td> <td>0.05</td> <td>PRDX2</td>	O96IV0	NGLY1	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	1.1	0.05	PRDX2
Q2587         FRD J         FRD J         FRD J         FRD J           Q2588         ARHGEFI         Rho guanine nucleotide exchang factor 1         1         0.006         PRDX2           P3487         RANBPI         Ran specific GTPase-activity protein         1         0.014         PRDX2           Q86VS8         HOOK3         Protein Hook homolog 3         1         0.014         PRDX2           Q9H3K6         BOLA2         BolA-like protein 2         1         0.018         PRDX2           Q9H3K6         BOLA2         BolA-like protein 2         1         0.014         PRDX3           Q96080         PRDX1         Proxiredoxin-1         3,1         0.002         PRDX3           Q66WKZ4         RABHFPI         Rabit family-interacting protein 1         2,7         0         PRDX3           Q6WKZ4         RABHFPI         Rabit family-interacting protein 1         2,7         0         PRDX3           Q6WKZ4         RABHFPI         Rabit family-interacting interacting interacting protein 1         2,7         0         PRDX3           Q6WKZ4         RABHFPI         Rabit family-interacting interacting int	013/51	FK BD5	Peptide In(1) IV dect/1 Seta Sidessamm//asparagine annuase	1	0.005	DR DY2
Q22885         ARTIGET1         1         0.006         PRDX2           Q286VS8         HOOK3         Protein Hook homolog 3         1         0.014         PRDX2           Q86VS8         BOLA2         BolA-like protein 2         1         0.018         PRDX2           Q913K6         BOLA2         BolA-like protein 2         1         0.018         PRDX2           Q0630         PRDX1         Peroxiredoxin-1         3.1         0         PRDX3           Q66800         PRDX1         Peroxiredoxin-1, minchondrial         3.1         0.02         PRDX3           Q66810         PRDX1         Peroxiredoxin-1, minchondrial         2,7         0         PRDX3           Q6WKZ4         RABIIFIPI         Rabi1 family-interacting protein 1         2,7         0         PRDX3           Q6WKZ4         RABIIFIPI         Rabi1 family-interacting protein 2         2,7         0.002         PRDX3           Q6WX4         RABIIFIPI         Rabi1 family-interacting famoling homolik happa variable 2D-24         2,7         0.002         PRDX3           Q6WX54         RABOP         For Appimerset I subunit RPB3         2,4         0.002         PRDX3           Q9518         ZRANB2         Zin. Gnger Ran-binding domain-containing protein	Q13431	ADJICEE1	Planet in the second se	1	0,003	PRDA2
P43487         RANBP1         Ranspectin c 1 Pass-activity protein         1         0.008         PHXX2           Q86VS8         HOOKS         Protein Hook homolog 3         1         0.014         PRDX2           Q9H3K6         BOLA2         BolA-like protein 2         1         0.034         PRDX2           Q9H3K6         BOLA2         CDH2         Cadherin-2         1         0.034         PRDX2           Q96305         PRDX1         Peroxiredoxin-5, mitochondrial         3,1         0.002         PRDX3           Q6WKZ4         RABIIPI         Rabii Ionily-interacting protein 1         2,7         0         PRDX3           GWWZ4         RAbii Ionily-interacting protein 1         2,7         0         PRDX3           S0398         GST21         Maleylacetoxetta tic somerase         2,6         0         PRDX3           P1474         MIF         Macrophage migration inhibitory factor         2,4         0.002         PRDX3           P05218         ZAKANB2         Zint finger Ran-binding domain-containing protein 2         2,3         0.001         PRDX3           Q95410         ERVK31         Endogenous stretority muse group X3 member 1         2,3         0.041         PRDX3           Q95411         LAboptosi-i	Q92888	AKHGEFI		1	0,006	PKDA2
Q86/S8         HOOK3         Protein Hook homolog 3         1         0.014         PRDX2           Q9413K6         BOLA2         BolA-like protein 2         1         0.034         PRDX2           P19022         CDH2         Cadherin-2         1         0.034         PRDX2           Q0630         PRDX1         Peroxitedoxin-5, mitochondrial         3,1         0         PRDX3           Q6WKZ4         RABUIFIPI         RabUI family-interacting protein 1         2,7         0         PRDX3           Q6WKZ4         RABUIFIPI         RabUI family-interacting protein 1         2,7         0         PRDX3           A0A07586R7         IGKV2D-24         Probable non-functional immunoglobulin kappa variable 2D-24         2,7         0,002         PRDX3           G3V3B9         GSTZ1         Maleylacetoacetate isomerase         2,6         0         PRDX3           P14174         MIF         Macephage migration inhibitory factor         2,3         0,001         PRDX3           P1387         POLR2C         DNA-directed RNA polymerase II subunit RPB3         2,4         0.002         PRDX3           Q95118         ZRANB2         Zinc finger Ran-binding domain-containing protein 2         2,3         0,001         PRDX3           Q96	P4348/	RANBPI	Ran-specific G I Pase-activating protein	1	0,008	PRDX2
QPH3K6         BOLA2         BolA-like protein 2         1         0.018         PRDX2           P19022         CDH2         Cadherin-2         1         0.034         PRDX3           P19024         CDH2         Cadherin-2         1         0.034         PRDX3           P30044         PRDX5         Peroxiredoxin-5, mitochondrial         3,1         0         PRDX3           P30044         PRDX5         Peroxiredoxin-5, mitochondrial         2,7         0         PRDX3           Q6WKZ4         RABIFPIP         RabIf amily-interacting protein 1         2,7         0         PRDX3           A0A075B6R9         IGKV2D-24         Probable non-functional immunoglobulin kappa variable 2D-24         2,7         0,002         PRDX3           P14174         MIF         Macrophage migration inhibitory factor         2,4         0,002         PRDX3           P19387         POLR2C         DNA-directed RNA polymerase II subunit RPB3         2,4         0,002         PRDX3           EFEVA0         MAP4         Microtubule associated protein         2,3         0,02         PRDX3           Q6410         ERVK3-1         Endogenous retrovirus group K3 member 1         2,2         0,006         PRDX3           Q60432         ZNRM1 <td>Q86VS8</td> <td>HOOK3</td> <td>Protein Hook homolog 3</td> <td>1</td> <td>0,014</td> <td>PRDX2</td>	Q86VS8	HOOK3	Protein Hook homolog 3	1	0,014	PRDX2
P1902         CDH2         Cadherin-2         1         0,034         PRDX2           Q06830         PRDX1         Peroxiredoxin-1         3,1         0         PRDX3           P30044         PRDX5         Peroxiredoxin-5, mitochondrial         3,1         0,002         PRDX3           Q6WKZ4         RAB11FIP1         Rab11 family-interacting protein 1         2,7         0         PRDX3           F8W9F9         WNK2         Non-specific serinc/hronine protein kinase         2,7         0,002         PRDX3           G3V3B9         GSTZ1         Maleylactocacetate isomerase         2,6         0         PRDX3           P1417         MIF         Macrophage migration inhibitory factor         2,4         0,002         PRDX3           095218         ZRANB2         Zine finger Ran-binding domain-containing protein 2         2,3         0,001         PRDX3           095431         AIAP4         Microtubule-associated protein         2,3         0,041         PRDX3           095431         AIAP4         Microtubule-associated protein         2,2         0         PRDX3           095431         AIAP4         Microtubule-associated protein         2,2         0,041         PRDX3           095431         AIAPGenous retrovin	Q9H3K6	BOLA2	BolA-like protein 2	1	0,018	PRDX2
Q06830PRDX1Peroxiredoxin-1.3,10PRDX3P30044PRDX5Peroxiredoxin-5, mitochondrial3,10,002PRDX3P30044RAb11FIP1Rab11 family-interacting protein 12,70PRDX3F8W9P9WNK2Non-specific serine/thronine protein kinase2,70PRDX3A0A075B6R9IGKV2D-24Probable non-functional immunoglobulin kappa variable 2D-242,70,002PRDX3G03V3B9GSTZ1Maleylacetoacctare isomerase2,60PRDX3P14174MIFMacrophage migration inbibitory factor2,40,002PRDX3P19387POLR2CDNA-directed RNA polymerase II subunit RPB32,40,002PRDX327540MAP4Microtrubule-associated protein2,30,001PRDX3296A10ERVK3-1Endogenous retrovirus group K3 member 12,30,041PRDX3206WE0LRSAM1E3 objuitin-protein ligase LRSAM12,20,005PRDX3206WE0LRSAM1E3 ubcinate delvdrogenase (ubiquitonel iron-sulfur subunit, mitochondrial2,10,004PRDX321929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX32194635CCNB1G2/mitotic-specific cyclin-B12,10,006PRDX321912SDH8Succinate delvdrogenase (ubiquitonel iron-sulfur subunit, mitochondrial2,10,006PRDX321912SDH8Succinate delvdrogenase (ubiquitonel iron-sulfur subunit, mitochondrial2,1 <td>P19022</td> <td>CDH2</td> <td>Cadherin-2</td> <td>1</td> <td>0,034</td> <td>PRDX2</td>	P19022	CDH2	Cadherin-2	1	0,034	PRDX2
P30044PRDX5Peroxiredoxin-5, mitochondrial3,10,002PRDX3Q6WKZ4RAB11FIP1Rab11 Family-interacting protein 12,70PRDX3Q6WKZ4RAB11FP1Rab11 Family-interacting protein kinase2,7002PRDX3A0A075B6R9IGKV2D-24Probable non-functional immunoglobulin kappa variable 2D-242,70,002PRDX3G3V3B9GSTZ1Maleryacetoacettate isomerase2,60PRDX3P14174MIFMacrophage migration inhibitory factor2,40,002PRDX3P19387POLR2CDNA-directed RNA polymerase II subunit RPB32,40,002PRDX3OP5218ZRANB2Zinc finger Ran-binding domain-containing protein 22,30,001PRDX327EVA0MAP4Microtrubule-associated protein2,30,02PRDX309531AIFM1Apogenous retrovirus group K3 member 12,30,041PRDX3095831AIFM1Apogenous retrovirus group K3 member 12,20,005PRDX3060322ZNKD2Protein ZNKD22,20,006PRDX3060323ZNKD2Protein ZNKD22,20,004PRDX301202EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3014635CCNB1G2/mitotic-specific cyclin-B12,10,006PRDX3014635MLT11Protein AF1q2,10,006PRDX301505MLLT11Protein AF1q2,10,006PRDX3	Q06830	PRDX1	Peroxiredoxin-1	3,1	0	PRDX3
Q6WKZ4         RAB11FIP1         Rab11 family-interacting protein 1         2,7         0         PRDX3           F8W9F9         WNK2         Non-specific serine/thronine protein kinase         2,7         0         PRDX3           A0A075B6R9         IGKV2D-24         Probable non-functional immunoglobulin kappa variable 2D-24         2,7         0,002         PRDX3           G3V3B9         GSTZ1         Maleylacetoacetate isomerase         2,6         0         PRDX3           P14174         MIF         Macrophage migration inhibitory factor         2,4         0,002         PRDX3           P19387         POLR2C         DNA-directed RNA polymerase II subunit RPB3         2,4         0,002         PRDX3           Q95218         ZRANB2         Zinc finger Ran-binding domain-containing protein 2         2,3         0,001         PRDX3           Q96A10         ERVK3-1         Endogenous retrovirus group K3 member 1         2,3         0,041         PRDX3           Q6WF01         ILRSAM1         Apoptosis-inducing factor 1, mitochondrial         2,2         0         PRDX3           Q6UVF0         LRSAM1         E3 ubiquitin-protein ligase LRSAM1         2,2         0,006         PRDX3           Q60232         ZNRD2         Protein ZNRD2         protein ZNRD2	P30044	PRDX5	Peroxiredoxin-5, mitochondrial	3,1	0,002	PRDX3
FW9F9         WNK2         Non-specific serind/theoning protein kinase         2,7         0         PRDX3           A0A075B6R9         IGKV2D-24         Probable non-functional immunoglobulin kappa variable 2D-24         2,7         0,002         PRDX3           G3V3B9         GSTZ1         Maleylacetoacetate isomerase         2,6         0         PRDX3           P14174         MIF         Macrophage migration inhibitory factor         2,4         0,002         PRDX3           P19387         POLR2C         DNA-directed RNA polymerase II subunit RPB3         2,4         0,002         PRDX3           Q95218         ZRANB2         Zinc finger Ran-binding domain-containing protein         2,3         0,001         PRDX3           Q96A10         ERVK3-1         Endogenous retrovirus group K3 member 1         2,3         0,021         PRDX3           Q6410         ERVK3-1         Endogenous retrovirus group K3 member 1         2,2         0,006         PRDX3           Q6UWE0         LRSAM1         E3 ubiquitin-protein ligas LRSAM1         2,2         0,006         PRDX3           Q60322         ZNRD2         Protein ZNRD2         2,2         0,004         PRDX3           Q12929         EPS8         Epidermal growth factor receptor kinase substrate 8         2,1	O6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	2.7	0	PRDX3
ADM/75         Instruction for the product number product numoe product number product number product number product number	F8W9F9	WNK2	Non-specific serine/threenine protein kinase	2.7	0	PR DX3
Abbr. Jobic         INST 2024         Product instructional minimized potume kappa variance 2024         2,1         0,002         PRDX3           G3V3B9         GST21         Malelylacetocacteate isomerase         2,6         0         PRDX3           P14174         MIF         Macrophage migration inhibitory factor         2,4         0,002         PRDX3           P19387         POLR2C         DNA-directed RNA polymerase II subunit RPB3         2,4         0,002         PRDX3           095218         ZRANB2         Zinc finger Ran-binding domain-containing protein 2         2,3         0,001         PRDX3           Q26A10         ERVK3-1         Endogenous retrovirus group K3 member 1         2,3         0,041         PRDX3           Q95818         AIFM1         Apoptosis-inducing factor 1, mitochondrial         2,2         0         PRDX3           Q64010         ERVK3-1         Endogenous retrovirus group K3 member 1         2,3         0,004         PRDX3           Q64UWE0         LRSAM1         Apoptosis-inducing factor 1, mitochondrial         2,2         0,006         PRDX3           Q60232         ZNRD2         Protein ZNRD2         2,2         0,004         PRDX3           Q12292         EPS8         Epidermal growth factor receptor kinase substrate 8	104075BCD9	ICKW2D 24	Prohable non-functional immunoglobulin kanna variable 2D 24	2,7	0.002	DP DV2
G3V 309         G51 Z1         Materplacetoacetate isomerase         2,6         0         PRDX3           P14174         MIF         Macrophage migration inhibitory factor         2,4         0,002         PRDX3           P19387         POLR2C         DNA-directed RNA polymerase II subunit RPB3         2,4         0,002         PRDX3           O95218         ZRANB2         Zinc finger Ran-binding domain-containing protein 2         2,3         0,001         PRDX3           Q96A10         ERVK3-1         Endogenous errorvirus group K3 member 1         2,3         0,02         PRDX3           Q95A10         ERVK3-1         Endogenous errorvirus group K3 member 1         2,2         0         PRDX3           Q95A10         ERVK3-1         Endogenous errorvirus group K3 member 1         2,2         0,005         PRDX3           Q640WE0         LRSAM1         E3 ubiquitin-protein ligase LRSAM1         2,2         0,006         PRDX3           Q60232         ZNRD2         Protein ZNRD2         2,2         0,014         PRDX3           Q1292         EPS8         Epidermal growth factor receptor kinase substrate 8         2,1         0,004         PRDX3           Q1292         EPS8         Epidermal growth factor receptor kinase substrate 8         2,1         0,0	Callabo	IGK V2D-24		2,/	0,002	PRDAJ
P14174MIFMacrophage migration inhibitory factor2,40,002PRDX3P19387POLR2CDNA-directed RNA polymerase II subunit RPB32,40,002PRDX3095218ZRANB2Zinc finger Ran-binding domain-containing protein 22,30,001PRDX3E7EVA0MAP4Microtubule-associated protein2,30,02PRDX3Q96A10ERVK3-1Endogenous retrovirus group K3 member 12,30,041PRDX3095881AIFM1Apoptosis-inducing factor 1, mitochondrial2,20PRDX3Q64UWE0LRSAM1E3 ubiquitin-protein ligase LRSAM12,20,006PRDX3Q60232ZNRD2Protein ZNRD22,20,004PRDX3Q12929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3Q13015MLLT11Protein AF1q2,10,006PRDX3Q13015MLLT11Protein AF1q2,10,006PRDX3Q5273RPS29405 ribosomal protein S292,10,006PRDX3Q60X51SERBP1Plasminogen activator inhibitor 1 RNA-binding protein 120,003PRDX3Q8NC51SERBP1Plasminogen activator inhibitor 1 RNA-binding protein 120,009PRDX3Q91544CNN2Calponin20,009PRDX3Q91545SERBP1Plasminogen activator inhibitor 1 RNA-binding protein 120,009PRDX3Q91541EIF4EBP11Eukaryotic transdation initiation factor 4E-bindin	G3V3D9	GSTZI	Maleylacetoacetate isomerase	2,6	0	PKDA5
P19387POLR2CDNA-directed RNA polymerase II subunit RPB32,40,002PRDX3O95218ZRANB2Zinc finger Ran-binding domain-containing protein 22,30,001PRDX3O95218ZRANB2Zinc finger Ran-binding domain-containing protein 22,30,001PRDX3Q96A10ERVK3-1Endogenous retrovirus group K3 member 12,30,041PRDX3Q95831AIFM1Apoptosis-inducing factor 1, mitochondrial2,20PRDX3Q60WE0LRSAM1E3 ubiquitin-protein ligase LRSAM12,20,006PRDX3Q60WE0LRSAM1E3 ubiquitin-protein ligase LRSAM12,20,004PRDX3Q12929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3Q13015MLLT11Protein AF1q2,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 120,003PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 120,005PRDX3Q9Y6A6DNAJC19Mitochondrial import in RNA-bind	P14174	MIF	Macrophage migration inhibitory factor	2,4	0,002	PRDX3
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E7EVA0MAP4Microtubule-associated protein2,30,02PRDX3Q96A10ERVK3-1Endogenous retrovirus group K3 member 12,30,041PRDX3O95831AIFM1Apoptosis-inducing factor 1, mitochondrial2,20PRDX3Q60WE0LRSAM1E3 ubiquitin-protein ligas LRSAM12,20,005PRDX3Q60WE0LRSAM1E3 ubiquitin-protein ligas LRSAM12,20,004PRDX3Q60WE0LRSAM1E3 ubiquitin-protein ligas LRSAM12,20,004PRDX3Q60232ZNRD2Protein ZNRD22,20,014PRDX3Q1292EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3Q1305CCN81G2/mitotic-specific cyclin-B12,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3Q8YCA1ERBP1Plasingogen activator inhibitor 1 RNA-binding protein20PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein20PRDX3Q8YCA1ERBP1Plasingogen activator inhibitor 1 RNA-binding protein20,005PRDX3Q95DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein Kinase1,90,002PRDX3Q926DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3	O95218	ZRANB2	Zinc finger Ran-binding domain-containing protein 2	2,3	0,001	PRDX3
Q96A10ERVK3-1Endogenous retrovirus group K3 member 12,30,041PRDX3O95831AIFM1Apoptosis-inducing factor 1, mitochondrial2,20PRDX3A0A087X1B1IKBKGNF-kappa-B essential modulator2,20,005PRDX3Q6UWE0LRSAM1E3 ubiquitin-protein ligase LRSAM12,20,006PRDX3O60232ZNRD2Protein ZNRD22,20,014PRDX3Q12929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3Q1305CCNB1G2/mitotic-specific cyclin-B12,10,006PRDX3Q1305MLLT11Protein AF1q2,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3Q9Y6A5SERBP1Plasminogen activator inhibitor 1 RNA-binding protein 1200PRDX3Q95DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13141ILKIntegrin-linked protein C11,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,004PRDX3	E7EVA0	MAP4	Microtubule-associated protein	2,3	0,02	PRDX3
O95831AIFM1Apoptosis-inducing factor 1, mitochondrial2,20PRDX3A0A087X1B1IKBKGNF-kappa-B essential modulator2,20,005PRDX3Q6UWE0LRSAM1E3 ubiquitin-protein ligase LRSAM12,20,006PRDX3O60232ZNRD2Protein ZNRD22,20,014PRDX3P21912SDHBSuccinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial2,10,004PRDX3Q12929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3Q13015CCNB1G2/mitotic-specific cyclin-B12,10,006PRDX3Q13015MLLT11Protein AF1q2,10,006PRDX3Q9K0A5TACC3Transforming acidic coiled-coil-containing protein 32,10,008PRDX3P62273RPS29408 ribosomal protein S292,10,006PRDX3Q8K051SERBP1Plasminogen activator inhibitor 1 RNA-binding protein 120,005PRDX3Q95DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q12948FOXC1Forkada box protein C11,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,004PRDX3	Q96A10	ERVK3-1	Endogenous retrovirus group K3 member 1	2,3	0,041	PRDX3
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Que with DExclusion in protein light Endinfit2,26,000FRDX3060232ZNRD2Protein ZNRD22,20,014PRDX3Q12929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3Q12929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3P14635CCNB1G2/mitotic-specific cyclin-B12,10,006PRDX3Q13015MLLT11Protein AF1q2,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3P62273RPS2940S ribosomal protein S292,10,016PRDX3B4DDF4CNN2Calponin20PRDX3Q950A6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein Kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	OGUWE0	LRSAM1	F3 ubiquitin-protein ligase LR SA M1	2.2	0.006	PR DX3
060232ZNKD2Protein ZNKD2Protein ZNKD2Protein ZNKD2Protein ZNKD2Protein ZNKD2Protein ZNKD2Protein ZNKD2P21912SDHBSuccinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial2,10,004PRDX3Q12929EPS8Epidermal growth factor receptor kinase substrate 82,10,004PRDX3P14635CCNB1G2/mitotic-specific cyclin-B12,10,006PRDX3Q13015MLLT11Protein AF1q2,10,006PRDX3Q9Y6A5TACC3Transforming acidic coile-coil-containing protein 32,10,006PRDX3P62273RPS2940S ribosomal protein S292,10,016PRDX3B4DDF4CNN2Calponin20PRDX3Q96DA6DNAJC19Plasminogen activator inhibitor 1 RNA-binding protein 120,005PRDX3Q13418ILKIntegrin-linked protein kinase20,009PRDX3Q13418ILKIntegrin-linked protein Kinase20,009PRDX3Q13418FOXC1Forkhead box protein C11,90,002PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	Q00 w L0	ZNIED2	Destric 7ND D2	2,2	0,000	DR DV2
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P14635CCNB1G2/mitotic-specific cyclin-B12,10,005PRDX3P11802CDK4Cyclin-dependent kinase 42,10,006PRDX3Q13015MLLT11Protein AF1q2,10,006PRDX3Q9Y6A5TACC3Transforming acidic coiled-coil-containing protein 32,10,006PRDX3P62273RPS2940S ribosomal protein S292,10,016PRDX3B4DDF4CNN2Calponin20PRDX3Q9SNC51SERBP1Plasminogen activator inhibitor 1 RNA-binding protein 120,003PRDX3Q96DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	Q12929	EPS8	Epidermal growth factor receptor kinase substrate 8	2,1	0,004	PRDX3
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P62273RPS2940S ribosonal protein S292,10,016PRDX3B4DDF4CNN2Calponin20PRDX3Q8NC51SERBP1Plasminogen activator inhibitor 1 RNA-binding protein20,003PRDX3Q13541EIF4EBP1Eukaryotic translation initiation factor 4E-binding protein 120,005PRDX3Q96DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein Kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3H0YNW5DUTDeoxyuridine 5'-triphosphate nucleotidohydrolase1,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	2,1	0,008	PRDX3
B4DDF4CNN2Calponin20PRDX3Q8NC51SERBP1Plasminogen activator inhibitor 1 RNA-binding protein20,003PRDX3Q13541EIF4EBP1Eukaryotic translation initiation factor 4E-binding protein 120,005PRDX3Q96DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3H0YNW5DUTDeoxyuridine 5'-triphosphate nucleotidohydrolase1,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	P62273	RPS29	40S ribosomal protein S29	2.1	0.016	PRDX3
Q8NC51SERBP1Plasminogen activator inhibitor 1 RNA-binding protein20PRDX3Q13541EIF4EBP1Eukaryotic translation initiation factor 4E-binding protein 120,003PRDX3Q96DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3H0YNW5DUTDeoxyuridine 5'-triphosphate nucleotidohydrolase1,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	B4DDF4	CNN2	Calponin	2	0	PR DX3
Q015541EIF4EBP1Eukaryotic translation initiation i r KNA-binding protein 120,005PRDX3Q96DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3H0YNW5DUTDeoxyuridine 5'-triphosphate nucleotidohydrolase1,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	08NC51	SER RD1	Diagninggen activator inhibitor 1 P NA hinding protein	2	0.002	DR DV2
Q13341EIF4EDP1Eukaryotic translation initiation factor 4E-binding protein 120,005PRDX3Q96DA6DNAJC19Mitochondrial import inner membrane translocase subunit TIM1420,009PRDX3Q13418ILKIntegrin-linked protein kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3H0YNW5DUTDeoxyuridine 5'-triphosphate nucleotidohydrolase1,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	012541	SERDET EIE4EDD1	Falsements and a lating in this is a factor of the line of the	2	0,005	DD DV2
Q26DA6DNAJC19Mitochondrial import inner membrane translocase subunit 11M1420,009PRDX3Q13418ILKIntegrin-linked protein kinase20,009PRDX3Q12948FOXC1Forkhead box protein C11,90,002PRDX3H0YNW5DUTDeoxyuridine 5'-triphosphate nucleotidohydrolase1,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	Q13541	EIF4EDP1	Eukaryouc translation initiation ractor 4E-binding protein 1	2	0,005	PKDA3
Q13418         ILK         Integrin-linked protein kinase         2         0,009         PRDX3           Q12948         FOXC1         Forkhead box protein C1         1,9         0,002         PRDX3           H0YNW5         DUT         Deoxyuridine 5'-triphosphate nucleotidohydrolase         1,9         0,002         PRDX3           Q8WVC0         LEO1         RNA polymerase-associated protein LEO1         1,9         0,014         PRDX3	Q96DA6	DNAJC19	Mitochondrial import inner membrane translocase subunit T1M14	2	0,009	PRDX3
Q12948         FOXC1         Forkhead box protein C1         1,9         0,002         PRDX3           H0YNW5         DUT         Deoxyuridine 5'-triphosphate nucleotidohydrolase         1,9         0,002         PRDX3           Q8WVC0         LEO1         RNA polymerase-associated protein LEO1         1,9         0,014         PRDX3	Q13418	ILK	Integrin-linked protein kinase	2	0,009	PRDX3
H0YNW5DUTDeoxyuridine 5'-triphosphate nucleotidohydrolase1,90,002PRDX3Q8WVC0LEO1RNA polymerase-associated protein LEO11,90,014PRDX3	Q12948	FOXC1	Forkhead box protein C1	1,9	0,002	PRDX3
Q8WVC0 LEO1 RNA polymerase-associated protein LEO1 1,9 0,014 PRDX3	H0YNW5	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase	1,9	0,002	PRDX3
	Q8WVC0	LEO1	RNA polymerase-associated protein LEO1	1,9	0,014	PRDX3

Q9C026	TRIM9	E3 ubiquitin-protein ligase TRIM9	1,9	0,015	PRDX3
P67936	TPM4	Tropomyosin alpha-4 chain	1,9	0,025	PRDX3
Q9BW83	IFT27	Intraflagellar transport protein 27 homolog	1,8	0,012	PRDX3
P35244	RPA3	Replication protein A 14 kDa subunit	1,8	0,02	PRDX3
P09497	CLTB	Clathrin light chain B	1,8	0,021	PRDX3
A8MYK1	MRPL23	39S ribosomal protein L23, mitochondrial	1,8	0,027	PRDX3
Q8TCF1	ZFAND1	AN1-type zinc finger protein 1	1,8	0,028	PRDX3
P47985	UQCRF\$1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	1,7	0,004	PRDX3
Q96B36	AKT1S1	Proline-rich AKT1 substrate 1	1,7	0,016	PRDX3
Q13151	HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	1,7	0,017	PRDX3
F5H345	HMBS	Hydroxymethylbilane synthase	1,7	0,02	PRDX3
O95248	SBF1	Myotubularin-related protein 5	1,7	0,028	PRDX3
015511	ARPC5	Actin-related protein 2/3 complex subunit 5	1,7	0,028	PRDX3
C9JAW5	C9JAW5	HIG1 domain-containing protein	1,7	0,039	PRDX3
Q9Y3D9	MRPS23	28S ribosomal protein S23, mitochondrial	1,7	0,04	PRDX3
P49914	MTHFS	5-formyltetrahydrofolate cyclo-ligase	1,7	0,049	PRDX3
Q9UN86	G3BP2	Ras GTPase-activating protein-binding protein 2	1,6	0	PRDX3
Q9Y265	RUVBL1	RuvB-like 1	1,6	0	PRDX3
A0A2R8Y811	RPS14	40S ribosomal protein S14	1,6	0	PRDX3
P35520	CBS	Cystathionine beta-synthase	1,6	0,013	PRDX3
P61758	VBP1	Prefoldin subunit 3	1,6	0,025	PRDX3
Q9H4L4	SENP3	Sentrin-specific protease 3	1,6	0,032	PRDX3
P10301	RRAS	Ras-related protein R-Ras	1,6	0,046	PRDX3
Q9H0H5	RACGAP1	Rac GTPase-activating protein 1	1,5	0	PRDX3
Q96F86	EDC3	Enhancer of mRNA-decapping protein 3	1,5	0,003	PRDX3
Q13123	IK	Protein Red	1,5	0,008	PRDX3
Q5XKP0	MICOS13	MICOS complex subunit MIC13	1,5	0,041	PRDX3
Q9P2X3	IMPACT	Protein IMPACT	1,5	0,042	PRDX3
Q16576	RBBP7	Histone-binding protein RBBP7	1,4	0,003	PRDX3
Q9NUQ3	TXLNG	Gamma-taxilin	1,4	0,005	PRDX3
Q9BR76	CORO1B	Coronin-1B	1,4	0,021	PRDX3
E9PM92	C11orf58	Small acidic protein	1,4	0,032	PRDX3
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	1,4	0,038	PRDX3
P30041	PRDX6	Peroxiredoxin-6	1,4	0,043	PRDX3
Q9NRX4	PHPT1	14 kDa phosphohistidine phosphatase	1,3	0	PRDX3
Q9Y5M8	SRPRB	Signal recognition particle receptor subunit beta	1,3	0	PRDX3
Q6IQ49	SDE2	Replication stress response regulator SDE2	1,3	0,002	PRDX3
Q9HB71	CACYBP	Calcyclin-binding protein	1,3	0,013	PRDX3
Q16204	CCDC6	Coiled-coil domain-containing protein 6	1,3	0,038	PRDX3
Q5VVQ6	YOD1	Ubiquitin thioesterase OTU1	1,3	0,044	PRDX3
P62826	RAN	GTP-binding nuclear protein Ran	1,2	0	PRDX3
Q92974	ARHGEF2	R ho guanine nucleotide exchange factor 2	1,2	0,005	PRDX3
Q9H936	SLC25A22	Mitochondrial glutamate carrier 1	1,2	0,005	PRDX3
P0DMV9	HSPA1B	Heat shock 70 kDa protein 1B	1,2	0,007	PRDX3
A0A087WUK2	HNRNPDL	Heterogeneous nuclear ribonucleoprotein D-like	1,2	0,009	PRDX3
Q15654	TRIP6	Thyroid receptor-interacting protein 6	1,2	0,013	PRDX3
Q13356	PPIL2	RING-type E3 ubiquitin-protein ligase PPIL2	1,2	0,016	PRDX3
Q6R327	RICTOR	Rapamycin-insensitive companion of mTOR	1,2	0,017	PRDX3
Q9H840	GEMIN7	Gem-associated protein 7	1,2	0,025	PRDX3
P32119	PRDX2	Peroxiredoxin-2	1,2	0,026	PRDX3
O00399	DCTN6	Dynactin subunit 6	1,2	0,027	PRDX3
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-	1,2	0,03	PRDX3
		succinocarboxamide synthase			
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	1,2	0,031	PRDX3
P61927	RPL37	60S ribosomal protein L37	1,2	0,031	PRDX3
H0Y4R1	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	1,2	0,04	PRDX3
P39019	RPS19	40S ribosomal protein S19	1,1	0	PRDX3
Q15181	PPA1	Inorganic pyrophosphatase	1,1	0,006	PRDX3
P82921	MRPS21	28S ribosomal protein S21, mitochondrial	1,1	0,017	PRDX3
Q07666	KHDRBS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	1,1	0,029	PRDX3
O14965	AURKA	Aurora kinase A	1,1	0,034	PRDX3
Q13247	SRSF6	Serine/arginine-rich splicing factor 6	1,1	0,041	PRDX3
P40222	TXLNA	Alpha-taxilin	1,1	0,046	PRDX3
Q9ULX3	NOB1	RNA-binding protein NOB1	1,1	0,05	PRDX3
P11586	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	1	0	PRDX3
O95336	PGLS	6-phosphogluconolactonase	1	0,017	PRDX3
Q15398	DLGAP5	Disks large-associated protein 5	1	0,024	PRDX3
P30044	PRDX5	Peroxiredoxin-5, mitochondrial	3,5	0,001	PRDX4
Q06830	PRDX1	Peroxiredoxin-1	3,4	0	PRDX4

H0YNW5	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase	3,2	0	PRDX4
A0A075B6R9	IGKV2D-24	Probable non-functional immunoglobulin kappa variable 2D-24	3,1	0	PRDX4
P62273	RPS29	40S ribosomal protein S29	3,1	0,001	PRDX4
P11802	CDK4	Cyclin-dependent kinase 4	3	0	PRDX4
P06132	UROD	Uroporphyrinogen decarboxylase	3	0	PRDX4
Q13015	MLLT11	Protein AF1q	2,9	0	PRDX4
Q6FI81	CIAPIN1	Anamorsin	2,9	0	PRDX4
Q9H840	GEMIN7	Gem-associated protein 7	2,8	0	PRDX4
Q9H2P9	DPH5	Diphthine methyl ester synthase	2,6	0	PRDX4
Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	2,5	0	PRDX4
F8W9F9	WNK2	Non-specific serine/threonine protein kinase	2,5	0	PRDX4
Q9NP97	DYNLRB1	Dynein light chain roadblock-type 1	2,5	0	PRDX4
G3V3B9	GSTZ1	Maleylacetoacetate isomerase	2,4	0	PRDX4
P19022	CDH2	Cadherin-2	2,4	0	PRDX4
B4DDF4	CNN2	Calponin	2,4	0	PRDX4
O60566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	2,4	0,001	PRDX4
P61758	VBP1	Prefoldin subunit 3	2,4	0,002	PRDX4
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	2,3	0,001	PRDX4
Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	2,3	0,009	PRDX4
A0A087X2D5	MRPL45	398 ribosomal protein L45, mitochondrial	2,2	0	PRDX4
Q8WVC2	RPS21	40S ribosomal protein S21	2,2	0,001	PRDX4
Q9BTE1	DCTN5	Dynactin subunit 5	2,2	0,001	PRDX4
H3BRE8	RPAP1	RNA polymerase II-associated protein 1	2,2	0,002	PRDX4
P19387	POLR2C	DNA-directed RNA polymerase II subunit RPB3	2,2	0,002	PRDX4
P0DMV9	HSPA1B	Heat shock 70 kDa protein 1B	2,1	0	PRDX4
095218	ZRANB2	Zinc finger Ran-binding domain-containing protein 2	2,1	0,001	PRDX4
P41250	GARSI	GlycinetRNA ligase	2,1	0,002	PRDX4
Q9NPH2	ISYNAI	Inositol-3-phosphate synthase I	2,1	0,003	PRDX4
P42//1	CDKN2A	Cyclin-dependent kinase inhibitor 2A	2	0	PRDX4
H/BXII	ESY12	Extended synaptotagmin-2	2	0,002	PRDX4
QSJRII	SKSF10	Serine/arginine-rich-splicing factor 10	2	0,004	PRDX4
AUAU8/AIDI	INDAG	NF-kappa-D essential modulator	2	0,006	PRDA4
Q60 WE0	C11arf58	E3 ubiquitin-protein ligase LKSAMI	2	0,007	PRDA4
C(0222	ZNIR D2	Destain ZNR D2	2	0,007	PRDA4
OBULNRC	C2BD2	Protein ZINED2	1.9	0,018	DP DV4
Q901086	HALIS8	HAUS augmin like complex subunit 8	1,9	0	PR DY/
P34897	SHMT2	Serine hydroxymethyltransferase mitochondrial	1,9	0	PR DX4
P22234	PAICS	Multifunctional protein A DF2 [Includes: Phosphorihosylaminoimidazole.	1.9	0.001	PR DX4
122251	111100	succinocarboxamide synthase	1,7	0,001	IRDAT
Q9BPW8	NIPSNAP1	Protein NipSnap homolog 1	1,9	0,004	PRDX4
P14635	CCNB1	G2/mitotic-specific cyclin-B1	1,9	0,007	PRDX4
P85037	FOXK1	Forkhead box protein K1	1,9	0,01	PRDX4
Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	1,9	0,016	PRDX4
O14964	HGS	Hepatocyte growth factor-regulated tyrosine kinase substrate	1,8	0	PRDX4
Q12933	TRAF2	TNF receptor-associated factor 2	1,8	0,009	PRDX4
O00629	KPNA4	Importin subunit alpha-3	1,8	0,011	PRDX4
Q99956	DUSP9	Dual specificity protein phosphatase 9	1,8	0,017	PRDX4
Q9Y265	RUVBL1	RuvB-like 1	1,7	0	PRDX4
P17252	PRKCA	Protein kinase C alpha type	1,7	0,001	PRDX4
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	1,7	0,01	PRDX4
Q13541	EIF4EBP1	Eukaryotic translation initiation factor 4E-binding protein 1	1,7	0,011	PRDX4
Q13418	ILK	Integrin-linked protein kinase	1,7	0,012	PRDX4
Q16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	1,7	0,012	PRDX4
Q9P2B4	CTTNBP2NL	CTTNBP2 N-terminal-like protein	1,7	0,013	PRDX4
Q96DH6	MSI2	RNA-binding protein Musashi homolog 2	1,7	0,013	PRDX4
Q96DA6	DNAJC19	Mitochondrial import inner membrane translocase subunit TIM14	1,7	0,013	PRDX4
Q8WVC0	LEO1	RNA polymerase-associated protein LEO1	1,7	0,018	PRDX4
Q9C026	TRIM9	E3 ubiquitin-protein ligase TRIM9	1,7	0,021	PRDX4
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	1,7	0,023	PRDX4
Q9HD26	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein	1,7	0,026	PRDX4
075616	ERAL1	GTPase Era, mitochondrial	1,7	0,027	PRDX4
P14174	MIF	Macrophage migration inhibitory factor	1,7	0,028	PRDX4
Q5VUJ6	LRCH2	Leucine-rich repeat and calponin homology domain-containing protein 2	1,7	0,029	PRDX4
P67936	TPM4	Tropomyosin alpha-4 chain	1,7	0,035	PRDX4
Q9NXR7	BABAM2	BRISC and BRCA1-A complex member 2	1,7	0,04	PRDX4
Q9Y3D9	MRPS23	28S ribosomal protein \$23, mitochondrial	1,7	0,04	PRDX4
Q9Y5Y2	NUBP2	Cytosolic Fe-S cluster assembly factor NUBP2	1,6	0	PRDX4
Q9ULX3	NOB1	RNA-binding protein NOB1	1,6	0,001	PRDX4

O15143	ARPC1B	Actin-related protein 2/3 complex subunit 1B	1,6	0,002	PRDX4
Q12948	FOXC1	Forkhead box protein C1	1,6	0,004	PRDX4
Q9Y5K6	CD2AP	CD2-associated protein	1,6	0,012	PRDX4
Q53H96	PYCR3	Pyrroline-5-carboxylate reductase 3	1,6	0,012	PRDX4
Q16204	CCDC6	Coiled-coil domain-containing protein 6	1,6	0,015	PRDX4
Q9BW83	IFT27	Intraflagellar transport protein 27 homolog	1,6	0,016	PRDX4
Q8NI60	COQ8A	Atypical kinase COQ8A, mitochondrial	1,6	0,017	PRDX4
Q6R327	RICTOR	Rapamycin-insensitive companion of mTOR	1,6	0,018	PRDX4
I3L2Z5	MAZ	Myc-associated zinc finger protein	1,6	0,022	PRDX4
P30041	PRDX6	Peroxiredoxin-6	1,6	0,025	PRDX4
O14617	AP3D1	AP-3 complex subunit delta-1	1,6	0,027	PRDX4
P35244	RPA3	Replication protein A 14 kDa subunit	1,6	0,029	PRDX4
P09497	CLTB	Clathrin light chain B	1,6	0,03	PRDX4
A8MYK1	MRPL23	39S ribosomal protein L23, mitochondrial	1,6	0,039	PRDX4
Q8TCF1	ZFAND1	AN1-type zinc finger protein 1	1,6	0,041	PRDX4
P53677	AP3M2	AP-3 complex subunit mu-2	1,5	0,003	PRDX4
P35520	CBS	Cystathionine beta-synthase	1,5	0,021	PRDX4
Q9BZE1	MRPL37	39S ribosomal protein L37, mitochondrial	1,5	0,022	PRDX4
U3KQC1	WDR18	WD repeat-containing protein 18	1,5	0,023	PRDX4
F5H345	HMBS	Hydroxymethylbilane synthase	1,5	0,028	PRDX4
P49903	SEPHSI ACTR 1P	Selenide, water dikinase l	1,5	0,038	PRDX4
P42025	ACIKIB	Beta-centractin	1,5	0,042	PRDX4
Q9N 123	GISEI	G2 and S phase-expressed protein 1	1,4	0	PRDX4
P3083/	R DR D1 A	Aldenyde denydrogenase X, mitochondria	1,4	0 001	PRDX4
AUAUC4DGQ6	MP DI 11	200 rik complementaria L 11 mitoch en driel	1,4	0,001	PRDX4
Q913B/	OTUR1	Ubiquitin thioseterese OTUB1	1,4	0,001	PRDX4
Q96F W1	ATEM1	Apoptoris inducing factor 1 mitochondrial	1,4	0,001	PRDX4
D/0937	R FC5	Replication factor C subunit 5	1,4	0,003	PR DX4
09BWD1	ACAT2	Acetyl CoA acetyltransferase cytosolic	1,4	0.015	PR DX4
099569	PKP4	Plakophilin_4	1,4	0.015	PR DX4
A0A 3B3IUD2	MSTO1	Protein misato homolog 1	1,1	0.025	PR DX4
E7EX48	NEK4	Serine/threonine-protein kinase Nek4	1,1	0.026	PR DX4
O9UBI6	GNG12	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12.	1,1	0.029	PR DX4
013573	SNW1	SNW domain-containing protein 1	1.4	0.031	PR DX4
O8N3C0	ASCC3	Activating signal cointegrator 1 complex subunit 3	1,4	0,032	PRDX4
Q9NV56	MRGBP	MRG/MORF4L-binding protein	1,4	0,033	PRDX4
O00291	HIP1	Huntingtin-interacting protein 1	1,4	0,035	PRDX4
O94992	HEXIM1	Protein HEXIM1	1,4	0,038	PRDX4
O95248	SBF1	Myotubularin-related protein 5	1,4	0,04	PRDX4
Q6P087	RPUSD3	Mitochondrial mRNA pseudouridine synthase RPUSD3	1,4	0,04	PRDX4
G3V1Q4	SEPTIN7	Septin-7	1,4	0,045	PRDX4
Q9NPD8	UBE2T	Ubiquitin-conjugating enzyme E2 T	1,4	0,047	PRDX4
Q7L5D6	GET4	Golgi to ER traffic protein 4 homolog	1,4	0,05	PRDX4
P35232	PHB	Prohibitin	1,3	0	PRDX4
P06733	ENO1	Alpha-enolase	1,3	0	PRDX4
P62937	PPIA	Peptidyl-prolyl cis-trans isomerase A	1,3	0,001	PRDX4
Q9UN37	VPS4A	Vacuolar protein sorting-associated protein 4A	1,3	0,001	PRDX4
P43487	RANBP1	Ran-specific GTPase-activating protein	1,3	0,001	PRDX4
Q96RT1	ERBIN	Erbin	1,3	0,002	PRDX4
P31930	UQCRC1	Cytochrome b-c1 complex subunit 1, mitochondrial	1,3	0,003	PRDX4
P35998	PSMC2	26S proteasome regulatory subunit 7	1,3	0,003	PRDX4
Q6PKG0	LARP1	La-related protein 1	1,3	0,004	PRDX4
A0A087X0K9	TJP1	Tight junction protein ZO-1	1,3	0,004	PRDX4
Q14C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	1,3	0,013	PRDX4
J3KN29	PSMD9	26S proteasome non-ATPase regulatory subunit 9	1,3	0,02	PRDX4
Q96F86	EDC3	Enhancer of mRNA-decapping protein 3	1,3	0,02	PRDX4
P26599	PTBP1	Polypyrimidine tract-binding protein 1	1,3	0,025	PRDX4
P63000	RAC1	Ras-related C3 botulinum toxin substrate 1	1,3	0,026	PRDX4
P47985	UQCRFS1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	1,3	0,03	PRDX4
Q13247	SRSF6	Serine/arginine-rich splicing factor 6	1,3	0,03	PRDX4
A0A3B3ITJ4	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	1,3	0,031	PRDX4
P14618	PKM	Pyruvate kinase PK M	1,3	0,033	PRDX4
P43686	PSMC4	265 proteasome regulatory subunit 6B	1,3	0,033	PRDX4
<u>Q5V VQ6</u>	YODI	Ubiquitin thioesterase U1 U1	1,3	0,045	PKDX4
Q4VCS5	AMOT	Angiomotin	1,3	0,045	PRDX4
Q9H4L4	SENP3	Sentrin-specific protease 3	1,3	0,047	PRDX4
Q715M8	SKPKB	Signal recognition particle receptor subunit beta	1,2	0	PKDX4
P11586	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	1,2	0	PKDX4

095456	PSMG1	Proteasome assembly chaperone 1	1.2	0.001	PR DX4
P22695	UOCRC2	Cytochrome b-c1 complex subunit 2 mitochondrial	1.2	0.004	PR DX4
P49593	PPM1F	Protein phosphatase 1F	1,2	0.008	PR DX4
014965	AURKA	Autora kinase A	1,2	0.026	PR DX4
014909 096B36	AKT1S1	Proline.rich AKT1 substrate 1	1,2	0.032	DR DY/
Q76D36	LISDAR	Heat shock compate 71 kDa protein	1,2	0,032	DP DV4
P11142	AL DUD	All h h h h h h h h h h h h h h h h h h	1,1	0 002	PRDA4
P05091	ALDH2	Aldehyde dehydrogenase, mitochondrial	1,1	0,002	PRDX4
Q1334/	EIF31	Eukaryotic translation initiation factor 3 subunit 1	1,1	0,004	PRDX4
Q2M1P5	KIF7	Kinesin-like protein KIF7	1,1	0,005	PRDX4
P19838	NFKB1	Nuclear factor NF-kappa-B p105 subunit	1,1	0,006	PRDX4
D6R938	CAMK2D	Calcium/calmodulin-dependent protein kinase	1,1	0,007	PRDX4
Q92974	ARHGEF2	Rho guanine nucleotide exchange factor 2	1,1	0,008	PRDX4
Q9BV44	THUMPD3	THUMP domain-containing protein 3	1,1	0,01	PRDX4
Q9UKK9	NUDT5	ADP-sugar pyrophosphatase	1,1	0,017	PRDX4
Q86WA6	BPHL	Valacyclovir hydrolase	1,1	0,02	PRDX4
Q9NXF7	DCAF16	DDB1- and CUL4-associated factor 16	1,1	0,021	PRDX4
K7EJQ8	HDHD2	Haloacid dehalogenase-like hydrolase domain-containing protein 2	1,1	0,029	PRDX4
P50542	PEX5	Peroxisomal targeting signal 1 receptor	1,1	0,03	PRDX4
075607	NPM3	Nucleoplasmin-3	1,1	0,033	PRDX4
P21964	COMT	Catechol O-methyltransferase	1,1	0,036	PRDX4
O6P1L8	MRPL14	39\$ ribosomal protein L14. mitochondrial	1.1	0.04	PRDX4
O6DK11	R PL7L1	60S ribosomal protein L7-like 1	11	0.046	PR DX4
D62195	DSMC5	26S protessome regulatory subunit 8	1	0.003	DR DY/
01/12/	DSC2	Desmoglein 2	1	0.016	DP DY/
Q14120	NUD122	Nuclear and complex metric Nuclear	1	0,016	DD DV4
Q8WUM0	NUP155	Nuclear pore complex protein Nup155	1	0,016	PKDA4
Q9H223	EHD4	EH domain-containing protein 4	1	0,026	PRDX4
A0A0G2JNZ2	SCRIB	Protein scribble homolog	1	0,029	PRDX4
BIALK7	ARHGEF7	Rho guanine nucleotide exchange factor 7	1	0,029	PRDX4
Q15398	DLGAP5	Disks large-associated protein 5	1	0,033	PRDX4
P23258	TUBG1	Tubulin gamma-1 chain	1	0,039	PRDX4
F5H008	VPS33B	Vacuolar protein sorting-associated protein 33B	1	0,04	PRDX4
Q53EL6	PDCD4	Programmed cell death protein 4	1	0,044	PRDX4
A0A075B6R9	IGKV2D-24	Probable non-functional immunoglobulin kappa variable 2D-24	3,3	0	PRDX5
Q4VCS5	AMOT	Angiomotin	3	0	PRDX5
P06132	UROD	Uroporphyrinogen decarboxylase	2,9	0	PRDX5
B4DDF4	CNN2	Calponin	2,9	0	PRDX5
Q13015	MLLT11	Protein AF1q	2,8	0,001	PRDX5
P62273	RPS29	40S ribosomal protein S29	2,8	0,003	PRDX5
O9H840	GEMIN7	Gem-associated protein 7	2,6	0	PRDX5
Q06830	PR DX1	Peroxiredoxin-1	2.5	0	PRDX5
P19105	MYL12A	Myosin regulatory light chain 12A	2.5	0.001	PR DX5
09NP97	DYNI R B1	Dynein light chain roadblock-type 1	2,5	0	PR DX5
HOVNIWS	DUT	Depreuriding 5' triphogaphata puglaatidabudralaga	2,1	0	DP DY5
EeWoEo	WNF2	Nen energine (the section energine material kinese	2,4	0.001	DRDX5
<u>rowyry</u>	WINK2	Non-specific serific/tifeonine protein kinase	2,4	0,001	PRDAS
Q15149	PLEC		2,4	0,004	PRDAS
Q9BR/6	COROIB	Coronin-IB	2,3	0	PRDX5
G3V3B9	GSTZ1	Maleylacetoacetate isomerase	2,3	0,001	PRDX5
P19022	CDH2	Cadherin-2	2,3	0,001	PRDX5
Q13573	SNW1	SNW domain-containing protein 1	2,3	0,002	PRDX5
O60566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	2,3	0,002	PRDX5
P51570	GALK1	Galactokinase	2,2	0	PRDX5
A0A0G2JNZ2	SCRIB	Protein scribble homolog	2,2	0	PRDX5
O15143	ARPC1B	Actin-related protein 2/3 complex subunit 1B	2,2	0,001	PRDX5
Q96AC1	FERMT2	Fermitin family homolog 2	2,2	0,005	PRDX5
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	2,1	0	PRDX5
O00629	KPNA4	Importin subunit alpha-3	2,1	0,001	PRDX5
E7EPN9	PRRC2C	Protein PRRC2C	2,1	0,001	PRDX5
O86WA6	BPHL.	Valacyclovir bydrolase	2.1	0.002	PRDX5
P19387	POLR 2C	DNA-directed RNA polymerase II subunit R PB3	2.1	0.004	PR DX5
013356	DDII 2	BING type F3 ubiquitin protein ligase DDU 2	2,1	0	DR DY5
094045	PACCAD1	Res CTDass activating protoin 1	2	0	DP DY5
O9LIN37	VDS/A	Vacualar protein sorting associated protein 4 A	2	0	DRDVS
OBTE1	DOTNS	vacuorar protein sorting-associated protein 4A	2	0.002	DDDVC
Q7D1E1		Zie Geer Den hie lie denst en state en tra	2	0,002	PRDAS
075218	ZKANB2	Zinc nnger Kan-binding domain-containing protein 2	2	0,003	PRDX5
Q8WVC2	KPS21	405 ribosomal protein 521	2	0,003	PKDX5
Q9BZE1	MRPL37	398 ribosomal protein L37, mitochondrial	2	0,004	PRDX5
Q9Y3D9	MRPS23	28S ribosomal protein S23, mitochondrial	2	0,017	PRDX5
Q9UN86	G3BP2	Ras GTPase-activating protein-binding protein 2	1,9	0	PRDX5
DC2870	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	1,9	0	PRDX5

A0A087X2D5	MRPL45	39\$ ribosomal protein L45, mitochondrial	1,9	0,001	PRDX5
P07196	NEFL	Neurofilament light polypeptide	1,9	0,001	PRDX5
Q7L2E3	DHX30	ATP-dependent RNA helicase DHX30	1,9	0,002	PRDX5
Q6P1L8	MRPL14	39S ribosomal protein L14, mitochondrial	1,9	0,009	PRDX5
P14174	MIF	Macrophage migration inhibitory factor	1,9	0,011	PRDX5
Q6UWE0	LRSAM1	E3 ubiquitin-protein ligase LRSAM1	1,9	0,012	PRDX5
Q16822	PCK2	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	1,9	0,013	PRDX5
O60232	ZNRD2	Protein ZNRD2	1,9	0,024	PRDX5
C9J8P9	CLTA	Clathrin light chain	1,9	0,044	PRDX5
Q8TCG1	CIP2A	Protein CIP2A	1,8	0,001	PRDX5
P09110	ACAA1	3-ketoacyl-CoA thiolase, peroxisomal	1,8	0,005	PRDX5
Q5JRI1	SRSF10	Serine/arginine-rich-splicing factor 10	1,8	0,007	PRDX5
Q96DH6	MSI2	RNA-binding protein Musashi homolog 2	1,8	0,008	PRDX5
Q15477	SKIV2L	Helicase SKI2W	1,8	0,009	PRDX5
Q9BPW8	NIPSNAP1	Protein NipSnap homolog 1	1,8	0,009	PRDX5
O43347	MSI1	RNA-binding protein Musashi homolog 1	1,8	0,01	PRDX5
Q9NXH9	TRMT1	tRNA	1,8	0,012	PRDX5
C9JRJ5	LIMD1	LIM domain-containing protein 1	1,7	0	PRDX5
Q96RP9	GFM1	Elongation factor G, mitochondrial	1,7	0,002	PRDX5
Q12948	FOXC1	Forkhead box protein C1	1,7	0,002	PRDX5
Q99569	PKP4	Plakophilin-4	1,7	0,002	PRDX5
Q53H96	PYCR3	Pyrroline-5-carboxylate reductase 3	1,7	0,011	PRDX5
K/ELV2	SEHIL	Nucleoporin SEH1	1,7	0,017	PRDX5
Q913B/	MRPLII	398 ribosomal protein L11, mitochondrial	1,6	0	PRDX5
Q9B125	HAUS8 CTRD2	HAUS augmin-like complex subunit 8	1,6	0	PRDX5
01(252	UNIA	C-terminal-binding protein 2	1,6	0 001	PRDA5
Q16552	SUCL C1	Alpha-Internexin	1,6	0,001	PRDAS
P 55577	FDC4	Enhancer of mP NA decemping protein 4	1,6	0,002	PRDA3
09V5K6	CD2AP	CD2 associated protein	1,6	0,003	PR DY5
Q915K0 Q8N3C0	ASCC3	Activating signal cointegrator 1 complex subunit 3	1,0	0.004	PR DX5
077406	MYH14	Myosin-14	1,0	0.005	PR DX5
014964	HGS	Hepatocyte growth factor-regulated tyrosine kinase substrate	1,6	0.005	PR DX5
075592	MYCBP2	F3 ubiquitin-protein ligase MYCBP2	1,6	0.005	PR DX5
013363	CTBP1	C-terminal-binding protein 1	1,6	0.01	PR DX5
A0A0A0MRT6	ABI1	Ablinteractor 1	1,6	0.012	PR DX5
P48047	ATP5PO	ATP synthase subunit O. mitochondrial	1,6	0,013	PRDX5
012933	TRAF2	TNF receptor-associated factor 2	1,6	0,016	PRDX5
P42345	MTOR	Serine/threonine-protein kinase mTOR	1,6	0,017	PRDX5
Q13418	ILK	Integrin-linked protein kinase	1,6	0,021	PRDX5
Q96DA6	DNAJC19	Mitochondrial import inner membrane translocase subunit TIM14	1,6	0,022	PRDX5
Q99956	DUSP9	Dual specificity protein phosphatase 9	1,6	0,027	PRDX5
Q9C026	TRIM9	E3 ubiquitin-protein ligase TRIM9	1,6	0,035	PRDX5
P55084	HADHB	Trifunctional enzyme subunit beta, mitochondrial	1,6	0,039	PRDX5
Q5VUJ6	LRCH2	Leucine-rich repeat and calponin homology domain-containing protein 2	1,6	0,043	PRDX5
Q13526	PIN1	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	1,5	0	PRDX5
Q96FW1	OTUB1	Ubiquitin thioesterase OTUB1	1,5	0	PRDX5
O43795	MYO1B	Unconventional myosin-Ib	1,5	0,001	PRDX5
P52272	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	1,5	0,002	PRDX5
Q15398	DLGAP5	Disks large-associated protein 5	1,5	0,002	PRDX5
Q9BW92	TARS2	ThreoninetRNA ligase, mitochondrial	1,5	0,004	PRDX5
A0A087WTZ5	UBXN1	UBX domain-containing protein 1	1,5	0,006	PRDX5
P82921	MRPS21	28S ribosomal protein S21, mitochondrial	1,5	0,006	PRDX5
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	1,5	0,008	PRDX5
O95785	WIZ	Protein Wiz	1,5	0,008	PRDX5
P46060	RANGAP1	Ran GTPase-activating protein 1	1,5	0,013	PRDX5
Q9Y2R4	DDX52	Probable ATP-dependent RNA helicase DDX52	1,5	0,013	PRDX5
H3BRE8	RPAP1	RNA polymerase II-associated protein 1	1,5	0,017	PRDX5
Q16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	1,5	0,022	PRDX5
B1ALK7	ARHGEF7	Rho guanine nucleotide exchange factor 7	1,5	0,024	PRDX5
Q9BY32	ITPA	Inosine triphosphate pyrophosphatase	1,5	0,026	PRDX5
P16403	H1-2	Histone H1.2	1,5	0,029	PRDX5
Q8NI60	COQ8A	Atypical kinase COQ8A, mitochondrial	1,5	0,029	PRDX5
A0A3B3IUD2	MSTO1	Protein misato homolog 1	1,5	0,029	PRDX5
Q8WVC0	LEO1	KNA polymerase-associated protein LEO1	1,5	0,031	PRDX5
P17028	ZNF24	Zinc tinger protein 24	1,5	0,035	PRDX5
A0A0A0MRM8	MYO6	Unconventional myosin-6	1,4	0	PRDX5
F8W B06	ATXN2	Ataxin-2	1,4	0	PRDX5
1 205 151	PSMG1	Proteasome assembly chaperone 1	1,4	0	PR DX5

Q9ULX3	NOB1	RNA-binding protein NOB1	1,4	0,001	PRDX5
Q86U42	PABPN1	Polyadenylate-binding protein 2	1,4	0,001	PRDX5
Q92974	ARHGEF2	Rho guanine nucleotide exchange factor 2	1,4	0,001	PRDX5
Q9Y5Y2	NUBP2	Cytosolic Fe-S cluster assembly factor NUBP2	1,4	0,002	PRDX5
Q9BSH4	TACO1	Translational activator of cytochrome c oxidase 1	1,4	0,002	PRDX5
P19838	NFKB1	Nuclear factor NF-kappa-B p105 subunit	1,4	0,002	PRDX5
Q9GZT3	SLIRP	SRA stem-loop-interacting RNA-binding protein, mitochondrial	1,4	0,003	PRDX5
P40937	RFC5	Replication factor C subunit 5	1,4	0,003	PRDX5
P23258	TUBG1	Tubulin gamma-1 chain	1,4	0,004	PRDX5
Q92888	ARHGEF1	Rho guanine nucleotide exchange factor 1	1,4	0,007	PRDX5
Q9P2B4	CTTNBP2NL	CTTNBP2N-terminal-like protein	1,4	0,008	PRDX5
Q16513	PKN2	Serine/threonine-protein kinase N2	1,4	0,01	PRDX5
Q96PK6	RBM14	RNA-binding protein 14	1,4	0,012	PRDX5
O60783	MRPS14	28S ribosomal protein S14, mitochondrial	1,4	0,013	PRDX5
Q13247	SRSF6	Serine/arginine-rich splicing factor 6	1,4	0,019	PRDX5
Q96GD0	PDXP	Pyridoxal phosphate phosphatase	1,4	0,021	PRDX5
Q6DKI1	RPL7L1	60S ribosomal protein L7-like 1	1,4	0,026	PRDX5
Q99959	PKP2	Plakophilin-2	1,4	0,026	PRDX5
Q9BW83	IFT27	Intraflagellar transport protein 27 homolog	1,4	0,03	PRDX5
Q6R327	RICTOR	Rapamycin-insensitive companion of mTOR	1,4	0,034	PRDX5
094760	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	1,4	0,042	PRDX5
P35244	RPA3	Replication protein A 14 kDa subunit	1,4	0,049	PRDX5
Q9NYZ3	GISEI	G2 and S phase-expressed protein 1	1,3	0,001	PRDX5
Q9BSD7	N I PCR	Cancer-related nucleoside-triphosphatase	1,3	0,002	PRDX5
Q13625	I P53BP2	Apoptosis-stimulating of p53 protein 2	1,3	0,002	PRDX5
P0//3/	PFN1 FXOC®	Profilin-1	1,3	0,002	PRDAS
Q81116	DRVCA	Exocyst complex component 8	1,5	0,005	PRDA5
00(PT1	EDDIN	Frotein kinase C alpha type	1,5	0,003	PRDA5
ESHOOR	VDS22R	Vieweler protein corting accepted protein 22B	1,5	0,006	DP DV5
OSWLIMO	NILID133	Nuclear pore complex protein Nup133	1,5	0,008	PRDX5
013464	ROCK1	R bo associated protein kingse 1	1,5	0.008	PR DY5
D28838	LAD3	Cutosal aminopentidase	1,5	0,000	PR DY5
A 5YK K 6	CNOT1	CCR4-NOT transcription complex subunit 1	1.3	0,009	PR DX5
086UK7	ZNF598	F3 ubiquitin-protein ligase ZNF598	1.3	0.01	PR DX5
P48634	PRRC2A	Protein PR RC2A	1.3	0.012	PR DX5
095373	IPO7	Importin-7	1.3	0.013	PR DX5
Q05655	PRKCD	Protein kinase C delta type	1.3	0,015	PRDX5
Q86V48	LUZP1	Leucine zipper protein 1	1.3	0,02	PRDX5
P05783	KRT18	Keratin, type I cytoskeletal 18	1,3	0,024	PRDX5
Q9Y3I0	RTCB	RNA-splicing ligase RtcB homolog	1,3	0,027	PRDX5
H3BPE1	MACF1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	1,3	0,034	PRDX5
Q13613	MTMR1	Myotubularin-related protein 1	1,3	0,039	PRDX5
Q01081	U2AF1	Splicing factor U2AF 35 kDa subunit	1,3	0,04	PRDX5
C9JZR2	CTNND1	Catenin delta-1	1,3	0,042	PRDX5
I3L2Z5	MAZ	Myc-associated zinc finger protein	1,3	0,049	PRDX5
P24752	ACAT1	Acetyl-CoA acetyltransferase, mitochondrial	1,2	0	PRDX5
P33240	CSTF2	Cleavage stimulation factor subunit 2	1,2	0,001	PRDX5
A0A087WW06	TTC28	Tetratricopeptide repeat protein 28	1,2	0,001	PRDX5
Q15126	PMVK	Phosphomevalonate kinase	1,2	0,001	PRDX5
P57740	NUP107	Nuclear pore complex protein Nup107	1,2	0,002	PRDX5
Q9P2R3	ANKFY1	Rabankyrin-5	1,2	0,002	PRDX5
Q16527	CSRP2	Cysteine and glycine-rich protein 2	1,2	0,003	PRDX5
Q8NCA5	FAM98A	Protein FAM98A	1,2	0,003	PRDX5
Q6P587	FAHD1	Acylpyruvase FAHD1, mitochondrial	1,2	0,004	PRDX5
A0A087WUK2	HNRNPDL	Heterogeneous nuclear ribonucleoprotein D-like	1,2	0,006	PRDX5
Q86Y56	DNAAF5	Dynein assembly factor 5, axonemal	1,2	0,007	PRDX5
P50213	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	1,2	0,008	PRDX5
Q15654	TRIP6	Thyroid receptor-interacting protein 6	1,2	0,009	PRDX5
P84103	SRSF3	Serine/arginine-rich splicing factor 3	1,2	0,013	PRDX5
Q9UNE7	STUB1	E3 ubiquitin-protein ligase CHIP	1,2	0,013	PRDX5
Q02241	KIF23	Kinesin-like protein KIF23	1,2	0,015	PRDX5
D6R938	CAMK2D	Calcium/calmodulin-dependent protein kinase	1,2	0,019	PRDX5
Q2TAL8	QRICH1	Glutamine-rich protein 1	1,2	0,021	PRDX5
Q13509	TUBB3	Tubulin beta-3 chain	1,2	0,023	PRDX5
Q9NQT5	EXOSC3	Exosome complex component RRP40	1,2	0,026	PRDX5
Q8N9T8	KRI1	Protein KRI1 homolog	1,2	0,03	PRDX5
P21912	SDHB	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1,2	0,039	PRDX5
Q8WWH5	TRUB1	Probable tRNA pseudouridine synthase 1	1,2	0,041	PRDX5

D00(22	DLD	Dit dada dalah dari seria dari dalah	1.1	0	DD DVC
P09622	DLD	Dinydrolipoyi denydrogenase, mitochondriai	1,1	0	PRDAS
P19525	EIF2AK2	Interferon-induced, double-stranded KNA-activated protein kinase	1,1	0	PRDX5
Q9Y5M8	SRPRB	Signal recognition particle receptor subunit beta	1,1	0	PRDX5
P39019	RPS19	40S ribosomal protein S19	1,1	0	PRDX5
O9Y2Z4	YAR S2	TyrosinetRNA ligase, mitochondrial	1,1	0,001	PRDX5
P58107	FPPK1	Fpiplakin	11	0.002	PR DX5
00010/02	DDVC	D L L ATD L L DNAL E DDVCC	1,1	0,002	DDDXC
Q9N 193	DDX56	Probable ATP-dependent KNA helicase DDX56	1,1	0,004	PRDX5
Q6P1N0	CC2D1A	Coiled-coil and C2 domain-containing protein 1A	1,1	0,005	PRDX5
P46778	RPL21	60S ribosomal protein L21	1,1	0,006	PRDX5
C9I9K3	R PSA	40\$ ribosomal protein \$A	11	0.006	PR DX5
4042D 000	SUCI A2	Surginate CoAlizers [ADD forming] subunit bets mittachen driel	1,1	0.000	DDDVs
AUAZK81DQ9	SUCLAZ	SuccinateCoA ligase [ADP-forming] subunit beta, mitochondriai	1,1	0,006	PKDA5
O00442	RTCA	RNA 3'-terminal phosphate cyclase	1,1	0,008	PRDX5
P62937	PPIA	Peptidyl-prolyl cis-trans isomerase A	1,1	0,008	PRDX5
O9P0K7	RAI14	Ankvcorbin	1,1	0,011	PRDX5
051875	DR R C 2R	Drotain DR R C 2B	11	0.012	DR DY5
Q)]02)	ALDUKAI		1,1	0,012	DDDXC
Q02252	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	1,1	0,014	PRDX5
Q9NQT4	EXOSC5	Exosome complex component RRP46	1,1	0,015	PRDX5
Q15750	TAB1	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	1,1	0,022	PRDX5
P50995	ANXA11	Annexin A11	1.1	0.022	PR DX5
092665	MP DS21	285 ribecomel protoin \$21 mitochondrial	1.1	0.022	DP DV5
Q92665	MKP351		1,1	0,025	PRDAS
Q12849	GRSF1	G-rich sequence factor 1	1,1	0,027	PRDX5
Q96F86	EDC3	Enhancer of mRNA-decapping protein 3	1,1	0,027	PRDX5
Q9UQ35	SRRM2	Serine/arginine repetitive matrix protein 2	1,1	0,027	PRDX5
O9RWF3	P BM/	R NA binding protein /	11	0.028	DR DYS
Q/DW15	RDM4	RNA-binding protein 4	1,1	0,028	PRDAJ
Q96N6/	DOCK/	Dedicator of cytokinesis protein 7	1,1	0,035	PRDX5
P00568	AK1	Adenylate kinase isoenzyme 1	1,1	0,036	PRDX5
P62266	RPS23	40S ribosomal protein S23	1,1	0,047	PRDX5
O7KZ85	SUPT6H	Transcription elongation factor SPT6	11	0.048	PR DX5
D04(27	TD:2	Callulation action at 2	1,1	0.048	DDDVs
P0463/	11755		1,1	0,048	PRDAS
F2Z388	RPL35	60S ribosomal protein L35	1,1	0,049	PRDX5
P62081	RPS7	40S ribosomal protein S7	1	0,001	PRDX5
P22570	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial	1	0,005	PRDX5
O8WY93	PALLD	Palladin	1	0.007	DR DY5
Q0WA75	ANIXA		1	0,007	DDDXC
P09525	ANXA4	Annexin A4	1	0,008	PRDX5
P35580	MYH10	Myosin-10	1	0,01	PRDX5
H7C5E4	XRN1	5'-3' exoribonuclease 1	1	0,011	PRDX5
013595	TR A 2 A	Transformer-2 protein homolog alpha	1	0.012	PR DX5
00/027	CCDD1	Cial and DNA his line and in his his his his	1	0,012	DDDVC
Q0485/	55DP1	Single-stranded DINA-binding protein, mitochondriai	1	0,015	PKDA5
Q12789	GTF3C1	General transcription factor 3C polypeptide 1	1	0,021	PRDX5
Q8WXF1	PSPC1	Paraspeckle component 1	1	0,022	PRDX5
P11172	UMPS	Uridine 5'-monophosphate synthase	1	0,025	PRDX5
EQDEL4	DIAT	A cotultransformed component of nuruwate debudrogenese complex	1	0.026	DP DV5
E/FEJ4	DLAI	Acception and the second of pyruvate denydrogenase complex	1	0,020	FRDA)
Q9BQ69	MACROD1	ADP-ribose glycohydrolase MACROD1	1	0,028	PRDX5
O14965	AURKA	Aurora kinase A	1	0,031	PRDX5
075691	UTP20	Small subunit processome component 20 homolog	1	0,038	PRDX5
P30520	4 DSS2	A denvlosuccinate synthetase isozyme ?	1	0.039	DR DY5
1 J0 J20	110332	A children and synthetiase isozyme 2		0,037	DDDV
D3Y1B5	IRAKI	Interleukin-1 receptor-associated kinase 1	1	0,046	PRDX5
P45985	MAP2K4	Dual specificity mitogen-activated protein kinase kinase 4	1	0,049	PRDX5
PRDX2-specific					
interactors					
P30048	PR DX 3	Thioredoxin-dependent peroxide reductase mitochondrial	5.8	0	PR DX1
D22110	DR DV2	Description 2	5,0	0	DR DV1
P32119	PRDAZ	Peroxiredoxin-2	5,/	0	PKDAI
Q9Y224	RTRAF	RNA transcription, translation and transport factor protein	5,4	0	PRDX1
P02790	HPX	Hemopexin	4,9	0	PRDX1
P62805	H4C1	Histone H4	4,1	0	PRDX1
060506	SVNCR ID	Heterogeneous nuclear ribonucleoprotein O	3.9	0	DR DY 1
D(0)00	D DI 124		3,7	0	DDDV1
P40429	KPL13A	605 ribosomal protein L13a	3,9	0	PRDXI
P63167	DYNLL1	Dynein light chain 1, cytoplasmic	3,8	0	PRDX1
O76094	SRP72	Signal recognition particle subunit SRP72	3,7	0	PRDX1
P05386	R PLP1	60S acidic ribosomal protein P1	3.4	0	PR DX1
D00167	CVRSA	Cutachtamab5	2.2	0	DD DV1
10010/	CIDJA NO SSS	Syteenionic by	3,3	-	r (DA1
096007	MOCS2	Molybdopterin synthase catalytic subunit	3,3	0	PRDX1
E9PKG1	PRMT1	Protein arginine N-methyltransferase 1	3,2	0	PRDX1
P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	3.2	0	PRDX1
P19338	NCI	Nucleolin	3.2	0	PR DY 1
11/JJ0 D(22//	DACK		3,2	0	DDDDV
P63244	RACK1	Receptor of activated protein C kinase 1	3	0	PRDX1
Q9Y3D6	FIS1	Mitochondrial fission 1 protein	2,9	0	PRDX1
P62244	RPS15A	40S ribosomal protein S15a	2.9	0	PRDX1
P05387	R DI D2	60\$ acidic tibosomal protein D2	2.9	0	PR DY 1
103307	1(1 L1 2	ovo actate noosoniai protein i 2	<u> </u>	v	INDAI

A0A0B4J1Z1	SRSF7	Serine/arginine-rich-splicing factor 7	2,9	0,001	PRDX1
Q6UW78	UQCC3	Ubiquinol-cytochrome-c reductase complex assembly factor 3	2,8	0	PRDX1
O00483	NDUFA4	Cytochrome c oxidase subunit NDUFA4	2.8	0	PR DX1
096CT7	CCDC124	Coiled coil domain containing protoin 12/	28	0	DP DV1
Q/0C1/	CCDC124	Coned-con domain-containing protein 124	2,0	0	FRDAT
P61353	RPL27	605 ribosomal protein L2/	2,7	0	PRDXI
Q92688	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B	2,7	0	PRDX1
P61106	RAB14	Ras-related protein Rab-14	2,7	0,002	PRDX1
A0A3B3ISV3	COL4A1	Collagen alpha-1(IV) chain	2.6	0	PR DX1
D00750	ANVAE		2,0	0	DR DV1
P08/38	ANAAS	Alinexin AS	2,6	0	PKDAI
P68133	ACTA1	Actin, alpha skeletal muscle	2,6	0,004	PRDX1
Q9NX55	HYPK	Huntingtin-interacting protein K	2,6	0,006	PRDX1
D6RA00	ENOPH1	Enolase-phosphatase E1	2,5	0	PRDX1
B9A018	USP39	U4/U6 U5 tri-spR NP-associated protein 2	2.5	0	PR DX1
0927(9	UDAC2	Ulistens desembles 2	2,5	0	DR DV1
Q)2/8)	IIDAC2		2,5	0	FRDAT
P12236	SLC25A6	ADP/ATP translocase 3	2,5	0	PRDXI
P26196	DDX6	Probable ATP-dependent RNA helicase DDX6	2,5	0	PRDX1
P35637	FUS	RNA-binding protein FUS	2,5	0,001	PRDX1
P18077	R PL35A	60S ribosomal protein L35a	2.4	0	PR DX1
D09211	GSTP1	Clutathione S. transferace D	2 /	0	DR DY1
F07211	G51F1		2,4	0	PRDAI
G5EA06	MRPS2/	285 ribosomal protein S2/, mitochondrial	2,4	0,002	PRDXI
P53602	MVD	Diphosphomevalonate decarboxylase	2,4	0,002	PRDX1
Q71UI9	H2AZ2	Histone H2A.V	2,3	0	PRDX1
O9H0U4	RAB1B	Ras-related protein Rab-1B	2.3	0	PRDX1
D36957	DIST	Dibudralinavellycine residue succinvitransferase component of 2-avaglutarate	2.3	0	DR DY1
r 36737	DL31	Dinydronpoynysme-residue succinyntansrerase component or 2-oxogiutarate	2,5	0	FRDAT
		denydrogenase complex, mitochondriai			
P62750	RPL23A	60S ribosomal protein L23a	2,3	0	PRDX1
C9J4Z3	RPL37A	60S ribosomal protein L37a	2,3	0	PRDX1
P27797	CALR	Calreticulin	2,3	0	PRDX1
P15121	AKR1B1	Aldo-keto reductase family 1 member B1	2.3	0	PR DX1
052000	LICD17D12	We have here 2 and 1 CoA sub-	2,0	0.002	DB DV1
<u>Q55GQ0</u>	HSDI/BIZ	very-long-chain 3-oxoacyl-CoA reductase	2,5	0,002	PRDAI
075223	GGCT	Gamma-glutamylcyclotransferase	2,3	0,002	PRDX1
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	2,3	0,004	PRDX1
P12955	PEPD	Xaa-Pro dipeptidase	2,3	0,007	PRDX1
A0A087WTM1	ROBO1	Roundahout homolog 1	2.2	0	PR DX1
Ool lovo	CORASDO	Colei economico productione e e e e e e e e e e e e e e e e e e	2,2	0	DR DV1
Q9H818	GORASP2	Goigi reassenioly-stacking protein 2	2,2	0	PRDAI
P50914	RPL14	60S ribosomal protein L14	2.2	0	PRDX1
			2,2	0	
P32969	RPL9	60\$ ribosomal protein L9	2,2	0	PRDX1
P32969 P51149	RPL9 RAB7A	60S ribosomal protein L9 Ras-related protein Rab-7a	2,2 2,2 2,2	0	PRDX1 PRDX1
P32969 P51149 P19174	RPL9 RAB7A PLCG1	60S ribosomal protein L9 Ras-related protein Rab-7a 1-phosphatidylinositol 4.5-bisphosphate phosphodiesterase gamma-1	2,2 2,2 2,2 2,2	0 0 0 0 0.002	PRDX1 PRDX1 PRDX1
P32969 P51149 P19174 O15144	RPL9 RAB7A PLCG1	60S ribosomal protein L9 Ras-related protein Rab-7a 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	2,2 2,2 2,2 2,2 2,2 2,2 2,2	0 0 0,002 0,002	PRDX1 PRDX1 PRDX1 PRDX1
P32969           P51149           P19174           O151144           Vanne X and X	RPL9 RAB7A PLCG1 ARPC2	60S ribosomal protein L9 Ras-related protein Rab-7a 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 Actin-related protein 2/3 complex subunit 2	2,2 2,2 2,2 2,2 2,2 2,2 2,2	0 0 0,002 0,002	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969           P51149           P19174           O15144           H3BRL3	RPL9 RAB7A PLCG1 ARPC2 UBFD1	60S ribosomal protein I.9 Ras-related protein Rab-7a 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 Actin-related protein 2/3 complex subunit 2 Ubiquitin domain-containing protein UBFD1	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2	0 0 0,002 0,002 0,003	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP	60S ribosomal protein I.9 Ras-related protein Rab-7a 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 Actin-related protein 2/3 complex subunit 2 Ubiquitin domain-containing protein UBFD1 S-methyl-5'-thioadenosine phosphorylase	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2	0 0 0,002 0,002 0,003 0,004	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2	0 0 0,002 0,002 0,003 0,004 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS	60S ribosomal protein E19 Ras-related protein Rab-7a 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 Actin-related protein 2/3 complex subunit 2 Ubiquitin domain-containing protein UBFD1 S-methyl-5'-thioadenosine phosphorylase Serpin B6 Ras-related protein R-Ras	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2	0 0 0,002 0,002 0,003 0,004 0 0	PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30700	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SER DINB1	60S ribosomal protein I.9 Ras-related protein Rab-7a 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 Actin-related protein 2/3 complex subunit 2 Ubiquitin domain-containing protein UBFD1 S-methyl-5'-thioadenosine phosphorylase Serpin B6 Ras-related protein R-Ras Lawkoryer adortase inhibitor	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2	0 0 0,002 0,002 0,003 0,004 0 0 0	PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30740	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SEAP	OS ribosomal protein L9     Ras-related protein Rab-7a     1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1     Actin-related protein 2/3 complex subunit 2     Ubiquitin domain-containing protein UBFD1     S-methyl-5'-thioadenosine phosphorylase     Serpin B6     Ras-related protein R-Ras     Leukocyte elastase inhibitor	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9NS69	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30740           Q15393           Q9N869           Q02750	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9NS69         Q02750         P49321	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q02750         P49321         P23921	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP R RM1	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diiposphate reductase large subunit	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q153933         Q9N869         Q02750         P49321         P23921         O9HLG3	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 PAB23	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Pac related protein Re-Na	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9N869         Q02750         P49321         P23921         Q9ULC3         Q27402	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 DP. PLCA	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9NS69         Q02750         P49321         P23921         Q9ULC3         O75400	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A	For information         60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q151393         Q02750         P49321         P23921         Q9ULC3         O75400         O95104	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4	60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O60547	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4 GMDS	For interview pretent and processing actors of the processing act	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30740           Q15393           Q9N869           Q02750           P49321           P23921           Q9ULC3           O75400           O95104           O60547           O00231	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4 GMDS PSMD11	Actin Protein L9         Ras-related protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q2NS69         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O600231         O043747	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4 GMDS PSMD11 AP1C1	Actin Protein L9         Ras-related protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP L complex subunit rearmand	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9NS69         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O60547         O00231         O43747	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4 GMDS PSMD11 APIG1 AUIG1	Action Protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O60547         O00231         O43747         O95433	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4 GMDS PSMD11 AP1G1 AHSA1	Active related protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9N869         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O00231         O43747         O95433         Q02878	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4 GMDS PSMD11 AP1G1 AHSA1 RPL6	File There in Perturbation         60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mR.NA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein L6	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9N869         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O60547         O9231         O43747         O95433         Q02878         P15880	RPL9 RAB7A PLCG1 ARPC2 UBFD1 MTAP SERPINB6 RRAS SERPINB1 SF3B3 TOMM22 MAP2K1 NASP RRM1 RAB23 PRPF40A SCAF4 GMDS PSMD11 AP1G1 AHSA1 RPL6 RPS2	Active related protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein L6	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9NS69         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O43747         O95433         Q02878         P15880         P06730	RPL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         AP1G1         AHSA1         RPL6         RPS2         EIF4E	Actin Protein L9         Ras-related protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         608 ribosomal protein S2         Evakaryotic translation initiation factor 4E	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9NS69         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O60547         O00231         O43747         O95433         Q02878         P15388	R.PL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         AP1G1         AHSA1         RPL6         RPL6         RPL6         RPL6         RPL6         RPL6         RPL6         RPL6         RPL0	Activity       Preserve         60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26\$ proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein S2         Eukaryotic translation initiation factor 4E         60S ribosomal protein P0	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P35740         Q15393         Q9NS69         Q02750         P49321         P23921         Q9ULC3         O75400         O06547         O00231         O43747         O95433         Q02878         P15880         P06730         P05388	R.PL9         R.AB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         R.RAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         R.RM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         AP1G1         AHSA1         RPL6         RPL6         RPL60         RPL60         RPL90         EUF4E	Activity       Prevented         60S ribosomal protein L9       Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein L6         40S ribosomal protein S2         Eukaryotic translation initiation factor 4E         60S acidic ribosomal protein PO         Eukaryotic translation i	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q9N869         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O60547         O00231         O43747         O95433         Q02878         P15880         P06730         P05388         K7ERF1	RPL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         AHSA1         RPL6         RPS2         EIF4E         RPLP0         EIF3K	Action Protein L9         Ras-related protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein L6         40S ribosomal protein S2         Eukaryotic translation initiation factor 3 subunit K	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P30740         Q15393         Q2NS69         Q02750         P49321         P23921         Q9ULC3         O75400         O95104         O60547         O00231         O43747         O95433         Q02878         P15880         P06730         P05388         K7ERF1         P35606	RPL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         APIG1         AHSA1         RPL6         RPL6         RPL6         RPL0         EIF4E         RPLP0         EIF3K         COPB2	Active Test Sector         60S ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein S2         Eukaryotic translation initiation factor 4E         60S acidic ribosomal protein P0         Eukaryotic translation initiation factor 3 subunit K         Coatomer subunit beta'	2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30740           Q15393           Q9NS69           Q02750           P49321           P23921           Q9ULC3           O75400           O95104           O60547           O00231           O43747           O95433           Q02878           P15388           K7ERF1           P35606           P11182	R.PL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         APIG1         AHSA1         RPL6         RPL6         RPL00         EIF3K         COPB2         DBT	Financial protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein L6         40S ribosomal protein P0         Eukaryotic translation initiation factor 4E         60S acidic ribosomal protein P0         Eukaryotic translation initiation factor 3 subunit K	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969         P51149         P19174         O15144         H3BRL3         Q13126         P35237         P10301         P35240         Q15393         Q9NS69         Q02750         P49321         P23921         Q9ULC3         O75400         O06547         O00231         O43747         O95433         Q02878         P15880         P06730         P05388         K7ERF1         P35606         P11182	R.PL9         R.AB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         APIG1         AHSA1         RPL6         RPS2         EIF4E         RPLP0         EIF3K         COPB2         DBT	Action Protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein L6         40S ribosomal protein S2         Eukaryotic translation initiation factor 4E         60S acidic ribosomal protein PO         Eukaryotic translation initiation factor 3 subunit K	2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30740           Q15393           Q9N869           Q02750           P49321           P23921           Q9ULC3           O75400           O95104           O60547           O00231           O43747           O95433           Q02878           P15880           P06730           P05388           K7ERF1           P35606           P11182           O5SY16	RPL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         AHSA1         RPL6         RPS2         EIF4E         RPLP0         EIF3K         COPB2         DBT	100       Free and the set of the set	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30740           Q15393           Q2NS69           Q02750           P49321           P23921           Q9ULC3           O75400           O95104           O60547           O00231           O43747           O95433           Q02878           P15880           P06730           P05388           K7ERF1           P35606           P11182           Q55Y16           O97570	RPL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         APIG1         AHSA1         RPL6         RPS2         EIF4E         RPLP0         EIF3K         COPB2         DBT         NOL9         PPMF1	Activation       Prevention         608 ribosomal protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein S2         Eukaryotic translation initiation factor 4E         60S acidic ribosomal protein P0         Eukaryotic translation initiation factor 3 subunit K         Coatomer subunit beta'         Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogen	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1           PRDX1 </td
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P30740           Q15393           Q9NS69           Q02750           P49321           P23921           Q9ULC3           O75400           O95104           O60547           O00231           O43747           O95433           Q02878           P15880           P06730           P05388           K7ERF1           P35606           P11182           Q5SY16           Q95SY16           Q97570	RPL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         AP1G1         AHSA1         RPL6         RPS2         EIF4E         RPLP0         EIF3K         COPB2         DBT         NOL9         PPME1	Action Protein L9         Ras-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein L6         40S ribosomal protein S2         Eukaryotic translation initiation factor 4E         60S acidic ribosomal protein P0         Eukaryotic translation inititation factor 3 subunit K	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1	0 0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1
P32969           P51149           P19174           O15144           H3BRL3           Q13126           P35237           P10301           P35237           P10301           P30740           Q15393           Q9NS69           Q02750           P49321           P23921           Q9ULC3           O75400           O06547           O00231           O43747           O95433           Q02878           P15880           P06730           P05388           K7ERF1           P35606           P11182           Q5SY16           Q9Y570           P00491	R.PL9         RAB7A         PLCG1         ARPC2         UBFD1         MTAP         SERPINB6         RRAS         SERPINB1         SF3B3         TOMM22         MAP2K1         NASP         RRM1         RAB23         PRPF40A         SCAF4         GMDS         PSMD11         AHSA1         RPL6         RPS2         EIF4E         RPLP0         EIF3K         COPB2         DBT         NOL9         PPME1         PNP         PRPE	Activity       Ass-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein Rab-7a         1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1         Actin-related protein 2/3 complex subunit 2         Ubiquitin domain-containing protein UBFD1         S-methyl-5'-thioadenosine phosphorylase         Serpin B6         Ras-related protein R-Ras         Leukocyte elastase inhibitor         Splicing factor 3B subunit 3         Mitochondrial import receptor subunit TOM22 homolog         Dual specificity mitogen-activated protein kinase kinase 1         Nuclear autoantigenic sperm protein         Ribonucleoside-diphosphate reductase large subunit         Ras-related protein Rab-23         Pre-mRNA-processing factor 40 homolog A         SR-related and CTD-associated factor 4         GDP-mannose 4,6 dehydratase         26S proteasome non-ATPase regulatory subunit 11         AP-1 complex subunit gamma-1         Activator of 90 kDa heat shock protein ATPase homolog 1         60S ribosomal protein S2         Eukaryotic translation initiation factor 4E         60S acidic ribosomal protein P0         Eukaryotic translation initiation factor 3 subunit K         Coatomer subunit beta'         Lipoamide acyltransfera	2,2 2,2 2,2 2,2 2,2 2,2 2,2 2,1 2,1 2,1	0 0 0 0,002 0,002 0,003 0,004 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX1

A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6	2	0,021	PRDX1
P04181	OAT	Ornithine aminotransferase, mitochondrial	1,9	0	PRDX1
Q14232	EIF2B1	Translation initiation factor eIF-2B subunit alpha	1,9	0	PRDX1
Q9UJS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	1,9	0	PRDX1
P53985	SLC16A1	Monocarboxylate transporter 1	1,9	0	PRDX1
O75489	NDUF\$3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	1,9	0,005	PRDX1
P84085	ARF5	ADP-ribosylation factor 5	1,9	0,012	PRDX1
E9PHS0	LANCL1	Glutathione S-transferase LANCL1	1,9	0,021	PRDX1
O60664	PLIN3	Perilipin-3	1,9	0,024	PRDX1
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	1,9	0,036	PRDX1
P10599	TXN	Thioredoxin	1,9	0,043	PRDX1
Q9UBF2	COPG2	Coatomer subunit gamma-2	1,8	0	PRDX1
Q15691	MAPRE1	Microtubule-associated protein RP/EB family member 1	1,8	0	PRDX1
A6NKB8	RNPEP	Aminopeptidase B	1,8	0	PRDX1
P00387	CYB5R3	NADH-cytochrome b5 reductase 3	1,8	0	PRDX1
P23396	RPS3	40S ribosomal protein S3	1,8	0	PRDX1
P41252	IARSI	IsoleucinetRNA ligase, cytoplasmic	1,8	0,001	PRDX1
014980	XPOI	Exportin-1	1,8	0,002	PRDXI
Q4J6C6	PREPL	Prolyl endopeptidase-like	1,8	0,006	PRDXI
P11388	TEPFOID	DNA topoisomerase 2-alpha	1,8	0,007	PRDXI
Q9N Y B0	I EKF2IP	Telomeric repeat-binding factor 2-interacting protein 1	1,8	0,007	PRDXI
P28288	ADCD3	A I P-binding cassette sub-ramily D member 3	1,8	0,009	PRDX1
E/E1Z4	DZ WZ	Cluteminess hidrawiseform mitachendeid	1,8	0,012	PRDX1
094925 EQDLINIZ	GL5 CSTM2	Clutathiana Standform, Mitochondriai	1,8	0,012	PRDX1
O9NVD1	DDV18	ATD dependent P NA belieses DDV18	1,0	0,014	PRDA1
Q9NVP1 D40616	API1	A DP riberylation factor like protein 1	1,0	0,013	PRDA1
D38159	RBMY	R NA binding matif protein Y chromosome	1,0	0.037	PR DY1
09P2B4	CTTNBP2NI	CTTNBP2 N-terminal-like protein	1,0	0	PR DX1
Q6PI48	DAR S2	AspartatetRNA ligase mitochondrial	1,7	0	PR DX1
P36542	ATP5F1C	ATP synthase subunit gamma, mitochondrial	1,7	0	PR DX1
P05141	SLC25A5	ADP/ATP translocase 2	1,7	0	PR DX1
O5T7C4	HMGB1	High mobility group protein B1	1,7	0,001	PRDX1
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	1,7	0,004	PRDX1
O00232	PSMD12	26S proteasome non-ATPase regulatory subunit 12	1,7	0,004	PRDX1
P27824	CANX	Calnexin	1,7	0,005	PRDX1
Q9BQG0	MYBBP1A	Myb-binding protein 1A	1,7	0,007	PRDX1
Q9ULW0	TPX2	Targeting protein for Xklp2	1,7	0,008	PRDX1
Q01085	TIAL1	Nucleolysin TIAR	1,7	0,01	PRDX1
P51398	DAP3	28S ribosomal protein S29, mitochondrial	1,7	0,014	PRDX1
Q96IU4	ABHD14B	Protein ABHD14B	1,7	0,016	PRDX1
O95163	ELP1	Elongator complex protein 1	1,7	0,017	PRDX1
Q9UBS4	DNAJB11	DnaJ homolog subfamily B member 11	1,7	0,018	PRDX1
P31153	MAT2A	S-adenosylmethionine synthase isoform type-2	1,6	0	PRDX1
P05455	SSB	Lupus La protein	1,6	0	PRDX1
P61313	RPL15	60S ribosomal protein L15	1,6	0	PRDX1
P51665	PSMD7	26S proteasome non-ATPase regulatory subunit 7	1,6	0	PRDX1
G8JLH9	STAT3	Signal transducer and activator of transcription	1,6	0	PRDX1
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	1,6	0	PRDX1
O75821	EIF3G	Eukaryotic translation initiation factor 3 subunit G	1,6	0	PRDX1
P16435	POR	NADPHcytochrome P450 reductase	1,6	0,003	PRDX1
P39023	RPL3	60S ribosomal protein L3	1,6	0,004	PRDX1
Q8TEX9	IPO4	Importin-4	1,6	0,006	PRDX1
Q8N3X1	FNBP4	Formin-binding protein 4	1,6	0,018	PRDX1
Q9Y4P1	ATG4B	Cysteine protease ATG4B	1,6	0,021	PRDX1
P00390	GSR	Glutathione reductase, mitochondrial	1,6	0,025	PRDX1
Q13542	EIF4EBP2	Eukaryotic translation initiation factor 4E-binding protein 2	1,6	0,025	PRDX1
Q514U8	RABGGTB	Geranylgeranyl transferase type-2 subunit beta	1,6	0,033	PRDX1
A6NGP5	JP12	Jupiter microtubule-associated homolog 2	1,6	0,033	PRDX1
P51991	HNRNPA3	Heterogeneous nuclear ribonucleoprotein A3	1,6	0,037	PRDX1
Q8N806	UBR7	Putative E3 ubiquitin-protein ligase UBR7	1,6	0,047	PRDX1
P43304	GPD2	Glycerol-3-phosphate dehydrogenase, mitochondrial	1,6	0,048	PRDXI
Q9B1 N0	5KXNI TWE2	Sumredoxin-1	1,6	0,048	PKDX1
Q61B20	1 WF2	IWINDIID-2	1,5	0	PRDX1
Q6IQ49	5DE2	Replication stress response regulator SDE2	1,5	0	PKDX1
0911080	EIFB DAGC	Electron transfer flavoprotein subunit beta	1,5	0	PKDX1
D(158)	PA2G4	Transforming protein P bo	1,5	0	PKDA1
P62024	DAFALIIDI	District antionalized and a second burden by TD and and the second	1,5	0	PKDX1
143034	PAFAHIBI	Platelet-activating factor acetylhydrolase IB subunit beta	1,5	U	PKDXI

Q00487	PSMD14	26S proteasome non-ATPase regulatory subunit 14	15	0.001	PR DX1
052112	ACK	Aculalization for the second second suburner in	1,5	0,002	DP DV1
01/521	DDP1	DNA damage kinding protein 1	1,5	0,002	DR DV1
Q16551	DDB1	DNA damage-binding protein 1	1,5	0,002	PRDAI
Q9GZS3	WDR61	WD repeat-containing protein 61	1,5	0,003	PRDXI
P30101	PDIA3	Protein disulfide-isomerase A3	1,5	0,003	PRDX1
Q9NPH2	ISYNA1	Inositol-3-phosphate synthase 1	1,5	0,004	PRDX1
P52597	HNRNPF	Heterogeneous nuclear ribonucleoprotein F	1,5	0,004	PRDX1
Q5VW32	BROX	BRO1 domain-containing protein BROX	1,5	0,007	PRDX1
Q96IZ0	PAWR	PRKC apoptosis WT1 regulator protein	1,5	0,009	PRDX1
Q92621	NUP205	Nuclear pore complex protein Nup205	1,5	0,012	PRDX1
P26599	PTBP1	Polypyrimidine tract-binding protein 1	1,5	0,018	PRDX1
H3BV80	R NPS1	RNA-binding protein with serine-rich domain 1	15	0.023	PR DX1
08NI27	THOC2	THO complex subunit 2	1,5	0.024	DR DY1
D42574	CASD2	Compare 2	1,5	0,024	DR DV1
P423/4	DOCID		1,5	0,026	PRDAI
Q9P28/	BCCIP	BRCA2 and CDKN1A-interacting protein	1,5	0,029	PRDXI
E9PGT1	TSN	Component 3 of promoter of RISC	1,5	0,031	PRDX1
Q9BSJ8	ESYT1	Extended synaptotagmin-1	1,5	0,032	PRDX1
Q9H9P8	L2HGDH	L-2-hydroxyglutarate dehydrogenase, mitochondrial	1,5	0,033	PRDX1
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	1,5	0,034	PRDX1
P07384	CAPN1	Calpain-1 catalytic subunit	1,5	0,037	PRDX1
Q9Y6Y0	IVNS1ABP	Influenza virus NS1A-binding protein	1,5	0,037	PRDX1
O9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	1,5	0,043	PRDX1
P27694	R PA 1	Replication protein A 70 kDa DNA-binding subunit	15	0.046	PR DX1
092973	TNPO1	Transportin-1	1,5	0	DR DY1
D22528	CEL1		1,1	0	DR DV1
P23320	DDC24		1,4	0	PRDAI
P6124/	RPS3A	40S ribosomal protein 53a	1,4	0	PRDXI
E9PN17	ATP5MG	ATP synthase subunit g, mitochondrial	1,4	0,001	PRDX1
A0A024R4M0	RPS9	40S ribosomal protein S9	1,4	0,001	PRDX1
O00203	AP3B1	AP-3 complex subunit beta-1	1,4	0,001	PRDX1
P60953	CDC42	Cell division control protein 42 homolog	1,4	0,001	PRDX1
P08133	ANXA6	Annexin A6	1,4	0,003	PRDX1
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1,4	0,004	PRDX1
Q96SB4	SRPK1	SRSF protein kinase 1	1,4	0,005	PRDX1
O5T4K5	CRTC2	CREB-regulated transcription coactivator 2	1.4	0.006	PR DX1
G3V529	DDX24	RNA belicase	1.4	0.019	PR DX1
0911109	CVR5P 1	NADU autochromo b5 reductore 1	1,1	0.027	DP DV1
	MD DC17	200 cite controlle by feddetase f	1,4	0,037	DD DV1
Q912K5	MKP51/	285 ribosomai protein 51/, mitocnondriai	1,4	0,037	PRDAI
Q9BZK/	IBLIXKI	F-box-like/ WD repeat-containing protein 1 BLIXRI	1,4	0,03/	PRDXI
096019	ACTL6A	Actin-like protein 6A	1,4	0,039	PRDX1
Q5JR04	MOV10	RNA helicase	1,4	0,039	PRDX1
K7EM73	CAPNS1	Calcium-activated neutral proteinase small subunit	1,4	0,04	PRDX1
O95394	PGM3	Phosphoacetylglucosamine mutase	1,3	0	PRDX1
P68104	EEF1A1	Elongation factor 1-alpha 1	1,3	0	PRDX1
P00338	LDHA	L-lactate dehydrogenase A chain	1,3	0	PRDX1
P06737	PYGL	Glycogen phosphorylase, liver form	1,3	0	PRDX1
P36578	R PL4	60S ribosomal protein L4	1.3	0	PR DX1
P08238	HSP90AB1	Heat shock protein HSP 90-beta	1 3	0	PR DX1
D525/5		Pha CDD dissociation inhibitor 1	1,5	0.001	DP DV1
E7ESV4	MTAI	Material and an MTA1	1,5	0,001	DR DV1
D/DI NI	D (DI NI	DNA FU(0126 Light signature Minches Light have been been been been been been been be	1,5	0,001	DD DV1
D4DLNI	D4DLNI WDD a.(	CDINA FLJ60124, nignly similar to Mitochondrial dicarboxylate carrier	1,5	0,001	PRDAI
Q9H7D7	WDR26	WD repeat-containing protein 26	1,3	0,002	PRDXI
P61923	COPZ1	Coatomer subunit zeta-1	1,3	0,002	PRDX1
P62269	RPS18	40S ribosomal protein S18	1,3	0,002	PRDX1
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	1,3	0,002	PRDX1
A0A3B3IRI2	CTPS1	CTP synthase	1,3	0,004	PRDX1
E7EV99	ADD1	Alpha-adducin	1,3	0,004	PRDX1
P56192	MARS1	MethioninetRNA ligase, cytoplasmic	1,3	0,005	PRDX1
O9Y678	COPG1	Coatomer subunit gamma-1	1,3	0,006	PRDX1
075832	PSMD10	26S proteasome non-ATPase regulatory subunit 10	1.3	0.007	PR DX1
X1WI28	R PI 10	60S ribosomal protein I 10	1.3	0.008	PR DX1
D50502	ST13	Hec70.interacting protein	1 2	0.012	DR DV1
001040	NAT10	DNA antiding protein	1,5	0.015	DD DV1
Q9HUAU	NATIO	RINA cylidine acetyltransferase	1,5	0,014	PRDAI
AUAUAUMKM9	NOLCI	Nucleolar and colled-body phosphoprotein 1	1,3	0,025	PKDXI
Q8N9Q2	SKEK11P1	Protein SKEK11P1	1,3	0,026	PKDX1
P52888	THOP1	Thimet oligopeptidase	1,3	0,032	PRDX1
Q9NUP9	LIN7C	Protein lin-7 homolog C	1,3	0,035	PRDX1
Q93008	USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	1,3	0,037	PRDX1
Q9Y262	EIF3L	Eukaryotic translation initiation factor 3 subunit L	1,3	0,043	PRDX1
Q96BW9	TAMM41	Phosphatidate cytidylyltransferase, mitochondrial	1,3	0,043	PRDX1

F5GZS6	SLC3A2	4F2 cell-surface antigen heavy chain	1,3	0,047	PRDX1
P49756	RBM25	RNA-binding protein 25	1,2	0	PRDX1
P61221	ABCE1	ATP-binding cassette sub-family E member 1	1,2	0	PRDX1
Q9H3P7	ACBD3	Golgi resident protein GCP60	1,2	0,001	PRDX1
Q07020	RPL18	60S ribosomal protein L18	1,2	0,001	PRDX1
O9NOW7	XPNPEP1	Xaa-Pro aminopeptidase 1	1,2	0,002	PRDX1
P55884	EIF3B	Eukarvotic translation initiation factor 3 subunit B	1.2	0,004	PRDX1
P62241	R PS8	40S ribosomal protein S8	1.2	0.005	PR DX1
P49736	MCM2	DNA replication licensing factor MCM2	1,2	0.005	PR DX1
D53618	COPR1	Costomer subunit beta	1.2	0.005	PR DY1
075521	BANE1	Barrier to autointegration factor	1,2	0,007	DP DV1
D15027	DAINI1	Darlierto-autointegration factor	1,2	0,007	DR DV1
P1372/	TODI	DNA consistences 1	1,2	0,011	PRDA1
P1138/	TOPI	DINA topoisomerase i	1,2	0,012	PRDAI
P153/4	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	1,2	0,012	PRDXI
QSQPM/	PSMF1	Proteasome inhibitor P131 subunit	1,2	0,017	PRDXI
P49750	YLPM1	YLP motif-containing protein 1	1,2	0,019	PRDX1
P20073	ANXA7	Annexin A7	1,2	0,025	PRDX1
Q00610	CLTC	Clathrin heavy chain 1	1,2	0,026	PRDX1
P33992	MCM5	DNA replication licensing factor MCM5	1,2	0,029	PRDX1
P31689	DNAJA1	DnaJ homolog subfamily A member 1	1,2	0,031	PRDX1
A0A0A0MRN5	OGFR	Opioid growth factor receptor	1,2	0,04	PRDX1
O15269	SPTLC1	Serine palmitoyltransferase 1	1,2	0,043	PRDX1
P82663	MRPS25	28S ribosomal protein S25, mitochondrial	1,1	0	PRDX1
P62424	RPL7A	60S ribosomal protein L7a	1,1	0	PRDX1
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	1,1	0	PRDX1
Q00325	SLC25A3	Phosphate carrier protein, mitochondrial	1,1	0	PRDX1
P34949	MPI	Mannose-6-phosphate isomerase	1,1	0,001	PRDX1
Q8NE71	ABCF1	ATP-binding cassette sub-family F member 1	1,1	0,001	PRDX1
E5RHG8	ELOC	Elongin-C	1.1	0,001	PRDX1
O9Y5P6	GMPPB	Mannose-1-phosphate guanyltransferase beta	1.1	0.002	PR DX1
O8WUH6	TMEM263	Transmembrane protein 263	11	0.002	PR DX1
P14324	FDPS	Farnesyl pyrophosphate synthase	11	0.002	PR DX1
015029	FETUD2	116 kDa US small puckas ribonuckanrotain component	1,1	0,002	DP DV1
Q13027	DD DE10	Drs m D NA massessing forster 19	1,1	0,003	DR DV1
Q90M34	SMARCC2	SWU/SNE complex suburit SMARCC2	1,1	0,003	PRDA1
Q81AQ2	SMARCC2	DNA minute la maria anna in Nal 2	1,1	0,004	PRDA1
P43246	MSH2	DINA mismatch repair protein Msh2	1,1	0,005	PRDAI
Q99460	PSMDI	265 proteasome non-ATP as regulatory subunit 1	1,1	0,006	PRDAI
Q9UNM6	PSMD13	265 proteasome non-ATPase regulatory subunit 13	1,1	0,009	PRDXI
P53004	BLVRA	Biliverdin reductase A	1,1	0,012	PRDXI
Q9U112	ATP6V1H	V-type proton AT Pase subunit H	1,1	0,013	PRDX1
Q9Y3Z3	SAMHD1	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	1,1	0,013	PRDX1
Q5T760	SRSF11	Serine/arginine-rich-splicing factor 11	1,1	0,019	PRDX1
F8W6I7	HNRNPA1	Helix-destabilizing protein	1,1	0,026	PRDX1
P62333	PSMC6	26S proteasome regulatory subunit 10B	1,1	0,03	PRDX1
P34932	HSPA4	Heat shock 70 kDa protein 4	1,1	0,032	PRDX1
P26583	HMGB2	High mobility group protein B2	1,1	0,039	PRDX1
P42224	STAT1	Signal transducer and activator of transcription 1-alpha/beta	1,1	0,046	PRDX1
P62314	SNRPD1	Small nuclear ribonucleoprotein Sm D1	1,1	0,049	PRDX1
P60891	PRPS1	Ribose-phosphate pyrophosphokinase 1	1	0	PRDX1
075396	SEC22B	Vesicle-trafficking protein SEC22b	1	0,004	PRDX1
O9BT78	COPS4	COP9 signalosome complex subunit 4	1	0.005	PR DX1
014240	FIF4A2	Fukarvotic initiation factor 4 A-II	- 1	0.011	PR DX1
09/903	DI DRD	Duridoval phoephate homeostasis protein	1	0.02	PR DY1
OSIWB7	WDEV1	WD report and EVVE domain containing protoin 1	1	0,02	DP DV1
Q000272	DEEA	DNA for exercision for the suburity sliph -	1	0,02	DR DV1
0002/3	CNU12	NUD2 lile securie 1	1	0,034	PRDA1
P55/69	SINU15	NHP2-like protein 1	1	0,038	PRDAI
Q8NHH9	AILZ	Atlastin-2	1	0,039	PRDXI
014965	AURKA	Aurora kinase A	1	0,044	PRDXI
Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	1	0,046	PRDX1
P32119	PRDX2	Peroxiredoxin-2	6,8	0	PRDX3
P00167	CYB5A	Cytochrome b5	4,4	0	PRDX3
O96007	MOCS2	Molybdopterin synthase catalytic subunit	3,7	0	PRDX3
P10301	RRAS	Ras-related protein R-Ras	3,7	0	PRDX3
Q9Y224	RTRAF	RNA transcription, translation and transport factor protein	3,7	0	PRDX3
Q9Y3D6	FIS1	Mitochondrial fission 1 protein	3,2	0	PRDX3
Q96CT7	CCDC124	Coiled-coil domain-containing protein 124	3,2	0	PRDX3
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	3	0	PRDX3
Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	3	0,001	PRDX3
O9NX55	НҮРК	Huntingtin-interacting protein K	2.9	0,003	PRDX3
~····		5	-,/	5,005	

E7EVA0	ΜΔΡ/	Microtubule associated protein	2.9	0.005	DR DY3
005921	ATT (1	As a second seco	2,9	0,005	DD DV2
075851	AIFMI	Apoptosis-inducing factor 1, infoctionaria	2,0	0	PRDAS
P53602	MVD	Diphosphomevalonate decarboxylase	2,8	0,001	PRDX3
Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	2,8	0,001	PRDX3
Q6IQ49	SDE2	Replication stress response regulator SDE2	2,7	0	PRDX3
Q9ULW0	TPX2	Targeting protein for Xklp2	2,7	0,001	PRDX3
O96A10	ERVK3-1	Endogenous retrovirus group K3 member 1	2.7	0,024	PRDX3
H0YNW5	DUT	Deoxyuridine S'-triphosphate nucleotidohydrolase	2.6	0	PR DX3
OONDUI2	ISVNIA 1	In easieral 2 mb earth and 1	2,0	0	DR DX2
Q9NPH2	ISINAI	Inositoi-3-phosphate synthase 1	2,6	0	PRDAS
Q13542	EIF4EBP2	Eukaryotic translation initiation factor 4E-binding protein 2	2,6	0,002	PRDX3
P12955	PEPD	Xaa-Pro dipeptidase	2,6	0,004	PRDX3
Q9C0C2	TNKS1BP1	182 kDa tankyrase-1-binding protein	2,6	0,007	PRDX3
O60664	PLIN3	Perilipin-3	2,5	0,002	PRDX3
O6PID6	TTC33	Tetratricopentide repeat protein 33	2.5	0.034	PR DX3
LI2DD L 2	LIPEDI	Ultimitie domain containing modelin UBED1	2,5	0	DR DV2
H JDKLJ	UBFDI		2,4	0	PRDAS
P4/985	UQCRESI	Cytochrome b-c1 complex subunit Rieske, mitochondrial	2,4	0	PRDX3
B7Z7F3	RANBP3	Ran-binding protein 3	2,4	0,001	PRDX3
P00491	PNP	Purine nucleoside phosphorylase	2,4	0,002	PRDX3
Q8N3X1	FNBP4	Formin-binding protein 4	2,3	0	PRDX3
Q9P2B4	CTTNBP2NL	CTTNBP2 N-terminal-like protein	2,3	0	PRDX3
09NU03	TXLNG	Gamma-taxilin	2.3	0	PR DX3
ORNES1	SED BD1	Plasminogen activator inhibitor 1 P NA hinding protein	2.2	0.001	DP DV3
Qanchi	SERDF1		2,5	0,001	PRDAJ
A4D150	KLRG2	Killer cell lectin-like receptor subfamily G member 2	2,3	0,003	PRDX3
P11802	CDK4	Cyclin-dependent kinase 4	2,3	0,004	PRDX3
P35244	RPA3	Replication protein A 14 kDa subunit	2,3	0,004	PRDX3
Q9P258	RCC2	Protein RCC2	2,2	0,001	PRDX3
O7Z4V5	HDGFL2	Hepatoma-derived growth factor-related protein 2	2.2	0,012	PRDX3
E7EV99	4 D D 1	Alpha-adducin	2.1	0	DR DY3
01/0/5			2,1	0	DD DV2
014965	AUKKA	Aurora kinase A	2,1	0	PRDAS
Q12948	FOXC1	Forkhead box protein C1	2,1	0,001	PRDX3
P14174	MIF	Macrophage migration inhibitory factor	2,1	0,01	PRDX3
A0A087WTM1	ROBO1	Roundabout homolog 1	2	0	PRDX3
F5GZS6	SLC3A2	4F2 cell-surface antigen heavy chain	2	0,006	PRDX3
P61758	VBP1	Prefoldin subunit 3	2	0.006	PRDX3
ACNCD5	IDT'2	Junitar migratubula associated homolog ?	2	0.007	DP DV2
Decree			2	0,007	DDDV2
P00590	GSK	Giutatnione reductase, mitocnondriai	2	0,009	PRDAS
015511	ARPC5	Actin-related protein 2/3 complex subunit 5	2	0,014	PRDX3
E9PDD6	BCL2L13	Bcl-2-like protein 13	2	0,02	PRDX3
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-	1,9	0,002	PRDX3
		succinocarboxamide synthase			
P41250	GARS1	GlycinetRNA ligase	1,9	0,004	PRDX3
013541	EIF4EBP1	Eukarvotic translation initiation factor 4E-binding protein 1	19	0.01	PR DX3
098266	NUDC	Nuclear migration protoin nudC	1.9	0.014	DP DV3
Q71200	CODOCA		1,9	0,014	DDDV2
Q81 V M0	CCDC50	Colled-coll domain-containing protein 50	1,9	0,014	PRDAS
J3KS31	ZNF207	BUB3-interacting and GLEBS motif-containing protein ZNF207	1,9	0,032	PRDX3
A0A1B0GUC3	FTO	Alpha-ketoglutarate-dependent dioxygenase FTO	1,8	0,025	PRDX3
P40222	TXLNA	Alpha-taxilin	1,7	0,002	PRDX3
P61927	RPL37	60S ribosomal protein L37	1,7	0,005	PRDX3
O6UW78	UOCC3	Ubiquinol-cvtochrome-c reductase complex assembly factor 3	1.7	0,01	PRDX3
ADAVT1	LIBA6	Ubiquitin-like modifier activating enzyme 6	17	0.022	DR DY3
OO(VP5	DPV	Lumphaking estimated killer T cell estimated meatrin kinese	1,7	0.022	DR DV2
Q76KD5	PDK	Lymphokine-activated kiner 1-cen-originated protein kinase	1,7	0,027	PRDAS
P13995	MTHFD2	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	1,7	0,029	PRDX3
		Includes: NAD-dependent methylenetetrahydrofolate dehydrogenase			
O94903	PLPBP	Pyridoxal phosphate homeostasis protein	1,6	0	PRDX3
P26599	PTBP1	Polypyrimidine tract-binding protein 1	1,6	0,012	PRDX3
Q99598	TSNAX	Translin-associated protein X	1,6	0,014	PRDX3
O9UHR 5	SAP30BP	SAP30-binding protein	16	0.02	PR DX3
012126	MTAD	S mothyl 5' thiosdenosing phosphoryless	1,0	0.02	DP DV3
Q13120	MIAP GALDI		1,0	0,03	PRDAJ
E7PGZI	CALDI		1,6	0,036	PKDA3
Q15181	PPA1	Inorganic pyrophosphatase	1,5	0	PRDX3
Q7Z2K8	GPRIN1	G protein-regulated inducer of neurite outgrowth 1	1,5	0,001	PRDX3
P31153	MAT2A	S-adenosylmethionine synthase isoform type-2	1,5	0,001	PRDX3
P62244	RPS15A	40S ribosomal protein S15a	1,5	0,003	PRDX3
071UI9	H2AZ2	Histone H2A.V	1.5	0.018	PR DX3
D85037	FOXK1	Forkbead hox protein K1	15	0.022	DR DY2
0011474	TN2KD D		1,5	0.022	DDDV2
Q7HA64	rN3KKP	Netosamine-5-kinase	1,5	0,03	PKDX3
A0A087WUT6	EIF5B	Eukaryotic translation initiation factor 5B	1,4	0,001	PRDX3
Q5T4K5	CRTC2	CREB-regulated transcription coactivator 2	1,4	0,014	PRDX3
Q5T6F2	UBAP2	Ubiquitin-associated protein 2	1,4	0,018	PRDX3

Q7L2J0	MEPCE	7SK snRNA methylphosphate capping enzyme	1,4	0,021	PRDX3
Q9NUP9	LIN7C	Protein lin-7 homolog C	1,4	0,026	PRDX3
P52888	THOP1	Thimet oligopeptidase	1,4	0,028	PRDX3
Q13137	CALCOCO2	Calcium-binding and coiled-coil domain-containing protein 2	1,4	0,028	PRDX3
P49903	SEPHS1	Selenide, water dikinase 1	1,4	0,031	PRDX3
Q16204	CCDC6	Coiled-coil domain-containing protein 6	1,4	0,034	PRDX3
E9PKG1	PRMT1	Protein arginine N-methyltransferase 1	1,3	0	PRDX3
P50914	RPL14	60S ribosomal protein L14	1,3	0,001	PRDX3
Q02878	RPL6	60S ribosomal protein L6	1,3	0,008	PRDX3
Q6PKG0	LARP1	La-related protein 1	1,3	0,008	PRDX3
Q16576	RBBP7	Histone-binding protein RBBP7	1,3	0,011	PRDX3
O9BO61	TRIR	Telomerase RNA component interacting RNase	1,3	0,014	PRDX3
08N902	SREK1IP1	Protein SREK1IP1	1,3	0,015	PRDX3
09GZS3	WDR61	WD repeat-containing protein 61	1.3	0.015	PR DX 3
096F86	EDC3	Enhancer of mRNA-decapping protein 3	1.3	0.018	PR DX3
P62266	R PS23	40S ribosomal protein \$23	13	0.02	PR DX3
P56385	ATP5MF	ATP synthase subunit e_mitochondrial	1,3	0.025	PR DX3
D/81/7	DDED	Probal and an appretidaça	1,5	0,025	DP DV2
09/170	DAWD	DR KC anomaticia WT1 normalitane materia	1,3	0,020	DR DV2
Q96120	PAWK	PKKC apoptosis w 11 regulator protein	1,5	0,032	PRDA3
Q915/0	PPMEI	Protein phosphatase methylesterase I	1,3	0,038	PRDX3
Q32MZ4	LKKFIPI	Leucine-rich repeat flightless-interacting protein 1	1,3	0,039	PRDX3
P40429	RPL13A	60S ribosomal protein L13a	1,2	0,001	PRDX3
P07195	LDHB	L-lactate dehydrogenase B chain	1,2	0,003	PRDX3
P34897	SHMT2	Serine hydroxymethyltransferase, mitochondrial	1,2	0,004	PRDX3
Q9BRP1	PDCD2L	Programmed cell death protein 2-like	1,2	0,006	PRDX3
J3KN29	PSMD9	26S proteasome non-ATPase regulatory subunit 9	1,2	0,011	PRDX3
P62851	RPS25	40S ribosomal protein S25	1,2	0,015	PRDX3
Q9H0U4	RAB1B	Ras-related protein Rab-1B	1,2	0,023	PRDX3
B4DDF4	CNN2	Calponin	1,2	0,031	PRDX3
O14949	UQCRQ	Cytochrome b-c1 complex subunit 8	1,2	0,046	PRDX3
P62826	RAN	GTP-binding nuclear protein Ran	1,1	0	PRDX3
Q8WUH6	TMEM263	Transmembrane protein 263	1,1	0,001	PRDX3
P18077	RPL35A	60S ribosomal protein L35a	1,1	0,004	PRDX3
P78346	RPP30	Ribonuclease P protein subunit p30	1,1	0,004	PRDX3
P62753	RPS6	40S ribosomal protein S6	1,1	0,014	PRDX3
P05388	RPLP0	60S acidic ribosomal protein P0	1,1	0,015	PRDX3
A0A0A0MR N5	OGER	Opioid growth factor receptor	11	0.022	PR DX 3
BIAMS2	SEPTIN6	Sentin 6 isoform CBA b	1,1	0.032	PR DX3
09NIS69	TOMM22	Mitochondrial import recentor subunit TOM22 homolog	1,1	0.039	DR DX3
D22281	WAP S1	Trustophan tP NA lizzes systeplasmic	1,1	0,002	DP DV 2
D(2888	P DI 20	60S ribosomal protein L 20	1	0,002	DP DV 2
001102	SI C25 A 22	Mitrach en dei al electemente consiste 1	1	0,005	DR DX2
Q/11/30	NAVE	NA D(D)/LL hudente entrerer	1	0,017	DR DX2
Q8INC W5	CDVN24	NAD(P)H-hydrate epimerase	1	0,02	PRDA3
P42//1	CDKNZA		1	0,03	PRDX3
Q9UJZ1	STOML2	Stomatin-like protein 2, mitochondrial	1	0,038	PRDX3
X1WI28	RPL10	60S ribosomal protein L10	1	0,04	PRDX3
Q9Y224	RTRAF	RNA transcription, translation and transport factor protein	5,1	0	PRDX4
P32119	PRDX2	Peroxiredoxin-2	5,1	0	PRDX4
P00167	CYB5A	Cytochrome b5	4,2	0	PRDX4
H0YNW5	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase	4	0	PRDX4
Q9NPH2	ISYNA1	Inositol-3-phosphate synthase 1	3,6	0	PRDX4
P10301	RRAS	Ras-related protein R-Ras	3,5	0	PRDX4
Q96CT7	CCDC124	Coiled-coil domain-containing protein 124	3,4	0	PRDX4
O96007	MOCS2	Molybdopterin synthase catalytic subunit	3,4	0	PRDX4
Q9P2B4	CTTNBP2NL	CTTNBP2 N-terminal-like protein	3,4	0	PRDX4
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	3,3	0	PRDX4
P41250	GARS1	GlycinetRNA ligase	3,3	0	PRDX4
O60664	PLIN3	Perilipin-3	3,2	0	PRDX4
P11802	CDK4	Cvclin-dependent kinase 4	3,2	0	PRDX4
O9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	3.2	0.001	PR DX4
Q9Y3D6	FIS1	Mitochondrial fission 1 protein	3	0	PRDX4
O9ULW0	TPX2	Targeting protein for Xklp?	3	0	PR DX4
O6UW78	UOCC3	Ubiquinol-cytochrome-c reductase compley assembly factor 3	3	0	PR DX4
D61758	VRD1	Drefoldin subunit 3	20	0	DR DV/
D/257/	CASD2	Company 2	2,0	0	DD DV4
CODDW/9	NIDENIA DI	Destein NinSauchamalan 1	2,8	0	PRDA4
Q/DF W 0	DTDD1	Delementaria di ne seconte la di ne mente della di la di ne seconte di ne seconte di la di ne seconte di la di ne seconte di la di ne seconte di ne seconte di la di ne seconte di n	2,8	0	PRDA4
F26599	P I BPI	Polypyrimidine tract-binding protein 1	2,8	0	PRDX4
Q9N569	10MM22	Mitochondrial import receptor subunit TOM22 homolog	2,8	0	PRDX4
Q9NX55	HYPK	Huntingtin-interacting protein K	2,8	0,003	PRDX4

H3BRL3	UBFD1	Ubiquitin domain-containing protein UBFD1	2,7	0	PRDX4
B7Z7F3	RANBP3	Ran-binding protein 3	2,6	0	PRDX4
O9H840	GEMIN7	Gem-associated protein 7	2.6	0	PR DX4
O(WK74	PAR11EID1	Pabl1 family interacting protoin 1	2,0	0	DP DV4
Q6WKZ4	CADITITITI OD DV/1001		2,0	0	PRDA4
Q8N9Q2	SKEKIIPI	Protein SREKIIPI	2,6	0	PRDX4
P30740	SERPINB1	Leukocyte elastase inhibitor	2,6	0	PRDX4
A0A087WTM1	ROBO1	Roundabout homolog 1	2,6	0	PRDX4
G5EA06	MRPS27	28\$ ribosomal protein \$27, mitochondrial	2,6	0,001	PRDX4
P53602	MVD	Diphosphomevalonate decarboxylase	2.6	0.001	PR DX4
09/EA/	SDDL 1	Dentain Serie dlu	2,0	0.002	DR DV/
Q96EA4	SPDLI	Protein Spinary	2,6	0,002	PKDA4
Q6PID6	11C33	Tetratricopeptide repeat protein 33	2,6	0,026	PRDX4
Q96A10	ERVK3-1	Endogenous retrovirus group K3 member 1	2,6	0,028	PRDX4
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase	2,5	0	PRDX4
Q6IQ49	SDE2	Replication stress response regulator SDE2	2,5	0	PRDX4
P34897	SHMT2	Serine hydroxymethyltransferase_mitochondrial	2.5	0	PR DX4
FODVC1	DD MT1	Dentria razinia N metholografiana 1	2,5	0	DR DV/
E9PKGI	PKMII	Protein arginine N-methyltransferase 1	2,5	0	PRDA4
Q13542	EIF4EBP2	Eukaryotic translation initiation factor 4E-binding protein 2	2,5	0,002	PRDX4
Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	2,5	0,002	PRDX4
P12955	PEPD	Xaa-Pro dipeptidase	2,5	0,003	PRDX4
H7BXI1	ESYT2	Extended synaptotagmin-2	2,4	0	PRDX4
075223	GGCT	Camma glutamylcyclotransferase	2.4	0	DR DY/
073223	DVAU D D1		2,4	0	DDDX
Q9NP9/	DINLKBI	Dynein light chain roadblock-type I	2,4	0	PKDX4
Q9H0U4	RAB1B	Ras-related protein Rab-1B	2,4	0	PRDX4
P42771	CDKN2A	Cyclin-dependent kinase inhibitor 2A	2,4	0	PRDX4
P12236	SLC25A6	ADP/ATP translocase 3	2,4	0	PRDX4
P56385	ATP5MF	ATP synthase subunit e mitochondrial	2.4	0.001	PR DX4
D0(122	LIBOD	I have been been been been been been been be	2,1	0,002	DRDX/
P06132	UKUD	Uroporphyrinogen decarboxylase	2,4	0,005	PKDX4
Q8WVC2	RPS21	40S ribosomal protein S21	2,3	0,001	PRDX4
Q9H2P9	DPH5	Diphthine methyl ester synthase	2,3	0,002	PRDX4
P49903	SEPHS1	Selenide, water dikinase 1	2,3	0,002	PRDX4
A6NGP5	IPT2	Jupiter microtubule-associated homolog 2	2,3	0,002	PRDX4
013126	ΜΤΔΡ	S-methyl-52-thioadenosine phosphorylase	2 3	0.003	DR DY/
Q15120			2,5	0,005	DDDX
014965	AUKKA	Aurora kinase A	2,2	0	PRDX4
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	2,2	0,001	PRDX4
Q9Y266	NUDC	Nuclear migration protein nudC	2,2	0,006	PRDX4
Q7Z4V5	HDGFL2	Hepatoma-derived growth factor-related protein 2	2,2	0,008	PRDX4
E7EV99	ADD1	Alpha-adducin	2.1	0	PR DX4
08N2V1	ENIRD4	Formin binding protain (	2.1	0	DP DV4
Qanazi	TINDF4		2,1	0	PRDA4
095831	AIFMI	Apoptosis-inducing factor 1, mitochondrial	2,1	0	PRDX4
P36542	ATP5F1C	ATP synthase subunit gamma, mitochondrial	2,1	0	PRDX4
Q9BTE1	DCTN5	Dynactin subunit 5	2,1	0,001	PRDX4
P47985	UQCRFS1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	2,1	0,001	PRDX4
P00491	PNP	Purine nucleoside phosphorylase	2.1	0.002	PR DX4
D05027	FOVV1	Full to the market K1	2,1	0,002	DRDX/
P8505/	FUAKI	Forknead box protein K1	2,1	0,005	PKDA4
A0AV11	UBA6	Ubiquitin-like modifier-activating enzyme 6	2,1	0,006	PRDX4
P07355	ANXA2	Annexin A2	2,1	0,028	PRDX4
P63000	RAC1	Ras-related C3 botulinum toxin substrate 1	2	0	PRDX4
P63167	DYNLL1	Dynein light chain 1, cytoplasmic	2	0,001	PRDX4
O9NUP9	LIN7C	Protein lin-7 homolog C	2	0.003	PR DX4
D84085	AD EC		2	0,005	DDDV/
P84085	ARFS	ADP-ribosylation factor 5	2	0,004	PRDA4
P35244	RPA3	Replication protein A 14 kDa subunit	2	0,004	PRDX4
O60547	GMDS	GDP-mannose 4,6 dehydratase	2	0,009	PRDX4
Q9HA64	FN3KRP	Ketosamine-3-kinase	2	0,009	PRDX4
P10599	TXN	Thioredoxin	2	0,028	PRDX4
090002	TNKS1RD1	182 kDa tankwrase 1 hinding protein	2	0.03/	DR DY4
Q/00/02	D DC20	406 sile some lange in 620	2	0,039	DDDV/
P622/3	KP529	405 ribosomai protein 529	2	0,038	PKDA4
P49642	PRIM1	DNA primase small subunit	1,9	0	PRDX4
Q9NUQ3	TXLNG	Gamma-taxilin	1,9	0,001	PRDX4
A0A087X2D5	MRPL45	39S ribosomal protein L45, mitochondrial	1,9	0,002	PRDX4
A4D1S0	KLRG2	Killer cell lectin-like receptor subfamily G member 2	1.9	0,002	PRDX4
P62304	SNR PF	Small nuclear ribonucleoprotein F	1 9	0.005	PR DX4
00/002	LIEVING	Destain HEVIM1	1,7	0,000	DDDV
074772	ITEAIMI		1,7	0,005	rrDA4
Q5JRI1	SRSF10	Serine/arginine-rich-splicing factor 10	1,9	0,006	PRDX4
E9PGT1	TSN	Component 3 of promoter of RISC	1,9	0,007	PRDX4
Q9BSI8					DD DX/
	ESYT1	Extended synaptotagmin-1	1,9	0,008	PRDX4
P25705	ESYT1 ATP5F1A	Extended synaptotagmin-1 ATP synthase subunit alpha, mitochondrial	1,9	0,008	PRDX4 PRDX4
P25705	ESYT1 ATP5F1A FOXC1	Extended synaptotagmin-1 ATP synthase subunit alpha, mitochondrial Forkhead box protein C1	1,9 1,8	0,008	PRDX4 PRDX4
P25705 Q12948	ESYT1 ATP5F1A FOXC1	Extended synaptotagmin-1 ATP synthase subunit alpha, mitochondrial Forkhead box protein C1	1,9 1,8 1,8	0,008	PRDX4 PRDX4 PRDX4 PRDX4

P3288THOPThems algographic1,00,00PEN24QMPITATG4BCynchreipotres ATG4B1.80,007PEN24QMD16MS12RNA basing protein Maush homolog 21.80,007PEN24P3464P84.AdCAMP actination refacters an inclusional plane 11.80,007PEN24P3464RATA4CAMP actination refacters and plane 10.8 (1.9)1.30,007PEN24P3470AtG11AtaAble actination finds parato 80.9 (1.9)1.30,007PEN24P3471AtG11AtaAble actination finds parato 80.9 (1.9)1.30,007PEN24P3472AtG11Atf12Atf12PEN24PEN24P3473AtG11Atf12Atf12PEN24PEN24P3474Atf12Atf12Standard status biorders atf121.70,008PEN24P3474PERPPatr12PERPPEN24PEN24PEN24P3474CD224Hasaa PLA2PEN24PEN24PEN24P3474PERPPatr244PEN24PEN24PEN24P3474PERPPatr244PEN24PEN24PEN24P3474PERPPatr244PEN24PEN24PEN24P3474PERPPatr244PEN24PEN24PEN24P3474PERPPatr244PEN24PEN24PEN24P3474PEN24PEN24PEN24PEN24PEN24P3474PEN24PEN24PEN24PEN24PEN24P347	U3KQC1	WDR18	WD repeat-containing protein 18	1,8	0,005	PRDX4
QPUPIAATG allCynetic preview ATG all1.80.907PLDXAPODDIAMS12RAMAchalle protect previnces miniches draft semant sph21.80.907PLDXAPODIARAMACARAB settered previnces miniches draft semant sph21.80.907PLDXAPALISARAMBRase fided previnces miniches draft semant sph21.80.907PLDXAPALISARAMBRase fided previnces miniches draft semant sph21.80.907PLDXAPALISARAMBRase fided previnces miniches draft semant sph21.70.907PLDXAPODIAALDELAlderly de dendorspresses miniches draft semant sph21.70.901PLDXAPODIAALDELAlderly de dendorspresses miniches draft semant sph21.70.901PLDXAPODIACARABCarabet sph2PLDXAPLDXAPLDXAPODIACARABCarabet sph2PLDXAPLDXAPLDXAPODIAPLDXA </td <td>P52888</td> <td>THOP1</td> <td>Thimet oligopeptidase</td> <td>1,8</td> <td>0,006</td> <td>PRDX4</td>	P52888	THOP1	Thimet oligopeptidase	1,8	0,006	PRDX4
QnOH6         MS12         NAhdming protein Mesoki konkey2         1.4         0.007         PED26           P02050         GS8         Gitamber referenze intecheringtal         1.4         0.007         PED26           P16464         PRAA         S-AMP-sattember referenze intecheringtal         1.4         0.007         PED26           P0100         AR184         APerlespiration factori like groning B         1.4         0.017         PED26           QRV12         AR184         APerlespiration factori like groning B         1.3         0.017         PED26           QRV12         AR184         Aperlespiration factori like groning B         1.7         0.010         PED26           QRV50         LADP1         Ladelenge dense in DD176A         1.7         0.001         PED26           QRV50         LADP1         Ladelenge dense in DD176A         1.7         0.001         PED26           QRV50         CD2A         CD2As ontopic action dense in DD176A         1.7         0.001         PED26           QRV51         PED2         Ped18         PED26         PED26         PED26           QRV51         PED24         Like action dense in dense	O9Y4P1	ATG4B	Cysteine protease ATG4B	1.8	0.007	PRDX4
PA0290         CSR.         Class the matrix introbuoting lays?         1.4         0.000         PLX24           PS4666         PKRAD2         I.A         0.000         PLX24           PS4066         RAB41         Ray enter options has a state s	0%DH6	MSI2	RNA-binding protein Musashi homolog 2	1.8	0.007	PR DX4
Pielde         PiEAA         CAME accord protoch biase config subana lights2         1.4         0.00         PEDXA           PNIOR         ARIAI         A Direchosystem functioning protoch Bia         1.4         0.02         PEDXA           QNIV12         ARIAB         A Direchosystem functioning protoch Bia         1.4         0.02         PEDXA           QNIV12         ARIAB         A Direchosystem function	P00390	GSR	Glutathione reductase, mitochondrial	1.8	0.009	PR DX4
PALINE         Rate aller present Rab: H         1.4         0.097         PRDMA           CPNVD1         ARLMA         ADPHologybics for aller present fills         1.4         0.017         PRDMA           EPDDE         BCL21.13         B61 2 dispersion 1.3         1.4         0.017         PRDMA           EPDDE         BCL21.13         B61 2 dispersion 1.3         1.7         0         PRDMA           PSP39         ATIC         Bifanctional partie Biosymbolic space fills         1.7         0.001         PRDMA           OpM343         NDVIIA1         Larching present         1.7         0.003         PRDMA           OpM343         NDVIIA1         Larching present         1.7         0.003         PRDMA           OPM32         CPL2         Dista particity present         1.7         0.003         PRDMA           OPM34         CPL26         Celled and present present         1.7         0.003         PRDMA           OPM34         CPL26         Celled and present present celled and present present         1.7         0.011         PRDMA           OPM34         CPL24         MADS         MedDama present celled and present present celled and pr	P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-?	1.8	0.009	PR DX4
OPNVD2         ALAB         ADP relonging interesting present as B         1.8         0.927         PRDx4           POPD06         DC121.3         Bel 2-kite present as present as an analysis of the present and	P61106	R A B14	Ras-related protein Rah-14	1.8	0.009	PR DX4
982706         BC.2113         Bc.24 parts protein 3         BC.25         PB.D34           PM9071         ATDH2         Addelpde belgebogeness minochood rule         1.7         0         PB.D34           PM9379         ATC         Bifrancinoal purite biosynthesis protein ATC.         1.7         0.081         PB.D34           QEPEGO         LARP         La reinsteg prosein 1         1.7         0.081         PB.D34           QEPEGO         LARP         La reinsteg prosein 1         1.7         0.085         PB.D34           QPD56         CD2AP         CD2-senscincel presein         1.7         0.086         PB.D34           QPD56         CD2AP         CD2-senscincel presein         1.7         0.086         PB.D34           QPD51         PARL         Protein biophysics methyleterrats 1         1.7         0.011         PB.D34           QPD34         CCD2A         Gebbos phases methyleterrats 1         1.7         0.035         PB.D34           QPD34         CAPA         Design 1 asteric constraint operation present 2.1         1.7         0.035         PB.D34           QPD34         MSP segnal field confid namic contraint operation present 2.1         1.7         0.035         PB.D34           QPD34         MSP segnal field confi	09NVI2	ARI 8B	A DP-ribosylation factor-like protein 8B	1.8	0.017	PR DX4
PONOP         ALDU2         Addenyck dwylanegonac, minchondral L.         1.7         0         PRDXA           D91939         ATTC         Binaccinol gurrent isopratesin protein ATCC         1.7         0.001         PRDXA           D91847         PRLP         Polytic adsynamic conducts exbans DNUFAA         1.7         0.001         PRDXA           D91847         PRLP         Polytic adsynamic conducts exbans DNUFAA         1.7         0.006         PRDXA           Q93756         CD2AP         CD2A concide adsynamic conducts exbans DNUFAA         1.7         0.006         PRDXA           Q93750         CD2AP         CD2A         CD2AN         CD2AN         CD2AN         CD2AN         PRDXA           Q1021         H2A2.2         Humore H3.2         Humore H3.2         HUMORE         1.7         0.011         PRDXA           Q1254         CD2AP         CC2DC.6         Calubic conducts and conducts exbans conducts exbans DNUE FA         1.7         0.011         PRDXA           Q1254         CL2AP         CD2AP         CD2AP         PD35         PRDXA           Q1253         FRDXA         GA1         FRDXA         GA1         FRDXA           Q1254         CAPAP         Signal coconution gurrent SPD4         GA1	EADD16	BCI 2I 13	Bcl.2 like protein 13	1.8	0.023	PR DX4
PM199         ATC         Biffer-transplanter biosynches protein ATC         17         0         PR DNA           ORMA3         NUTURA         17         0.001         PR DNA           QPKK00         LARP         Laesbord portein         17         0.003         PR DNA           QPM140         Laesbord portein         17         0.004         PR DNA           QPM210         RKP127         Set alsowed portein 12, set to bond information         1.7         0.006         PR DNA           QPU211         RKP127         Set alsowed portein 12, set to bond information         1.7         0.001         PR DNA           QPU304         CCDC06         Celdybord information containing protein 0         1.7         0.013         PR DNA           QPU304         CCDC05         Celdybrid carbodybro inform formation for	D05091	ALDH2	Aldebyde debydrogenase, mitochondrial	1.7	0,025	DR DY/
Addets         1.7         2001         PRDM           ADMERGIN         1.7         2001         PRDM           PRKGD         1.4.8.1         1.7         0.001         PRDM           PRKH         PRDM         PRDM         1.7         0.001         PRDM           PRKH         PRDM         PRDM         1.7         0.004         PRDM           QMEXE         CD2Associand protein         1.7         0.004         PRDM           QMEXE         CD2AS         0.004         PRDM         1.7         0.004         PRDM           QMEXE         CCD2C6         Celled-oid-lomain-constaining protein 6         1.7         0.011         PRDM           QMEXE         CANN         Caluat analysis admint         1.7         0.013         PRDM           QMEXE         CANN         Caluat analysis admint         1.7         0.015         PRDM           QMEXE         CANN         Caluat analysis admint         1.7         0.015         PRDM           QMEXE         DREXE         DREXE         DREXE         1.7         0.015         PRDM           QMEXE         DREXE         DREXE         DREXE         1.6         0.0018         PRDM	D21929	ATIC	Bifunctional puring biosynthesis protoin ATIC	1,7	0	DP DV/
0.0000000         1.0         0.00000000000000000000000000000000000	000482	NDUEA (	Cutacherene e suidese suburit NDUEA (	1,7	0 001	PRDA4
QBFXA00         LAAM         La Halla presint         1.7         0.001         PR.DMA           QPTS61         CD.2.10         CD.2.essexited presint         1.7         0.006         PR.DMA           QPTS61         CD.2.10         CD.2.essexited presint         1.7         0.006         PR.DMA           QPG519         CD.2.4.2         CD.2.4.1.2         0.001         PR.DMA           QPG519         CD.2.4.2         Control preside preside and end preside and e	000485 0(DVC0	I A D D1	Cytochrome c oxidase subunit NDO FA4	1,7	0,001	PRDA4
PADP.         PADP.         PADP.         PADP.         PADA.           QPSS64         CD2A.us         CD2A.us         1.7         0.006         PR.DXA           QPSS64         CD2A.us         SP.Sebound protein L37, mitochondrial         1.7         0.006         PR.DXA           QPS264         CD2A.us         SP.Sebound protein L37, mitochondrial         1.7         0.011         PR.DXA           QPS50         PPME1         Protein phopdiname entrylesteract         1.7         0.015         PR.DXA           QPS50         PPME1         Protein phopdiname entrylesteract         1.7         0.015         PR.DXA           QPS44         CAPVA         Calabitic tashysis uslamin         1.7         0.015         PR.DXA           QPS41         ElftPBPL         Eakarysokis translation factors F2-binding protein         1.7         0.019         PR.DXA           QPS13         ZPAT27         H3         D.9         PR.DXA         QPAT4         QP	Q6PKG0	DDED	Da-leader protein 1	1,7	0,001	PRDA4
QPDSA         CDA/A         CDA/A         CDA/A         PRDA           QPDZE1         MARLES         S5 mbosonal protein 13,7 minecolonial         1,7         0,008         PRDAX           QPDZ1         MARLES         CDA/A         1,7         0,011         PRDAX           QPDA         PRDAX         1,7         0,011         PRDAX           QPDA         PADEI         Protein phophase medy enters 1         1,7         0,011         PRDAX           QPDA         Exhance structure internation from the internation of the the internatinter	P4814/	PREP		1,/	0,003	PRDA4
QPR/L1         MIA 1.57         SP monoming protein 1.4, minicebondrul         L7         0.008         PRIXA           Qia209         CCDC6         Galea cold domain containing protein 6         1.7         0.011         PRIXA           Qia209         CCDC6         Galea cold domain containing protein 6         1.7         0.011         PRIXA           Qia209         CCDC6         Galea cold domain containing protein 1         1.7         0.015         PRIXA           Q13541         Elf-HildP1         Ead arrow containing protein 24 Mag protein         1.7         0.018         PRIXA           Q13541         Elf-HildP1         Ead arrow containing protein 24 Mag         1.6         0.001         PRIXA           Q27454         MAYS         Mitobondrul antrirital-ganding protein         1.7         0.045         PRIXA           Q27454         MAYS         Mitobondrul antrirital-ganding protein         1.6         0.001         PRIXA           Q27454         MAYS         Mitobondrul antrirital-ganding protein         1.6         0.001         PRIXA           Q27454         MAYS         Start Mag and arteria straining protein 2.0         1.6         0.001         PRIXA           Q2150         StCCAM13         Cacharen frind protein friad orterin frind strain from anita ortanini	Q915K6	CD2AP	CD2-associated protein	1,/	0,006	PRDX4
Q2019         112.42         Interest 12.4.V         1.7         0.018         PRUXA           Q4599         CCDC 6.         Codele-oid domin constaining protein 6         1.7         0.011         PRUXA           Q47530         PPMEL         Protein protein factory for transformation factoring from the 1.7         0.015         PRUXA           P4458         SRP         Signific factory for transformation factoring from the 2.015 (2017)         1.7         0.015         PRUXA           Q4531         Elf-LBPI         Balanyet crassing and GLBBs more formating protein 2.012 (2017)         1.7         0.039         PRUXA           Q5433         ZNF207         BUBS interacting and GLBBs more formating protein 2.1         1.6         0.001         PRUXA           Q5129         SIC-SA13         Calcium-Inding mitochendrial carter protein Arala?         1.6         0.001         PRUXA           Q5129         SIC-SA13         Calcium-Inding mitochendrial carter protein Arala?         1.6         0.001         PRUXA           Q4119         VLD Calponin         Calponin         1.6         0.003         PRUXA           Q4114         CRRFIP         Leadonin containing protein 2         1.6         0.021         PRUXA           Q2114         CRRFIP         Separio 6.16/070 CRA15 <td< td=""><td>Q9BZEI</td><td>MRPL3/</td><td>39S ribosomal protein L3/, mitochondrial</td><td>1,/</td><td>0,006</td><td>PRDX4</td></td<>	Q9BZEI	MRPL3/	39S ribosomal protein L3/, mitochondrial	1,/	0,006	PRDX4
QL204         CCD4.6         Constant constraining protein 6         1.7         0.011         PRDX4           QPTS70         PTME1         Protein phosphatism end/ubscena.1         1.7         0.015         PRDX4           QPTS44         CAPN1         Calpital-caralytic subatifit         1.7         0.015         PRDX4           QPS454         EIF4EPP1         Eakaryotic translation inticitor factor 42-binding protein ZPG77         1.7         0.039         PRDX4           QPTA41         MVS         MUB0-interaction particle XPG77         1.7         0.045         PRDX4           QPTA41         MVS         Mucohondrial antritral-gaining protein CRF277         1.6         0.001         PRDX4           QPTA51         IPO4         Importin 4         1.6         0.001         PRDX4           QPUIDS         SCD51A1         Eakine Schoodrial arritrate protein Aralaz         1.6         0.001         PRDX4           QPUIDS         Isoparate mon-ATPase regulatory submin*9         1.6         0.003         PRDX4           QPUIDS         Experime         Isoparate Mucohonin containing protein argument in a submin*8         1.6         0.017         PRDX4           QPUIDS         Experime         Isoparate Mucohonin containing protein in argument in a submin*8         1.6	Q/1019	H2AZ2	Histone H2A.V	1,7	0,008	PRDX4
QP1570         PMR11         Prototise phoophases moting hearing 1         1.7         0.011         PRDX4           P49458         SRP9         Signal recognition particle VDx protein         1.7         0.015         PRDX4           P49458         SRP9         Signal recognition particle VDx protein         1.7         0.015         PRDX4           P49458         SRP9         Signal recognition particle VDx protein APLAC         1.7         0.015         PRDX4           JSS31         ZNF207         BUB3-interacting and CLBBs modif-constituting protein 2NF207         1.7         0.039         PRDX4           PS127         SIR/NN86         Serpin B6         1.6         0.001         PRDX4           QUIS0         SIC.25A13         Calcium Inding mitochondrul carrier protein Aralu?         1.6         0.003         PRDX4           QUIN1         PMD002         Calponin         1.6         0.003         PRDX4           QUIV31         PMD012         Deprotisane M20-emain-contraining protein 2         1.6         0.001         PRDX4           QUV44         LRRTPIP         Laccine-citk repart flight-cites recenting protein 1         1.6         0.017         PRDX4           QUV44         LRRTPIP         Laccine-citk recenting protein 1         1.6         0.022 <td>Q16204</td> <td>CCDC6</td> <td>Coiled-coil domain-containing protein 6</td> <td>1,7</td> <td>0,011</td> <td>PRDX4</td>	Q16204	CCDC6	Coiled-coil domain-containing protein 6	1,7	0,011	PRDX4
P07384         CAPNI         Captanic carabjex is submit         1.7         0.055         PRDXA           Q1354.1         EIF4BPI         Export of translation intritor factor 42-binding protein 1         1.7         0.018         PRDXA           Q1354.1         EIF4BPI         EuRorent containing protein ZPZ07         1.7         0.038         PRDXA           Q274.34         M475         Mutochondrial antivitari signaling protein CR207         1.7         0.045         PRDXA           Q274.34         M475         Mutochondrial antivitari signaling protein CR207         1.6         0.001         PRDX4           Q21150         SLC25.11.2         Calcium-binding mitochondrial carrier protein Arala         1.6         0.001         PRDX4           Q21150         SLC25.11.2         Calcium-binding mitochondrial carrier protein Arala         1.6         0.001         PRDX4           Q21151         PDA20         Poputase M20 domain contraining protein 2         1.6         0.001         PRDX4           Q21151         PMD20         Poputase M20 domain contraining protein 2         1.6         0.0021         PRDX4           Q21154         PMD716         Septin 7         1.6         0.017         PRDX4           Q21494         UQCRQ C         Crotowore Hightelsis interacting protein	Q9Y570	PPME1	Protein phosphatase methylesterase 1	1,7	0,011	PRDX4
Physis         SRP         Signal accognition particle 24D2 protein         1.7         0.015         PRDX4           QISs1         EIFEEBP         Eakaryotic critics of 24-binding protein [a 1, 7         0.039         PRDX4           JSXS1         ZN1207         BUB3-interacting and CLEBS motif-containing protein ZNE207         1, 7         0.045         PRDX4           JSXS1         ZN1207         BURDMA         Statistic and the animal animal signaling protein animal signaling protein Aralar2         1, 6         0.001         PRDX4           QUIS0         SLC52A13         Calcium-binding mitochondrial carrier protein Aralar2         1, 6         0.000         PRDX4           BJNDP4         CNN2         Calponin         Calponin         1, 6         0.001         PRDX4           BJNDP5         CNN2         Calponin         Concinent Argent glubaci-interacting protein 1         1, 6         0.001         PRDX4           QUAQ4         ERRTP1         Locine-chargent glubaci-interacting protein 1         1, 6         0.021         PRDX4           QUAQ5         ErrTP1N6         September SMD10         1, 6         0.021         PRDX4           QUAQ4         ERRTP1         Locine-chargent glubaci-interacting protein 1         1, 6         0.021         PRDX4           QUAQ5 <td>P07384</td> <td>CAPN1</td> <td>Calpain-1 catalytic subunit</td> <td>1,7</td> <td>0,015</td> <td>PRDX4</td>	P07384	CAPN1	Calpain-1 catalytic subunit	1,7	0,015	PRDX4
Q1541         IFFAEP         Fakaryoic translation initiation factor 4.E-binding protein         1,7         0,013         PRDX4           Q274.54         MAYS         Mice-bondrial anviral signaling protein         1,7         0,043         PRDX4           Q274.54         MAYS         Mice-bondrial anviral signaling protein         1,6         0,001         PRDX4           Q274.54         MAYS         Mice-bondrial anviral signaling protein         1,6         0,001         PRDX4           QPUIS0         SLC25A13         Calcium-binding mitochondrial carrier protein Analo2         1,6         0,001         PRDX4           JBNDPF         CNN2         Calcium-inchengen mitochondrial carrier protein Analo2         1,6         0,003         PRDX4           Q2N24         LRRFIPI         Leucinor-inchengen mitochondrial carrier protein Analo2         1,6         0,017         PRDX4           Q2N24         LRRFIPI         Leucinor-ich in protein kinase Chil OS-Home         1,6         0,021         PRDX4           Q2NQ4         LRRFIPI         Leucinoric RA-b         1,6         0,021         PRDX4           Q2NQ4         SEPTIN in 6x60 CGN-CILIKL IFLAN         North Child Seried Child Seried Seried Seried Seried Second Child Seried Seried Seried Second Child Seried Seried Seried Second Second Child Seried Seried Seried Second Second Second Second Se	P49458	SRP9	Signal recognition particle 9 kDa protein	1,7	0,015	PRDX4
JSK51         ZNF 207         BUB3-interacting and LEBS modif-containing protein ZNF207         1,7         0.043         PRDX4           PS327         SERPINB6         Sepin B6         1,6         0.001         PRDX4           PS327         SERPINB6         Sepin B6         1,6         0.001         PRDX4           QUIS0         SLC2A113         Calcium-binding microhondrial carrier protein Aralar2         1,6         0.001         PRDX4           QUIS0         SLC2A113         Calcium-binding microhondrial carrier protein Aralar2         1,6         0.003         PRDX4           BADDF4         CNN2         Calponia         Calponia         1,6         0.001         PRDX4           QUX24         LRRTP1         Learine rich repeat Biplates-interacting protein 2         1,6         0.017         PRDX4           QUX24         LRRTP1         Sepint 6: anche Cher 2-1 comptex submit 8         1,6         0.021         PRDX4           QUX24         SEPTTN6         Sepint 6: anche Cher 2-1 Comptex submit 8         1,6         0.022         PRDX4           QUX24         LRRTP1         Learine rich repeat Biplates 3/mainter 2/mainter 2/ma	Q13541	EIF4EBP1	Eukaryotic translation initiation factor 4E-binding protein 1	1,7	0,018	PRDX4
QZZ434         M475         Mitochondrial antroinal-signaling protein         1.7         0.945         PRDX4           QZTEX9         IPO4         Importin-4         1.6         0.001         PRDX4           QUIS0         SLC2XA13         Calcium-binding mitochondrial carrier protein Aralar2         1.6         0.003         PRDX4           JBADDF4         CANp2         Calpoin         1.6         0.003         PRDX4           QUIS0         SLC2XA11         LR REIPI         Laccine rich repert flightless-interacting protein 1         1.6         0.001         PRDX4           QUIX24         LR REIPI         Laccine rich repert flightless-interacting protein 1         1.6         0.001         PRDX4           QUIX24         LR REIPI         Laccine rich repert flightless interacting protein in a contain second in a cont	J3K\$31	ZNF207	BUB3-interacting and GLEBS motif-containing protein ZNF207	1,7	0,039	PRDX4
P3527         F5R/N186         Serpin B6         1.6         0.001         PRDX4           QPUTEX9         IPO4         Importin-4         1.6         0.001         PRDX4           QPUL90         SLC23A13         Calcium-binding mitochendrial carrier protein Arala2         1.6         0.003         PRDX4           BADDF4         CN2         Calponin         1.6         0.005         PRDX4           BADDF4         CN2         Calponin         1.6         0.001         PRDX4           QMX24         LRRP11         Laucine rich repear flightes-interacting protein 2         1.6         0.001         PRDX4           QMX24         SEPTIN         Septin-7         Septin-7         Septin-7         NUX4         0.012         PRDX4           QMX42         SEPTIN         Septin-6, looform CAA_b         1.6         0.021         PRDX4           BIAMS2         SEPTIN         Septin-7, Septin-7         Septin-Septi	Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	1,7	0,045	PRDX4
QPTLX9         IPO-4         Importin-4         1.6         0.001         PRDX4           QVUIS0         SLC25A13         Calcium-Minding mitochondrial carter protein Analar2         1.6         0.003         PRDX4           JAND27         PSMD9         26 proteasome non-ATPase regulatory subunit 9         1.6         0.003         PRDX4           QUINS1         FM20D2         Peptidase M20 domain-containing protein 2         1.6         0.001         PRDX4           QUAL24         LRRTPI         Laccine rich repeat fightless interacting protein 1         1.6         0.013         PRDX4           QUAL24         LRRTPIN         Septin 7.         1.6         0.021         PRDX4           QUAL3         UCCRQ         Crochrome b-c1 complex subunit 8         1.6         0.021         PRDX4           JIANS2         SEPTIN6         Septin 6.10560 (CA-CHEK) PE-1 SV-1::sy010777(CHK), ILMAN Scrinc/Hronoine-protein kinase Chk IOS+Homo suption SV-5060 CA-CHEK INPE-1         SV-2:sy01777(CHK), ILMAN Scrinc/Hronoine-protein kinase Chk IOS+HOM Scrinc/HroNine-protein kinase Chk IOS+HOM Scrinc/Hronoine-protein k	P35237	SERPINB6	Serpin B6	1,6	0,001	PRDX4
QPUIB0         SLC2A13         Calcum-binding mitochondrial carrier protein Arala?         1.6         0.001         PRDX4           JSN292         PSMD9         265 protessome non-AT2Par regulatory submit 9         1.6         0.003         PRDX4           BADDFA         CNN2         Calponin         1.6         0.006         PRDX4           QSWIX1         LRRTP1         Leacine-rich repeat flightless-instracting protein 1         1.6         0.017         PRDX4           GVI4Q         SEPTIN7         Septin-7         Septin-7         1.6         0.021         PRDX4           BIAMS2         SEPTIN6         Septin 6, isoform CRA_b         1.6         0.021         PRDX4           BIAMS2         SEPTIN6         Septin 6, isoform CRA_b         1.6         0.021         PRDX4           BIAMS2         SEXTIN7         Septin 6, isoform CRA_b         1.6         0.028         PRDX4           BIAMS2         SEXTIN7         Septin 6, isoform CRA_b         1.6         0.028         PRDX4           BIAMS2         SEXTIN7         Septin 6, isoform CRA_b         1.6         0.028         PRDX4           BIAMS2         SEXTIN7         Septin 6, isoform CRA_b         1.6         0.028         PRDX4           BIAMS2	Q8TEX9	IPO4	Importin-4	1,6	0,001	PRDX4
J3KN2         PMD9         268 protessome non-ATPase regulatory submit 9         1.6         0.003         PRDX4           BADDF4         CNN2         Cajoonin         Containing protein 2         1.6         0.003         PRDX4           QSIM24         LRRFIP1         Leuction-rich repeat flightless-interacting protein 1         1.6         0.013         PRDX4           QSIM24         LRRFIP1         Leuction-rich repeat flightless-interacting protein 1         1.6         0.021         PRDX4           QH949         UQCRQ         Cynochrome 5-1 complex subunit 8         1.6         0.021         PRDX4           QHN87         SEPTINK         Septin 6, incorma CA, A brain-richronoline- protein kinass Chkl OS-Homos tapien CNS-906 GNN-CILELI PE-1         0.022         PRDX4           J3KN87         J3KN87         PRDX4         PRDX4         0.028         PRDX4           P30041         PRDX6         Peroxitedosin-6         1.6         0.028         PRDX4           P31452         DVSP3         Dual specificity protein phosphatase 3         1.5         0         PRDX4           P31458         RCD3A         La-Licettactedopricen RAo-A         1.5         0.01         PRDX4           P3149         RAFA         Kas-related proterin RAo-A         1.5         0.01 <td>Q9UJS0</td> <td>SLC25A13</td> <td>Calcium-binding mitochondrial carrier protein Aralar2</td> <td>1,6</td> <td>0,001</td> <td>PRDX4</td>	Q9UJS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	1,6	0,001	PRDX4
BADDF4         CNN2         Calponin         1.6         0.003         PRDX4           QSINS1         PM2020         Prepriates W20 domains commaining protein in protein protein in prot	J3KN29	PSMD9	26S proteasome non-ATPase regulatory subunit 9	1,6	0,003	PRDX4
QRINS1PM20D2Peptidase M20 domain-containing protein 21,60,006PRDX4Q33MZ4LRRFIP1Lacticne rich repeat flighdes-interacting protein 11,60,013PRDX4Q34D42SEPTIN7Septin5Septin51,60,021PRDX4OH949UQCRQCyrochrome 5-1 complex subunit 81,60,021PRDX4JIANS2SEPTIN6Septin 6,105/mr CRA. b1,60,022PRDX4JJKN87SEPTIN6Septin 6,05/mr CRA. b1,60,028PRDX4JAKN87SEPTIN6Septin 50/mr CRA. b1,60,028PRDX4JAKN87PRDX6Peroxitedoxin-61,60,028PRDX4A0A2R97H5SEC38Protein transport protein SEC231,60,029PRDX4P61580RH0ATransforming protein RbaA1,50PRDX4P51452DUS75Daul specificity protein phophatast 31,50PRDX4P51451SEC238LDPHAL-Lactact deprdsgenas A chain1,50,001PRDX4P5141SLC5A5ADP/ATP translocase 21,50,001PRDX4P51451SEC355ADP/ATP translocase 21,50,003PRDX4P5141SLC5A5ADP/ATP translocase 21,50,003PRDX4P5141SLC5A5ADP/ATP translocase 21,50,003PRDX4P5141SLC5A5ADP/ATP translocase 21,50,003PRDX4P5141SLC5A5ADP/ATP translocase 21,50,003 <td>B4DDF4</td> <td>CNN2</td> <td>Calponin</td> <td>1,6</td> <td>0,003</td> <td>PRDX4</td>	B4DDF4	CNN2	Calponin	1,6	0,003	PRDX4
Q324Z4LR.RFIP1Leachner/therspert flighdess-interacting protein 11.60.013PRDX4G3Y1Q4SEPTIN7Septin 7Septin 80.021PRDX4014949UQCRQCytochrome b~1 complex subunit 81.60.021PRDX4B1AMS2SEPTIN6Septin 6, isoferm CRA b1.60.021PRDX4B1AMS2JJKN87xrtJJKN87JJKN87, JHMAN Seriner/threonine-protein kinase Chk1 OS-Homo spino1.60.021PRDX4B1AMS2SEPTIN6Septin 6, isoferm CRA bSeptin 60.000 CN-CHEK1 PE-1Velocita CN-CHEK1 PE-1SW=2>crt[ZETPR0[JETEPR_HUMAN Seriner/threonine-protein kinase Chk1 OS-Homo spino XS-9606 CN-CHEK1 PE-10.028PRDX4P30041PRDX6Protein transport protein SEC231.60.028PRDX4P30452DUSP3Dual specificity protein phosphatzae 31.50PRDX4P31452DUSP3Dual specificity protein phosphatzae 31.50PRDX4P0358LDHALactate delydrogenase A chain1.50PRDX4P3149RAB7ARas-Pracha protein hisba/Ta1.50.001PRDX4P3149RAB7ARas-Pracha protein hisba/Ta1.50.001PRDX4P3149RAB7AATP synthase subunit g, nitochondrial1.50.002PRDX4P3149RAB7ABysthase subunit g, nitochondrial1.50.003PRDX4P3149PAG14Protessome inhibitor P31 subunit 21.50.003PRDX4P3149PSD5A356 sthosonal protein	Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	1,6	0,006	PRDX4
GYUQ4         Septin 7         1.6         0.017         PRDX4           014949         UQCRQ         Cytochrome b-c1 complexibunit 8         1.6         0.021         PRDX4           BIAMS2         SEPTTN6         Septin 6, isoform CRA b         1.6         0.021         PRDX4           J3KN87         J3KN87         >vrlJ3KN87/J3KN87/J1UMAN Scrine/threonine-protein kinase Chk1 OS-Homo         1.6         0.022         PRDX4           J3KN87         J3KN87         Septin 7.6         1.6         0.022         PRDX4           SV2-52/FITPRIG SEPTIGE/FEPFIFE/FEFFIFE/FFFFFFFF	Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	1,6	0,013	PRDX4
014949UQCRQCyrochrome b-c1 complex subunit 81.60.021PRDX4BIAMS2SEPTIN6Septin 6, isoform CRA b1.60.021PRDX4BIAMS7JJKN87SriftSKN97/JKN87	G3V1Q4	SEPTIN7	Septin-7	1,6	0,017	PRDX4
BIAMS2         SEPTING         Septin 6, isoform CRA b         1,6         0,021         PRDX4           J3KN87         J3KN87         svtf[JSKN87], BKN87, HUAAN Serinchenine-protein kinase Chki IOS-Homo supieren OX-960 GN-CHEKI PE-1 SV-1;>sp[OI477]CHK1 [HUMAN Serinc/ threonine-protein kinase Chki IOS-Homo supiers OX-960 GN-CHEKI PE-1 SV-2;>ttf[ZEP0E]CEPDE, HUMAN Serinc/threonine-protein k         1,6         0,022         PRDX4           P30041         PRDX6         Precoxitedosin-6         1,6         0,028         PRDX4           P3041         PRDX6         Precoxitedosin-6         1,6         0,028         PRDX4           P3042         DUSP3         Dual specificity protein SC23         1,5         0         PRDX4           P61546         RHOA         1,5         0         PRDX4           P61543         DLGPAT         L-actated dystogenase Achin         1,5         0         PRDX4           P51419         RAEFA         Rae-related protein Rab-7a         1,5         0         PRDX4           P59531         DPM1F         Protesin phosphatzse I         1,5         0,001         PRDX4           P62543         WDR61         WD repeat-containing protein 61         1,5         0,003         PRDX4           QQVDX7         PSM1F         Protessome Inhibbord Protein 2,3         0,	O14949	UOCRO	Cvtochrome b-c1 complex subunit 8	1.6	0.021	PRDX4
J3KN87         J3KN87         >triJ3KN87/J3KN87/J3KN87/J4KN87, HUMAN Serine/hreonine-protein kinase Ch4/OS-Homo spleins OX=906 CN=CHEK1 PE=1 SV=1;2+gIO/477/CIK1_HUMAN Serine/ threonine-protein knase Ch4/OS-Homo spleins OX=9060 CN=CHEK1 PE=1         1,6         0,022         PRDX4           920041         PRDX6         Prestriedonin-6         1,6         0.023         PRDX4           A0A2R87H5         SEC238         Protein transport protein SEC23         1,6         0.028         PRDX4           P51452         DUSP3         Dual specificity protein phospharase 3         1,5         0         PRDX4           P03586         RH0A         Transforming protein RhoA         1,5         0         PRDX4           P03181         DHA         L-lactate dehytoregnase A chain         1,5         0         PRDX4           P05141         SLC25A5         ADP/ATP translocase 2         1,5         0,001         PRDX4           P05141         SLC25A5         ADP/ATP translocase 2         1,5         0,001         PRDX4           PSPN17         ATPSMG         ATP synthase subunit g, mitochondrial         1,5         0,002         PRDX4           QSQPM7         PSMF1         Proteins protein 613         1,5         0,003         PRDX4           QVH752         MXH1         Protesame inhibitor P13	B1AMS2	SEPTIN6	Septin 6. isoform CRA b	1.6	0.021	PRDX4
Jantos         Japiers XX-9606 GN-CHEK1 PE=1 SV=1;>sp[O14757](CHK1_HUMAN Serine/ threonine-protein kinase Chk1 OS=Homo sapiens XX-9606 GN-CHEK1 PE=1 SV=2;>ref12F2PE9[E1796, HUMAN Serine/threonine-protein k         Inc         Ones         PRDX4           P30041         PRDX6         Peroxitedoxin-6         1.6         0.028         PRDX4           P30041         PRDX6         Peroxitedoxin-6         1.6         0.029         PRDX4           P51452         DUSP3         Dual specificity protein phosphatase 3         1.5         0         PRDX4           P61586         RHOA         1.5         0         PRDX4           P61586         RHOA         1.5         0         PRDX4           P61514         L1-factate dehydrogenase A chain         1.5         0         PRDX4           P05141         SLC25A5         ADP/ATP translocase 2         1.5         0         PRDX4           P9593         PMIF         Protein phosphatase 1F         1.5         0.001         PRDX4           P9593         PMIF         Protein phosphatase 1F         1.5         0.002         PRDX4           QSQPM7         PSMF1         Protein phosphatase 1F         1.5         0.003         PRDX4           QSPM53         WDR61         WD repeat-containing protein 61	I3KN87	13KN87	>tr/J3KN87/J3KN87 HUMAN Serine/threonine-protein kinase Chk1 OS=Homo	1.6	0.022	PR DX4
P30041         PRDX6         Proxitedoxin-6         1,6         0,028         PRDX4           P3041         PRDX5         SEC23B         Protein transport protein SEC23         1,6         0,039         PRDX4           P51452         DUSP3         Dual specificity protein phosphatase 3         1,5         0         PRDX4           P61586         RHOA         Transforming protein Rab-A         1,5         0         PRDX4           P51149         RAB7A         Ras-related protein Rab-7a         1,5         0         PRDX4           P05141         SLC2SA5         ADP/ATP translocase 2         1,5         0,001         PRDX4           P95939         PPMIF         Protein phosphatarae IF         1,5         0,001         PRDX4           PSPN17         ATPSMG         ATP synthase subunit g, mitochondrial         1,5         0,003         PRDX4           Q2C233         WDR61         Wore preat-constraining protein 61         1,5         0,003         PRDX4           Q2C234         WRP13         395 ribosomal protein 51sa         1,5         0,008         PRDX4           Q2H974         QTRT2         Queuiter KNA-Hospytransferza eccescory subunit 2         1,5         0,028         PRDX4           Q2H974         Q			sapiens OX=9606 GN=CHEK1 PE=1 SV=1;>sp O14757 CHK1_HUMAN Serine/ threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=2;>tr[E7EPP6]E7EPP6_HUMAN Serine/threonine-protein k			
A0A288/FH5         SEC23B         Protein transport protein SEC23         1.6         0.039         PRDX4           P51452         DUBP3         Dual specificity protein phosphatase 3         1.5         0         PRDX4           P01386         RHOA         Transforming protein RhoA         1.5         0         PRDX4           P00338         LDHA         L-lactate dehydrogenase A chain         1.5         0         PRDX4           P01141         SLC25A5         ADP/ATP translocase 2         1.5         0         PRDX4           P05141         SLC25A5         ADP/ATP translocase 2         1.5         0,001         PRDX4           P49593         PPM1F         Protein phosphatase 1F         1.5         0,001         PRDX4           Q5QPM7         PSMF1         Protein chondrial         1.5         0,002         PRDX4           Q5QPM7         PSMF1         Protein slisa         1.5         0,003         PRDX4           Q62244         RPS15A         405 ribosomal protein S15a         1.5         0,008         PRDX4           Q9HYK5         MRPL39         395 ribosomal protein S15a         1.5         0,018         PRDX4           Q9HY74         Q1RT2         Queuine (RNA-ribosytransferase accesory subunit 2 </td <td>P30041</td> <td>PRDX6</td> <td>Peroxiredoxin-6</td> <td>1,6</td> <td>0,028</td> <td>PRDX4</td>	P30041	PRDX6	Peroxiredoxin-6	1,6	0,028	PRDX4
P51452DUSP3Dual specificity protein phosphatase 31,50PRDX4P61586R10ATransforming protein RhoA1,50PRDX4P61586LDHAL-lactate dehydrogenase A chain1,50PRDX4P51141SLC25A5ADP/ATP translocase 21,50PRDX4P615141SLC25A5ADP/ATP translocase 21,50,001PRDX4E9PN17ATP5MGATP synthase subunit g, mitochondrial1,50,001PRDX4GQPM7PSMF1Proteasome inhibitor PI31 subunit1,50,002PRDX4Q6253WDR61WD repeat-containing protein 611,50,003PRDX4Q92742RTR12Queuine rRNA-ribosytransferase accessory subunit 21,50,008PRDX4Q91474QTR12Queuine rRNA-ribosytransferase accessory subunit 21,50,018PRDX4Q75306NDUFS2NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial1,50,028PRDX4Q16186ADRM1Proteasomal ubiquitin receptor ADRM11,50,028PRDX4Q16190STX5Syntaxin-51,50,038PRDX4Q16190FTDN2Prefoldin subunit 21,50,038PRDX4Q16192CDH2CAbherin-21,50,038PRDX4Q16190STX5Syntaxin-51,50,038PRDX4Q16190STM2CAbherin-21,50,038PRDX4Q13190STX5Syntaxin-51,50,038 <td>A0A2R8YFH5</td> <td>SEC23B</td> <td>Protein transport protein SEC23</td> <td>1,6</td> <td>0,039</td> <td>PRDX4</td>	A0A2R8YFH5	SEC23B	Protein transport protein SEC23	1,6	0,039	PRDX4
P61586         RHOA         Transforming protein RboA         1,5         0         PRDX4           P00338         LDHA         L-lactate dehydrogenase A chain         1,5         0         PRDX4           P00338         LDHA         R.as-related protein Rab-7a         1,5         0         PRDX4           P05141         SLC25A5         ADP/ATP translocase 2         1,5         0,001         PRDX4           P45933         PPM1F         Protein phosphatase 1F         1,5         0,001         PRDX4           P45937         ATP SMG         ATP synthase subunit g, mitochondrial         1,5         0,002         PRDX4           QSQPM7         PSMF1         Protecasome inhibitor PI31 subunit         1,5         0,003         PRDX4           QSQPM7         MR61         WD repeat-containing protein 615         1,5         0,003         PRDX4           Q9C523         WDR61         WD repeat-containing protein 515a         1,5         0,008         PRDX4           Q9HYK5         MRPL39         39S ribosomal protein 139, mitochondrial         1,5         0,008         PRDX4           Q9HYK5         MRPL39         39S ribosomal protein 139, mitochondrial         1,5         0,028         PRDX4           Q15100         NDLF32	P51452	DUSP3	Dual specificity protein phosphatase 3	1,5	0	PRDX4
P00338         LDHA         L-lactate dehydrogenase A chain         1,5         0         PRDX4           P51149         RAB7A         Ras-related protein Rab-7a         1,5         0         PRDX4           P51141         SLC25A5         ADP/ATP translocase 2         1,5         0,001         PRDX4           P49593         PPM1F         Protesin phosphatase IF         1,5         0,001         PRDX4           EVPN17         ATP Synthase subunit g, mitochondrial         1,5         0,002         PRDX4           QSQPM7         PSMF1         Proteasome inhibitor P131 subunit         1,5         0,003         PRDX4           QSQPM7         PSMF1         Proteasome inhibitor P131 subunit         1,5         0,003         PRDX4           QSQPM7         MRPL39         395 ribosomal protein 154         1,5         0,008         PRDX4           Q9H974         QTR72         Queuine tRNA-ribosyltransfersas accessory subunit 2         1,5         0,018         PRDX4           Q16186         ADRM1         Proteasomal ubiquitin receptor ADRM1         1,5         0,028         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,038         PRDX4           Q13190         STX5         Syntaxin-5	P61586	RHOA	Transforming protein RhoA	1,5	0	PRDX4
P51149RAB7ARasrelated protein RAb-7a1,50PRDX4P05141SLC25A5ADP/ATP translocase 21,50PRDX4P05153PPM1FProtein phosphatase 1F1,50,001PRDX4E9PN17ATP5MGATP synthase subunit g, mitochondrial1,50,001PRDX4Q9CQ75PDM1FProtein phosphatase 1F1,50,002PRDX4Q9CQ75PDM61WD repeat-containing protein 611,50,003PRDX4Q9C253WDR61WD repeat-containing protein 611,50,003PRDX4Q9C375MRP139395 ribosomal protein 515a1,50,008PRDX4Q9H974QTR72Queuine RNA-ribosyltransferase accessory subunit 21,50,018PRDX4Q9H974QTR72Queuine RNA-ribosyltransferase accessory subunit 21,50,028PRDX4Q13190STX5Syntaxin-51,50,028PRDX4Q13190STX5Syntaxin-51,50,038PRDX4Q1902CDH2Cadherin-21,50,038PRDX4P19022CDH2Cadherin-21,50,038PRDX4Q9UHV9PFDN2Prefoldin subunit 21,50,04PRDX4Q9UHV9PFDN2Prefoldin subunit 21,50,04PRDX4Q9UHV9PDN2Cadherin-21,50,038PRDX4Q9U44THUMPD3THSM11,40PRDX4Q9U44PBDM326S proteasome non-ATPase regulatory subuni	P00338	LDHA	L-lactate dehydrogenase A chain	1,5	0	PRDX4
P05141         SLC25A5         ADP/ATP translocse 2         1,5         0         PRDX4           P49593         PPM1F         Protein phosphatase 1F         1,5         0,001         PRDX4           P299171         ATP synthase subunit g, mitochondrial         1,5         0,002         PRDX4           Q5QPM7         PSMF1         Proteasome inhibitor P131 subunit         1,5         0,003         PRDX4           Q6C2S3         WDR61         WD repeat-containing protein 61         1,5         0,003         PRDX4           Q62C4S3         RPS15A         405 ribosomal protein 139, mitochondrial         1,5         0,008         PRDX4           Q9MYK5         MRPL39         395 ribosomal protein 139, mitochondrial         1,5         0,018         PRDX4           Q9H974         QTRT2         Queuine tRNA-ribosyltransferase accessory subunit 2         1,5         0,018         PRDX4           Q16186         ADRM1         Protezsomal ubiquitin receptor ADRM1         1,5         0,028         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           Q9UHV9         PFDN2 <t< td=""><td>P51149</td><td>RAB7A</td><td>Ras-related protein Rab-7a</td><td>1,5</td><td>0</td><td>PRDX4</td></t<>	P51149	RAB7A	Ras-related protein Rab-7a	1,5	0	PRDX4
P49593PPMLFProtein phosphatase 1F1,50,001PRDX4E9PN17ATP SynCATP synthase subunit g, mitochondrial1,50,001PRDX4Q5QPM7PSMF1Protexasome inhibitor P131 subunit1,50,003PRDX4Q6CZ33WDR61WD repeat-containing protein 611,50,003PRDX4Q62Z44RPS15A40S ribosomal protein 15a1,50,003PRDX4Q9HY7QTRT2Queuine tRNA-ribosyltransferase accessory subunit 21,50,018PRDX4Q9H974QTRT2Queuine tRNA-ribosyltransferase accessory subunit 21,50,018PRDX4Q1816ADRM1Proteasomal ubiquitin receptor ADRM11,50,028PRDX4Q1310STX5Syntaxin-51,50,038PRDX4Q19102CDH2Cadherin-21,50,038PRDX4Q9UHV9PFDN2Prefoldin subunit 21,50,038PRDX4Q9UHV9PFDN2Prefoldin subunit 21,50,038PRDX4Q00487PSMD1426S proteasome non-ATPase regulatory subunit 31,40,001PRDX4Q9W44THUMP03THUMP domain-containing protein 31,40,001PRDX4Q9W54RPLP060S caicia ribosomal protein 71,40,001PRDX4Q9W54RPLP0G5 proteasome non-ATPase regulatory subunit 31,40,001PRDX4Q9W54THUMP03THUM domain-containing protein 31,40,001PRDX4Q9W54PLP0 </td <td>P05141</td> <td>SLC25A5</td> <td>ADP/ATP translocase 2</td> <td>1,5</td> <td>0</td> <td>PRDX4</td>	P05141	SLC25A5	ADP/ATP translocase 2	1,5	0	PRDX4
EPPN17         ATP SMG         ATP synthase subunit g, mitochondrial         1,5         0,001         PRDX4           QSQPM7         PSMF1         Proteasome inhibitor PI31 subunit         1,5         0,002         PRDX4           Q9GZS3         WD R61         WD repeat-containing protein 61         1,5         0,003         PRDX4           Q9GZS3         MRPL39         395 ribosomal protein S15a         1,5         0,008         PRDX4           Q9HYK5         MRPL39         395 ribosomal protein 123, mitochondrial         1,5         0,018         PRDX4           Q9H974         QTRT2         Queuine tRNA-ribosyltransferase accessory subunit 2         1,5         0,022         PRDX4           Q75306         NDUFS2         NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial         1,5         0,022         PRDX4           Q16186         ADRM1         Protessomal ubiquitin receptor ADRM1         1,5         0,022         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,038         PRDX4           Q19042         CDH2         Cadherin-2         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,048         PRDX4           <	P49593	PPM1F	Protein phosphatase 1F	1,5	0,001	PRDX4
QSQPM7         PSMF1         Proteasome inhibitor PI31 subunit         1,5         0,002         PRDX4           Q9G2S3         WDR61         WD repeat-containing protein 61         1,5         0,003         PRDX4           P62244         RPS15A         40S ribosomal protein 139, mitochondrial         1,5         0,008         PRDX4           Q9NYK5         MRPL39         39S ribosomal protein 139, mitochondrial         1,5         0,018         PRDX4           Q9H974         QTR72         Queuine tRNA-ribosyltransferase accessory subunit 2         1,5         0,018         PRDX4           Q18166         ADRM1         Proteasomal ubiquitin receptor ADRM1         1,5         0,02         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,02         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,03         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,03         PRDX4           Q19192         CDH2         Cadherin-2         1,5         0,03         PRDX4           Q9UHV9         PSDN2         Prefoldin subunit 2         1,5         0,04         PRDX4           Q9U1V9         PSND14         26S proteasome non-ATPase regula	E9PN17	ATP5MG	ATP synthase subunit g, mitochondrial	1,5	0,001	PRDX4
Q9GZS3         WDR61         WD repeat-containing protein 61         1,5         0,003         PRDX4           P62244         RPS15A         405 ribosomal protein S15a         1,5         0,003         PRDX4           Q9NYK5         MRPL39         395 ribosomal protein L39, mitochondrial         1,5         0,008         PRDX4           Q9H974         QTR72         Queuine tRNA-ribosyltransferase accesory subunit 2         1,5         0,018         PRDX4           Q75306         NDUFS2         NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial         1,5         0,02         PRDX4           Q18196         ADRM1         Proteasomal ubiquitin receptor ADRM1         1,5         0,02         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,02         PRDX4           Q04186         ADRM1         Proteasomal ubiquitin receptor ADRM1         1,5         0,02         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,02         PRDX4           Q14190         FTO         Alpha-ketoglutraate-dependent dioxygenase FTO         1,5         0,03         PRZ4           Q9UHY9         PFDN2         Prefoldin subunit 2         1,5         0,04         PRDX4	Q5QPM7	PSMF1	Proteasome inhibitor PI31 subunit	1,5	0,002	PRDX4
Pé2244RPS15A408 ribosomal protein S15a1,50,003PRDX4Q9NYK5MRPL39395 ribosomal protein L39, mitochondrial1,50,008PRDX4Q9H974QTR72Queuine tRNA-ribosyltransferase accessory subunit 21,50,018PRDX4O75306NDUFS2NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial1,50,022PRDX4Q16186ADRM1Proteasomal ubiquitin receptor ADRM11,50,028PRDX4Q13190STX5Syntaxin-51,50,038PRDX4A0A1B0GUC3FTOAlpha-ketoglutarate-dependent dioxygenase FTO1,50,038PRDX4P1902CDH2Cadherin-21,50,038PRDX4Q9UHV9PFDN2Prefoldin subunit 21,50,04PRDX4O00487RPL37605 ribosomal protein L371,50,04PRDX4P68104EEF1A1Elongation factor 1-alpha 11,40PRDX4Q9BV44THUMPD3THUMP domain-containing protein 31,40,001PRDX4P68371TUBB4BTubulin beta-4B chain1,40,002PRDX4Q9EVK5NUDT5ADP-sugar prophosphatas1,40,004PRDX4Q9UK59PND0Projeugamed cell death protein 41,40,002PRDX4Q92598TSNAXTranslin-associated protein X1,40,002PRDX4Q92598TSNAXTranslin-associated protein X1,40,024PRDX4	Q9GZS3	WDR61	WD repeat-containing protein 61	1,5	0,003	PRDX4
Q9NYK5         MRPL39         39S ribosomal protein L39, mitochondrial         1,5         0,008         PRDX4           Q9H974         QTRT2         Queuine tRNA-ribosyltransferase accessory subunit 2         1,5         0,018         PRDX4           O73306         NDUFS2         NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial         1,5         0,02         PRDX4           Q16186         ADRM1         Proteasomal ubiquitin receptor ADRM1         1,5         0,028         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,029         PRDX4           Q01180GUC3         FTO         Alpha-ketoglutrate-dependent dioxygenase FTO         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           Q0487         PSMD14         268 proteasome non-ATPase regulatory subunit 14         1,4         0         PRDX4           P68104         EFF1A1         Elongation factor 1-alpha 1         1,4         0,001         PRDX4           Q9BV44         THUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           Q9BV44         THUMP35         Ges proteasome nor-ATPase regulatory subunit 3         1,4         0,0	P62244	RPS15A	40S ribosomal protein S15a	1,5	0,003	PRDX4
Q9H974         QTRT2         Queuine tRNA-ribosyltransferase accessory subunit 2         1,5         0,018         PRDX4           Q75306         NDUFS2         NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial         1,5         0,02         PRDX4           Q16186         ADRM1         Proteasomal ubiquitin receptor ADRM1         1,5         0,028         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,029         PRDX4           Q19022         CDH2         Cadherin-2         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           Q0487         PSMD14         265 proteasome non-ATPase regulatory subunit 14         1,4         0         PRDX4           Q9BV44         FHUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           Q9BV44         THUMP domain-containing protein 3         1,4         0,001         PRDX4           Q9BV44         THUMP3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           Q98X31         TUBB4	Q9NYK5	MRPL39	39S ribosomal protein L39, mitochondrial	1,5	0,008	PRDX4
O75306         NDUFS2         NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial         1,5         0,02         PRDX4           Q16186         ADRM1         Proteasomal ubiquitin receptor ADRM1         1,5         0,028         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,029         PRDX4           A0A1B0GUC3         FTO         Alpha-ketoglutarate-dependent dioxygenase FTO         1,5         0,03         PRDX4           P19022         CDH2         Cadherin-2         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           P61927         RPL37         60S ribosomal protein L37         1,5         0,04         PRDX4           P68104         EEF1A1         Elongation factor 1-alpha 1         1,4         0         PRDX4           Q9BV44         THUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           P63388         RPLP0         60S acidic ribosomal protein 4         1,4         0,002         PRDX4           Q9BV44         THUMP103         THUMP domain-containing protein 3         1,4         0,002         PRDX4           Q9S388         RP	Q9H974	QTRT2	Queuine tRNA-ribosyltransferase accessory subunit 2	1,5	0,018	PRDX4
Q16186         ADR.M1         Proteasonal ubiquitin receptor ADRM1         1,5         0,028         PRDX4           Q13190         STX5         Syntaxin-5         1,5         0,029         PRDX4           A0A1B0GUC3         FTO         Alpha-ketoglutarate-dependent dioxygenase FTO         1,5         0,03         PRDX4           P19022         CDH2         Cadherin-2         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           P61927         RPL37         608 ribosomal protein L37         1,5         0,04         PRDX4           O04487         PSMD14         265 proteasome non-ATPase regulatory subunit 14         1,4         0         PRDX4           P68104         EEF1A1         Elongation factor 1-alpha 1         1,4         0,001         PRDX4           Q9BV44         THUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           P68371         TUBB4B         Tubulin beta-4B chain         1,4         0,002         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           Q92G29         PNPO         Pyridoxal 5-phosph	075306	NDUF\$2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	1,5	0,02	PRDX4
Q13190         STX5         Syntaxin-5         1,5         0,029         PRDX4           A0A1B0GUC3         FTO         Alpha-ketoglutarate-dependent dioxygenase FTO         1,5         0,03         PRDX4           P19022         CDH2         Cadherin-2         1,5         0,038         PRDX4           Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           P61927         RPL37         60S ribosomal protein L37         1,5         0,04         PRDX4           O00487         PSMD14         26S proteasome non-ATPase regulatory subunit 14         1,4         0         PRDX4           O43242         PSMD3         26S proteasome non-ATPase regulatory subunit 3         1,4         0,001         PRDX4           Q9BV44         THUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           P68371         TUBB4B         Tubulin beta-4B chain         1,4         0,002         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           Q9UKK9         NUDT5         ADP-sugar p	O16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	1,5	0.028	PRDX4
Quints         Optimized         Optimized <thoptized< th=""> <thoptized< th="">         Optized</thoptized<></thoptized<>	013190	STX5	Syntaxin-5	15	0.029	PR DX4
International approximation approximatintexpectentedupproximation approximation approximation approximati	A0A1B0GUC3	FTO	Alpha-ketoglutarate-dependent dioxygenase FTO	1.5	0.03	PR DX4
Q9UHV9         PFDN2         Prefoldin subunit 2         1,5         0,038         PRDX4           P61927         RPL37         60S ribosomal protein L37         1,5         0,04         PRDX4           000487         PSMD14         26S proteasome non-ATPase regulatory subunit 14         1,4         0         PRDX4           P68104         EEF1A1         Elongation factor 1-alpha 1         1,4         0         PRDX4           Q9BV44         THUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           P68308         RPLP0         60S acidic ribosomal protein P0         1,4         0,002         PRDX4           P05388         RPLP0         60S acidic ribosomal protein P0         1,4         0,003         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           Q9E15         SCLY         Selenocysteine lyase         1,4         0,002         PRDX4           Q95958         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	P19022	CDH2	Cadherin-2	1.5	0.038	PR DX4
RPL37FielderFielderFielderFielderFielderP61927RPL3760S ribosomal protein L371,50,04PRDX4O00487PSMD1426S proteasome non-ATPase regulatory subunit 141,40PRDX4P68104EEF1A1Elongation factor 1-alpha 11,40PRDX4Q43242PSMD326S proteasome non-ATPase regulatory subunit 31,40,001PRDX4Q9BV44THUMPD3THUMP domain-containing protein 31,40,002PRDX4P68371TUBB4BTubulin beta-4B chain1,40,002PRDX4Q9UKK9NUDT5ADP-sugar pyrophosphatase1,40,004PRDX4Q9E115SCLYSelenocysteine lyase1,40,022PRDX4Q9598TSNAXTranslin-associated protein X1,40,026PRDX4	09UHV9	PFDN2	Prefoldin subunit 2	15	0.038	PR DX4
ACKLIt StructureIt StructureI	P61927	R DI 27	60\$ ribosomal protein I 37	1.5	0,030	PR DY/
COURSEFSMEDIAZess processione non-AT rase regulatory subunit 141,40PRDX4P68104EEF1A1Elongation factor 1-alpha 11,40PRDX4O43242PSMD326S proteasome non-AT Pase regulatory subunit 31,40,001PRDX4Q9BV44THUMPD3THUMP domain-containing protein 31,40,001PRDX4P05388RPLP060S acidic ribosomal protein P01,40,002PRDX4Q53EL6PDCD4Programmed cell death protein 41,40,004PRDX4Q9UKK9NUDT5ADP-sugar pyrophosphatase1,40,004PRDX4J3QQZ9PNPOPyridoxal 5'-phosphate synthase1,40,02PRDX4Q9155SCLYSelenocysteine lyase1,40,024PRDX4Q9598TSNAXTranslin-associated protein X1,40,026PRDX4	000/87	DSMD14	26 protosomo pop ATDeso regulatoru (	1,5	0,04	DD DV4
Product         LEFTA1         Elongation factor 1-appna 1         1,4         0         PRDX4           O43242         PSMD3         26S proteasome non-ATPase regulatory subunit 3         1,4         0,001         PRDX4           Q9BV44         THUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           P05388         RPLP0         60S acidic ribosomal protein P0         1,4         0,002         PRDX4           P68371         TUBB4B         Tubulin beta-4B chain         1,4         0,004         PRDX4           Q53EL6         PDCD4         Programmed cell death protein 4         1,4         0,004         PRDX4           J3QQZ9         PNPO         Pyridoxal 5'-phosphatase         1,4         0,002         PRDX4           Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	D(9104	FOND14	200 processome non-A 1 Pase regulatory subunit 14	1,4	0	PRDA4
O43242         F3MD5         Zebs protectasome non-A 1 rase regulatory subunit 5         1,4         0,001         PRDX4           Q9BV44         THUMPD3         THUMP domain-containing protein 3         1,4         0,001         PRDX4           P05388         RPLP0         60S acidic ribosomal protein P0         1,4         0,002         PRDX4           P68371         TUBB4B         Tubulin beta-4B chain         1,4         0,003         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           J3QQZ9         PNPO         Pyridoxal 5'-phosphate synthase         1,4         0,02         PRDX4           Q9515         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q95988         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	042242	DEM D2	200 meteorementer en ATDese semiletermenter 2	1,4	0.001	DD DV
Q2DV44         FITUMPD5         I HUMP domain-containing protein 5         1,4         0,001         PRDX4           P05388         RPLP0         60S acidic ribosomal protein P0         1,4         0,002         PRDX4           P68371         TUBB4B         Tubulin beta-4B chain         1,4         0,003         PRDX4           Q53EL6         PDCD4         Programmed cell death protein 4         1,4         0,004         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           J3QQ29         PNPO         Pyridoxal 5'-phosphate synthase         1,4         0,02         PRDX4           Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	043242 00PW//	romD3	265 proteasome non-A 1 Pase regulatory subunit 3	1,4	0,001	PKDX4
PU5388         KPLP0         60S acidic ribosomal protein P0         1,4         0,002         PRDX4           P68371         TUBB4B         Tubulin beta-4B chain         1,4         0,003         PRDX4           Q53EL6         PDCD4         Programmed cell death protein 4         1,4         0,004         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           J3QQZ9         PNPO         Pyridoxal 5'-phosphate synthase         1,4         0,002         PRDX4           Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q9598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	Q9BV44	THUMPD3	1 HUMP domain-containing protein 3	1,4	0,001	PKDX4
P68371         TUBB4B         Tubulin beta-4B chain         1,4         0,003         PRDX4           Q53EL6         PDCD4         Programmed cell death protein 4         1,4         0,004         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           J3QQZ9         PNPO         Pyridoxal 5'-phosphate synthase         1,4         0,002         PRDX4           Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	P05388	KPLP0	605 acidic ribosomal protein P0	1,4	0,002	PKDX4
Q53EL6         PDCD4         Programmed cell death protein 4         1,4         0,004         PRDX4           Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           J3QQZ9         PNPO         Pyridoxal 5'-phosphate synthase         1,4         0,02         PRDX4           Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	P68371	TUBB4B	Iubulin beta-4B chain	1,4	0,003	PRDX4
Q9UKK9         NUDT5         ADP-sugar pyrophosphatase         1,4         0,004         PRDX4           J3QQZ9         PNPO         Pyridoxal 5'-phosphate synthase         1,4         0,02         PRDX4           Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	Q53EL6	PDCD4	Programmed cell death protein 4	1,4	0,004	PRDX4
J3QQZ9         PNPO         Pyridoxal 5'-phosphate synthase         1,4         0,02         PRDX4           Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	Q9UKK9	NUDT5	ADP-sugar pyrophosphatase	1,4	0,004	PRDX4
Q96115         SCLY         Selenocysteine lyase         1,4         0,024         PRDX4           Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	J3QQZ9	PNPO	Pyridoxal 5'-phosphate synthase	1,4	0,02	PRDX4
Q99598         TSNAX         Translin-associated protein X         1,4         0,026         PRDX4	Q96I15	SCLY	Selenocysteine lyase	1,4	0,024	PRDX4
	Q99598	TSNAX	Translin-associated protein X	1,4	0,026	PRDX4

O9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	1.4	0,027	PRDX4
096GK7	FAHD2A	Fumarylacetoacetate hydrolase domain-containing protein 2A	1.4	0.044	PR DX4
014694	USP10	Ubiquitin carboxyl-terminal hydrolase 10	1.3	0.001	PR DX4
092688	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B	13	0.002	PR DX4
D6R 938	CAMK2D	Calcium/calmodulin-dependent protein kinase	13	0.002	PR DX4
09BR P1	PDCD2I	Programmed cell death protein 2-like	1,3	0.003	PR DX4
Q9UHD1	CHORDC1	Cysteine and histidine-rich domain-containing protein 1	13	0.005	PR DX4
Q98T25	HAUSS	HAUS augmin, like complex subunit 8	1,5	0.007	DR DY4
D63244	R ACK1	Receptor of activated protein C kinase 1	1,5	0.008	DR DY4
D12225	SI C25A4	ADD/ATD translosses 1	1,5	0,008	PRDX4
P12233	SLC23A4	ADP/ATP transiocase 1	1,5	0,02	PRDA4
Q81 V IVIO	ULAT1	Uistana contralmente marchana proteini 50	1,5	0,02	PRDA4
014929	OTUDO	Pristone acetyntransierase type B catalytic subunit	1,5	0,024	PRDA4
Q8INGMU	UIUD6D	Deubiquitinase OTOD6B	1,3	0,035	PRDA4
P00492	HPRII	Hypoxanthine-guanine phosphoribosyltransferase	1,3	0,042	PRDX4
Q96HS1	PGAM5	Serine/threonine-protein phosphatase PGAMS, mitochondrial	1,3	0,043	PRDX4
HOYLH3	RABGGIA	Geranylgeranyl transferase type-2 subunit alpha	1,3	0,044	PRDX4
Q92576	PHF3	PHD finger protein 3	1,3	0,047	PRDX4
Q86W42	THOC6	THO complex subunit 6 homolog	1,3	0,048	PRDX4
095394	PGM3	Phosphoacetylglucosamine mutase	1,2	0	PRDX4
P17858	PFKL	ATP-dependent 6-phosphofructokinase, liver type	1,2	0	PRDX4
Q92769	HDAC2	Histone deacetylase 2	1,2	0,001	PRDX4
P22102	GART	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine- -glycine ligase	1,2	0,001	PRDX4
P25398	RPS12	40S ribosomal protein S12	1.2	0,001	PRDX4
O9UNM6	PSMD13	26S proteasome non-ATPase regulatory subunit 13	1.2	0.002	PR DX4
P31040	SDHA	Succinate debydrogenase [ubiquinone] flavonrotein subunit, mitochondria]	1.2	0.002	PR DX4
P61313	R PI 15	608 ribosomal protein L 15	1,2	0.003	PR DX4
P22695	LIOCRC2	Cytochrome b-c1 complex subunit 2 mitochondrial	1.2	0.004	PR DX4
075400	DP DE40A	Dra mP NA processing factor (0 homolog A	1,2	0.004	DP DV4
073400	DI DPD	Duridanal akaankata kamaaataala maatain	1,2	0,004	PRDX4
D/972(	MCM2	DNA ambienting linearing frates MCM2	1,2	0,004	PRDX4
015728	MCM2	Event 6 alaba and 2 alaba and 2 alaba and 2 alaba	1,2	0,004	PRDA4
Q15/38	NSDHL	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	1,2	0,006	PRDX4
015144	ARPC2	Actin-related protein 2/3 complex subunit 2	1,2	0,007	PRDX4
P31930	UQCRC1	Cytochrome b-cl complex subunit 1, mitochondrial	1,2	0,008	PRDX4
				0.000	1111 1217 /
P21964	COMT	Catechol O-methyltransferase	1,2	0,008	PRDX4
<u>P21964</u> <u>O95373</u>	IPO7	Catechol O-methyltransferase Importin-7	1,2 1,2	0,008	PRDX4 PRDX4
P21964           O95373           Q14232	IPO7 EIF2B1	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha	1,2 1,2 1,2	0,008 0,01 0,011	PRDX4 PRDX4 PRDX4
P21964           O95373           Q14232           Q9UJZ1	EIF2B1 STOML2	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial	1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015	PRDX4 PRDX4 PRDX4 PRDX4
P21964           O95373           Q14232           Q9UJZ1           P47755	COMT IPO7 EIF2B1 STOML2 CAPZA2	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2	1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964           O95373           Q14232           Q2UJZ1           P47755           P04181	IPO7 EIF2B1 STOML2 CAPZA2 OAT	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964           O95373           Q14232           Q2UJZ1           P47755           P04181           K7EJQ8	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,017 0,019 0,025	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964           O95373           Q14232           Q9UJZ1           P47755           P04181           K7EJQ8           Q7L2J0	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,03	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964           O95373           Q14232           Q9UJZ1           P47755           P04181           K7EJQ8           Q7L2J0           Q13177	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,03 0,032	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964           O95373           Q14232           Q9UJZ1           P47755           P04181           K7EJQ8           Q7L2J0           Q13177           O00231	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,03 0,032 0,034	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11 Alpha-taxilin	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,03 0,032 0,034 0,035	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11 Alpha-taxilin Eukaryotic translation initiation factor 3 subunit L	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,03 0,032 0,032 0,034 0,035 0,044	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11 Alpha-taxilin Eukaryotic translation initiation factor 3 subunit L cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,03 0,032 0,034 0,035 0,044 0,001	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11 Alpha-taxilin Eukaryotic translation initiation factor 3 subunit L cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier Amidophosphoribosyltransferase	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,032 0,032 0,034 0,035 0,044 0,001 0,002	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11 Alpha-taxilin Eukaryotic translation initiation factor 3 subunit L cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier Amidophosphoribosyltransferase Eukaryotic translation initiation factor 5B	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,032 0,034 0,035 0,034 0,035 0,044 0,001 0,002 0,002	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11 Alpha-taxilin Eukaryotic translation initiation factor 3 subunit L cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier Amidophosphoribosyltransferase Eukaryotic translation initiation factor 5B Phosphatidate cytidylyltransferase, mitochondrial	1,2 1,2 1,2 1,2 1,2 1,2 1,2 1,2	0,008 0,01 0,011 0,015 0,017 0,019 0,025 0,032 0,034 0,035 0,034 0,035 0,044 0,001 0,002 0,002 0,003	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1	0,008 0,01 0,011 0,015 0,017 0,025 0,03 0,032 0,034 0,035 0,044 0,001 0,002 0,002 0,003 0,003	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF3B TAMM41 AKR1B1 KIF7	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008 0,01 0,011 0,015 0,017 0,025 0,03 0,032 0,034 0,035 0,044 0,001 0,002 0,003 0,003 0,003 0,004	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2MIP5         P46778	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein KIF7	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,003           0,004	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2MIP5         P46778         Q9Y5Y2	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2	Catechol O-methyltransferase Importin-7 Translation initiation factor eIF-2B subunit alpha Stomatin-like protein 2, mitochondrial F-actin-capping protein subunit alpha-2 Ornithine aminotransferase, mitochondrial Haloacid dehalogenase-like hydrolase domain-containing protein 2 7SK snRNA methylphosphate capping enzyme Serine/threonine-protein kinase PAK 2 26S proteasome non-ATPase regulatory subunit 11 Alpha-taxilin Eukaryotic translation initiation factor 3 subunit L cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier Amidophosphoribosyltransferase Eukaryotic translation initiation factor 5B Phosphatidate cytidylyltransferase, mitochondrial Aldo-keto reductase family 1 member B1 Kinesin-like protein KIF7 60S ribosomal protein L21 Cytosolic Fe-S cluster assembly factor NUBP2	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,003           0,004           0,004	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2MIP5         P46778         Q9Y5Y2         P50914	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         608 ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         608 ribosomal protein L14	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,004           0,004	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y522         P50914         P35232	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,002           0,003           0,003           0,003           0,004           0,004           0,004	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y5Y2         P50914         P35232         P08574	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,025           0,032           0,034           0,035           0,044           0,002           0,003           0,003           0,003           0,004           0,004           0,004           0,004           0,004           0,004	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y5Y2         P50914         P35232         P08574         P31153	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome cl, heme protein, mitochondrial         Schoered L4         Seadenosylmethionine synthase isoform type-2	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,025           0,03           0,032           0,034           0,005           0,001           0,002           0,002           0,003           0,004           0,004           0,004           0,004           0,004           0,004           0,001	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y3Y2         P50914         P3153         P155800	COM1 IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A RPS2	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         408 ribosomal protein S2	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,025           0,03           0,032           0,034           0,035           0,044           0,002           0,003           0,002           0,003           0,004           0,004           0,004           0,004           0,001           0,004           0,004           0,001           0,001	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y3Y2         P50914         P35232         P08574         P15880         O13618	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A RPS2 CUL3	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithline aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1         1,1	0,008           0,01           0,011           0,015           0,017           0,025           0,03           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,004           0,004           0,004           0,004           0,004           0,004           0,012           0,017	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y22         P50914         P35232         P08574         P31153         P15880         Q13618         P62851	COM1           IPO7           EIF2B1           STOML2           CAPZA2           OAT           HDHD2           MEPCE           PAK2           PSMD11           TXLNA           EIF3L           B4DLN1           PPAT           EIF5B           TAMM41           AKR1B1           KIF7           RPL21           NUBP2           RPL14           PHB           CYC1           MAT2A           RPS2           CUL3           RPS25	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S25	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1	0,008           0,01           0,011           0,015           0,017           0,025           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,003           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,001           0,012           0,017           0,021	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y5Y2         P50914         P35232         P08574         P31153         P15880         Q13618         P62851         H0YDU8	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A RPS2 CUL3 RPS25 PPP5C	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         75K snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S25         Serine/threonine-protein phosphatase	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,025           0,031           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,010           0,012           0,017           0,021           0,022	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y5Y2         P50914         P35232         P08574         P31153         P15880         Q13618         P62851         H0YDU8         Q5T760	COM1 IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A RPS2 CUL3 RPS25 PPP5C SRSF11	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S25         Serine/threonine-protein phosphatase         Serine/threonine-protein phosphatase <td>1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1</td> <td>0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,004           0,004           0,004           0,004           0,017           0,017           0,021           0,022</td> <td>PRDX4 PRDX4</td>	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,004           0,004           0,004           0,004           0,017           0,017           0,021           0,022	PRDX4 PRDX4
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2MIP5         P46778         Q9Y5Y2         P50914         P35232         P08574         P31153         P15880         Q13618         P62851         H0YDU8         Q95T760         Q92922	COM1           IPO7           EIF2B1           STOML2           CAPZA2           OAT           HDHD2           MEPCE           PAK2           PSMD11           TXLNA           EIF3L           B4DLN1           PPAT           EIF5B           TAMM41           AKR1B1           KIF7           RPL21           NUBP2           RPL14           PHB           CYC1           MAT2A           RPS2           CUL3           RPS25           PP5C           SRSF11           SMARCC1	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S2         Serine/threonine-protein phosphatase         Serine/threonine-protein phosphatase	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1	0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,004           0,004           0,004           0,004           0,001           0,004           0,004           0,004           0,001           0,012           0,017           0,021           0,022           0,023           0,023	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y5Y2         P50914         P35232         P08574         P3153         P15880         Q13618         P62851         H0YDU8         Q51760         Q92922         O14C84	COM1           IPO7           EIF2B1           STOML2           CAPZA2           OAT           HDHD2           MEPCE           PAK2           PSMD11           TXLNA           EIF3L           B4DLN1           PPAT           EIF5B           TAMM41           AKR1B1           KIF7           RPL21           NUBP2           RPL14           PHB           CYC1           MAT2A           RPS2           CUL3           RPS25           PPP5C           SRSF11           SMARCC1           CAPU1	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S25         Serine/arginine-rick-splicing factor 11         SWI/SNF complex subunit SMARCC1         GTDrace crimicus moteria ad VDS9 domain containing noteria 1 <td>1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1   </td> <td>0,008           0,01           0,011           0,015           0,017           0,025           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,001           0,012           0,017           0,017           0,021           0,023           0,023           0,023           0,024</td> <td>PRDX4 PR</td>	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1	0,008           0,01           0,011           0,015           0,017           0,025           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,001           0,012           0,017           0,017           0,021           0,023           0,023           0,023           0,024	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y5Y2         P30914         P35232         P08574         P31153         P15880         Q13618         P62851         H0YDU8         Q51760         Q92922         Q14C86         A0A1BOCTC2	COM1           IPO7           EIF2B1           STOML2           CAPZA2           OAT           HDHD2           MEPCE           PAK2           PSMD11           TXLNA           EIF3L           B4DLN1           PPAT           EIF5B           TAMM41           AKR1B1           KIF7           RPL21           NUBP2           RPL14           PHB           CYC1           MAT2A           RPS2           CUL3           RPS25           PPP5C           SRSF11           SMARCC1           GAPVD1	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S2         Serine/threonine-protein phosphatase         Serine/arginine-rich-splicing factor 11 </td <td>1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1          1,1          1,1    <td>0,008           0,01           0,011           0,015           0,017           0,025           0,03           0,032           0,034           0,035           0,044           0,002           0,003           0,002           0,003           0,004           0,004           0,004           0,004           0,001           0,004           0,004           0,001           0,017           0,017           0,021           0,022           0,023           0,024           0,027           0,037</td><td>PRDX4           PRDX4           PRDX4<!--</td--></td></td>	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1          1,1          1,1 <td>0,008           0,01           0,011           0,015           0,017           0,025           0,03           0,032           0,034           0,035           0,044           0,002           0,003           0,002           0,003           0,004           0,004           0,004           0,004           0,001           0,004           0,004           0,001           0,017           0,017           0,021           0,022           0,023           0,024           0,027           0,037</td> <td>PRDX4           PRDX4           PRDX4<!--</td--></td>	0,008           0,01           0,011           0,015           0,017           0,025           0,03           0,032           0,034           0,035           0,044           0,002           0,003           0,002           0,003           0,004           0,004           0,004           0,004           0,001           0,004           0,004           0,001           0,017           0,017           0,021           0,022           0,023           0,024           0,027           0,037	PRDX4           PRDX4 </td
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y5Y2         P50914         P35232         P08574         P31153         P15880         Q13618         P62851         H0YDU8         Q5T760         Q29222         Q14C86         A0A1B0GTG2         O15143	COM1 IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF3B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A RPS2 CUL3 RPS2 CUL3 RPS25 PPP5C SRSF11 SMARCC1 GAPVD1 ALDH7A1 ACRC1P	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithline aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S2         Serine/Arginine-rich-splicing factor 11         SWI/SNF complex subunit SMARCC1	1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,1         1	0,008           0,01           0,011           0,015           0,017           0,025           0,03           0,032           0,034           0,035           0,044           0,002           0,003           0,002           0,003           0,004           0,004           0,004           0,004           0,017           0,017           0,017           0,017           0,021           0,022           0,023           0,021           0,021           0,022           0,023           0,027           0,034           0,032	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y3Y2         P50914         P35232         P08574         P31153         P15880         Q13618         P62851         H0YDU8         Q5T760         Q92922         Q14C86         A0A1B0GTG2         O15143	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF5B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A RPS2 CUL3 RPS25 PP5C SRSF11 SMARCC1 GAPVD1 ALDH7A1 ARPC1B	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithline aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L4         Prohibitin         Cytochrome c1, heme protein, mitochondrial         S-adenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S25         Serine/threonine-protein phosphatase         Serine/arginine-rich-splicing factor 11<	1,2         1,1         1	0,008           0,01           0,011           0,015           0,017           0,025           0,03           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,003           0,004           0,004           0,004           0,004           0,017           0,017           0,017           0,023           0,027           0,034           0,037           0,038	PRDX4 PR
P21964         O95373         Q14232         Q9UJZ1         P47755         P04181         K7EJQ8         Q7L2J0         Q13177         O00231         P40222         Q9Y262         B4DLN1         Q06203         A0A087WUT6         Q96BW9         P15121         Q2M1P5         P46778         Q9Y322         P08574         P31153         P15880         Q13618         P62851         H0YDU8         Q5T760         Q92922         Q14C86         A0A1B0GTG2         O15143         P40926         O20210	COMT IPO7 EIF2B1 STOML2 CAPZA2 OAT HDHD2 MEPCE PAK2 PSMD11 TXLNA EIF3L B4DLN1 PPAT EIF3B TAMM41 AKR1B1 KIF7 RPL21 NUBP2 RPL14 PHB CYC1 MAT2A RPS2 CUL3 CUL3 RPS2 CUL3 RPS2 CUL3 CUL3 RPS2 CUL3 RPS2 CUL3 CUL3 RPS2 CUL3 CUL3 RPS2 CUL3 CUL3 RPS2 CUL3 CUL	Catechol O-methyltransferase         Importin-7         Translation initiation factor eIF-2B subunit alpha         Stomatin-like protein 2, mitochondrial         F-actin-capping protein subunit alpha-2         Ornithine aminotransferase, mitochondrial         Haloacid dehalogenase-like hydrolase domain-containing protein 2         7SK snRNA methylphosphate capping enzyme         Serine/threonine-protein kinase PAK 2         26S proteasome non-ATPase regulatory subunit 11         Alpha-taxilin         Eukaryotic translation initiation factor 3 subunit L         cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier         Amidophosphoribosyltransferase         Eukaryotic translation initiation factor 5B         Phosphatidate cytidylyltransferase, mitochondrial         Aldo-keto reductase family 1 member B1         Kinesin-like protein KIF7         60S ribosomal protein L21         Cytosolic Fe-S cluster assembly factor NUBP2         60S ribosomal protein L14         Prohibitin         Cytochrome c1, heme protein, mitochondrial         Sadenosylmethionine synthase isoform type-2         40S ribosomal protein S2         Cullin-3         40S ribosomal protein S25         Serine/threonine-protein phosphatase         Serine/threonine-protein and VPS9 domain-	1,2         1,1         1	0,008           0,01           0,011           0,015           0,017           0,019           0,032           0,034           0,035           0,044           0,001           0,002           0,003           0,004           0,004           0,004           0,004           0,004           0,004           0,004           0,010           0,012           0,017           0,017           0,021           0,022           0,023           0,027           0,034           0,037           0,038           0	PRDX4           PRDX4 </td

P13639	EEF2	Elongation factor 2	1	0	PRDX4
O00303	EIF3F	Eukaryotic translation initiation factor 3 subunit F	1	0,002	PRDX4
P62888	RPL30	60S ribosomal protein L30	1	0,004	PRDX4
P62495	ETF1	Eukaryotic peptide chain release factor subunit 1	1	0,005	PRDX4
P49411	TUFM	Flongation factor Tu mitochondrial	1	0.027	PR DX4
O53H12	AGK	Acylglycerol kinase mitochondrial	- 1	0.04	PR DX4
Q9V224	RTRAF	R NA transcription translation and transport factor protein	6.9	0,01	PR DY5
Q71224 D22110	DDDV2	Description, translation and transport factor protein	5.2	0	PRDA)
P32119	PRDA2	Peroxiredoxin-2	5,2	0	PRDAS
P0016/	CYBSA	Cytochrome b5	4,1	0	PRDX5
Q96C17	CCDC124	Coiled-coil domain-containing protein 124	3,3	0	PRDX5
O96007	MOCS2	Molybdopterin synthase catalytic subunit	3,3	0	PRDX5
P10301	RRAS	Ras-related protein R-Ras	3,3	0	PRDX5
H0YNW5	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase	3,2	0	PRDX5
Q9P2B4	CTTNBP2NL	CTTNBP2 N-terminal-like protein	3,1	0	PRDX5
Q9Y3D6	FIS1	Mitochondrial fission 1 protein	2,9	0	PRDX5
Q6UW78	UQCC3	Ubiquinol-cytochrome-c reductase complex assembly factor 3	2,8	0	PRDX5
O9ULW0	TPX2	Targeting protein for Xklp2	2,8	0	PRDX5
P63167	DYNLL1	Dynein light chain 1. cytoplasmic	2.7	0	PR DX5
09NX55	HYPK	Huntingtin-interacting protein K	2.7	0.005	PR DX5
OORDWA	NIDSNA D1	Dratain NinSnan hamalag 1	2,7	0,005	DP DV5
Q9DP W8	CD EV 11D1	Protein Nipsnap nomolog 1	2,6	0 001	PRDA3
Q8N9Q2	SKEKIIPI		2,5	0,001	PRDX5
Q96AC1	FERM12	Fermitin family homolog 2	2,5	0,002	PRDX5
O60664	PLIN3	Perilipin-3	2,5	0,003	PRDX5
P53602	MVD	Diphosphomevalonate decarboxylase	2,4	0,001	PRDX5
Q9H840	GEMIN7	Gem-associated protein 7	2,4	0,001	PRDX5
P55084	HADHB	Trifunctional enzyme subunit beta, mitochondrial	2,4	0,004	PRDX5
Q9NP97	DYNLRB1	Dynein light chain roadblock-type 1	2,3	0,001	PRDX5
Q6IQ49	SDE2	Replication stress response regulator SDE2	2,2	0	PRDX5
P62244	RPS15A	40S ribosomal protein S15a	2,2	0	PRDX5
O9BZE1	MRPL37	39S ribosomal protein L37. mitochondrial	2.2	0.001	PR DX5
O8WVC2	R PS21	40S ribosomal protein S21	2.2	0.003	PR DX5
D19105	MVI 12 A	Muorin rogulatory light chain 12A	2,2	0,003	DP DV5
A0A0D (11771	CD CE7	Sector (activity light chain 12A	2,2	0,003	PRDA)
AUAUD4J1Z1	SKSF/	Serine/arginine-rich-splicing ractor /	2,2	0,004	PRDAS
Q13126	MIAP	S-methyl-5-thioadenosine phosphorylase	2,2	0,006	PRDAS
P06132	UROD	Uroporphyrinogen decarboxylase	2,2	0,006	PRDX5
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	2,2	0,009	PRDX5
B4DDF4	CNN2	Calponin	2,1	0	PRDX5
Q9NS69	TOMM22	Mitochondrial import receptor subunit TOM22 homolog	2,1	0	PRDX5
P19338	NCL	Nucleolin	2,1	0	PRDX5
Q9GZS3	WDR61	WD repeat-containing protein 61	2,1	0	PRDX5
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	2,1	0,002	PRDX5
Q9BYN0	SRXN1	Sulfiredoxin-1	2,1	0,018	PRDX5
O14965	AURKA	Aurora kinase A	2	0	PRDX5
095373	IPO7	Importin-7	2	0	PR DX5
H3BRI3	LIBED1	Ubiquitin domain-containing protein LIBED1	2	0.004	PR DX5
O9BTE1	DCTNS	Dynactin subunit 5	2	0.004	PR DY5
D00/01	DUIN	Dynactini subunit y	2	0,004	DDDV5
P00491	PINP		2	0,004	PRDAS
E9PHS0	LANCLI	Glutathione S-transferase LANCLI	2	0,018	PRDX5
E9PKGI	PRMII	Protein arginine N-methyltransferase 1	1,9	0	PRDX5
Q12948	FOXC1	Forkhead box protein C1	1,9	0,001	PRDX5
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	1,9	0,004	PRDX5
P26599	PTBP1	Polypyrimidine tract-binding protein 1	1,9	0,004	PRDX5
P84085	ARF5	ADP-ribosylation factor 5	1,9	0,01	PRDX5
P35244	RPA3	Replication protein A 14 kDa subunit	1,9	0,01	PRDX5
P68133	ACTA1	Actin, alpha skeletal muscle	1,9	0,03	PRDX5
P15880	RPS2	40S ribosomal protein S2	1,8	0	PRDX5
P46778	RPL21	60S ribosomal protein L21	1.8	0	PRDX5
P40429	R PL 13A	60S ribosomal protein L13a	1.8	0	PR DX5
A0A087WTM1	ROBO1	Roundshout homolog 1	1,8	0	PR DY5
D(22((	D DC22		1,0	0.001	DDDV5
F07200	RF323	405 fibosofiai protein 525	1,8	0,001	PRDA)
F2Z388	KPL55	505 ribosomai protein L35	1,8	0,001	PRDAS
Q96DH6	M812	KNA-binding protein Musashi homolog 2	1,8	0,006	PRDX5
G5EA06	MRP\$27	28S ribosomal protein S27, mitochondrial	1,8	0,01	PRDX5
P62304	SNRPE	Small nuclear ribonucleoprotein E	1,8	0,013	PRDX5
Q86WA6	BPHL	Valacyclovir hydrolase	1,8	0,015	PRDX5
Q5JRI1	SRSF10	Serine/arginine-rich-splicing factor 10	1,8	0,016	PRDX5
P53597	SUCLG1	SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	1,7	0,001	PRDX5
P04181	OAT	Ornithine aminotransferase, mitochondrial	1,7	0,001	PRDX5
			. –	0.001	DD DWC
P63244	RACK1	Receptor of activated protein C kinase 1	1.7	0,001	PRDX5

Q9Y5K6	CD2AP	CD2-associated protein	1,7	0,002	PRDX5
O15143	ARPC1B	Actin-related protein 2/3 complex subunit 1B	1,7	0.018	PRDX5
P00390	GSR	Glutathione reductase mitochondrial	17	0.022	PR DX5
015/77	CKINOL		1,7	0,022	DDDVC
Q154//	SKIV2L	Helicase SK12W	1,/	0,025	PRDAS
Q13542	EIF4EBP2	Eukaryotic translation initiation factor 4E-binding protein 2	1,7	0,031	PRDX5
O95168	NDUFB4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	1,6	0	PRDX5
O02878	R PL6	60S ribosomal protein L6	1.6	0.001	PR DX5
AGAGLIER DAG	ENIALI	Describer and the lange of the second s	1,0	0,001	DDDVC
AUAUUIKKM6	ENAH	Protein enabled homolog	1,6	0,001	PRDAS
O95861	BPNT1	3'(2'),5'-bisphosphate nucleotidase 1	1,6	0,003	PRDX5
P82930	MRPS34	28S ribosomal protein \$34, mitochondrial	1,6	0,004	PRDX5
096115	SCLY	Selenocysteine lyase	1.6	0.006	PR DX5
Q70117	MD DI /C		1,0	0,000	DDDVC
A0A08/X2D5	MKPL45	395 ribosomal protein L45, mitochondrial	1,6	0,01	PRDX5
Q4VCS5	AMOT	Angiomotin	1,6	0,013	PRDX5
Q9Y4P1	ATG4B	Cysteine protease ATG4B	1,6	0,019	PRDX5
P16403	H1.2	Histone H1 2	1.6	0.031	PR DX5
D0720/	CADNII		1,0	0,001	DDDVC
P0/384	CAPNI	Calpain-1 catalytic subunit	1,6	0,034	PRDAS
Q9NXH9	TRMT1	tRNA	1,6	0,039	PRDX5
P14174	MIF	Macrophage migration inhibitory factor	1,6	0,045	PRDX5
E9PDD6	BCL2L13	Bcl-2-like protein 13	1.6	0.045	PR DX5
077/05	UDCEL2	If the protein 15	1,0	0,019	DDDVC
Q/Z4V5	HDGFL2	Hepatoma-derived growth factor-related protein 2	1,6	0,048	PRDX5
P61313	RPL15	60S ribosomal protein L15	1,5	0	PRDX5
P36542	ATP5F1C	ATP synthase subunit gamma, mitochondrial	1,5	0	PRDX5
F9PFI4	DLAT	A cetyltransferase component of pyruvate dehydrogenase complex	15	0.001	PR DX5
Dacaaz	CED DINID (	c : DC	1,5	0,001	DDDVC
P3523/	SERPINB6	Serpin B6	1,5	0,001	PRDX5
C9J9K3	RPSA	40S ribosomal protein SA	1,5	0,001	PRDX5
G5E9W7	MRPS22	28S ribosomal protein \$22, mitochondrial	1,5	0,002	PRDX5
P63000	RAC1	Bas-related C3 botulinum toxin substrate 1	15	0.002	PR DX5
0.000	ICICI IDO/		1,5	0,002	DDDW
Q8TEX9	IPO4	Importin-4	1,5	0,002	PRDX5
P61353	RPL27	60S ribosomal protein L27	1,5	0,004	PRDX5
Q7L2J0	MEPCE	7SK snRNA methylphosphate capping enzyme	1,5	0,011	PRDX5
0711119	H2A72	Histone H2A V	15	0.022	PR DX5
Q/101/	1121122		1,5	0,022	DDDVC
Q9Y2R5	MRPS17	285 ribosomal protein S17, mitochondrial	1,5	0,028	PRDX5
Q9H7N4	SCAF1	Splicing factor, arginine/serine-rich 19	1,5	0,032	PRDX5
P42345	MTOR	Serine/threonine-protein kinase mTOR	1,5	0,035	PRDX5
G3V104	SEDTIN7	Sentin-7	1.5	0.038	DR DYS
03/104	JLI IIIN/		1,5	0,030	DDDV
Q16/62	151	I hiosulfate sulfurtransferase	1,5	0,039	PRDX5
Q6P1L8	MRPL14	39S ribosomal protein L14, mitochondrial	1,5	0,048	PRDX5
P23921	RRM1	Ribonucleoside-diphosphate reductase large subunit	1,4	0	PRDX5
D12236	SLC25A6	A DP/A TP translocase 3	1 /	0	DR DYS
F12236	SLC2JA6	ADF/ATF transiocase 5	1,4	0	PRDA)
P62081	RPS/	408 ribosomal protein 87	1,4	0	PRDX5
P34897	SHMT2	Serine hydroxymethyltransferase, mitochondrial	1,4	0,001	PRDX5
P50914	RPL14	60S ribosomal protein L14	1,4	0,001	PRDX5
D62750	R DI 23Δ	60S ribosomal protein I 23a	1 /	0.001	DR DYS
102/J0	RI L23/I		1,1	0,001	DDDW
P51452	DUSP3	Dual specificity protein phosphatase 3	1,4	0,001	PRDX5
P62269	RPS18	40S ribosomal protein S18	1,4	0,001	PRDX5
P43897	TSFM	Elongation factor Ts, mitochondrial	1,4	0,001	PRDX5
Ο9ΝΟΤ/	FYOSCS	Exosome complex component R R D/A	1 /	0.001	DR DYS
Q/11Q11	ENOUG		1,1	0,001	DDDVC
P225/0	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial	1,4	0,001	PRDX5
P62495	ETF1	Eukaryotic peptide chain release factor subunit 1	1,4	0,002	PRDX5
P68371	TUBB4B	Tubulin beta-4B chain	1,4	0,004	PRDX5
07L106	BZW1	Basic leucine zipper and W2 domain-containing protein 1	1.4	0.005	PR DX5
000	A DLID1/D	Description A DUID1/D	1.4	0.00/	DDDVC
Q96104	ADHD14D	Ploteni ADHD14D	1,4	0,006	PKDA3
094973	AP2A2	AP-2 complex subunit alpha-2	1,4	0,007	PRDX5
P12277	CKB	Creatine kinase B-type	1,4	0,013	PRDX5
O86XI2	NCAPG2	Condensin-2 complex subunit G2	1,4	0.024	PRDX5
D(2829	P DI 22	(08 ribosomal protain I 22	1.4	0.025	DP DV5
0102027	NTE CE 4		1,4	0,02)	DDDW
Q13613	MIMRI	Myotubularin-related protein 1	1,4	0,03	PRDX5
O00629	KPNA4	Importin subunit alpha-3	1,4	0,033	PRDX5
Q9UHQ9	CYB5R1	NADH-cytochrome b5 reductase 1	1,4	0,034	PRDX5
O5VW32	BROX	BRO1 domain-containing protein BROX	14	0.041	PR DX5
075207	NIDUECO		1,7	0,011	DDDDV
075306	NDUF52	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	1,4	0,046	PKDX5
P68104	EEF1A1	Elongation factor 1-alpha 1	1,3	0	PRDX5
B4DLN1	B4DLN1	cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier	1,3	0	PRDX5
O8WUH6	TMEM263	Transmembrane protein 263	13	0	PR DX5
D05091	ALDU2	Aldahuda dahudaagaagaa mita-har daial	1.2	0.001	DD DVC
r 03071	ALUH2	Aldenyde denydrogenase, mitochondrial	1,5	0,001	PRDAS
Q92688	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B	1,3	0,002	PRDX5
O00442	RTCA	RNA 3'-terminal phosphate cyclase	1,3	0,003	PRDX5
P11172	UMPS	Uridine 5'-monophosphate synthase	1.3	0.005	PR DX5
08/11/2	DA PDN1	Delus denulases him dine meneralin 2	1,5	0.005	DDDVC
Q00U42	FADEINI	roryadenyrate-billding protein 2	1,5	0,005	PRDA)

APD90       K1R.c21       Klife cell lector-like recorport allowing Gaussiber 2       1.3       0.006         DR439       CAMK2D       Calcium, clannohilm-depender portek Kusse       1.3       0.01         P81401       SR37       Sternikerginner-förpherich politerig faster 3       1.3       0.01         EPR147       GSTM24       Giannafanon-Stranderse Ma 2       1.3       0.01         Q00401       CTTC       Calcium Aption Stranderse Ma 2       1.3       0.01         Q00401       CTTC       Calcium Aption Stranderse Ma 2       1.3       0.021         Q00401       CTTC       Calcium Aption Stranderse Ma 1       0.3       0.021         Q00401       CTTC       Calcium Aption Stranderse Ma 1       0.3       0.021         Q01212       UTDS1       Particip PR45CA       0.3       0.021         Q0212       UTDS1       Debring Stranderse Ma 1       0.3       0.021         Q01404       UTPA1       Debring Stranderse Ma 1       0.3       0.021         Q01404       UTPA1       Debring Stranderse Ma 1       0.3       0.001         Q01404       UTPA1       Debring Stranderse Ma 1       0.2       0.001         Q01404       UTPA1       Haber 2A       0.001       0.011 <th>K18.C2         Kille of Hexeques update 1         1.3         0.06         PFDNS           SINAL         Inside 3-phosphare ymbas 1         1.3         0.01         PFDNS           SIST         Strain formaling inter of 1.0         1.3         0.01         PFDNS           SIST         Strain formaling inter of 1.0         1.3         0.01         PFDNS           CITC         Calman gluan sylpost ratio 1.0         1.3         0.016         PFDNS           SIST         Strain intrain for face of 1.0         1.3         0.016         PFDNS           COTT         Calman gluan sylpost ratio 1.0         1.3         0.016         PFDNS           SIST         Strain intrain face of 1.0         1.3         0.016         PFDNS           CONS         Consort strain sylpost ratio 1.0         1.3         0.011         PFDNS           SIST         Strain intrain strain strain</th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th>	K18.C2         Kille of Hexeques update 1         1.3         0.06         PFDNS           SINAL         Inside 3-phosphare ymbas 1         1.3         0.01         PFDNS           SIST         Strain formaling inter of 1.0         1.3         0.01         PFDNS           SIST         Strain formaling inter of 1.0         1.3         0.01         PFDNS           CITC         Calman gluan sylpost ratio 1.0         1.3         0.016         PFDNS           SIST         Strain intrain for face of 1.0         1.3         0.016         PFDNS           COTT         Calman gluan sylpost ratio 1.0         1.3         0.016         PFDNS           SIST         Strain intrain face of 1.0         1.3         0.016         PFDNS           CONS         Consort strain sylpost ratio 1.0         1.3         0.011         PFDNS           SIST         Strain intrain strain						
QPNP1P12         [SYNA]         Ionolo-3-phagebagebag predicts in his         1.3         0.001           DB4103         SRAST         Scientify and incredicts in high in the first of 3         1.3         0.011           DB4103         SRAST         Scientify and incredicts in high in the first of 3         0.011           XIW128         RPL 0         655 month predicts in the first incredict in the interm in the interm in the interm interm in the interm int	ISYNAI         Inselied-3-polyhets rubase1         1.3         0.008         PRDXS           CAMKED         CAMMAD         0.01         PRDXS           SRST         Serine/arginitier rich splicing factor 3         1.3         0.01         PRDXS           SRST         Genarchance 5-ranar factors Mo 2         1.3         0.012         PRDXS           CUTC         Calmar by control 1.0         1.3         0.016         PRDXS           CGCT         Gename gluture/coleranofraze         1.3         0.016         PRDXS           CGCC         Gename gluture/coleranofraze         1.3         0.016         PRDXS           CGPD2         Contoner subunit her         1.3         0.017         PRDXS           DRMSC         Delyndystasteride factor factors         1.2         0.01         PRDXS           DRMSC         Delyndystasteride factors         1.2         0.01         PRDXS           DRTA         Calanthano Faranafactors factors         1.2         0.01         PRDXS           DRTA         Delyndystasteride factors         1.2         0.01         PRDXS           DRTA         Delyndystasteride factors         1.2         0.01         PRDXS           DRTA         Delyndystasteride factors	A4D1S0	KLRG2	Killer cell lectin-like receptor subfamily G member 2	1,3	0,006	PRDX5
DAR 928         C.A.G.M.CAD         C.A.G.M.CAD         0.04           PM1403         SKR3         Schnolorghim-chronolynch opticing         1.3         0.04           PM1407         GSTM2         Charabhams-Stranofizza Mu 2         1.3         0.04           SWR22         RFL10         GSTribesong Propering L10         1.3         0.046           Q00610         C.T.C         Clarinith barry chain 1         0.3         0.046           Q12323         FIR318         Transfaction Initiation factor of L72.8 ubunit dpla         1.3         0.051           Q1234         FIR318         Transfaction Initiation factor 147.8 ubunit dpla         1.3         0.052           Q1234         D11857         Delphydroganar/Charactica Multiation factor 147.8 ubunit dplan         1.3         0.041           Q1234         Dillafor         Delphydroganar/Charactica Multiation factor 147.8 ubunit dblands dplan         1.3         0.042           Q12491         Dillafor         Delphydroganar/Charactica Multiation factor 147.8 ubunit dblands dplant         1.2         0.001           Q12491         DSP10         Clarattion factor 147.8 ubunit dbland         1.2         0.001           Q12491         DSP10         Delphydroganar/Charactica Multiation factor 147.8 ubunit dbland         1.2         0.001	CAME20 CAUE20 CA	Q9NPH2	ISYNA1	Inositol-3-phosphate synthase 1	1,3	0,008	PRDX5
P4108SR50Sentic Application Sector1,30,01XIWIZARPL06000000000000000000000000000000000000	SRS3Senie Agmine chi pilaing factors31,30,01PRXSRPLA000114000 stransformer Mu31,30,012PRXSRPLA00011400 stransformal protein L101,30,016PRXSCGCTCannabasine initions factor BL2 Bachani alpha1,30,016PRXSDRRACA1,30,016PRXSPRXSCGRB2Cannabasine initions factor BL2 Bachani alpha1,30,014PRXSDRRACADevises PRRCA1,30,015PRXSDRRACADevises prace factors algo initions factor BL2 Bachani scontaining 51,20,01PRXSDRRACADelysoperame/reductare SDR initions factor BL20,011PRXSPRXSDRRACADelysoperame/reductare SDR initions factors factors algo inition scontaining 51,20,011PRXSDRRACADelysoperame/reductare SDR initions factors factor	D6R938	CAMK2D	Calcium/calmodulin-dependent protein kinase	1,3	0,01	PRDX5
B79HN         GTM2         Clastificace Stratigner Ma 2         1.3         0.012           QM0610         CLTC         Clarkin heary chain 1         1.3         0.016           QM222         ECGT         Clarkin heary chain 1         1.3         0.016           QH232         ECGT         Clarkin heary chain 1         0.016         0.024           QH232         HT281         Transfactor for CL28 hearing the chain 1         0.016         0.024           QH364         CPR62CA         Contorn rubanity bearing the chain 1         0.016         0.024           QF394         DH1857         Delvelogessaccholocates SDR family member 7         1.3         0.016           QF394         DH1857         Delvelogessaccholocates SDR family member 7         1.2         0.001           QF404         USP10         Classitiones stratifyras PL         1.2         0.001           QF404         DSP10         Classitiones stratifyras PL         1.2         0.001           QF404         DSP10         Transforming protein Rbn         1.2         0.001           QF404         DSP10         Transforming protein Rbn         1.2         0.001           QF126         RH10         Transforming protein Rbn         1.2         0.001	GATAM         1,3         0,01         PRXS           RPLA0         6,37 mbsomal protects PLXS         1,3         0,016         PRXSS           CLTC         Clarbin bary chain 1         1,3         0,016         PRXSS           CGCT         Gama plarms/protects PLXS         1,3         0,016         PRXSS           EFE3H         Transfation intriton factor CF2B suburit alpha         1,3         0,011         PRXSS           COPPID         Catomer suburit bea'         1,3         0,031         PRXSS           COPPID         Catomer suburit bea'         1,3         0,041         PRXSS           DIFKS         Delphagomans/chatomes Suburit member 7         1,3         0,041         PRXSS           DIFKD         Charabines Stransfrase P         1,2         0,001         PRXSS           DIFRD         Habosid bablogmans/chatomes tabea domain containing 7         1,2         0,001         PRXSS           DIFN         Displaint andors/relating interior habos         1,2         0,001         PRXSS           RHAD         Transforming portic RhoA         1,2         0,001         PRXSS           RHAD         Transforming portic RhoA         1,2         0,001         PRXSS           RHAD         Transforming	P84103	SRSF3	Serine/arginine-rich splicing factor 3	1,3	0,01	PRDX5
XIVI28         R.P.10         6057         6057         6057         6057           OP323         GCC         Camme gatamy hysterina fraces         1.3         0.016           OP323         GCC         Camme gatamy hysterina fraces         1.3         0.016           P4854         PRSCA         Pressin PRSCA         0.33         0.025           P3566         COP92         Contours subunk ben'         1.3         0.031           QP3341         DHRS         Dedregorase/federaces OR Raily nember 7         1.3         0.041           QR8W7         HDD15         Halacid schologenase (like problem demain containing 5         1.2         0.011           QR8W7         HDG15         Halacid schologenase (like problem demain containing 5         1.2         0.001           QR4W1         USP0         Ubintric achosy derminal hystelses 10         1.2         0.001           QR4W1         HDG         Schologenase (like schologenase)         1.2         0.001           P45586         RHOA         Transforming protein 5.7         microbondraid         1.2         0.001           P45597         FASIN         Fransforming protein 5.7         microbondraid         1.2         0.002           Q15450         TKHD3         Pachyschysch	RPL30         46% fibesonal procental 10         1.3         0.012         PRXX5           CITC         Carthrin kerry dual 1         1.3         0.016         PRXX5           CGCT         Garma phynelycoleraniferas         1.3         0.016         PRXX5           PRR2A2         Prostin PLRC2A         1.3         0.024         PRXX5           OCV022         Caronar subanit for all 7.3 maly member 7         1.3         0.041         PRXX5           DIHAS7         Dedystopmace/roducture SNR family member 7         1.3         0.041         PRXX5           DIHAS7         Dedystopmace/roducture SNR family member 7         1.3         0.041         PRXX5           DIHAS7         Dedystopmace/roducture SNR family member 7         1.3         0.041         PRXX5           DIHAS7         Dedystopmace/roducture SNR family member 7         1.3         0.041         PRXX5           DIHAS7         Dedystopmace/roducture SNR family member 7         1.2         0.001         PRXX5           DIHAS7         Dedystopmace/roducture SNR family member 7         1.2         0.001         PRXX5           DINAS7         Dedystopmace/roducture SNR family member 7         1.2         0.001         PRXX5           DINAS7         Dedystopmace/roducture SNR family member 7 <td>E9PHN7</td> <td>GSTM2</td> <td>Glutathione S-transferase Mu 2</td> <td>1,3</td> <td>0,01</td> <td>PRDX5</td>	E9PHN7	GSTM2	Glutathione S-transferase Mu 2	1,3	0,01	PRDX5
Q0000         CLC         Claimsplantwickermaticsum         1.3         0.016           Q1421         ELT         Translation instance factor 42 Barbania lapha         1.3         0.016           Q1422         ELT         Translation instance factor 42 Barbania lapha         1.3         0.031           P1864A         PRASCA         1.3         0.031           Q1979A         Dublystogan Architectures VDR Mainly atember 7         1.3         0.031           P1867A         Accipturatin thiosettaxe 1         1.2         0.001           Q167A         GERTIP         Classinger-science functional factor	CLUC         Clarkin heary chain 1         13         0.016         PBDX5           GCGT         Gamm-glumm/skytems/stream         1.3         0.016         PBDX5           EU7281         Translario initiation factor 47.28 mkmin alpha         1.3         0.024         PBDX5           COPB2         Contoner shwm/that/         1.3         0.035         PBDX5           DIRKS7         Dophytogenase refunctors SVR family member 7         1.3         0.041         PRDX5           LYPLA1         Acciptrogenase refunctors SVR family member 7         1.2         0.001         PRDX5           LYPL0         Glustationes Stransfraze P         1.2         0.001         PRDX5           LYPL0         Glustationes Stransfraze P         1.2         0.001         PRDX5           LWPL0         Glustationes Transforming protein L30         1.2         0.001         PRDX5           RH0A         Transforming protein L30         1.2         0.001         PRDX5           RH15         MStrans instation familia         1.2         0.001         PRDX5           RH15         Pachytogenase domaing protein L30         1.2         0.001         PRDX5           RH14         1.2         0.001         PRDX5         PRDX5         PRDX5	X1WI28	R PL10	60S ribosomal protein L10	13	0.012	PR DX5
CVS21         CGCT         General part project         10         0.014           Q4824         EFEB         Translation induction factor of E2 submit alpha         1.3         0.014           Q4824         EFEB         Translation induction factor if E2 submit alpha         1.3         0.014           Q4864         EFEB         Product PARCA         1.3         0.014           PS666         COURS         Concourt submit Netri         1.3         0.015           ESGRAD         LYHALA         Acyleptotic blockstranse I         1.3         0.014           Q4804         LYHALA         Acyleptotic blockstranse I         1.2         0.01           Q4874         USP10         Ubaquin carchock emmail hybolize 10         1.2         0.001           Q4874         USP10         Ubaquin carchock emmail hybolize 10         1.2         0.001           Q4874         USP10         Ubaquin carchock emmail hybolize 10         1.2         0.001           Q4874         RH120         G487 floosang hybolizes in monochand a         1.2         0.001           Q1875         TRU13         Party ador ymmatine table and hybolize 10         1.2         0.001           Q1714         CONA         Transladophant prestin Bandong A         1.2         0.	6.6G T         6.6m appropring/spacementers         1.0         0.016         FRUX5           BEBZB         Translamin initiation force BC 2B solumi apha         1.3         0.016         FRUX5           ERREGA         Translamin initiation force BC 2B solumi apha         1.3         0.015         FRUX5           EOVED         Contamer ubown the Yi         1.3         0.015         FRUX5           DINEST         Contamer ubown the Yi         1.3         0.015         FRUX5           DINEST         Contamer ubown the Yi         1.3         0.016         FRUX5           EDEDD         Halassi dhalogenase/file phylobs domain containing 5         1.2         0.011         FRUX5           EDEDD         Ubigotin corbory terminal hydrolus (branch containing 5         1.2         0.001         FRUX5           ISP10         Ubigotin corbory terminal hydrolus (branch containing 5         1.2         0.001         FRUX5           ISP10         Ubigotin corbory terminal hydrolus (branch containing 5         1.2         0.001         FRUX5           ISP10         Ubigotin corbory terminal hydrolus (branch containing 5         1.2         0.001         FRUX5           ISP10         Ubigotin corbory terminal hydrolus (branch containing 5         1.2         0.001         FRUX5	000610	CLTC	Clathrin beauw chain 1	1,3	0.012	PR DY5
0.7420         Color.         Color.         Color.         0.078           0.7420         ET28b         Translate in initiation factor if 2.8 should alpha         1.3         0.078           798636         COPPE         Contomer should bea'         1.3         0.078           0.7430         DFRRS7         Dehdrogenast-reductars SDR fmilly member 7         1.3         0.041           0.7810         Dehdrogenast-reductars SDR fmilly member 7         1.3         0.041           0.7810         Illasted dehalogenast-fide phylase domain containing 5         1.2         0.001           0.7840         USP10         Usiquitin carboxyl steminal lykolase 10         1.2         0.001           0.7845         RTL30         Offstemant force if 1.30         1.2         0.001           0.7845         RTL30         Offstemant force if 1.30         1.2         0.001           0.7845         RTL91         Fars force inftrance         1.2         0.001           0.7845         RTL91         Fars force inftrance         1.2         0.001           0.7845         RTL91         Fars force inftrance inftran	GAA.1         Column guntaphyciontalisentes         1.3         0.046         PRXX3           ET2B1         Trianalation initioafic facer dT2B suburial pha         1.3         0.024         PRXX3           COP22         Columner suburial board         1.3         0.034         PRXX3           DHRS7         Dehydiogenaci/reductas SDR (mity member 7         1.3         0.045         PRXX5           DIP11.3         Actionation suburial board         1.3         0.041         PRXX5           DIP12.4         Actiopacon inductas SDR (mity member 7         1.3         0.041         PRXX5           DIP13.0         Ublaquian carboart seminal hydrolas to         1.2         0.001         PRXX5           DIP12.0         Ublaquian carboart seminal hydrolas to         1.2         0.001         PRXX5           RID4.0         Trainoforming protein Lo         1.2         0.001         PRXX5           RID3.1         Trainoforming protein RoAchandrial         1.2         0.001         PRXX5           RID4.1         Trainoforming protein RoAchandrial         1.2         0.001         PRXX5           RID4.3         Frainoforming protein RoAchandrial         1.2         0.001         PRXX5           RRD4.1         RAchanyres initiation cores Alan         1.2 <td>075222</td> <td>CLIC</td> <td>Charman heavy chann 1</td> <td>1,5</td> <td>0,016</td> <td>PRDA)</td>	075222	CLIC	Charman heavy chann 1	1,5	0,016	PRDA)
QL0.2         L12.81         Iransizon inconcil.26 substant ippa.         1.3         0.016           PN666         COPE2         Constant substant berz?         1.3         0.031           QN909         DHRSC         Delyndrogastac fordcasts SDR family member 7         1.3         0.031           DV9017         HDDIDS         Halocid delabalizames like hydrolast duration containing 5         1.2         0           DV9211         GSTP1         Glanthions * transforms P         1.2         0.001           QN049         USP10         Usapinitic control periodic labolizate 10         1.2         0.001           QN1497         HBEC14         3bydroxylobsbaryrl-CoA hydrolast, mitochondrial         1.2         0.001           QN1497         HBEC14         3bydroxylobsbaryrl-CoA hydrolast, mitochondrial         1.2         0.001           QN1498         RHDA         Transforming protein Nanochondrial         1.2         0.001           QN2455         TRIP13         Pacty acid ynothic for mitochondrial         1.2         0.002           QN2460         EFAB73         Pacty acid ynothic for mitochondrial         1.2         0.003           QN2400         EFAP34         Pacty acid ynothic for mitochondrial         1.2         0.022           QN2400         EF	L12.81       Iranstron instration 2.60 or 0.2 distorts appa       1.3       0.014       PRDXS         COP82       Coassoner submit betz'       1.3       0.031       PRDXS         COP82       Coassoner submit betz'       1.3       0.031       PRDXS         DIRKS'       Delpdrogeness/refeatures SDR finity member 7       1.3       0.041       PRDXS         LIP1A.1       Acyl protein theorem like hydroles domain containing 5       1.2       0.001       PRDXS         GSTP1       Glutarthione's transferss P       1.2       0.001       PRDXS         USP10       Ubiquitin carboxy terminal hydrolase, mitochondrial       1.2       0.001       PRDXS         RHOA       Transforming protein RhoA       1.2       0.001       PRDXS         RHOA       Transforming protein S, minochondrial       1.2       0.000       PRDXS         RHP3       Delpdroly circans forcer 3 honosog       1.2       0.000       PRDXS         RRP3       Parity acid ymbase       1.2       0.000       PRDXS         RRP40A       Transforming protein S, minochondrial       1.2       0.000       PRDXS         RRP41       Laker yood in protein S, minochondrial       1.2       0.000       PRDXS         RRP41       Laker yood in tho	0/5225	GGCI	Gamma-giutamyicyciotransferase	1,5	0,016	PRDAS
P4864         PRKC2A         Postell PKRC2A         1.3         0.024           P5606         COPE2         Castomer submit beta'         1.3         0.031           QPU394         DHKS7         Dedynegonase/reductase SDR family member 7         1.3         0.031           QPUSVT         HDHD5         Halaccid dehalogenase like hydrolase domain centaining 5         1.2         0.011           QPUSVT         HDHD5         Halaccid dehalogenase like hydrolase domain centaining 5         1.2         0.001           QL4644         USP10         Ubigatin carboxyl-terminal hydrolase 10         1.2         0.001           PCSS86         RFD3         667 rehosomal protein 1.50         1.2         0.001           PCSS86         RFD3         Fara forming protein 180A         1.2         0.001           P48327         FASN         Fara forming protein 3.0         1.2         0.001           P48326         Pachytros (Ockdopin protein 2.0 bonolog         1.2         0.001           QYE484         RFP3         285 (dobsonal protein 2.0 bonolog A         1.2         0.002           QYE484         RFP3         285 (dobsonal protein 3.0 bonolog A         1.2         0.001           QYE484         RFP3         285 (dobsonal protein 3.0 bonolog A         1.2 </td <td>PRRC2A         Destain PRRC2A         1.3         0.024         PRDX5           COPB2         Costomer silounitetra'         1.3         0.031         PRDX5           DPHRS7         Delydrogenase/reductures DR family member 7         1.3         0.031         PRDX5           DPHRS7         Delydrogenase/reductures DR family member 7         1.3         0.031         PRDX5           DPHRS7         Delydrogenase/reductures DR family member 7         1.2         0.001         PRDX5           DSTP1         Glarathione S*randfrase P         1.2         0.001         PRDX5           DSTP1         Glarathione S*randfrase P         1.2         0.001         PRDX5           DSTP1         Glarathione arrise members Arrise Deloged         1.2         0.001         PRDX5           RPL03         G45 refuberoal protein 1.50         1.2         0.001         PRDX5           FARD3         Farat sold synthase         1.2         0.006         PRDX5           FRB3         Perplath prodyl-faration factore ARD1         1.2         0.008         PRDX5           CDKNAA         Cynich depander faration factore ATD1         1.2         0.011         PRDX5           CDKNAA         Cynich depandera faration factore ATD1         1.2         0.025</td> <td>Q14232</td> <td>EIF2B1</td> <td>Translation initiation factor eIF-2B subunit alpha</td> <td>1,3</td> <td>0,016</td> <td>PRDX5</td>	PRRC2A         Destain PRRC2A         1.3         0.024         PRDX5           COPB2         Costomer silounitetra'         1.3         0.031         PRDX5           DPHRS7         Delydrogenase/reductures DR family member 7         1.3         0.031         PRDX5           DPHRS7         Delydrogenase/reductures DR family member 7         1.3         0.031         PRDX5           DPHRS7         Delydrogenase/reductures DR family member 7         1.2         0.001         PRDX5           DSTP1         Glarathione S*randfrase P         1.2         0.001         PRDX5           DSTP1         Glarathione S*randfrase P         1.2         0.001         PRDX5           DSTP1         Glarathione arrise members Arrise Deloged         1.2         0.001         PRDX5           RPL03         G45 refuberoal protein 1.50         1.2         0.001         PRDX5           FARD3         Farat sold synthase         1.2         0.006         PRDX5           FRB3         Perplath prodyl-faration factore ARD1         1.2         0.008         PRDX5           CDKNAA         Cynich depander faration factore ATD1         1.2         0.011         PRDX5           CDKNAA         Cynich depandera faration factore ATD1         1.2         0.025	Q14232	EIF2B1	Translation initiation factor eIF-2B subunit alpha	1,3	0,016	PRDX5
P5606         Cols         Cossmar submit beta'         1,3         0.031           QP394         DHRS D         Ody5         3.3         0.045           ESRGR0         LVPLA1         Acylprotein thesetters I         1,3         0.045           QP8WW         HDHD5         Haloxid GMalagoraselike bindendas domain-containing S         1,2         0           P0211         GSTP1         Glutahions S-transferase P         1,2         0.001           Qu6494         UBiquito antopy terminal Myleolase 10         1,2         0.001           Qu6494         UBiquito antopy terminal Myleolase 10         1,2         0.001           Qu6484         RP10.0         GST shoonal protein 1,50         1,2         0.001           P02327         FASN         Fatty said yanthase         1,2         0.002           Qu6484         RR19.1         Patry and yanthase         1,2         0.006           Qu728.9         MR1870         PercinRN Any protein S-n microchondrial         1,2         0.006           Qu7240         EFR420         Estaryand yanthase         1,3         0.021           Qu7240         EFR42         Estaryand yanthase         1,3         0.022           Qu7244         Qu8240         AnxAAA <td< td=""><td>COPB2         Costnerr submit Fetr<sup>1</sup>         1,3         0,031         PRDX5           DIRKS7         Delydrogenest chronic the Sectors as 1         1,3         0,041         PRDX5           LYPL A1         Acyl protein the Sectors as 1         1,3         0,041         PRDX5           GSTP1         Glutathinon S-transferase P         1,2         0,001         PRDX5           GSTP1         Glutathinon S-transferase P         1,2         0,001         PRDX5           IIBC1         3-bydroxy isohuryr) CoA hydrolase, nincohondrial         1,2         0,001         PRDX5           RHOA         Transforming protein Jo         1,2         0,001         PRDX5           RHOA         Transforming protein S, nincohondrial         1,2         0,001         PRDX5           RHS7         285 rhosonal protein S, nincohondrial         1,2         0,007         PRDX5           FRB93         Pepridyl prodyl circarasi nonceare F RB73         1,2         0,008         PRDX5           FRB40A         PenraRNA oprocessi filter of Ahondog A         1,2         0,008         PRDX5           CORNA         Calue Aproned Maxino Insci Inhibitor 2A         1,2         0,018         PRDX5           QRIC11         Glutaranise richis nor inhibitor 2A         1,2</td><td>P48634</td><td>PRRC2A</td><td>Protein PRRC2A</td><td>1,3</td><td>0,024</td><td>PRDX5</td></td<>	COPB2         Costnerr submit Fetr <sup>1</sup> 1,3         0,031         PRDX5           DIRKS7         Delydrogenest chronic the Sectors as 1         1,3         0,041         PRDX5           LYPL A1         Acyl protein the Sectors as 1         1,3         0,041         PRDX5           GSTP1         Glutathinon S-transferase P         1,2         0,001         PRDX5           GSTP1         Glutathinon S-transferase P         1,2         0,001         PRDX5           IIBC1         3-bydroxy isohuryr) CoA hydrolase, nincohondrial         1,2         0,001         PRDX5           RHOA         Transforming protein Jo         1,2         0,001         PRDX5           RHOA         Transforming protein S, nincohondrial         1,2         0,001         PRDX5           RHS7         285 rhosonal protein S, nincohondrial         1,2         0,007         PRDX5           FRB93         Pepridyl prodyl circarasi nonceare F RB73         1,2         0,008         PRDX5           FRB40A         PenraRNA oprocessi filter of Ahondog A         1,2         0,008         PRDX5           CORNA         Calue Aproned Maxino Insci Inhibitor 2A         1,2         0,018         PRDX5           QRIC11         Glutaranise richis nor inhibitor 2A         1,2	P48634	PRRC2A	Protein PRRC2A	1,3	0,024	PRDX5
QP1394         DHRS7         Dehydrogenase/reductase SDR family member 7         1.3         0.045           SDRGR0         LTPLA1         Acyl proseni thiosermar 1         1.3         0.041           QPBXW7         H1011D5         Halaccid dehalogenase like hydrolase domain containing 5         1.2         0.001           QPL644         USP10         Ubiquitin carboxyl-seminal hydrolase 10         1.2         0.001           P02836         RF10.0         GR infosomal protein L30         1.2         0.001           P02856         RF10.7         Park infosomal protein L30         1.2         0.001           P02567         FASIN         Faray del ymbase         1.2         0.002           QD5645         TR1P13         Parkinero chroping for of honolog A         1.3         0.008           QD5460         PRH740         Parkinero chroping for of honolog A         1.2         0.001           QD5460         PRH740         Parkinero chroping for of honolog A         1.2         0.002           QD5460         PRH740         Farkary for intraintering for thionolog A         1.2         0.014           QD7420         EH47.4         Ekakry for intraintering for thionolog A         1.2         0.022           QD7420         EH47.42         Ekakry for in	DHEST         Dehydrogenase/idextass.DBR family member 7         1.5         0.0941         PRDX5           HIDHD5         Halocat dehalogenase/ike producat domain, containing 5         1.2         0         PRDX5           HIDHD5         Halocat dehalogenase/ike producat domain, containing 5         1.2         0.001         PRDX5           USP10         Uliquinti carboxyl-terminal physiolose 10         1.2         0.001         PRDX5           HIBCH         3 hydroxyinoburyl-cohat physion incohondrial         1.2         0.001         PRDX5           RPL30         605 ribocanal protein 1.50         1.2         0.001         PRDX5           RADA         1.2         0.001         PRDX5           FASN         Fatty scid symbase         1.2         0.006         PRDX5           FASN         Fatty scid symbase         1.2         0.006         PRDX5           FABP3         Peatyrsech chydroine protein 2 homolog         1.2         0.008         PRDX5           FABP3         Las cologin protein 5.7         micochandria         1.2         0.008         PRDX5           CDNNAA         Cynlin deproduct factor 6.711         1.2         0.001         PRDX5           CDNNAA         Cynlin deprodulan protein 13         1.2         0.022	P35606	COPB2	Coatomer subunit beta'	1,3	0,031	PRDX5
ESKGR0         LVPLA1         Acytprotein thiosestress 1         1.2         0           P02211         GSTP1         Glutahous 5-transferss P         1.2         0           P02211         GSTP1         Glutahous 5-transferss P         1.2         0.001           Q4044         USP10         Ubiquitic archyoryterminal Hydrolas 10         1.2         0.001           QeNVY1         HIBCH         3-hydroxytoburyrt-CoAhydrolas, mitochondrial         1.2         0.001           P02356         RH0A         Transforming protein NAo         1.2         0.001           Q05465         TRIP13         Patry acidy protein 2-honolog         1.2         0.001           Q05480         FRBF9A         Peric/RA/ Hydrohydrobytic is trans inconstrain K100         1.2         0.001           Q05400         ERFF4A         Eaturyrtic initiation facrore KAII         1.2         0.011           Q12711         CDKNA         Peric/RA/ Hydrobytic is trans inohonoly A         1.2         0.012           Q12741         QRLCHI         Glutamine chi protein 1         1.2         0.012           Q17741         HMCBI         High mobility group rotein 1         1.2         0.022           Q17741         HMCBI         High mobility group rotein 1         1.2	LYP.A1.       Acylprotech thloserterse 1       1.3       0.04       PRDX5         IDIDDS       ILalcad debalgence like hydrale admin.containing 5       1.2       0.001       PRDX5         GSTP1       Gluathinos Stranferase P       1.2       0.001       PRDX5         IBRCH       3-brd/oryiceburyth-CoA hydrolas. mitochondrial       1.2       0.001       PRDX5         RHOA       Transforming protein RhoA       1.2       0.001       PRDX5         RHOA       Transforming protein RhoA       1.2       0.001       PRDX5         RHS7       285 ribosomal protein S-7, mitochondrial       1.2       0.008       PRDX5         RRP37       285 ribosomal protein S-7, mitochondrial       1.2       0.008       PRDX5         RRP44       Prem RA Approcessing factor 40-banolog A       1.2       0.008       PRDX5         RRP44       Prem RA Approcessing factor 40-banolog A       1.2       0.001       PRDX5         RRP44       Prem RA Approcessing factor 40-banolog A       1.2       0.011       PRDX5         RRP44       Adaryscic initiation factor 41-B1       1.2       0.021       PRDX5         RRCH1       Glutamine-circh protein 1       1.2       0.021       PRDX5         RAKA       Amacin As	Q9Y394	DHRS7	Dehydrogenase/reductase SDR family member 7	1,3	0,035	PRDX5
QBEXPT         HD1D5         Halocial dishalognase like hydrolase donain containing 5         1,2         0           Q14694         USP10         Ubiquitin carboxyl cranufastay for 10         1,2         0,001           Q41694         USP10         HB1CH         3-byd axisylase intrakay for an intrakay	HDHD5       Haloard dehalogenze like pirolaze domain containing 5       1,2       0       PRDX5         GSTP1       Gluchtions 5-transferse P       1,2       0,001       PRDX5         LBPG1       Jaydroxyiolowyi-CoAlydrodzas 10       1,2       0,001       PRDX5         RPL30       605 ribosonal precin L30       1,2       0,001       PRDX5         RHOA       Transforming procein RhoA       1,2       0,001       PRDX5         RHS7       285 ribosonal procein S, micechondral       1,2       0,001       PRDX5         RHS7       285 ribosonal procein S, micechondral       1,2       0,007       PRDX5         RHS7       285 ribosonal procein S, micechondral       1,2       0,007       PRDX5         RHS7       285 ribosonal procein S, micechondral       1,2       0,007       PRDX5         RL11       Guernen RNA processing factor 40 homolog A       1,2       0,007       PRDX5         CDNN2A       Cyclin-degenoder Kinase inhibitor 2A       1,2       0,017       PRDX5         GALK1       Galaexin instain inhibitor 2A       1,2       0,022       PRDX5         GALK1       Galaexin instain inhibitor 2A       1,2       0,032       PRDX5         GALK1       Galaexin instainhibitor 2A <t< td=""><td>E5RGR0</td><td>LYPLA1</td><td>Acyl-protein thioesterase 1</td><td>1,3</td><td>0,041</td><td>PRDX5</td></t<>	E5RGR0	LYPLA1	Acyl-protein thioesterase 1	1,3	0,041	PRDX5
P0221         GSTP         Ginzhions Armafrang P         1,2         0,001           Q16494         USP(0)         Ubiquino chorsy terminal phytohas 10         1,2         0,001           QRNYI         HIGCH         3hythoxytioburyty Cohythytas, mitochondrial         1,2         0,001           P6356         RH 50         Transforming protein RboA         1,2         0,001           P6357         FAN         Fariy skid synthase         1,2         0,001           Q15455         TRHP13         Parkytes Chorspin forcin 21 homolog         1,2         0,008           Q15450         RKBP3         Perkid-projed lei-trans inomeras FRB73         1,2         0,001           Q15400         PRH7640         PressRNA-processing factor 40 homolog A         1,2         0,011           Q12414         LHKAP3         D4 sing homoling group protein B         1,2         0,012           Q12414         GRICHI         Glatamise indhitoir 2A         1,2         0,023           Q1714         HKGB1         High mobiling group protein B         1,2         0,023           Q1724         HKAS1         Anaccin A5         1,2         0,033           Q17550         GALKI         Galaxinsa         1,2         0,032           Q175	GSTP1         Claratione Sranderase P         1.2         0.01         PRDXS           USP10         Ublaquita cabous learnial liphosides 10         1.2         0.01         PRDXS           HIBCH         Hydroxynsburyn-PCaA bydrolase, mixolondral         1.2         0.01         PRDXS           RH0A         Transforming protein RboA         1.2         0.01         PRDXS           SRMD         Fatry acid ynchase         1.2         0.005         PRDXS           FASN         Fatry acid ynchase         1.2         0.006         PRDXS           RRP3         285 ribosomal protein RboA         1.2         0.008         PRDXS           RRP4         Predisd'prod/y clast nationeraser RBT3         1.2         0.008         PRDXS           RRP4A         Predisd'prod/y clast nationeraser RBT3         1.2         0.017         PRDXS           CDKNAA         Cyclin dependent kinase inhibitor 2A         1.2         0.017         PRDXS           CDKNAA         Cyclin dependent kinase inhibitor 2A         1.2         0.027         PRDXS           ADKCHI         1.2         0.037         PRDXS         ADXA         ADXA         ADXA         ADXA         ADXA         ADXA         ADXA         ADXA         ADXA         ADXA<	Q9BXW7	HDHD5	Haloacid dehalogenase-like hydrolase domain-containing 5	1,2	0	PRDX5
QH694         US90         Ubiquitin carboxyl-crimical hydrolase 10         1.2         0.001           PR2588         RPL30         668 ribosomal protein L30         1.2         0.001           PR258         RH10A         Transforming protein RhoA         1.2         0.001           PR257         FAN         Farty acid synthase         1.2         0.0061           QV268         TR1P13         Pachytene checkpoint protein 2 homolog A         1.2         0.0086           QV278.7         MR187         Pergriticyl protein 2 homolog A         1.2         0.0081           QV278.0         RR187.40         Pergriticyl protein 2 homolog A         1.2         0.0081           QV278.0         RR187.40         Processing factor 3 homolog A         1.2         0.0081           QV274.0         RR147.42         Eukaryotic initiation factor 4 A11         1.2         0.012           QV270.4         RR147.42         Calcarabinase         1.2         0.025           QV271.4         RR147.43         Anaxa 5         Anaxa 5         0.022           QV276.4         HM169.61         L         0.02         0.025           QV273.5         SACML1         Pacarobin 1         L         0.012           QV273.5 <td< td=""><td>USPID         Ubaptin carbon-jereminal hydrolase in         1.2         0.001         PRDXS           RPL30         605 ribosomal protein L30         1.2         0.001         PRDXS           RPL30         605 ribosomal protein L30         1.2         0.001         PRDXS           RPL30         Fatary acid yrnhase         1.2         0.001         PRDXS           RPL30         Fatary acid yrnhase         1.2         0.001         PRDXS           RPL31         Pachytene checkpoint protein S. mitochondrial         1.2         0.008         PRDXS           RRP30         Peptid/probyl cistrans iomerase FKB73         1.2         0.008         PRDXS           RRP40A         Personal protein S. mitochondral         1.2         0.014         PRDXS           QRICH1         Gluzanine-rich protein 1         1.2         0.014         PRDXS           QRICH1         Gluzanine-rich protein 1         1.2         0.022         PRDXS           GALK1         Galaxchinase         1.2         0.023         PRDXS           SACML         Photophatylinostol-3-phophatase SAC1         1.2         0.031         PRDXS           SACML         Photophatase TGA         1.1         0.017         PRDXS           SACATA</td><td>P09211</td><td>GSTP1</td><td>Glutathione S-transferase P</td><td>1,2</td><td>0,001</td><td>PRDX5</td></td<>	USPID         Ubaptin carbon-jereminal hydrolase in         1.2         0.001         PRDXS           RPL30         605 ribosomal protein L30         1.2         0.001         PRDXS           RPL30         605 ribosomal protein L30         1.2         0.001         PRDXS           RPL30         Fatary acid yrnhase         1.2         0.001         PRDXS           RPL30         Fatary acid yrnhase         1.2         0.001         PRDXS           RPL31         Pachytene checkpoint protein S. mitochondrial         1.2         0.008         PRDXS           RRP30         Peptid/probyl cistrans iomerase FKB73         1.2         0.008         PRDXS           RRP40A         Personal protein S. mitochondral         1.2         0.014         PRDXS           QRICH1         Gluzanine-rich protein 1         1.2         0.014         PRDXS           QRICH1         Gluzanine-rich protein 1         1.2         0.022         PRDXS           GALK1         Galaxchinase         1.2         0.023         PRDXS           SACML         Photophatylinostol-3-phophatase SAC1         1.2         0.031         PRDXS           SACML         Photophatase TGA         1.1         0.017         PRDXS           SACATA	P09211	GSTP1	Glutathione S-transferase P	1,2	0,001	PRDX5
QNVTY1         HIICH         3-bydroxytokuryy1CoA bydrózse, minochondrial         1.2         0.001           PR2888         RH.50         Transforming protein KboA         1.2         0.001           Ph9327         FAN         Farsy sid synthase         1.2         0.001           QV2848         MKP7         285 fibesomal protein 57, micoChondrial         1.2         0.007           QV2847         MKP7         285 fibesomal protein 57, micoChondrial         1.2         0.008           QV2849         MKP7         285 fibesomal protein 57, micoChondrial         1.2         0.008           QV2840         PErddl-Protein Chornelog A         1.2         0.008           QV2424         EIF4A2         Caluration Christian factor 40 homolog A         1.2         0.011           QV27LA         QRICHI         Glaturation-factor 4A-VI         1.2         0.021           QV27LA         QRICHI         Glaturation-factor 4A-VI         1.2         0.022           QV75A         ANXA5         Annexin A5         1.2         0.023           QV75A         ANXA5         Annexin A5         1.2         0.033           QV333         GBP1         Ra GTPace activiring protein binding protein 1         1.2         0.033           QV33	HIBCH         3-bylanystohurypt-CaA bylardase, mitochondrial         1.2         0.001         PRDX5           RPL30         665 ribosomal protein RbaA         1.2         0.001         PRDX5           FASN         Fatry acid synthase         1.2         0.001         PRDX5           FASN         Fatry acid synthase         1.2         0.006         PRDX5           RRPT3         285 ribosomal protein Sr, intochondrial         1.2         0.008         PRDX5           FRP30         Perptish-perolic trans.intochondrial         1.2         0.008         PRDX5           CDKN2A         Cyclin dependent kinase inhibitor 2A         1.2         0.011         PRDX5           CDKN2A         Cyclin dependent kinase inhibitor 2A         1.2         0.017         PRDX5           GAIKI         Gilatarokinerikon facer 4A-11         1.2         0.017         PRDX5           GAIKI         Gilatarokinerikon facer 4D         1.2         0.025         PRDX5           GAIKI         Gilatarokinerikon facer 4D         1.2         0.032         PRDX5           SACMIL         Phosphatity intoid-3-phosphatase SAC1         1.2         0.032         PRDX5           SACMIL         Phosphatity intoid-3-phosphatase SAC1         1.1         0.01         P	O14694	USP10	Ubiquitin carboxyl-terminal hydrolase 10	1.2	0,001	PRDX5
QCI:1.1         IPS         Optimization         IP         Optimization           P6388         RPL30         605 thoosand protein L30         1.2         0.001           P6386         RH0A         Transforming pretein RhoA         1.2         0.001           Q15645         TLNP13         Pachytene checkpoint protein 2 homolog         1.2         0.006           Q272R.3         MRRS7         285 ribosand protein 7, Sinchechadrial         1.2         0.008           Q0688         FKBP3         Peptish/proyl cit-trans ionerase FKBP3         1.2         0.001           Q14240         Elf+A.2         Eukaryotic initiation factor 4A-11         1.2         0.011           Q17C4         HMCR1         Clumanine-rich protein 1         1.2         0.022           Q17C4         HMCR1         Halp conduity gooup protein B1         1.2         0.022           Q17S4         HMCR1         Hancein AS         1.2         0.025           Q07S5         QANASA         Annexin AS         1.2         0.022           Q17S4         HMCR1         Hancein Associant protein 1         1.2         0.033           Q1323         GBP1         Ra SCT Prose-schafterican binotion protein 1         1.2         0.031           Q1323<	RPL30         605 ribosani protein RhoA         1.2         0.001         PRDS5           RH0A         Transforming protein RhoA         1.2         0.001         PRDS5           RH0A         Transforming protein RhoA         1.2         0.001         PRDS5           RH71         Pachytene checkpoint protein RhoA         1.2         0.001         PRDS5           RR757         285 ribosani protein Rhondy a         1.2         0.008         PRDS5           FR893         Peptidy probl cistrans homerase FKB73         1.2         0.008         PRDS5           CRN2A         Cyclin drependen thrase inhibitor 2A         1.2         0.011         PRDS5           QRICH1         Glatzoninza         Galactokinza         1.2         0.017         PRDS5           CRNXA         Cyclin drependen thrase inhibitor 2A         1.2         0.017         PRDS5           QRICH1         Galactokinza         1.2         0.017         PRDS5           CALKI         Galactokinza         1.2         0.025         PRDS5           CALKI         Galactokinza         1.2         0.032         PRDS5           GARI         Ra GTPus-activiting protein fal         1.2         0.033         PRDS5           GARI <t< td=""><td>O6NVY1</td><td>HIRCH</td><td>3-bydroxyisobutyryl-CoA bydrolase mitochondrial</td><td>1.2</td><td>0.001</td><td>PR DX5</td></t<>	O6NVY1	HIRCH	3-bydroxyisobutyryl-CoA bydrolase mitochondrial	1.2	0.001	PR DX5
Packase         N.1.20         Both Robating protein Roba         1.2         0.001           P49352         FASN         Fatty acid synthase         1.2         0.001           P49327         FASN         Fatty acid synthase         1.2         0.006           QV2EA9         MRPS7         288 ribosomal protein S7, mitochondrial         1.2         0.007           QV2EA9         MRPS7         288 ribosomal protein S7, mitochondrial         1.2         0.008           QV2EA9         MRPS7         288 ribosomal protein S7, mitochondrial         1.2         0.008           QV2EA0         PEPidd/Approtein S7, mitochondrial         1.2         0.001           QV2EA0         PEPidd/Approtein S7, mitochondrial         1.2         0.001           QV2EA0         Optile dependent linase inhibitor 2A         1.2         0.012           QV2TA1         CRNNAA         Ancein A5         1.2         0.022           QV3T35         GALKI         Galactokinase         1.2         0.032           QV3T35         ADXAM         Ancein A5         1.2         0.032           QV3S8         TIGAR         Frances-2:chiphophatase SAC1         1.0         0.01           QV3S8         TIGAR         Frances-2:chiphophatase TIGAR	NLD:0         bit of modeling preterin Robot         1.2         0.001         PRLDX5           FASN         Fatz sticl synthate         1.2         0.001         PRLDX5           FASN         Fatz sticl synthate         1.2         0.005         PRLDX5           FASN         Fatz sticl synthate         1.2         0.006         PRLDX5           MRPS7         285 ribosomal protein S, incohendrial         1.2         0.008         PRLDX5           FRBP3         Peptidy-peptic/terms isomerase FRB73         1.2         0.011         PRLDX5           CDKN2A         Cyclin dependent kinase inhibitor 2A         1.2         0.017         PRDX5           GALK1         Galactokinase         1.2         0.025         PRDX5           GALK1         Galactokinase         1.2         0.025         PRDX5           GALK1         Galactokinase         1.2         0.025         PRDX5           SACML1         Phosphatitylinostol 3-phosphate SAC1         1.2         0.025         PRDX5           SACML2         DPRDY1T Brankosca 2         1.1         0         PRDX5           SACML3         Aprest praintylinostola 3-phosphate SAC1         1.2         0.032         PRDX5           SACML4         Model Shobosmal	D(2888	P DI 20	(08 ribecomal protein L 20	1.2	0,001	DP DV5
PH358         NLVA         Instatorming protein Adox         1.2         0,001           Q15645         TR/P13         Packytene checkpoint protein 2 homolog         1.2         0,006           Q272R.9         MRPS7         285 riboscomal protein 5, "incohecoharial         1.2         0,007           Q00688         FRB73         Pepridyl-prolyl cist trans ionersare FRB73         1.2         0,008           Q12420         El FA2         Exharyoric initiation factor 4AII         1.2         0,011           P42711         CDKN2A         Cyclin-dependent kinase inhibitor 2A         1.2         0,012           Q1714.4         QRICHI         Glutarnine rich protein 1         1.2         0,012           Q1774.4         HMCBI         High mobility group protein B1         1.2         0,022           P08758         ANXA5         Anneein A5         1.2         0,023           Q87075         SACMLI         Phoophatase SACI         1.2         0,033           Q98W92         TARS2         Threorine-rRNA ligge, mitochondrial         1.2         0,033           Q98W92         TARS2         Threorine-rRNA ligge, mitochondrial         1.1         0,001           Q9784         SLC25A         ADP/ATP transloceas         1.1         0,001	ATRA         Instruction         1.2         0.001         PRL03S           FASN         Farty acid synchrosis         1.2         0.001         PRL03S           TRIP13         Pachyreac checkpoint protein 2 homolog         1.2         0.006         PRL03S           RRP57         285 ribosomal protein 57, mitochondrial         1.2         0.008         PRD05S           PRFF40A         PremRN-Approtein Sing struction homolog 4         1.2         0.001         PRD05S           QRICH1         Gluzamine-rich protein 1         1.2         0.017         PRD05S           QRICH1         Gluzamine-rich protein 1         1.2         0.017         PRD05S           QRICH1         Gluzamine-rich protein 1         1.2         0.017         PRD05S           ANXA5         Annexin A5         1.2         0.022         PRD3S           SACML1         Phosphatidylinositol-3-phosphatase SAC1         1.2         0.032         PRD3S           SIZCSA5         ADP/AT Prandocase 2         1.1         0.01         PRD3S           SIZCSA5         ADP/AT Prandocase 2         1.1         0.001         PRD3S           Tyrosine-4RNA ligase, mitochondrial         1.1         0.001         PRD3S           SIGA5         ADP/AT Prand	P(159)	RTL30	Transforming protein E50	1,2	0,001	PRDA)
P4932         PASN         Patry acid synthase         1,2         0,001           QS565         TRUP13         Packytene chckpoint protein 2 homolog         1,2         0,006           QV2R2         MRN7         285 ribosomal protein 57, mitochondrial         1,2         0,006           QV2R40         MRN7         285 ribosomal protein 57, mitochondrial         1,2         0,008           QV5400         PRP40A         Pre mRNA processing factor 40 homolog A         1,2         0,011           P1271         CDKN2A         Cyclin dependent tinates inhibitor 2A         1,2         0,012           Q2TAL8         QRICH         Glatcokinase         1,2         0,021           Q3TS3         GALKI         Galacokinase         1,2         0,023           Q9N756         GALKI         Galacokinase         1,2         0,032           Q9N757         SACMIL         Phosphatidylinostoi-3phospharas SAC1         1,2         0,032           Q9N838         TRGAR         Precise-2c Alia         1,4         0,001           Q9N242         TARS2         Threcone-2c Aliagas, mitochondrial         1,1         0,001           Q9N288         TIGAR         Fraccos-2c Aliagas, mitochondrial         1,1         0,001 <td< td=""><td>PASN         Fairy add ynthase         1.2         0.001         PRD33           TRIP13         Pachytres checkpoint protein 2 homolog         1.2         0.006         PRD35           FRBP3         Pstidyl Fopdyl icrams insomers rRIP3         1.2         0.008         PRD35           FRBP3         PremRNA processing factor 40 homolog A         1.2         0.014         PRD35           CDKN2A         Cyclins-dependent kinase inhibitor 2A         1.2         0.014         PRD35           CDKN2A         Cyclins-dependent kinase inhibitor 2A         1.2         0.014         PRD35           CDKN1A         Galaxrotic inhizitor factor 4A 01         1.2         0.027         PRD35           GALK1         Galaxrotic inhizitor factor 4A 01         1.2         0.025         PRD35           GALK1         Galaxrotic inhizitor factor 4A 01         1.2         0.025         PRD35           SACML1         Phighylephyletylephy</td><td>P61586</td><td>KHOA</td><td>Iransforming protein KhoA</td><td>1,2</td><td>0,001</td><td>PRDX5</td></td<>	PASN         Fairy add ynthase         1.2         0.001         PRD33           TRIP13         Pachytres checkpoint protein 2 homolog         1.2         0.006         PRD35           FRBP3         Pstidyl Fopdyl icrams insomers rRIP3         1.2         0.008         PRD35           FRBP3         PremRNA processing factor 40 homolog A         1.2         0.014         PRD35           CDKN2A         Cyclins-dependent kinase inhibitor 2A         1.2         0.014         PRD35           CDKN2A         Cyclins-dependent kinase inhibitor 2A         1.2         0.014         PRD35           CDKN1A         Galaxrotic inhizitor factor 4A 01         1.2         0.027         PRD35           GALK1         Galaxrotic inhizitor factor 4A 01         1.2         0.025         PRD35           GALK1         Galaxrotic inhizitor factor 4A 01         1.2         0.025         PRD35           SACML1         Phighylephyletylephy	P61586	KHOA	Iransforming protein KhoA	1,2	0,001	PRDX5
Q1565         TRIP13         Peckprene checkpoint protein 2 homolog         1,2         0,006           Q002R2         MR P57         285 ribosomal potein 57, micehondrial         1,2         0,008           Q00588         FK BP3         Pepridylprodyl cistrans isomerase FKBP3         1,2         0,008           Q14240         EFKA2         Exkaryotic initiation factor 40 homolog A         1,2         0,011           P42771         CDKN2A         Cyclin-dependent kinase inhibitor 2A         1,2         0,012           QTTAL8         QRLC111         Glutamine rich protein 1         1,2         0,025           P35750         CALK1         Galaccolinase         1,2         0,025           QNTTG         SACML1         Palsorial phosphatase SAC1         1,2         0,025           Q98W92         TAR52         Threonine-rRNA ligate, mitochondrial         1,2         0,033           Q98W92         TAR52         Threonine-rRNA ligate, mitochondrial         1,1         0,001           Q97S78         RPL4         60 ribosomal poteins TA         1,1         0,001           Q97S45         RPL4         60 ribosomal poteins TA         1,1         0,001           Q97S45         RPL4         60 ribosomal potesin L5         1,1         0,00	TRIP13       Pactyresc checkpoint protein 2 homolog       1.2       0.006       PRDS5         MRP57       285 ribosonal protein 57, mitochondrial       1.2       0.008       PRDS5         PRFH0A       Prem RNA Processing factor 40 homolog A       1.2       0.008       PRDS5         EIF+A2       Eakaryotic initiation factor 4AII       1.2       0.014       PRDS5         CDKN2A       Cyclini-dependent kinase inhibitor 2A       1.2       0.014       PRDS5         CDKN2A       Cyclini-dependent kinase inhibitor 2A       1.2       0.022       PRDS5         CAIKAI       Galaxanikarase       1.2       0.022       PRDS5         SACMIL       Phospharitifyinositol-3-phospharase SACI       1.2       0.025       PRDS5         G3BP1       Ras GTPase-activating protein-binding protein 1       1.2       0.031       PRDS5         G3BP1       Ras GTPase-activating protein-binding protein 1       1.2       0.033       PRDS5         G1AKS2       ThreonineRNA higase, mitochondrial       1.1       0.001       PRDS5         G1AKA       Gobspondurates TIGAR       1.1       0.001       PRDS5         SOKD       Sorbiciol delydrogenac       1.1       0.001       PRDS5         SPK1       Protezsome assenbl	P49327	FASN	Fatty acid synthase	1,2	0,001	PRDX5
QPU2R9         MR P57         28 stribosomal protein S7, mitochondrial         1,2         0,007           QP00688         FK BP3         1,2         0,008           Q75400         PR DF40A         Pre-mR NA-processing factor 40 homolog A         1,2         0,001           Q1240         El F4A2         Eukaryotic initiation factor 4A:II         1,2         0,011           Q2TTC4         QR ICH1         Glutamine-rich protein 1         1,2         0,012           QTTC4         HM GB1         High mobility group protein B1         1,2         0,022           PS750         GALK1         Galactokinase         1,2         0,022           QPS754         ANXA5         Annexin A5         1,2         0,025           QPN715         SACMLL         Phosphatich/Insorting protein 1         1,2         0,032           QPBW92         TAKS2         Threonine-refNA liggs, mitochondrial         1,2         0,031           QPN24         TAKS2         Threonine-refNA liggs, mitochondrial         1,1         0,001           QPN24         TAKS2         Threonine-refNA liggs, mitochondrial         1,1         0,001           QPN24         TAKS2         Threonine-refNA liggs, mitochondrial         1,1         0,001           QPN28	MRPS         285 ribosomal protein SZ mitochondrial         1.2         0.007         PRDSS           FKBP3         Depuids/pop/text raras isomerars FKBP3         1.2         0.008         PRDXS           EIFA42         Endarrotic initiation facor 4-AUI         1.2         0.014         PRDSS           CDKN2A         Cyclin-dependent kinase inhibitor 2A         1.2         0.014         PRDSS           CDKN2A         Cyclin-dependent kinase inhibitor 2A         1.2         0.012         PRDSS           GALKI         Galaxotic kinitation facor 4A-OII         1.2         0.025         PRDSS           GALKI         Galaxotic kinitation facor 4A-OII         1.2         0.025         PRDSS           SACMIL         Phophidiylinositol-3-phopharas ACI         1.2         0.031         PRDSS           SACMIL         Phophidiylinositol-3-phopharas ACI         1.2         0.032         PRDSS           SILC25AS         ADP/ATP translocase 2         NRDS         1.1         0.001         PRDSS           SILC25AS         ADP/ATP translocase 2         NRDS         1.1         0.001         PRDSS           SORD         Soribonand protein L4         1.1         0.001         PRDSS           SORD         Soribonand protein L5A         1.1 <td>Q15645</td> <td>TRIP13</td> <td>Pachytene checkpoint protein 2 homolog</td> <td>1,2</td> <td>0,006</td> <td>PRDX5</td>	Q15645	TRIP13	Pachytene checkpoint protein 2 homolog	1,2	0,006	PRDX5
Q0068         FK BP3         Pepridy/proph/icit-trans ionerase FK BP3         1,2         0,008           Q14240         EIF4A2         Eakaryotic initiation factor 4A-II         1,2         0,011           P4271         CDKN2A         Cyclin-dependent kinass inhibitor 2A         1,2         0,011           Q2TALS         QRICH1         Glutaminerich protein 1         1,2         0,017           QSTTC4         HMGB1         High mobility group protein B1         1,2         0,025           P05750         GALKI         Galexchinase         1,2         0,025           QWTJ5         SACM1L         Phosphradylinosito.3-phospharase SAC1         1,2         0,031           Q13283         G3BP1         Ras GTPs-accitrating protein 1         1,2         0,031           Q98092         TAKS2         ThreoninRNA kingase, nitochondrial         1,1         0,001           Q97578         RPL4         60 Stribosomal protein 1.4         1,1         0,001           Q97824         TAKS2         ThreoninRNA kingase, nitochondrial         1,1         0,001           Q9724         YAKS2         ThrotinRNA kingase, nitochondrial         1,1         0,001           Q97858         PKL         ATP-dependente /phosphortextokinase, inever type         1	FKBP3         PeptidyLprob/f cir-maxis ionerzse FKBP3         1,2         0,008         PRDX5           PRFH40A         Pre-mRNA-processing factor 40-h0molog A         1,2         0,011         PRDX5           CDKN2A         Cyclin-dependent kinase inhibitor 2A         1,2         0,012         PRDX5           CDKN2A         Cyclin-dependent kinase inhibitor 2A         1,2         0,017         PRDX5           CMRGHI         Glutamine-rich protein B1         1,2         0,017         PRDX5           CALK1         Galactolinase         1,2         0,025         PRDX5           ANXA5         Annexin A5         1,2         0,03         PRDX5           SACM1L         Phosphatrighinostol-3-phosphazes SAC1         1,2         0,03         PRDX5           G3BP1         Ras GTPase-activating protein-binding protein 1         1,2         0,03         PRDX5           SIC25A5         ADP/ATP translocase 2         1,1         0         PRDX5           SIC25A5         ADP/ATP translocase 2         1,1         0,001         PRDX5           SIC26A5         ATP dependent 5-phosphostares TIGAR         1,1         0,001         PRDX5           SIC26A5         ADP/ATP translocase 2         1,1         0,001         PRDX5 <t< td=""><td>Q9Y2R9</td><td>MRPS7</td><td>28S ribosomal protein S7, mitochondrial</td><td>1,2</td><td>0,007</td><td>PRDX5</td></t<>	Q9Y2R9	MRPS7	28S ribosomal protein S7, mitochondrial	1,2	0,007	PRDX5
075400         PR Fei0A         Pre-mRNA processing factor 40 homolog A         1,2         0.001           9124240         EIFsA2         Endstroytic initiation forces 4A-II         1,2         0.011           912771         CDKN2A         Cyclin-dependent kinase inhibitor 2A         1,2         0.012           9217C4         HM GBI         High mobility group protein B1         1,2         0.022           951570         GALK1         Galacokinase         1,2         0.022           908738         ANXA5         Annexin A5         1,2         0.023           Q13283         G38P1         Ras GT Pase activating protein b1         1,2         0.031           Q13283         G38P1         Ras GT Pase activating protein b1         1,2         0.032           Q9W922         TARS2         Threconine-relNA ligase, mitochondraf         1,1         0.001           Q9K924         TGAR         Fractose 2,4-bisphosphatase TGAR         1,1         0.001           Q9X24         Yenks         Tortion-relNA ligase, mitochondraf         1,1         0.001           Q9X24         Yenks         Tortion-relNA ligase, mitochondraf         1,1         0.001           Q9X54         PFKL         ATP-dependent 6-phosphofractokinase, liver type         1,1	PR.PF40A         Pre-mR.NA-processing factor 40 homolog A         1.2         0.008         PRDXS           EIFAA2         Exaksrytein initiation factor 4A-HI         1.2         0.014         PRDXS           CDKN2A         Cyclin-dependent kinase inhibitor 2A         1.2         0.012         PRDXS           QRICHI         Glutamine rich protein 1         1.2         0.022         PRDXS           GALKI         Galactokinase         1.2         0.023         PRDXS           SACMIL         Pophysitrkylinositol-3-phospharas 5AC1         1.2         0.03         PRDXS           G3BP1         Ras GTPas-activaling protein 1         1.2         0.03         PRDXS           SACMIL         Phosphatirkylinositol-3-phospharas 5AC1         1.2         0.03         PRDXS           SACAS         ADPATP translocase 2         1.1         0.01         PRDXS           SIC25A5         ADPATP translocase 2         1.1         0.01         PRDXS           Yrosine-r&NA ligase, mitochondrial         1.1         0.001         PRDXS           MASZ         Tyrosine-r&NA ligase, mitochondrial         1.1         0.001         PRDXS           SRG         Sorbiol didylogenase         1.1         0.001         PRDXS           SRD	Q00688	FKBP3	Peptidyl-prolyl cis-trans isomerase FKBP3	1,2	0,008	PRDX5
Q14200       EIFA42       Evaluation factor AAT       1.2       0.011         P42771       CDKN2A       Cyclin-dependent kinase inhibitor 2A       1.2       0.014         Q2TAL&       QRECH1       Clutamine-rich protein 1       1.2       0.022         QST7C4       HMGB1       High mobility group protein B1       1.2       0.025         QST7C4       HMGB1       High mobility group protein B1       1.2       0.025         QST7T5       SACM1L       Phospharize SAC1       1.2       0.032         QPNT95       SACM1L       Phospharize group protein 1       1.2       0.033         QPSW2       TARS2       Throonine-rRANA ligase, mitochondrial       1.2       0.031         QPSW2       TARS2       Throonine-rRANA ligase, mitochondrial       1.1       0.001         QPSV24       YARS2       Tyrosine-rRNA ligase, mitochondrial       1.1       0.001         QPSV24       YARS2       Tyrosine-rGNA ligase, mitochondrial </td <td>EIFA2         Eakryotic initiation Eacro 4A-H         1.2         0.014         PRDX5           CDKN2A         Cyclin-dependent kinase inhibitor 2A         1.2         0.017         PRDX5           CMRGHI         Glutamine-rich protein B1         1.2         0.022         PRDX5           ANKA5         Anesin A5         1.2         0.025         PRDX5           SACMIL         Phosphatidylinositol-3-phosphatase SAC1         1.2         0.032         PRDX5           SACMIL         Phosphatidylinositol-3-phosphatase SAC1         1.2         0.032         PRDX5           SACMIL         Phosphatidylinositol-3-phosphatase SAC1         1.2         0.032         PRDX5           SACMA1         Ass GTPas-activating protein infing protein 1         1.2         0.032         PRDX5           SIC2A5A         ADP/ATP translocase 2         1.1         0.001         PRDX5           TridGAR         Fructose 2.6-biphosphatase TIGAR         1.1         0.001         PRDX5           SIC2A5         Arborente chAN ligase, micochondrial         1.1         0.001         PRDX5           SICA6         Protessome assembly chaperone 1         1.1         0.001         PRDX5           SICA6         Protessome assembly chaperone 1         1.1         0.001</td> <td>O75400</td> <td>PRPF40A</td> <td>Pre-mRNA-processing factor 40 homolog A</td> <td>1,2</td> <td>0,008</td> <td>PRDX5</td>	EIFA2         Eakryotic initiation Eacro 4A-H         1.2         0.014         PRDX5           CDKN2A         Cyclin-dependent kinase inhibitor 2A         1.2         0.017         PRDX5           CMRGHI         Glutamine-rich protein B1         1.2         0.022         PRDX5           ANKA5         Anesin A5         1.2         0.025         PRDX5           SACMIL         Phosphatidylinositol-3-phosphatase SAC1         1.2         0.032         PRDX5           SACMIL         Phosphatidylinositol-3-phosphatase SAC1         1.2         0.032         PRDX5           SACMIL         Phosphatidylinositol-3-phosphatase SAC1         1.2         0.032         PRDX5           SACMA1         Ass GTPas-activating protein infing protein 1         1.2         0.032         PRDX5           SIC2A5A         ADP/ATP translocase 2         1.1         0.001         PRDX5           TridGAR         Fructose 2.6-biphosphatase TIGAR         1.1         0.001         PRDX5           SIC2A5         Arborente chAN ligase, micochondrial         1.1         0.001         PRDX5           SICA6         Protessome assembly chaperone 1         1.1         0.001         PRDX5           SICA6         Protessome assembly chaperone 1         1.1         0.001	O75400	PRPF40A	Pre-mRNA-processing factor 40 homolog A	1,2	0,008	PRDX5
P42771         CDKN2A         Cyclin-dependent kinase inhibitor 2A         1.2         0.014           Q2TAL48         QRICH1         Glutamine-rich protein 1         1.2         0.017           QTTC4         HIKGBH         High protein 1         1.2         0.025           P51570         GALK1         Galactokinase         1.2         0.025           QWT35         SANASA         Annesin AS         1.2         0.033           Q13283         G3BP1         Ras GTPase-activating protein binding protein 1         1.2         0.033           Q98W92         TARS2         Throonin-eRNA ligase, mitochondrial         1.2         0.031           Q98W82         TIGAR         Fructose-2,e-bisphosphatase TIGAR         1,1         0.001           Q97244         VARS2         Tyrosin-eRNA ligase, mitochondrial         1,1         0.001           Q97264         SORD         Sorbiol dehydrogenase         1,1         0.001           Q97264         SORD         Sorbiol dehydrogenase         1,1         0.001           Q97365         PSMG1         Protessome assembly chaperoae 1         1,1         0.007           Q13595         TRAZA         Transformer-2 protein honolog alpha         1,1         0.012           Q373	CDKN2A         Cyclin-dependent kinase inhibitor 2A         1,2         0,014         PRDX5           QRICH1         Glutzmine-rich protein 1         1,2         0,017         PRDX5           GALK1         Glatzenkinase         1,2         0,025         PRDX5           GALK1         Glatzenkinase         1,2         0,025         PRDX5           SACM11         Phosphatidylinositol-3-phospharase SAC1         1,2         0,033         PRDX5           G3BP1         Ras GTPas-activating protein-binding protein 1         1,2         0,033         PRDX5           SACM11         Phosphatidylinositol-3-phospharase SAC1         1,2         0,033         PRDX5           SIAC25A5         ADP/ATP translocase 2         1,1         0,011         PRDX5           Trosine-erKNA ligase, mitochondrial         1,1         0,001         PRDX5           Trosine-erKNA ligase, mitochondrial         1,1         0,001         PRDX5           PKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,001         PRDX5           SRG10         Protessome assembly chapterone 1         1,1         0,001         PRDX5           SRC24C         Protein transport protein Sc24C         1,1         0,012         PRDX5           T	O14240	EIF4A2	Eukarvotic initiation factor 4A-II	1.2	0,011	PRDX5
12.1.1       Optimizing the protein fails       1.2       0.017         QTTALS       QRICHL       Gluttamine-rich protein 1       1.2       0.022         QSTTC4       HMGBI       High mobility group protein B1       1.2       0.025         P08758       ANXA5       Annexin A5       1.2       0.025         QWTJ5       SACM1L       Phosphatidylinositol-3-phosphatase SAC1       1.2       0.033         Q13283       G3BP1       Ras CTPass-activating protein-binding protein 1       1.2       0.032         Q98W92       TAR52       ThreoninerRNA ligase, mitochondrial       1.2       0.033         Q91244       SLC25A5       ADP/ATP translocase 2       1.1       0.001         Q97824       TAR52       TrosinerRNA ligase, mitochondrial       1.1       0.001         Q97824       TAR52       Trosine-rRNA ligase, mitochondrial       1.1       0.001         Q97824       TAR52       Trosine-rRNA ligase, mitochondrial       1.1       0.001         Q97824       TAR52       Trosine-rRNA ligase, mitochondrial       1.1       0.001         Q97824       YAR55A       GB Tobosomal protein L54       1.1       0.001         Q9785       SNG1       Proteasome assembly chaperone 1       1.1	CALLENT         Claim dependent and motion Data         1.2         0.017         PRDX3           HMGBI         High mobility group protein B1         1.2         0.025         PRDX5           CALKI         Galactohirase         1.2         0.025         PRDX5           ANXA5         Annexin A5         1.2         0.035         PRDX5           SACMIL         Phosphatidylinositol-3-phopharase SAC1         1.2         0.03         PRDX5           SACMIL         Phosphatidylinositol-3-phopharase SAC1         1.2         0.03         PRDX5           SIC23A5         ADP/A7D translocase 2         1.1         0         PRDX5           SIC23A5         ADP/A7D translocase 2         1.1         0         PRDX5           TGGAR         Fractose 2,6-biphopharase TIGA R         1.1         0.001         PRDX5           SVARS         Trostine-4RNA ligase, mitochondrial         1.1         0.001         PRDX5           SVARS         Trostine-4RNA ligase, mitochondrial         1.1         0.001         PRDX5           SVARS         Trostine-4RNA ligase, mitochondrial         1.1         0.001         PRDX5           SVARS         SockD         Sorbitol delydrogenas         1.1         0.001         PRDX5	P42771	CDKN2A	Cyclin-dependent kingse inhibitor 2 A	1.2	0.014	PR DX5
Q217LA         Q40X111         Guammerization protein B1         1,2         0,07           Q517C4         HMGB         High mobility group protein B1         1,2         0,025           P51570         GALK1         Galactokinase         1,2         0,025           Q9N7C4         ANXA5         Annexin A5         1,2         0,032           Q9BW92         TARS2         Threonin-rRNA ligax, mitochondrial         1,2         0,033           Q9BW92         TARS2         Threonin-eRNA ligax, mitochondrial         1,2         0,033           Q9BW92         TARS2         Threonin-eRNA ligax, mitochondrial         1,1         0,001           Q9N288         TIGAR         Fructose 2,6-bisphosphatase TIGAR         1,1         0,001           Q9N284         TIGAR         Fructose 2,6-bisphosphatase TIGAR         1,1         0,001           Q9N285         PFKL         ATP-depender 6 f-phosphortockinas, liver type         1,1         0,001           Q9N266         PSMG1         Proteasone assembly chaperone 1         1,1         0,007           Q0756         OSML         Softbosonal protein L25a         1,1         0,007           Q1555         TRA2A         Transformer-2 protein homolog alpha         1,1         0,01	QRLC111         Guidantier (n) protein 1         1,2         Quidantier (n) protein 3           HMGB1         High mobiling group protein B1         1,2         Quidantier (n) protein 3           GALK1         Galactokinase         1,2         Quidantier (n) protein 3         1,2         Quidantier (n) protein 3           SACM1L         Phospharddylinositol-3-phospharase \$AC1         1,2         Quidantier (n) protein 3         PRDX5           G3BP1         Ras GTPase-activating protein inform 1         1,2         Quidantier (n) protein 3         PRDX5           SLC25A5         ADP/ATP translocase 2         1,1         Quidantier (n) protein 4         1,1         Quidantier (N) PRDX5           TIGAR         Fructose 2,6-bisphospharase TIGAR         1,1         Quidantier (N) PRDX5         PRDX5           SRC2A5A         ADP/ATP translocase 2         1,1         Quidantier (N) PRDX5         PRDX5           TIGAR         Fructose 2,6-bisphospharase TIGAR         1,1         Quidantier (N) PRDX5         PRDX5           SRC4D         ATP-dependent 6-phosphortockinase, Invertype         1,1         Quidantier (N) PRDX5         PRDX5           SRAD         Sorbiol dehydrogenase         1,1         Quidantier (N) PRDX5         PRDX5           SRAD         Sorbiol dehydrogenase         1,1         Qu	02TAL8	OP ICH1	Clutamina rich protain 1	1.2	0.017	DP DV5
QD1/C4         Fight modulity group protein b1         1.2         0.025           P05750         GALKI         Galactockinase         1.2         0.025           P08758         ANXA5         Annexin A5         1.2         0.032           Q98TJ5         SACMIL         Phosphatrkylinositol-3-phospharase SAC1         1.2         0.032           Q98W92         TARS2         Threonine-tRNA ligase, mitochondrial         1.2         0.032           Q98W92         TARS2         Threonine-tRNA ligase, mitochondrial         1.1         0.001           Q9NQ88         TIGAR         Fractose-2,6-bisphospharase TIGAR         1.1         0.001           Q9Y224         YARS2         Trosine-tRNA ligase, mitochondrial         1.1         0.001           Q9Y24         YARS2         Trosine-tRNA ligase, mitochondrial         1.1         0.001           Q9Y24         YARS2         Trosine-tRNA ligase, mitochondrial         1.1         0.001           Q9Y25         YARS2         Trosine-tRNA ligase, mitochondrial         1.1         0.001           Q9Y24         YARS2         Trosine-tRNA ligase, mitochondrial         1.1         0.001           Q9Y25         SORD         Sorbitol dehydrogenase         1.1         0.001	HANGDI         High modility group protein D1         1,2         0,022         PRDX5           GALK1         Galactokinase         1,2         0,025         PRDX5           ANXA5         Annexin A5         1,2         0,035         PRDX5           SACMIL         Phosphards/inositol-3-phopharase SAC1         1,2         0,035         PRDX5           SCAMIL         Phosphards/inositol-3-phopharase SAC1         1,2         0,032         PRDX5           SCAMA         Anse GTPase-activating protein J         1,2         0,033         PRDX5           SCC25A5         ADP/A7D translocse 2         1,1         0         PRDX5           RPL4         608 ribosomal protein L4         1,1         0,001         PRDX5           YAR52         TreconinerRNA ligase, mitochondrial         1,1         0,001         PRDX5           PSMG1         Protexaome assembly chaperone 1         1,1         0,001         PRDX5           PSMG4         Protexaome assembly chaperone 1         1,1         0,001         PRDX5           SC24AC         Protein regulated inducer of neuric outgrowth 1         1,1         0,007         PRDX5           SL24AC         Transformer 2 protein homolog alpha         1,1         0,017         PRDX5 <tr< td=""><td>Q2IAL8</td><td>UNCRI</td><td>Util and the protein 1</td><td>1,2</td><td>0,017</td><td>PRDA)</td></tr<>	Q2IAL8	UNCRI	Util and the protein 1	1,2	0,017	PRDA)
PS15/0       GALK1       Galactoknase       1,2       0,025         QPNTJ5       SACMIL       Phosphatidylinositol3-phospharase SAC1       1,2       0,032         Q13283       G3BP1       Ras GTPase-activating protein-binding protein 1       1,2       0,032         Q13283       G3BP1       Ras GTPase-activating protein-binding protein 1       1,2       0,032         Q9BW92       TAR52       Threonine-tRNA ligase, mitochondrial       1,1       0,001         Q9NQ88       TIGAR       Fractose-2,6-bisphospharase TIGAR       1,1       0,001         Q9NQ88       TIGAR       Fractose-2,6-bisphospharase TIGAR       1,1       0,001         Q9NQ84       TIGAR       Fractose-2,6-bisphospharase TIGAR       1,1       0,001         Q9N284       TIGAR       Fractose-2,6-bisphospharase TIGAR       1,1       0,001         Q9N285       PKL       ATP-dependent 6-phosphartexet, liver trype       1,1       0,001         Q9N286       PSMG1       Proteasome assembly chaperone 1       1,1       0,003         Q00796       SORD       Sorbtol dehydrogenase       1,1       0,001         Q13395       TRA2A       Transformer-2 protein homolog alpha       1,1       0,01         Q13395       TRA2A	CALKI         Calactokinase         1,2         0,025         PRDX5           ANXA5         Annexin A5         1,2         0,035         PRDX5           SACMLI         Phosphatidyfinositol-sphorphatase SAC1         1,2         0,032         PRDX5           G3BP1         Ras GTPuse activating protein-binding portein 1         1,2         0,032         PRDX5           TARS2         Threonine-cRNA ligase, mitochondrial         1,2         0,033         PRDX5           SLC25A5         ADP/ATP translocase 2         1,1         0,001         PRDX5           TIGAR         Fractorese 2,6-bisphosphatase TIGAR         1,1         0,001         PRDX5           YARS2         Tyrosine-tRNA ligase, mitochondrial         1,1         0,001         PRDX5           PKL         ATP-dependent 6-phosphofractokinase, liver type         1,1         0,001         PRDX5           SRCAC         Protein transport protein Sc24C         1,1         0,001         PRDX5           SRC4C         Protein transport protein Sc24C         1,1         0,001         PRDX5           SL24C         Protein transport protein Sc24C         1,1         0,01         PRDX5           SL24C         Protein transport protein Sc24C         1,1         0,017         PRDX5 <td>Q51/C4</td> <td>HMGBI</td> <td>High mobility group protein B1</td> <td>1,2</td> <td>0,022</td> <td>PRDX5</td>	Q51/C4	HMGBI	High mobility group protein B1	1,2	0,022	PRDX5
P08758         ANXA5         Annexin A5         1,2         0.025           QPNT15         SACMIL         Phospharidylinositol-3-phosphatass SAC1         1,2         0.03           QJ3283         G3BP1         Ras GTPaxe-activating protein-binding protein 1         1,2         0.032           QPBW92         TARS2         Threonine-4RNA ligase, mitochondrial         1,1         0           P36578         RPL4         605 ribosomal protein L4         1,1         0.001           QPNQ88         TIGAR         Fructores-2.6 siphsphatast TIGAR         1,1         0.001           QP1224         YARS2         Tyrosine-4RNA ligase, mitochondrial         1,1         0.001           QP3758         PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0.001           QP376         SORD         Sorbirol dehydrogenase         1,1         0.003           Q00776         SORD         Sorbirol dehydrogenase         1,1         0.007           Q13595         TRA2A         Transformer-2 protein bonolog alpha         1,1         0.012           Q45795         MYO1B         Unconventional myosin-1b         1,1         0.012           Q45745         ZNF503         Zinc finger protein 503         1,1         0.012	ANXA5       Anexia A5       1,2       0.025       PRDX5         SACMIL       Phosphatidylinositol-3-phosphatase SAC1       1,2       0.032       PRDX5         G3BP1       Ras GTPase-activating protein-binding protein 1       1,2       0.032       PRDX5         SLC25A5       ADP/ATP randocase 2       1,1       0       PRDX5         TIGAR       Fructores 2,6-bisphosphatase TIGAR       1,1       0,001       PRDX5         TIGAR       Fructores 2,6-bisphosphatase TIGAR       1,1       0,001       PRDX5         SCRD       Sorbitol dehydrogenase intochondrial       1,1       0,001       PRDX5         SORD       Sorbitol dehydrogenase       1,1       0,001       PRDX5         SC24C       Protein-regulared inducer of neuric ourgrowth 1       1,1       0,011       PRDX5         SILRP       Grainine molegi alpha       1,1       0,012       PRDX5 <tr< td=""><td>P51570</td><td>GALK1</td><td>Galactokinase</td><td>1,2</td><td>0,025</td><td>PRDX5</td></tr<>	P51570	GALK1	Galactokinase	1,2	0,025	PRDX5
QPNTJ5         SACM11.         Phosphatidylinositol-3-phosphatase SAC1         1,2         0,03           QJB283         G3BP1         Ras CTPase-activating protein-binding protein 1         1,2         0,032           Q9BW92         TARS2         ThreoninetRNA ligase, mitochondrial         1,1         0           P05141         SLC25A5         ADP/ATP translocase 2         1,1         0,001           Q9NQ88         TIGAR         Furctose-2,6-bisphospharase TIGAR         1,1         0,001           Q9Y224         YARS2         Tyrosine-tRNA ligase, mitochondrial         1,1         0,001           Q9Y224         YARS2         Tyrosine-tRNA ligase, mitochondrial         1,1         0,001           Q9Y254         YARS2         Tyrosine-tRNA ligase, mitochondrial         1,1         0,001           Q9756         SORD         Sorbiol dehydrogenase         1,1         0,004           P18077         RPL35A         605 ribosonal protein L5a         1,1         0,001           G54531         SEC24C         Protein transport protein Sec24C         1,1         0,012           Q722248         GPRIN1         G protein-regulard inducer of neurite outgrowth 1         1,1         0,012           Q722245         GPRD1         Grometin-regulard inducer of	SACM11.         Phosphatidylinositol-3phosphatase SAC1         1,2         0.03         PRDX5           G3BP1         Ras GTDsze-activating protein-ibniding protein         1,2         0.032         PRDX5           TARS2         ThreoninetRNA ligase, mitochondrial         1,2         0.033         PRDX5           SLC2SA5         ADP/ATP translocase 2         1,1         0         PRDX5           TIGAR         Fructose-2,6-bisphosphatase TIGAR         1,1         0,001         PRDX5           YARS2         TyrosinetRNA ligase, mitochondrial         1,1         0,001         PRDX5           SKRD         ATP-dependent 6-phosphotyroructokinase, liver type         1,1         0,001         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,004         PRDX5           SRC2AC         Protein transport protein 52a         1,1         0,007         PRDX5           SLC2AC         Protein transport protein 52a         1,1         0,017         PRDX5           TRA2A         Transformer-2 protein homolog alpha         1,1         0,017         PRDX5           SLRP         SR A stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,017         PRDX5           SLRP         SR A stem-loop-interacting RNA-binding pro	P08758	ANXA5	Annexin A5	1,2	0,025	PRDX5
Q1328         G3BP1         Ras CTPase-activating protein-binding protein 1         1,2         0,032           Q9BW92         TAR52         Threonine-rtRNA ligase, mitochondrial         1,1         0           P36573         RPL4         605 ribosonal protein L4         1,1         0,001           Q9NQ88         TIGAR         Fractores-2.6-bisphospharase TIGAR         1,1         0,001           Q9Y24         YAR52         Tyrosine-rtRNA ligase, mitochondrial         1,1         0,001           Q9Y24         YAR52         Tyrosine-rtRNA ligase, mitochondrial         1,1         0,001           Q9Y24         YAR52         Tyrosine-rtRNA ligase, mitochondrial         1,1         0,001           Q9Y25         PSKIG         Porteasome assembly chaperone 1         1,0         0,003           Q00796         SORD         Sorbitol dehydrogenase         1,1         0,001           Q13595         TRA2A         Transformer-2 protein homolog alpha         1,1         0,012           Q13595         TRA2A         Transformer-2 protein homolog alpha         1,1         0,012           Q722K8         GPR1N1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,012           Q722K8         GPR1N1         G protein-regulated induce	G3BP1         RasCTPase-activating protein-binding protein 1         1,2         0,032         PRDXS           TARS2         Thronine-RNN ligase, mitochondrial         1,2         0,033         PRDXS           SLC25AS         ADP/ATP translocase 2         1,1         0         PRDXS           TICAR         Tructose 2,-obsphospharase TIGAR         1,1         0,001         PRDXS           YARS2         TyrosinetRNA ligase, mitochondrial         1,1         0,001         PRDXS           PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,001         PRDXS           SORD         Sorbitol dehydrogenase         1,1         0,001         PRDXS           SC24C         Protestim asport protein 5ce24C         1,1         0,001         PRDXS           MYO1B         Unconventional myosin-Ib         1,1         0,011         PRDXS           MYO1B         Unconventional myosin-Ib         1,1         0,012         PRDXS           ZIRPS03         Zinc finger protein 503         1,1         0,021         PRDXS           ZIRPS03         Zinc finger protein 503         1,1         0,021         PRDXS           ZNF503         Zinc finger protein 543         1,1         0,033         PRDXS <t< td=""><td>Q9NTJ5</td><td>SACM1L</td><td>Phosphatidylinositol-3-phosphatase SAC1</td><td>1,2</td><td>0,03</td><td>PRDX5</td></t<>	Q9NTJ5	SACM1L	Phosphatidylinositol-3-phosphatase SAC1	1,2	0,03	PRDX5
Q9BW92         TARS2         Threoninc-rRNA ligse, mitochondrial         1,2         0,033           P05141         SLC25A5         ADP/ATP translocase 2         1,1         0           P05478         RPL4         605 ribosonal protein 1.4         1,1         0,001           Q9Y024         YAR52         Tyrosine-rRNA ligse, mitochondrial         1,1         0,001           Q9Y224         YAR52         Tyrosine-recRNA ligse, mitochondrial         1,1         0,001           Q97565         PFKL         ATP-dependents f-phosphofructokinase, liver type         1,1         0,003           Q00796         SORD         Sorbitol dehydrogenase         1,1         0,004           P18077         RPL55A         605 ribosomal protein L55a         1,1         0,007           Q13595         TRA2A         Transforme-2 protein homolog alpha         1,1         0,012           Q72728         GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,012           Q9267T3         SLIRP         SR A stem-loop-interacting RNA-binding protein mitochondrial         1,1         0,023           Q9267T3         SLIRP         SR A stem-loop-interacting RNA-binding protein GI//G[S]/G[T] subunit beta-2         1,1         0,033           Q9267T3         <	TAR2       Threonine-cRNA ligase, mitochondrial       1,2       0,033       PRDX5         SLC25A5       ADP/ATP translocase 2       1,1       0,001       PRDX5         RPL4       605 ribosomal protein L4       1,1       0,001       PRDX5         TIGAR       Fructose-2,6-bisphosphatzse TIGAR       1,1       0,001       PRDX5         YAR52       Tyrosine-rRNA ligase, mitochondrial       1,1       0,001       PRDX5         SORD       ATP-dependent 6-phosphofructokinase, liver type       1,1       0,003       PRDX5         SORD       Sorbitol didyrdrogenase       1,1       0,004       PRDX5         SORD       Sorbitol didyrdrogenase       1,1       0,007       PRDX5         SEC24C       Protein transport protein Sec24C       1,1       0,01       PRDX5         AP2B1       AP2 complex subunit beta       1,1       0,01       PRDX5         MYOIB       Unconventional myosin-Ib       1,1       0,01       PRDX5         SLIRP       SRA stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,021       PRDX5         SUR503       Zine finger protein 503       1,1       0,032       PRDX5         NNNS       Salita acid synthase       1,1       0,031       <	Q13283	G3BP1	Ras GTPase-activating protein-binding protein 1	1,2	0,032	PRDX5
P05141SLC25A5ADP/ATP translocase 21,10P36578RPL460S ribosomal protein L41,10,001Q9NQ28TLGARFructose 2,6-bisphosphatase TLGAR1,10,001Q9N224YARS2Tyrosine-tRNA ligase, mitochondrial1,10,001Q97545PSMG1Protesamon assembly chaperone 11,10,001Q00756SORDSorbitoi dehydrogenase1,10,003Q00776SORDSorbitoi dehydrogenase1,10,007Q13975TRA2AFransformer-2 protein Sc24C1,10,011Q13959TRA2ATransformer-2 protein bonolog alpha1,10,012Q722K8GPRINIG protein-regulared inducer of neurite outgrowth 11,10,012Q722K8GPRINIG protein-regulared inducer of neurite outgrowth 11,10,023Q9273SLIRPSRA stem-loop-interacting RNA-binding protein, mitochondrial1,10,023Q92358TUBG1Tubuling annma-1 chain1,10,032P54386ALDH18A1Delta-1-pyrroline-5-carboxylate synthase1,10,033P54386ALDH18A1Delta-1-pyrroline-5-carboxylate synthase1,10,031Q98175HAUSHAUS sugmin-like complex subunit 810,001Q98175HAUS8HAUS sugmin-like complex subunit 810,001Q98176NANSSialie acid synthase10,032P54386ALDH18A1Delta-1-pyrroline-5-carboxylate synthase10,031Q98175 </td <td>SIC2SA5       ADP/ATP translocuse 2       1,1       0       PRDX5         RPL4       60S ribosonal protein L4       1,1       0,001       PRDX5         TIGAR       1,1       0,001       PRDX5         YAR52       Tyrosine-rRNA ligase, mitochondrial       1,1       0,001       PRDX5         PFKL       ATP-dependent 6-phosphofructokinase, liver type       1,1       0,001       PRDX5         SORD       Sorbiol dehydrogenase       1,1       0,003       PRDX5         SORD       Sorbiol dehydrogenase       1,1       0,007       PRDX5         SIC24C       Protextome assembly chapterone 1       1,1       0,007       PRDX5         SIC24C       Protein insport protein 5ec24C       1,1       0,001       PRDX5         AP2B1       AP-2 complex subunit beta       1,1       0,011       PRDX5         GPRIN1       G protein-regulated inducer of neutrice outgrowth 1       1,1       0,012       PRDX5         SILRP       SRA stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,021       PRDX5         SUN503       Zinc finger protein 503       1,1       0,022       PRDX5         SUN503       Zinc finger protein 503       1,1       0,032       PRDX5</td> <td>Q9BW92</td> <td>TARS2</td> <td>ThreoninetRNA ligase, mitochondrial</td> <td>1,2</td> <td>0,033</td> <td>PRDX5</td>	SIC2SA5       ADP/ATP translocuse 2       1,1       0       PRDX5         RPL4       60S ribosonal protein L4       1,1       0,001       PRDX5         TIGAR       1,1       0,001       PRDX5         YAR52       Tyrosine-rRNA ligase, mitochondrial       1,1       0,001       PRDX5         PFKL       ATP-dependent 6-phosphofructokinase, liver type       1,1       0,001       PRDX5         SORD       Sorbiol dehydrogenase       1,1       0,003       PRDX5         SORD       Sorbiol dehydrogenase       1,1       0,007       PRDX5         SIC24C       Protextome assembly chapterone 1       1,1       0,007       PRDX5         SIC24C       Protein insport protein 5ec24C       1,1       0,001       PRDX5         AP2B1       AP-2 complex subunit beta       1,1       0,011       PRDX5         GPRIN1       G protein-regulated inducer of neutrice outgrowth 1       1,1       0,012       PRDX5         SILRP       SRA stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,021       PRDX5         SUN503       Zinc finger protein 503       1,1       0,022       PRDX5         SUN503       Zinc finger protein 503       1,1       0,032       PRDX5	Q9BW92	TARS2	ThreoninetRNA ligase, mitochondrial	1,2	0,033	PRDX5
P36578         RPL4         60S ribosonal protein L4         1,1         0,001           QPNQ88         TIGAR         Fructores 2,6-bisphosphatzes TIGAR         1,1         0,001           QPN224         YARS2         Tyrosine -rtRN All gase, mitochondrial         1,1         0,001           QPN226         YARS2         Tyrosine -rtRN All gase, mitochondrial         1,1         0,001           QPN264         PSMG1         Proteasome assembly chaperone 1         1,1         0,001           Q90796         SQRD         Sorbitol delydrogenase         1,1         0,001           Q00796         SQRD         Sorbitol delydrogenase         1,1         0,001           Q18595         TRA2A         Transformer-2 protein homolog alpha         1,1         0,011           Q6310         AP2B1         AP2 complex subunit beta         1,1         0,012           Q722K8         GPRIN1         G protein regulated inducer of neurite ourgowth 1         1,1         0,012           Q722K8         GPRIN1         G protein subunit beta         1,1         0,021           Q96F45         XN503         Zinc finger protein 503         1,1         0,023           Q98R45         NANS         Silia caid syntrhase         1,1         0,031	RPL4         60S ribosomal protein L4         1,1         0,001         PRDX5           TIGAR         Fructose-2,6-bisphophatase TIGAR         1,1         0,001         PRDX5           YARS2         TyrosineRNA ligase, mitochondrial         1,1         0,001         PRDX5           PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,001         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,004         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,007         PRDX5           SEC24C         Protein transport protein Sc24C         1,1         0,01         PRDX5           SEC24C         Transformer-2 protein beta         1,1         0,01         PRDX5           GPRIN1         G protein-regulated inducer of neurite ourgrowth 1         1,1         0,017         PRDX5           SURP503         Zinc finger protein 503         1,1         0,021         PRDX5           SURS1         Tubulin gamma-1 chain         1,1         0,023         PRDX5           CNF503         Zinc finger protein 503         1,1         0,033         PRDX5           GNAS1         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033	P05141	SLC25A5	ADP/ATP translocase 2	1,1	0	PRDX5
Q9NQ88         TIGAR         Fructosc-2,6-bisphosphatase TIGAR         1,1         0,001           Q9Y224         YARS2         Tyrosinc-rRNA ligase, mitochondrial         1,1         0,001           P17858         PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,003           Q00796         SORD         Sorbiol dehydrogenase         1,1         0,004           Q10777         RPL35A         60S ribosomal protein L35a         1,1         0,007           Q13595         TRA2A         Transformer-2 protein homolog alpha         1,1         0,011           Q63775         MYO1B         Unconventional myosin-1b         1,1         0,012           Q722K8         GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,012           Q96F45         ZNF503         Zinc finger protein 503         1,1         0,023           Q923258         TUBG1         Tubulin gamma-1 chain         1,1         0,032           Q94F45         NANS         Sialic acid synthase         1,1         0,032           Q95F45         NAS         Sialic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1 </td <td>TIGAR       Fructose-2,6-bisphosphatase TIGAR       1,1       0,001       PRDX5         YARS2       TyrosinetRNA ligase, mitochondrial       1,1       0,001       PRDX5         PSKL       ATP-dependent 6-phosphortcockinase, liver type       1,1       0,001       PRDX5         PSMG1       Proteasome assembly chaperone 1       1,1       0,003       PRDX5         SORD       Sorbitol dehydrogenase       1,1       0,004       PRDX5         SEC24C       Protein transport protein Sec24C       1,1       0,007       PRDX5         SEC24C       Protein transport protein fomolog alpha       1,1       0,01       PRDX5         MYO1B       Uncorrectional myosin-lb       1,1       0,01       PRDX5         SURP       SRA stem-loop-interexting RNA-binding protein, mitochondrial       1,1       0,012       PRDX5         SURG1       Tubulin gamma-1 chain       1,1       0,021       PRDX5         NANS       Sialic acid synthase       1,1       0,022       PRDX5         NANS       Sialic acid synthase       1,1       0,032       PRDX5         SURG1       Tubulin gamma-1 chain       1,1       0,032       PRDX5         NANS       Sialic acid synthase       1,1       0,032       <t< td=""><td>P36578</td><td>RPL4</td><td>60S ribosomal protein L4</td><td>1,1</td><td>0,001</td><td>PRDX5</td></t<></td>	TIGAR       Fructose-2,6-bisphosphatase TIGAR       1,1       0,001       PRDX5         YARS2       TyrosinetRNA ligase, mitochondrial       1,1       0,001       PRDX5         PSKL       ATP-dependent 6-phosphortcockinase, liver type       1,1       0,001       PRDX5         PSMG1       Proteasome assembly chaperone 1       1,1       0,003       PRDX5         SORD       Sorbitol dehydrogenase       1,1       0,004       PRDX5         SEC24C       Protein transport protein Sec24C       1,1       0,007       PRDX5         SEC24C       Protein transport protein fomolog alpha       1,1       0,01       PRDX5         MYO1B       Uncorrectional myosin-lb       1,1       0,01       PRDX5         SURP       SRA stem-loop-interexting RNA-binding protein, mitochondrial       1,1       0,012       PRDX5         SURG1       Tubulin gamma-1 chain       1,1       0,021       PRDX5         NANS       Sialic acid synthase       1,1       0,022       PRDX5         NANS       Sialic acid synthase       1,1       0,032       PRDX5         SURG1       Tubulin gamma-1 chain       1,1       0,032       PRDX5         NANS       Sialic acid synthase       1,1       0,032 <t< td=""><td>P36578</td><td>RPL4</td><td>60S ribosomal protein L4</td><td>1,1</td><td>0,001</td><td>PRDX5</td></t<>	P36578	RPL4	60S ribosomal protein L4	1,1	0,001	PRDX5
Q9Y224         YA RS2         TyrosineRNA ligase, mitochondrial         1,1         0,001           P17558         PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,003           Q907924         YA RS2         TyrosineRNA ligase, mitochondrial         1,1         0,001           Q95456         PSMG1         Proteasome assembly chaperone 1         1,1         0,003           Q00796         SORD         Sorbitol delydrogenase         1,1         0,006           G5EA31         SEC24C         Protein transport protein Sec24C         1,1         0,001           Q43595         TRA2A         Transformer-2 protein homolog alpha         1,1         0,011           Q43795         MY01B         Unconventional myosin-1b         1,1         0,012           Q47254         GPRNNI         G protein-regulated inducer of neurite outgrowth 1         1,1         0,012           Q45275         MY01B         Unconventional myosin-1b         1,1         0,021           Q4545         ZNF503         Zinc finger protein 503         1,1         0,023           Q4545         NANS         Sialic acid synthase         1,1         0,032           Q4545         NANS         Sialic acid synthase         1,1         0,03	YARS2         Tyrosine-rRNA ligase, mitochondrial         1,1         0,001         PRDX5           PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,001         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,003         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,004         PRDX5           SEC24C         Protein transport protein Sc24C         1,1         0,007         PRDX5           AP2B1         AP2 complex subunit beta         1,1         0,01         PRDX5           AV01B         Unconventional myosin-1b         1,1         0,012         PRDX5           SLLRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021         PRDX5           SLLRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,022         PRDX5           NANS         Sialic cid synthase         1,1         0,023         PRDX5           NANS         Sialic cid synthase         1,1         0,033         PRDX5           NANS         Sialic cid synthase         1,1         0,032         PRDX5           NANS         Sialic cid synthase         1,1         0,033         PRDX5	O9NO88	TIGAR	Fructose-2.6-bisphosphatase TIGAR	1.1	0.001	PR DX5
Q1121         1110         0,001           P17858         PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,001           0959456         PSMG1         Protessome assembly chaperone 1         1,1         0,004           Q00796         SORD         Sorbitol dehydrogenase         1,1         0,005           G5EA31         SEC24C         Protein transport protein Sc24C         1,1         0,007           Q13595         TR.A2A         Transformer-2 protein homolog alpha         1,1         0,011           P63010         AP2B1         AP-2 complex subunit beta         1,1         0,012           Q722K8         GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,012           Q96F45         ZNF503         Zinc finger protein 503         1,1         0,023           P23258         TUBG1         Tubulin gamma-1 chain         1,1         0,032           Q96F45         ZNF503         Zinc finger protein 503         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001	International information         International information         International information           PFKL         ATP-dependent 6-phosphofructokinase, liver type         1,1         0,001         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,004         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,005         PRDX5           SEC24C         Protein transport protein L35a         1,1         0,007         PRDX5           SEC24C         Protein transport protein bomolog alpha         1,1         0,011         PRDX5           AP2B1         AP-2 complex subunit beta         1,1         0,011         PRDX5           GRRINI         G protein-regulated inducer of neurite ourgrowth 1         1,1         0,012         PRDX5           SLRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,023         PRDX5           TUBG1         Tubulin gamma-1 chain         1,1         0,024         PRDX5           CGNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDX5           ANS         Sialic acid synthase         1,1         0,039         PRDX5           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit b	09Y274	YAR S2	TyrosinetRNA ligase mitochondrial	11	0.001	PR DX5
F1753         F17L         All + appendent of prospanni actomates, invertype         1,1         0,001           0095456         PSMG1         Proteasome assembly chapterone 1         1,1         0,003           000796         SORD         Sorbitol dehydrogenase         1,1         0,004           P18077         RPL35A         605 ribosomal protein L35a         1,1         0,007           GSEA31         SEC24C         Protein transport protein Sec24C         1,1         0,01           P63010         AP2B1         AP-2 complex subunit beta         1,1         0,01           Q67274         GILR         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017           Q962T3         SLIRP         SR A stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021           Q96Z454         ZNF503         Zinc finger protein 503         1,1         0,032           P23258         TUBG1         Tubulin gamma-1 chain         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(1)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001           P62701         RP54X	FIRE         Fire         Fire         Fire         Fire         Fire         Fire         Fire           PSMG1         Protessone assembly chaperone 1         1,1         0,003         PRDXS           SORD         Sorbitol dehydrogenase         1,1         0,004         PRDXS           SORD         Sorbitol dehydrogenase         1,1         0,007         PRDXS           SEC24C         1,1         0,007         PRDXS           TRA2A         Transformer-2 protein homolog alpha         1,1         0,01         PRDXS           MYO1B         Unconventional myosin-1b         1,1         0,01         PRDXS           SURP         SR A stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,017         PRDXS           SURP         SR A stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,024         PRDXS           NANS         Sialic acid synthase         1,1         0,024         PRDXS           NANS         Sialic acid synthase         1,1         0,032         PRDXS           RPS44         408 ribosomal protein S24         1         0,031         PRDXS           RPS44         408 ribosomal protein S4, X isoform         1         0,001         PRDXS <td>D17858</td> <td>DEKI</td> <td>ATD dependent 6 phoenhofrusteleinges liver tune</td> <td>1,1</td> <td>0,001</td> <td>DP DV5</td>	D17858	DEKI	ATD dependent 6 phoenhofrusteleinges liver tune	1,1	0,001	DP DV5
Opsishe         FSMC1         Protession & assembly chaperone 1         1,1         0,003           Q00796         SOR D         Sorbiol dehydrogenase         1,1         0,004           P18077         RPL35A         608 ribosomal protein L35a         1,1         0,007           Q13595         TRA2A         Transformer-2 protein homolog alpha         1,1         0,017           Q13595         TRA2A         Transformer-2 protein homolog alpha         1,1         0,012           Q43795         MYO1B         Unconventional myosin-Ib         1,1         0,012           Q722K8         GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,021           Q96F45         ZINF503         Zinc finger protein 503         1,1         0,021           Q96F45         ZINF503         Zinc finger protein 503         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001           P62701         RPS4X         405 ribosomal protein S4, Xisoform         1         0,001           P62701         RPS4X         405 ribosomal protein S4,	FSMC1         1,1         0,003         PRDX5           SORD         Sorbitol dehydrogenase         1,1         0,004         PRDX5           RPL35A         608 ribosomal protein L35a         1,1         0,007         PRDX5           SEC24C         Protein transport protein Sc24C         1,1         0,001         PRDX5           TRA2A         Transformer-2 protein homolog alpha         1,1         0,01         PRDX5           MYO1B         Unconventional myosin-Ib         1,1         0,017         PRDX5           CPRINI         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017         PRDX5           ZINF503         Zinc finger protein 503         1,1         0,021         PRDX5           TUBGI         Tubulin gamma-1 chain         1,1         0,024         PRDX5           NANS         Sialic acid synthase         1,1         0,032         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,031         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1         0,006         PRDX5           AVS         HAUS augmin-1-ke complex subunit 8         1         0,001         PRDX5           ALDH18A1	005/5/	PENC1	Determinent of phosphore uctokinase, nyer type	1,1	0,001	PRDA)
Q00/96         SORD         Sorbtol dehydrogenase         1,1         0,004           P18077         RPL35A         608 ribosomal protein L35a         1,1         0,005           GSEA31         SEC24C         Protein transport protein Sec24C         1,1         0,017           Q13595         TR.A2A         Transformer-2 protein homolog alpha         1,1         0,01           P63010         AP2B1         AP-2 complex subunit beta         1,1         0,012           Q722K8         GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017           Q96ZT3         SLIRP         SR.A stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021           Q96F45         ZNF503         Zinc finger protein 503         1,1         0,023           P23288         TUBC1         Tubulin gamma-1 chain         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         A LDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001           P62701         RP54X         403 ribosomal protein S24         1         0,001           P62701         RP54X         405 ribosomal	SORD         Sorbitol dehydrogenase         1,1         0,004         PRDX5           SEC24C         Protein transport protein Sec24C         1,1         0,005         PRDX5           SEC24C         Protein transport protein Sec24C         1,1         0,01         PRDX5           AP281         AP-2 complex subunit beta         1,1         0,01         PRDX5           GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017         PRDX5           SLRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021         PRDX5           TUBGI         Tobulin gamma-1 chain         1,1         0,021         PRDX5           NANS         Stalic acid synthase         1,1         0,032         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,033         PRDX5           RPS24         405 ribosomal protein S4, X isoform         1         0,001         PRDX5           RPS44         405 ribosomal protein S4, X isoform         1         0,018         PRDX5           RPS44         405 ribosomal protein S4, X isoform         1         0,018         PRDX5           NDUFA4         Cytochrome c oxidase subunit 8         1         0,029<	095456	PSMGI		1,1	0,003	PRDAS
P18077       RPL35A       605 ribosomal protein L35a       1,1       0,005         G5EA31       SEC24C       Protein transport protein Sc24C       1,1       0,01         Q13595       TR.A2A       Transformer-2 protein homolog alpha       1,1       0,01         P63010       AP2B1       AP-2 complex subunit beta       1,1       0,01         Q43795       MYO1B       Unconventional myosin-Ib       1,1       0,012         Q7Z2K8       GPR1N1       G protein-regulated inducer of neurite outgrowth 1       1,1       0,017         Q9G2T3       SLIRP       SR A stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,023         P23258       TUBG1       Tubulin gamma-1 chain       1,1       0,024         Q9R455       NANS       Stalic acid synthase       1,1       0,032         P62879       GNB2       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033         P54886       ALDH18A1       Delta-1-pyrroline-5-carboxylate synthase       1,1       0,001         P62701       RP54X       405 ribosomal protein S24       1       0,001         Q9R125       HAUS8       HAUS8 augmin-like complex subunit 8       1       0,012         Q9BT25       HAUS	RPL35A       60S ribosomal protein L35a       1,1       0,005       PRDXS         SEC24C       Protein transport protein sec24C       1,1       0,007       PRDXS         TRA2A       Transformer-2 protein homolog alpha       1,1       0,01       PRDXS         AP2B1       AP-2 complex subunit beta       1,1       0,01       PRDXS         MYO1B       Unconventional myosin-Ib       1,1       0,017       PRDXS         SLRP       SRA stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,017       PRDXS         ZNF503       Zinc finger protein 503       1,1       0,023       PRDXS         GNB2       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033       PRDXS         ALDH18A1       Delta-1-pyrroline-5-carboxylate synthase       1,1       0,001       PRDXS         RPS24       40S ribosomal protein 524       1       0,001       PRDXS         ATPSMG       ATP synthase subunit g, mitochondrial       1       0,011       PRDXS         HAUS8       HAUS8 augmin-like complex subunit 8       1       0,012       PRDXS         MYSMG       ATP synthase subunit 10UFA4       1       0,012       PRDXS         ADS ribosomal protein 54, X isoform	Q00796	SORD	Sorbitol dehydrogenase	1,1	0,004	PRDX5
G5EA31         SEC24C         Protein transport protein Sec24C         1,1         0,007           Q13595         TR A2A         Transformer-2 protein homolog alpha         1,1         0,01           Q43091         AP2E         AP2 complex subunit beta         1,1         0,01           Q43795         MY01B         Unconventional myosin-Ib         1,1         0,012           Q722K8         GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,012           Q96F45         ZNF503         Zinc finger protein 503         1,1         0,023           Q923258         TUBG1         Tubulin gamma-1 chain         1,1         0,024           Q9NR45         NANS         Sialic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I//G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1         0,001           P62701         RPS4X         405 ribosomal protein S24         1         0,001           P62701         RPS4X         405 ribosomal protein S4, X isoform         1         0,012           Q9BT25         HAUS8         HAUS augmin-like complex subunit 8 <t< td=""><td>SEC24C       Protein transport protein Sec24C       1,1       0,007       PRDX5         TRA2A       Transformer-2 protein homolog alpha       1,1       0,01       PRDX5         MP2B1       AP-2 complex subunit beta       1,1       0,01       PRDX5         MYO1B       Unconventional myosin-Ib       1,1       0,012       PRDX5         GPRIN1       G protein-regulated inducer of neurite outgrowth 1       1,1       0,021       PRDX5         SLIRP       SRA stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,023       PRDX5         TUBG1       Tubulin gamma-1 chain       1,1       0,024       PRDX5         SNANS       Sialic acid synthase       1,1       0,032       PRDX5         GNB2       Guanine nucleoride-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033       PRDX5         RPS24       405 ribosomal protein S24       1       0,001       PRDX5         RPS44       405 ribosomal protein S4, Xi soform       1       0,011       PRDX5         PPS6C       Serine/threonine-protein phosphatase       1       0,012       PRDX5         NDUFA4       Cytochrome c oxidase subunit NDUFA4       1       0,027       PRDX5         RAB1A       Ras-related protein</td><td>P18077</td><td>RPL35A</td><td>60S ribosomal protein L35a</td><td>1,1</td><td>0,005</td><td>PRDX5</td></t<>	SEC24C       Protein transport protein Sec24C       1,1       0,007       PRDX5         TRA2A       Transformer-2 protein homolog alpha       1,1       0,01       PRDX5         MP2B1       AP-2 complex subunit beta       1,1       0,01       PRDX5         MYO1B       Unconventional myosin-Ib       1,1       0,012       PRDX5         GPRIN1       G protein-regulated inducer of neurite outgrowth 1       1,1       0,021       PRDX5         SLIRP       SRA stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,023       PRDX5         TUBG1       Tubulin gamma-1 chain       1,1       0,024       PRDX5         SNANS       Sialic acid synthase       1,1       0,032       PRDX5         GNB2       Guanine nucleoride-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033       PRDX5         RPS24       405 ribosomal protein S24       1       0,001       PRDX5         RPS44       405 ribosomal protein S4, Xi soform       1       0,011       PRDX5         PPS6C       Serine/threonine-protein phosphatase       1       0,012       PRDX5         NDUFA4       Cytochrome c oxidase subunit NDUFA4       1       0,027       PRDX5         RAB1A       Ras-related protein	P18077	RPL35A	60S ribosomal protein L35a	1,1	0,005	PRDX5
Q13595         TR.A2A         Transformer-2 protein homolog alpha         1,1         0,01           P63010         AP2B1         AP2 complex subunit beta         1,1         0,01           Q43795         MYO1B         Unconventional myosin-Ib         1,1         0,012           Q722K8         GPRIN1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017           Q9GZT3         SLIRP         SR.A stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,023           Q9GF45         ZNF503         Zinc finger protein 503         1,1         0,024           Q9NR45         NANS         Sialic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001           P62701         RPS4X         405 ribosomal protein S4, X isoform         1         0,001           P9PT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,012           Q9BT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,027           O00483         NDUFA4 <td< td=""><td>TRA2A         Transformer-2 protein homolog alpha         1,1         0,01         PRDXS           AP2B1         AP-2 complex suburit beta         1,1         0,01         PRDXS           MYO1B         Unconventional myosin-Ib         1,1         0,012         PRDXS           SLIRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021         PRDXS           ZNF503         Zinc finger protein 503         1,1         0,024         PRDXS           TUBG1         Tubulin gamma-1 chain         1,1         0,024         PRDXS           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,032         PRDXS           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,033         PRDXS           RPS4X         405 ribosomal protein S4,X isoform         1         0,001         PRDXS           HAUS8         HAUS augmin-like complex subunit 8         1         0,011         PRDXS           HAUS8         HAUS augmin-like complex subunit 8         1         0,012         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,022         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         <td< td=""><td>G5EA31</td><td>SEC24C</td><td>Protein transport protein Sec24C</td><td>1,1</td><td>0,007</td><td>PRDX5</td></td<></td></td<>	TRA2A         Transformer-2 protein homolog alpha         1,1         0,01         PRDXS           AP2B1         AP-2 complex suburit beta         1,1         0,01         PRDXS           MYO1B         Unconventional myosin-Ib         1,1         0,012         PRDXS           SLIRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021         PRDXS           ZNF503         Zinc finger protein 503         1,1         0,024         PRDXS           TUBG1         Tubulin gamma-1 chain         1,1         0,024         PRDXS           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,032         PRDXS           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,033         PRDXS           RPS4X         405 ribosomal protein S4,X isoform         1         0,001         PRDXS           HAUS8         HAUS augmin-like complex subunit 8         1         0,011         PRDXS           HAUS8         HAUS augmin-like complex subunit 8         1         0,012         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,022         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4 <td< td=""><td>G5EA31</td><td>SEC24C</td><td>Protein transport protein Sec24C</td><td>1,1</td><td>0,007</td><td>PRDX5</td></td<>	G5EA31	SEC24C	Protein transport protein Sec24C	1,1	0,007	PRDX5
P63010       AP2B1       AP-2 complex subunit beta       1,1       0,01         043795       MY01B       Unconventional myosin-1b       1,1       0,012         Q7Z2K8       GPR1N1       G protein-regulated inducer of neurite outgrowth 1       1,1       0,017         Q9GZT3       SLIRP       SRA stem-loop-interacting RNA-binding protein, mitochondrial       1,1       0,021         Q9GF45       ZNF503       Zinc finger protein 503       1,1       0,023         P23258       TUBG1       Tubulin gamma-1 chain       1,1       0,024         Q9NR45       NANS       Sialic acid synthase       1,1       0,032         P62879       GNB2       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033         P54886       ALDH18A1       Delta-1-pyrroline-5-carboxylate synthase       1,1       0,001         P62701       RPS4X       40S ribosomal protein S24       10       0,001         P09T17       ATP5MG       ATP synthase subunit g, mitochondrial       1       0,001         Q9BT25       HAUS8       HAUS augmin-like complex subunit 8       1       0,022         Q00483       NDUFA4       Cytochrome c oxidase subunit NDUFA4       0,032       026         Q9HAV4       XP	AP2B1AP-2 complex subunit beta1,10,01PRDX5MY01BUnconventional myosin-lb1,10,012PRDX5GPRIN1G protein-regulated inducer of neurite outgrowth 11,10,017PRDX5SLIRPSR A stem-loop-interacting RNA-binding protein, mitochondrial1,10,021PRDX5ZNF503Zinc finger protein 5031,10,021PRDX5TUBG1Tubulin gamma-1 chain1,10,023PRDX5NANSSialic acid synthase1,10,032PRDX5ALDH18A1Delta-1-pyrroline-5-carboxylate synthase1,10,039PRDX5RPS24405 ribosomal protein S4,410,001PRDX5RPS4X406 ribosomal protein S4,410,011PRDX5HAUS8HAUS augmin-like complex subunit 810,011PRDX5PPSCSerine/threonine-protein phosphatase10,022PRDX5NDUFA4Cytochrome c oxidase subunit NDUFA410,032PRDX5XPO5Exportin-510,038PRDX5CBLE3 ubiquitin protein Igare CBL10,038PRDX5XPO5Exportin-510,038PRDX5CBLE3 ubiquitin-protein ligase CBL10,045PRDX5CBLE3 ubiquitin-protein ligase CBL10,045PRDX5XPO5Exportin-510,045PRDX5XPO5Exportin-510,045PRDX5CBLE3 ubiquitin-protein ligase CBL4,50 <td>Q13595</td> <td>TRA2A</td> <td>Transformer-2 protein homolog alpha</td> <td>1,1</td> <td>0,01</td> <td>PRDX5</td>	Q13595	TRA2A	Transformer-2 protein homolog alpha	1,1	0,01	PRDX5
043795         MY01B         Unconventional myosin-Ib         1,1         0,012           Q7Z2K8         GPR1N1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017           Q9G7T3         SLIR P         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021           Q96F45         ZNF503         Zinc finger protein 503         1,1         0,022           Q23258         TUBG1         Tubulin gamma-1 chain         1,1         0,032           P23258         NANS         Sialic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001           P62701         RP54X         405 ribosomal protein S24         1         0,001           P62701         RP54X         405 ribosomal protein S4, Xi soform         1         0,002           P62701         RP54X         405 ribosomal protein S4, Xi soform         1         0,018           H0YDU8         PP5C         Serine/threonine-protein phosphatase         1         0,022           P62802         RABIA         Ras-related	MYO1B         Unconventional myosin-lb         1,1         0,012         PRDX5           GPR1N1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017         PRDX5           SLIRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021         PRDX5           ZNF503         Zinc finger protein 503         1,1         0,022         PRDX5           TUBG1         Tubulin gamma-1 chain         1,1         0,023         PRDX5           SANS         Sialic acid synthase         1,1         0,032         PRDX5           GNB2         Guanine nucleotide-binding protein G(1)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDX5           RPS24         40S ribosomal protein S24         1         0,001         PRDX5           RPS44         40S ribosomal protein S4, X isoform         1         0,001         PRDX5           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011         PRDX5           HAUS8         HAUS8 augmin-like complex subunit 8         1         0,027         PRDX5           NDUFA4         Cytochrome c oxidase subunit 8         1         0,027         PRDX5           RAB1A         Ras-related protein Rab-1A         1         <	P63010	AP2B1	AP-2 complex subunit beta	1,1	0,01	PRDX5
Q7Z2K8         GPR1N1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017           Q9GZT3         SLIRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021           Q9GZT3         ZINF 503         Zinc finger protein 503         1,1         0,023           P23258         TUBG1         Tubulin gamma-1 chain         1,1         0,024           Q9NR45         NANS         Sialic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001           P62701         RPS24         40S ribosomal protein S24         1         0,001           P62701         RPS4X         40S ribosomal protein S4, X isoform         1         0,001           Q9DT25         HAUS8         HAUS augmin-like complex subunit g, mitochondrial         1         0,012           Q924         Qyorchrome coxidase subunit g, mitochondrial         1         0,027         Q00483           MOYDU8         PPP5C         Serine/threonine-protein phosphatase         1         0,032           Q6PKG0         LA	GPR1N1         G protein-regulated inducer of neurite outgrowth 1         1,1         0,017         PRDX5           SLIR.P         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021         PRDX5           ZNF503         Zinc finger protein 503         1,1         0,023         PRDX5           TUBG1         Tubulin gamma-1 chain         1,1         0,032         PRDX5           NANS         Sialic acid synthase         1,1         0,032         PRDX5           GGNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,003         PRDX5           RPS24         40S ribosomal protein S4, X isoform         1         0,001         PRDX5           RPS4X         40S ribosomal protein S4, X isoform         1         0,011         PRDX5           HAUS8         HAUS augmin-like complex subunit 8         1         0,012         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,027         PRDX5           RAB1A         Ras-related protein Rab-1A         1         0,038         PRDX5           LARP1         La-related protein Rab-1A	O43795	MYO1B	Unconventional myosin-Ib	1,1	0,012	PRDX5
Q9GZT3         SLIRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021           Q9GZT3         ZNF503         Zinc finger protein 503         1,1         0,023           P23258         TUBG1         Tubulin gamma-1 chain         1,1         0,024           Q9NR45         NANS         Sialic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pytroline-5-carboxylate synthase         1,1         0,001           P62701         RPS4X         40S ribosomal protein S24         1         0,001           P62701         RPS4X         40S ribosomal protein S4, X isoform         1         0,001           P62701         RPS4X         40S ribosomal protein S4, X isoform         1         0,001           Q9BT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,018           H0YDU8         PPP5C         Serine/threonine-protein phosphatase         1         0,022           Q00483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,038           Q9H205         RAB1A         Ras-related protein 1	SLIRP         SRA stem-loop-interacting RNA-binding protein, mitochondrial         1,1         0,021         PRDX5           ZNF503         Zinc finger protein 503         1,1         0,023         PRDX5           TUBG1         Tubulin gamma-1 chain         1,1         0,024         PRDX5           NANS         Sialic acid synthase         1,1         0,032         PRDX5           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039         PRDX5           RPS24         40S ribosomal protein S24         1         0,001         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1         0,001         PRDX5           RPS4X         40S ribosomal protein S4, X isoform         1         0,001         PRDX5           ATPSMG         ATP synthase subunit g, mitochondrial         1         0,011         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,027         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,038         PRDX5           LARP1         La-related protein Rab-1A         1<	O7Z2K8	GPRIN1	G protein-regulated inducer of neurite outgrowth 1	1,1	0,017	PRDX5
Q20115         Outcome of the constraint of prime within the prin the prin the prime within the prin the prime within the prime	Diricit         Offer         Problem         Problem           ZNF503         Zinc finger protein 503         1,1         0,023         PRDX5           TUBG1         Tubulin gamma-1 chain         1,1         0,024         PRDX5           NANS         Sialic acid synthase         1,1         0,032         PRDX5           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039         PRDX5           RPS24         405 ribosomal protein S24         1         0,001         PRDX5           RPS4X         405 ribosomal protein S24         1         0,001         PRDX5           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011         PRDX5           HAUS8         HAUS augmin-like complex subunit 8         1         0,018         PRDX5           DVFA4         Cytochrome c oxidase subunit NDUFA4         1         0,022         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,038         PRDX5           LARP1         La-related protein Rab-1A         1         0,038         PRDX5           GLS	O9GZT3	SLIR P	SR A stem-loop-interacting RNA-binding protein mitochondrial	11	0.021	PR DX5
Q28143         Zitk Iniger protein 505         1,1         0,023           P23258         TUBG1         Tubulin gamma-1 chain         1,1         0,024           Q9NR45         NANS         Sialic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,001           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1         0,001           P62701         RPS4X         40S ribosomal protein S4, X isoform         1         0,006           E9PN17         ATP5MG         ATP synthase subunit g, mitochondrial         1         0,018           H0YDU8         PPP5C         Serine/threonine-protein phosphatase         1         0,027           000483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,032           Q6PKG0         LARP1         La-related protein Rab-1A         1         0,038           Q9HAV4         XPO5         Exportin-5         1 </td <td>Zhix Bige protein 303       1,1       0,023       FRDX5         TUBG1       Tubulin gamma-1 chain       1,1       0,024       PRDX5         NANS       Sialic acid synthase       1,1       0,032       PRDX5         GNB2       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033       PRDX5         ALDH18A1       Delta-1-pyrroline-5-carboxylate synthase       1,1       0,003       PRDX5         RPS24       40S ribosomal protein S24       1       0,001       PRDX5         RPS4X       40S ribosomal protein S4, X isoform       1       0,006       PRDX5         ATP5MG       ATP synthase subunit g, mitochondrial       1       0,011       PRDX5         HAUS8       HAUS augmin-like complex subunit 8       1       0,018       PRDX5         PPP5C       Serine/threonine-protein phosphatase       1       0,027       PRDX5         NDUFA4       Cytochrome c oxidase subunit NDUFA4       1       0,032       PRDX5         LARP1       La-related protein Rab-1A       1       0,038       PRDX5         LARP1       La-related protein flase-GBL       1       0,045       PRDX5         CBL       Glutaminase kidney isoform, mitochondrial       1       0,045</td> <td>Q96E45</td> <td>ZNES02</td> <td>7ing Engar protain 502</td> <td>1,1</td> <td>0.023</td> <td>DP DV5</td>	Zhix Bige protein 303       1,1       0,023       FRDX5         TUBG1       Tubulin gamma-1 chain       1,1       0,024       PRDX5         NANS       Sialic acid synthase       1,1       0,032       PRDX5         GNB2       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033       PRDX5         ALDH18A1       Delta-1-pyrroline-5-carboxylate synthase       1,1       0,003       PRDX5         RPS24       40S ribosomal protein S24       1       0,001       PRDX5         RPS4X       40S ribosomal protein S4, X isoform       1       0,006       PRDX5         ATP5MG       ATP synthase subunit g, mitochondrial       1       0,011       PRDX5         HAUS8       HAUS augmin-like complex subunit 8       1       0,018       PRDX5         PPP5C       Serine/threonine-protein phosphatase       1       0,027       PRDX5         NDUFA4       Cytochrome c oxidase subunit NDUFA4       1       0,032       PRDX5         LARP1       La-related protein Rab-1A       1       0,038       PRDX5         LARP1       La-related protein flase-GBL       1       0,045       PRDX5         CBL       Glutaminase kidney isoform, mitochondrial       1       0,045	Q96E45	ZNES02	7ing Engar protain 502	1,1	0.023	DP DV5
P2253s       10BG1       110BG1       10001       0,024         Q9NR45       NANS       Sialic acid synthase       1,1       0,032         P62879       GNB2       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033         P54886       ALDH18A1       Delta-1-pyrroline-5-carboxylate synthase       1,1       0,039         E7ETK0       RPS24       40S ribosomal protein S24       1       0,001         P62701       RPS4X       40S ribosomal protein S4, X isoform       1       0,006         E9PN17       ATP5MG       ATP synthase subunit g, mitochondrial       1       0,011         Q9BT25       HAUS8       HAUS augmin-like complex subunit 8       1       0,018         H0YDU8       PPP5C       Serine/threonine-protein phosphatase       1       0,027         000483       NDUFA4       Cytochrome c oxidase subunit NDUFA4       1       0,032         Q6PKG0       LARP1       La-related protein Rab-1A       1       0,038         Q9HAV4       XPO5       Exportin-5       1       0,038         O94925       GLS       Glutaminase kidney isoform, mitochondrial       1       0,044         O94925       GLS       Glutaminase kidney isoform, mitochondrial	TOBG1         Tubbin gamma renain         1,1         0,024         PRDXS           NANS         Sialic acid synthase         1,1         0,032         PRDXS           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDXS           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039         PRDXS           RPS24         40S ribosomal protein S24         1         0,001         PRDXS           RPS4X         40S ribosomal protein S4, X isoform         1         0,001         PRDXS           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011         PRDXS           HAUS8         HAUS augmin-like complex subunit 8         1         0,018         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,029         PRDXS           RAB1A         Ras-related protein Rab-1A         1         0,038         PRDXS           XPO5         Exportin-5         1         0,038         PRDXS           GLS         Glutaminase kidney isoform, mitochondrial         1         0,045         PRDXS           CBL         E3 ubiquitin-protein ligase CBL         1         0,045         PRDXS </td <td>Q/014)</td> <td>TUDCI</td> <td>The line mage protein 505</td> <td>1,1</td> <td>0,023</td> <td>PRDA)</td>	Q/014)	TUDCI	The line mage protein 505	1,1	0,023	PRDA)
Q9NR45         NANS         Stalic acid synthase         1,1         0,032           P62879         GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033           P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039           F7ETK0         RPS24         40S ribosomal protein S24         1         0,001           P62701         RPS4X         40S ribosomal protein S4, X isoform         1         0,006           E9PN17         ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011           Q9BT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,012           Q9BT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,027           000483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,032           QeFKG0         LARP1         La-related protein Rab-1A         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,044           A0A1B0GW38         CBL         E3 ubiquitin-protein ligase CBL         1         0,045 <td>NANS         Staltc acid synthase         1,1         0,032         PRDXS           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDXS           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039         PRDXS           RPS24         40S ribosomal protein S24         1         0,001         PRDXS           RPS4X         40S ribosomal protein S4, X isoform         1         0,011         PRDXS           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,018         PRDXS           HAUS8         HAUS augmin-like complex subunit 8         1         0,027         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,029         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,038         PRDXS           LARP1         La-related protein Rab-1A         1         0,038         PRDXS           LARP1         La-related protein 1         1         0,038         PRDXS           SVO5         Exportin-5         1         0,049         PRDXS           GLS         Glutaminase kidney isoform, mitochondrial         1         0,045         PRDX5</td> <td>P23238</td> <td>TUBGI</td> <td>1ubulin gamma-1 chain</td> <td>1,1</td> <td>0,024</td> <td>PRDAS</td>	NANS         Staltc acid synthase         1,1         0,032         PRDXS           GNB2         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2         1,1         0,033         PRDXS           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039         PRDXS           RPS24         40S ribosomal protein S24         1         0,001         PRDXS           RPS4X         40S ribosomal protein S4, X isoform         1         0,011         PRDXS           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,018         PRDXS           HAUS8         HAUS augmin-like complex subunit 8         1         0,027         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,029         PRDXS           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,038         PRDXS           LARP1         La-related protein Rab-1A         1         0,038         PRDXS           LARP1         La-related protein 1         1         0,038         PRDXS           SVO5         Exportin-5         1         0,049         PRDXS           GLS         Glutaminase kidney isoform, mitochondrial         1         0,045         PRDX5	P23238	TUBGI	1ubulin gamma-1 chain	1,1	0,024	PRDAS
P62879       GNB2       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2       1,1       0,033         P54886       ALDH18A1       Delta-1-pyrroline-5-carboxylate synthase       1,1       0,039         E7ETK0       RPS24       40S ribosomal protein S24       1       0,001         P62701       RPS4X       40S ribosomal protein S4, X isoform       1       0,006         E9PN17       ATP5MG       ATP synthase subunit g, mitochondrial       1       0,011         Q9BT25       HAUS8       HAUS augmin-like complex subunit 8       1       0,027         000483       NDUFA4       Cytochrome c oxidase subunit NDUFA4       1       0,022         P62820       RAB1A       Ras-related protein Rab-1A       1       0,038         Q9HAV4       XPO5       Exportin-5       1       0,038         Q9425       GLS       Glutaminase kidney isoform, mitochondrial       1       0,045         PRDX3 -specific interactors       1       0,045           P02790       HPX       Hemopexin       4,5       0	GNB2         Guanine nucleotide-binding protein G(I)/G(T) subunit beta-2         1,1         0,033         PRDX5           ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039         PRDX5           RPS24         40S ribosomal protein S24         1         0,001         PRDX5           RPS4X         40S ribosomal protein S4, X isoform         1         0,006         PRDX5           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011         PRDX5           PMS5         Serine/threonine-protein phosphatase         1         0,027         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,038         PRDX5           RAB1A         Ras-related protein Rab-1A         1         0,038         PRDX5           LARP1         La-related protein 1         1         0,038         PRDX5           SYO5         Exportin-5         1         0,038         PRDX5           GLS         Glutaminase kidney isoform, mitochondrial         1         0,04         PRDX5           CBL         E3 ubiquitin-protein ligase CBL         1         0,045         PRDX5           CBL         E3 ubiquitin-protein ligase CBL         4,9         0         PRDX1 </td <td>Q9NR45</td> <td>NANS</td> <td>Sialic acid synthase</td> <td>1,1</td> <td>0,032</td> <td>PRDX5</td>	Q9NR45	NANS	Sialic acid synthase	1,1	0,032	PRDX5
P54886         ALDH18A1         Delta-1-pyrroline-5-carboxylate synthase         1,1         0,039           E7ETK0         RPS24         40S ribosomal protein S24         1         0,001           P62701         RPS4X         40S ribosomal protein S4, X isoform         1         0,006           E9PN17         ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011           Q9B725         HAUS8         HAUS augmin-like complex subunit 8         1         0,018           H0YDU8         PPP5C         Serine/threonine-protein phosphatase         1         0,027           000483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,032           Q6FKG0         LARP1         La-related protein Rab-1A         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,034           Q9425         GLS         Glutaminase kidney isoform, mitochondrial         1         0,045           PRDX3 -specific interactors         1         0,045         1         0,045           PRDX3         H4C1         Histone H4         4,9         0         1           P02790 </td <td>ALDH18A1         Delta-1-pytroline-5-carboxylate synthase         1,1         0,039         PRDX5           RP524         405 ribosomal protein S24         1         0,001         PRDX5           RP54X         405 ribosomal protein S4, X isoform         1         0,006         PRDX5           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011         PRDX5           HAUS8         HAUS augmin-like complex subunit 8         1         0,018         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,027         PRDX5           RAB1A         Ras-related protein Rab-1A         1         0,038         PRDX5           LARP1         La-related protein 1         1         0,038         PRDX5           SCB         Glutaminase kidney isoform, mitochondrial         1         0,038         PRDX5           CBL         E3 ubiquitin-protein ligase CBL         1         0,045         PRDX5           <b>tctor</b>         -         -         -         -         -           H4C1         Histone H4         4,9         0         PRDX1           HPX         Hemopexin         4,5         0         PRDX1           SYNCRIP         Heterogeneous nuclea</td> <td>P62879</td> <td>GNB2</td> <td>Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2</td> <td>1,1</td> <td>0,033</td> <td>PRDX5</td>	ALDH18A1         Delta-1-pytroline-5-carboxylate synthase         1,1         0,039         PRDX5           RP524         405 ribosomal protein S24         1         0,001         PRDX5           RP54X         405 ribosomal protein S4, X isoform         1         0,006         PRDX5           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011         PRDX5           HAUS8         HAUS augmin-like complex subunit 8         1         0,018         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,027         PRDX5           RAB1A         Ras-related protein Rab-1A         1         0,038         PRDX5           LARP1         La-related protein 1         1         0,038         PRDX5           SCB         Glutaminase kidney isoform, mitochondrial         1         0,038         PRDX5           CBL         E3 ubiquitin-protein ligase CBL         1         0,045         PRDX5 <b>tctor</b> -         -         -         -         -           H4C1         Histone H4         4,9         0         PRDX1           HPX         Hemopexin         4,5         0         PRDX1           SYNCRIP         Heterogeneous nuclea	P62879	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	1,1	0,033	PRDX5
E7ETK0         R PS24         40S ribosomal protein S24         1         0,001           P62701         R PS4X         40S ribosomal protein S4, X isoform         1         0,006           E9PN17         A TP 5MG         ATP synthase subunit g, mitochondrial         1         0,011           Q9BT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,018           H0YDU8         PPP5C         Serine/threonine-protein phosphatase         1         0,027           000483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,032           P62820         R AB1A         Ras-related protein Rab-1A         1         0,032           Q9HAV4         XPO5         Exportin-5         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,044           A0A1B0GW38         CBL         E3 ubiquitin-protein ligase CBL         1         0,045           PRDX3 -specific interactors         PR         PR         PR         PR         PR           P02790         HPX         Hemopexin         4,5         0	RPS24         40S ribosomal protein S24         1         0,001         PRDX5           RPS4X         40S ribosomal protein S4, X isoform         1         0,006         PRDX5           ATP5MG         ATP synthase subunit g, mitochondrial         1         0,011         PRDX5           HAUS8         HAUS augmin-like complex subunit 8         1         0,018         PRDX5           PPP5C         Serine/threonine-protein phosphatase         1         0,027         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,032         PRDX5           RAB1A         Ras-related protein Rab-1A         1         0,032         PRDX5           LARP1         La-related protein 1         1         0,038         PRDX5           SCBL         Glutaminase kidney isoform, mitochondrial         1         0,048         PRDX5           GLS         Glutaminase kidney isoform, mitochondrial         1         0,04         PRDX5           cBL         E3 ubiquitin-protein ligase CBL         1         0,045         PRDX5           cBL         E3 ubiquitin-protein ligase CBL         4,9         0         PRDX1           HPX         Hemopexin         4,5         0         PRDX1           SYNCRIP </td <td>P54886</td> <td>ALDH18A1</td> <td>Delta-1-pyrroline-5-carboxylate synthase</td> <td>1,1</td> <td>0,039</td> <td>PRDX5</td>	P54886	ALDH18A1	Delta-1-pyrroline-5-carboxylate synthase	1,1	0,039	PRDX5
P62701         R PS4X         40S ribosomal protein S4, X isoform         1         0,006           E9PN17         ATP 5MG         ATP synthase subunit g, mitochondrial         1         0,011           Q9BT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,018           H0YDU8         PPP5C         Serine/threonine-protein phosphatase         1         0,027           000483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,032           P62800         RAB1A         Ras-related protein Rab-1A         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,038           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,044           O94925         GLS         Glutaminase Kidney isoform, mitochondrial         1         0,045           PRDX3 -specific interactors         1         0,045         1         0,045           PROX3         H4C1         Histone H4         4,9         0         1           P02790         HPX         Hemopexin         4,5         0	RPS4X40S ribosomal protein S4, X isoform10,006PRDXSATP5MGATP synthase subunit g, mitochondrial10,011PRDXSHAUS8HAUS augmin-like complex subunit 810,018PRDXSPPP5CSerine/threonine-protein phosphatase10,027PRDXSNDUFA4Cytochrome c oxidase subunit NDUFA410,029PRDXSRAB1ARas-related protein Rab-1A10,032PRDXSLARP1La-related protein 110,038PRDXSSZDOSExportin-510,038PRDXSGLSGlutaminase kidney isoform, mitochondrial10,04PRDXSCBLE3 ubiquitin-protein ligase CBL10,045PRDXSH4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	E7ETK0	RPS24	40S ribosomal protein S24	1	0,001	PRDX5
E9PN17ATP 5MGATP synthase subunit g, mitochondrial10,011Q9BT25HAUS8HAUS augmin-like complex subunit 810,018H0YDU8PPP5CSerine/threonine-protein phosphatase10,027000483NDUFA4Cytochrome c oxidase subunit NDUFA410,029P62820RAB1ARas-related protein Rab-1A10,032Q6PKG0LARP1La-related protein 110,038Q9HAV4XPO5Exportin-510,038O94925GLSGlutaminase kidney isoform, mitochondrial10,04A0A1B0GW38CBLE3 ubiquitin-protein ligase CBL10,045PRDX3 -specific interatorsP62805H4C1Histone H44,90	ATP5MGATP synthase subunit g, mitochondrial10,011PRDX5HAUS8HAUS augmin-like complex subunit 810,018PRDX5PPP5CSerine/threonine-protein phosphatase10,027PRDX5NDUFA4Cytochrome c oxidase subunit NDUFA410,029PRDX5RABIARas-related protein Rab-1A10,032PRDX5LARP1La-related protein 110,038PRDX5STO5Exportin-510,038PRDX5GLSGlutaminase kidney isoform, mitochondrial10,04PRDX5CBLE3 ubiquitin-protein ligase CBL10,045PRDX5H4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RABI4Ras-related protein Rab-1440PRDX1	P62701	RPS4X	40S ribosomal protein S4, X isoform	1	0,006	PRDX5
Q9BT25         HAUS8         HAUS augmin-like complex subunit 8         1         0,018           H0YDU8         PPP5C         Serine/threonine-protein phosphatase         1         0,027           O00483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,029           P62820         RAB1A         Ras-related protein Rab-1A         1         0,032           Q6PKG0         LARP1         La-related protein 1         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,048           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,045           PRDX3-specific interactors          1         0,045         1           P62805         H4C1         Histone H4         4,9         0           P02790         HPX         Hemopexin         4,5         0	HAUS8HAUS augmin-like complex subunit 810,018PRDX5PPP5CSerine/threonine-protein phosphatase10,027PRDX5NDUFA4Cytochrome c oxidase subunit NDUFA410,029PRDX5RAB1ARas-related protein Rab-1A10,032PRDX5LARP1La-related protein 110,038PRDX5SYO5Exportin-510,038PRDX5GLSGlutaminase kidney isoform, mitochondrial10,04PRDX5cBLE3 ubiquitin-protein ligase CBL10,045PRDX5H4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	E9PN17	ATP5MG	ATP synthase subunit g, mitochondrial	1	0,011	PRDX5
HOYDUS         PPP5C         Serine/threonine-protein phosphatase         1         0,027           000483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,029           P62820         RABIA         Ras-related protein Rab-1A         1         0,032           Q6PKG0         LARP1         La-related protein 1         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,038           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,045           PRDX3 -specific interactors           1         0,045           P62805         H4C1         Histone H4         4,9         0           P02790         HPX         Hemopexin         4,5         0	PPP5C         Serine/threonine-protein phosphatase         1         0,027         PRDX5           NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,029         PRDX5           RAB1A         Ras-related protein Rab-1A         1         0,032         PRDX5           LARP1         La-related protein 1         1         0,038         PRDX5           XPO5         Exportin-5         1         0,038         PRDX5           GLS         Glutaminase kidney isoform, mitochondrial         1         0,044         PRDX5           CBL         E3 ubiquitin-protein ligase CBL         1         0,045         PRDX5 <b>tetors</b>	O9BT25	HAUS8	HAUS augmin-like complex subunit 8	1	0,018	PRDX5
NDUCo         NDU FA4         Cytochrome c oxidase subunit NDUFA4         1         0,027           000483         NDUFA4         Cytochrome c oxidase subunit NDUFA4         1         0,029           P62820         RAB1A         Ras-related protein Rab-1A         1         0,032           Q6PKG0         LARP1         La-related protein Rab-1A         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,038           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,045           PRDX3 -specific interactors          1         0,045           PRO250         H4C1         Histone H4         4,9         0           P02790         HPX         Hemopexin         4,5         0	NTOCOrtholymitesine provent p	HOYDUS	PPP5C	Serine/threenine-protein phosphatase	1	0.027	PR DX5
Conversion         File Cytotinoine Contract Studimit (ADOTA*)         1         0,022           P62820         R ABIA         Ras-related protein Rab-1A         1         0,032           Q6PKG0         LARP1         La-related protein Rab-1A         1         0,032           Q9HAV4         XPO5         Exportin-5         1         0,038           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,044           A0A1B0GW38         CBL         E3 ubiquitin-protein ligase CBL         1         0,045           PRDX3 -specific interactors         P         P         P         P         P         Hemopexin         4,5         0	RABIARas-related protein Rab-1A10,022PRDX5LARP1La-related protein 110,032PRDX5LARP1La-related protein 110,038PRDX5SYPO5Exportin-510,038PRDX5GLSGlutaminase kidney isoform, mitochondrial10,04PRDX5CBLE3 ubiquitin-protein ligase CBL10,045PRDX5tetorsH4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	000/83	NDUEA/	Cutochrome a oxidece cubunit NDUFA /	1	0,029	DP DV5
P62820         RABIA         Ras-related protein Rab-IA         1         0,032           Q6PKG0         LARP1         La-related protein 1         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,038           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,04           A0A1B0GW38         CBL         E3 ubiquitin-protein ligase CBL         1         0,045           PRDX3 -specific interactors         P         P         P         P         P         P         P         P         O	RABIARas-related protein Rab-1A10,052PRDXSLARP1La-related protein 110,038PRDX5XPO5Exportin-510,038PRDX5GLSGlutaminase kidney isoform, mitochondrial10,04PRDX5CBLE3 ubiquitin-protein ligase CBL10,045PRDX5actorsH4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	D(2820	D A D1 A	Described and a second Delt 14	1	0,022	PRDA)
Q6PKG0         LARP1         La-related protein 1         1         0,038           Q9HAV4         XPO5         Exportin-5         1         0,038           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,04           A0A1B0GW38         CBL         E3 ubiquitin-protein ligase CBL         1         0,045           PRDX3 -specific interactors         P         P         P         P         P         P         P         P         P         O	LARP1La-related protein 110,038PRDX5XPO5Exportin-510,038PRDX5GLSGlutaminase kidney isoform, mitochondrial10,04PRDX5CBLE3 ubiquitin-protein ligase CBL10,045PRDX5actorsH4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	P62820	KADIA	Kas-related protein Kab-IA	1	0,032	PRDAS
Q9HAV4         XPO5         Exportin-5         1         0,038           O94925         GLS         Glutaminase kidney isoform, mitochondrial         1         0,04           A0A1B0GW38         CBL         E3 ubiquitin-protein ligase CBL         1         0,045           PRDX3 -specific interactors         P         P         P         P         O           P02790         HPX         Hemopexin         4,5         0	XPO5         Exportin-5         1         0,038         PRDX5           GLS         Glutaminase kidney isoform, mitochondrial         1         0,04         PRDX5           CBL         E3 ubiquitin-protein ligase CBL         1         0,045         PRDX5           actors	Q6PKG0	LARPI	La-related protein 1	1	0,038	PRDX5
094925GLSGlutaminase kidney isoform, mitochondrial10,04A0A1B0GW38CBLE3 ubiquitin-protein ligase CBL10,045 <b>PRDX3 -specific interactors</b> P62805H4C1Histone H44,90P02790HPXHemopexin4,50	GLSGlutaminase kidney isoform, mitochondrial10,04PRDX5CBLE3 ubiquitin-protein ligase CBL10,045PRDX5actorsH4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	Q9HAV4	XPO5	Exportin-5	1	0,038	PRDX5
A0A1B0GW38         CBL         E3 ubiquitin-protein ligase CBL         1         0,045           PRDX3 -specific interactors         P62805         H4C1         Histone H4         4,9         0           P02790         HPX         Hemopexin         4,5         0	CBLE3 ubiquitin-protein ligase CBL10,045PR.DX5actorsH4C1Histone H44,90PR.DX1HPXHemopexin4,50PR.DX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PR.DX1SRP72Signal recognition particle subunit SR.P724,20PR.DX1RAB14Ras-related protein Rab-1440PR.DX1	O94925	GLS	Glutaminase kidney isoform, mitochondrial	1	0,04	PRDX5
PRDX3 -specific interactors           P62805         H4C1         Histone H4         4,9         0           P02790         HPX         Hemopexin         4,5         0	actorsH4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	A0A1B0GW38	CBL	E3 ubiquitin-protein ligase CBL	1	0,045	PRDX5
P62805         H4C1         Histone H4         4,9         0           P02790         HPX         Hemopexin         4,5         0	H4C1Histone H44,90PRDX1HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	PRDX3 -specific i	nteractors				
P02790 HPX Hemopexin 4,5 0	HPXHemopexin4,50PRDX1SYNCRIPHeterogeneous nuclear ribonucleoprotein Q4,20PRDX1SRP72Signal recognition particle subunit SRP724,20PRDX1RAB14Ras-related protein Rab-1440PRDX1	P62805	H4C1	Histone H4	4,9	0	PRDX1
	SYNCRIP     Heterogeneous nuclear ribonucleoprotein Q     4,2     0     PRDX1       SRP72     Signal recognition particle subunit SRP72     4,2     0     PRDX1       RAB14     Ras-related protein Rab-14     4     0     PRDX1	P02790	HPX	Hemopexin	4.5	0	PRDX1
O60506 SYNCRIP Heterogeneous nuclear ribonucleoprotein O 4.2 0	SRP72     Signal recognition particle subunit SRP72     4,2     0     PRDX1       RAB14     Ras-related protein Rab-14     4     0     PRDX1	O60506	SYNCRID	Heterogeneous nuclear ribonucleoprotein O	4.2	0	PR DX1
72000 SPD71 Single recognition particle schwii (2) D72104 (2) (2) (2) (2) (2) (2) (2) (2) (2) (2)	RAB14     Ras-related protein Rab-14     4     0     PRDX1	076094	SP D72	Signal recognition particle suburit CD D72	4.2	0	DP DV1
V/00/7 SK7/2 Signal recognition particle subunit SK7/2 4,2 0	KAD14 Kas-related protein Kab-14 4 0 PRDX1	D(110)	DAD1/	Described accession Data 14	4,2	0	PRDAI
P61106 KABI4 Kas-related protein Kab-14 4 0		P61106	KAB14	Kas-related protein Kab-14	4	U	PKDX1

P42704	I R PPR C	Leucine-rich PDR motif-containing protein mitochondrial	3.9	0	PR DX1
D05297	P DI D2	(0S acidia ribasamal protein D2	2 /	0	DP DV1
P(21/7	NTLT2	Descializione de la constructione de la constr	3,4	0	DR DV1
<u>P6516/</u>	DINLLI	Dynem nght en ann 1, eytopiasme	3,5	0	PRDAI
Q4J6C6	PREPL	Prolylendopeptidase-like	3,3	0	PRDXI
Q14257	RCN2	Reticulocalbin-2	3,3	0	PRDX1
P40616	ARL1	ADP-ribosylation factor-like protein 1	3,1	0	PRDX1
P35637	FUS	RNA-binding protein FUS	3,1	0	PRDX1
O95163	ELP1	Elongator complex protein 1	3,1	0	PRDX1
Q15388	TOMM20	Mitochondrial import receptor subunit TOM20 homolog	3,1	0,002	PRDX1
P05386	RPLP1	60S acidic ribosomal protein P1	3	0	PRDX1
P63244	RACK1	Receptor of activated protein C kinase 1	2,9	0	PRDX1
P78417	GST01	Glutathione S-transferase omega-1	2.9	0	PR DX1
08N5K1	CISD2	CDCSH iron-sulfur domain-containing protein 2	2.9	0.003	DR DY1
D(1252	D DI 27	(05 rik scenaril materia L 27	2,9	0,005	DR DV1
P61555	RPL2/		2,0	0	PRDAI
P26196	DDX6	Probable A I P-dependent R NA helicase DDX6	2,8	0	PRDXI
P35606	СОРВ2	Coatomer subunit beta'	2,7	0	PRDX1
P16435	POR	NADPHcytochrome P450 reductase	2,7	0	PRDX1
Q9UBF2	COPG2	Coatomer subunit gamma-2	2,7	0	PRDX1
P40429	RPL13A	60S ribosomal protein L13a	2,7	0	PRDX1
E9PHS0	LANCL1	Glutathione S-transferase LANCL1	2,7	0,001	PRDX1
Q8N2K0	ABHD12	Lysophosphatidylserine lipase ABHD12	2,7	0,003	PRDX1
O94925	GLS	Glutaminase kidnev isoform, mitochondrial	2.6	0	PRDX1
P23588	EIF4B	Fukaryotic translation initiation factor 4B	2.6	0	PR DX1
P50502	ST13	Hec70 interacting protein	2,6	0	DR DY1
OOLIPP 4	ATVN10	Atomic 10	2,6	0	DR DV1
Q90BB4	ATANIO	Ataxin-10	2,6	0	PRDAI
Q0/820	MCLI	Induced myeloid leukemia cell differentiation protein Mcl-1	2,6	0,001	PRDXI
P51148	RAB5C	Ras-related protein Rab-5C	2,6	0,005	PRDX1
Q9NVP1	DDX18	ATP-dependent RNA helicase DDX18	2,5	0	PRDX1
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	2,5	0	PRDX1
Q96CS3	FAF2	FAS-associated factor 2	2,5	0	PRDX1
P98194	ATP2C1	Calcium-transporting ATPase type 2C member 1	2,5	0,001	PRDX1
Q14690	PDCD11	Protein RRP5 homolog	2,5	0,001	PRDX1
P68133	ACTA1	Actin, alpha skeletal muscle	2,5	0,003	PRDX1
077.434	MAVS	Mitochondrial antiviral-signaling protein	2.5	0.003	PR DX1
D11388	TOP2A	DNA topoisomerase 2 alpha	2,5	0	DR DY1
OPTEVO	IDO/	Importin 4	2,4	0	DR DV1
Q81EX)	IIDAC2	Tiportin-4	2,4	0	DR DV1
Q92/69	HDAC2	Histone deacetylase 2	2,4	0	PRDAI
P19338	NCL	Nucleolin	2,4	0	PRDXI
G5EA06	MRPS27	28S ribosomal protein S27, mitochondrial	2,4	0,001	PRDX1
E7ETZ4	BZW2	Basic leucine zipper and W2 domain-containing protein 2	2,4	0,001	PRDX1
Q92621	NUP205	Nuclear pore complex protein Nup205	2,3	0	PRDX1
O14980	XPO1	Exportin-1	2,3	0	PRDX1
P62314	SNRPD1	Small nuclear ribonucleoprotein Sm D1	2,3	0	PRDX1
P27797	CALR	Calreticulin	2,3	0	PRDX1
Q9H3P7	ACBD3	Golgi resident protein GCP60	2,3	0	PRDX1
O9ULC3	RAB23	Ras-related protein Rab-23	2.3	0.001	PR DX1
050NY5	PFX19	Perovin-19	2.3	0.004	PR DX1
092008	LISDON	Probable ubiquitin cathory I terminal hydrolase EA F Y	2,5	0,001	DP DV1
Q/3008	LAD S1	Ladausing and NA lises antenlamia	2,2	0	DR DV1
P41232	IAK31	Isoleucinetriva ligase, cytoplasmic	2,2	0	PRDAI
0953/3	IPO/	Importin-/	2,2	0	PRDXI
Q15393	SF3B3	Splicing factor 3B subunit 3	2,2	0	PRDXI
Q9H0A0	NAT10	RNA cytidine acetyltransferase	2,2	0	PRDX1
075832	PSMD10	26S proteasome non-ATPase regulatory subunit 10	2,2	0	PRDX1
Q92688	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B	2,2	0	PRDX1
K7ERF1	EIF3K	Eukaryotic translation initiation factor 3 subunit K	2,2	0	PRDX1
Q5SY16	NOL9	Polynucleotide 5'-hydroxyl-kinase NOL9	2,2	0,001	PRDX1
Q96EY7	PTCD3	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	2,2	0,001	PRDX1
P28288	ABCD3	ATP-binding cassette sub-family D member 3	2.2	0.001	PR DX1
08NI27	THOC2	THO complex subunit ?	2.2	0.001	PR DX1
096008	TOMM40	Mitachandrial impart recentor subunit TOM/0 homolog	2,2	0.017	DP DV1
D09759	ANIVAC	Amonia AS	2,2	0,01/	DDDV1
100/30 OCUW022	AINAA)		2,1	0	PRDAI
Q5V W32	BROX	BKO1 domain-containing protein BKOX	2,1	0	PRDX1
Q5V166	MTARC1	Mitochondrial amidoxime-reducing component 1	2,1	0	PRDX1
Q9H8Y8	GORASP2	Golgi reassembly-stacking protein 2	2,1	0	PRDX1
P06730	EIF4E	Eukaryotic translation initiation factor 4E	2,1	0	PRDX1
O00203	AP3B1	AP-3 complex subunit beta-1	2,1	0	PRDX1
P61923	COPZ1	Coatomer subunit zeta-1	2,1	0	PRDX1
Q8TC07	TBC1D15	TBC1 domain family member 15	2,1	0	PRDX1
O94826	TOMM70	Mitochondrial import receptor subunit TOM70	2,1	0	PRDX1
		· · ·			

D/303/	DA FA H1B1	Platelet activating factor acetylbydrolase IB subunit beta	2.1	0	DR DY1
001085	TIAI 1	Nucleolycin TLAR	2,1	0.001	PR DY1
Q01005	MVRRD1 A	Mucholysin Third	2,1	0,001	DP DV1
R3KUS5	LISD30	Ubiquitin carboxyl-terminal bydrolace	2,1	0,001	PR DY1
08N/V1	MMGT1	Membrane magnesium transporter 1	2,1	0.002	DR DX1
D6R A00	FNOPH1	Fnolsse-nhosphatase F1	2,1	0.002	PR DX1
095104	SCAF4	SR-related and CTD-associated factor 4	2,1	0.002	PR DX1
08N335	GPD1L	Glycerol-3-phosphate debydrogenase 1-like protein	2,1	0.002	PR DX1
A0A 3B3ISV3	COL4A1	Collagen alpha-1(IV) chain	2.1	0.002	PR DX1
053G00	HSD17B12	Verv-long-chain 3-oxoacyl-CoA reductase	2.1	0.003	PR DX1
A0A0A0MS29	MFF	Mitochondrial fission factor	2,1	0,004	PRDX1
Q8N806	UBR7	Putative E3 ubiquitin-protein ligase UBR7	2,1	0,006	PRDX1
P36957	DLST	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate	2	0	PRDX1
		dehydrogenase complex, mitochondrial			
O75381	PEX14	Peroxisomal membrane protein PEX14	2	0	PRDX1
O94874	UFL1	E3 UFM1-protein ligase 1	2	0	PRDX1
Q9Y678	COPG1	Coatomer subunit gamma-1	2	0	PRDX1
O00410	IPO5	Importin-5	2	0	PRDX1
P12236	SLC25A6	ADP/ATP translocase 3	2	0	PRDX1
P14324	FDPS	Farnesyl pyrophosphate synthase	2	0	PRDX1
Q92973	TNPO1	Transportin-1	2	0	PRDX1
P98175	RBM10	RNA-binding protein 10	2	0	PRDX1
Q9BVP2	GNL3	Guanine nucleotide-binding protein-like 3	2	0,001	PRDX1
015269	SPTLC1	Serine palmitoyltransferase 1	2	0,001	PRDX1
075489	NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	2	0,002	PRDX1
Q8N6T3	ARFGAP1	ADP-ribosylation factor GTPase-activating protein 1	2	0,003	PRDX1
O15144	ARPC2	Actin-related protein 2/3 complex subunit 2	2	0,003	PRDX1
Q9NQ29	LUC7L	Putative RNA-binding protein Luc7-like 1	2	0,003	PRDX1
Q9H9P8	L2HGDH	L-2-hydroxyglutarate dehydrogenase, mitochondrial	2	0,003	PRDX1
P19174	PLCG1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	2	0,003	PRDX1
Q9BSJ8	ESYT1	Extended synaptotagmin-1	2	0,003	PRDX1
P51809	VAMP7	Vesicle-associated membrane protein 7	2	0,015	PRDX1
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	14,7	0	PRDX1
094905	ERLIN2	Erlin-2	1,9	0	PRDX1
P153/4	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	1,9	0	PRDXI
P49321	NASP	Nuclear autoantigenic sperm protein	1,9	0	PRDX1
E/E314	TMDO	Metastasis-associated protein M I A I	1,9	0	PRDA1
P42166	CVR5P 2	NADH cutechrome b5 reductore 2	1,9	0	PRDA1
P35237	SER DINB4	Sernin B4	1,9	0.001	PR DY1
098679	ALIPI	Linid droplet-regulating VI DL assembly factor AUP1	1.9	0.002	PR DX1
096019	ACTL6A	Actin-like protein 6A	1.9	0.003	PR DX1
B9A018	USP39	U4/U6.U5 tri-snRNP-associated protein 2.	1.9	0.003	PR DX1
O9BZK7	TBL1XR1	F-box-like/WD repeat-containing protein TBL1XR1	1.9	0.003	PR DX1
O5IR04	MOV10	RNA helicase	1,9	0,004	PRDX1
P51398	DAP3	28\$ ribosomal protein \$29. mitochondrial	1,9	0,005	PRDX1
Q13190	STX5	Syntaxin-5	1,9	0,005	PRDX1
E9PKG1	PRMT1	Protein arginine N-methyltransferase 1	1,9	0,006	PRDX1
P84085	ARF5	ADP-ribosylation factor 5	1,9	0,011	PRDX1
Q9NQG6	MIEF1	Mitochondrial dynamics protein MID51	1,9	0,014	PRDX1
P13667	PDIA4	Protein disulfide-isomerase A4	1,9	0,017	PRDX1
Q14964	RAB39A	Ras-related protein Rab-39A	1,9	0,039	PRDX1
P08243	ASNS	Asparagine synthetase [glutamine-hydrolyzing]	1,8	0	PRDX1
Q9UIG0	BAZ1B	Tyrosine-protein kinase BAZ1B	1,8	0	PRDX1
O00268	TAF4	Transcription initiation factor TFIID subunit 4	1,8	0	PRDX1
P09211	GSTP1	Glutathione S-transferase P	1,8	0	PRDX1
G8JLH9	STAT3	Signal transducer and activator of transcription	1,8	0	PRDX1
Q8TC12	RDH11	Retinol dehydrogenase 11	1,8	0	PRDX1
Q9HAV4	XPO5	Exportin-5	1,8	0,001	PRDX1
O00231	PSMD11	26S proteasome non-ATPase regulatory subunit 11	1,8	0,001	PRDX1
P31689	DNAJA1	DnaJ homolog subfamily A member 1	1,8	0,001	PRDX1
O75131	CPNE3	Copine-3	1,8	0,001	PRDX1
Q5VYK3	ECPAS	Proteasome adapter and scaffold protein ECM29	1,8	0,004	PRDX1
Q9P287	BCCIP	BRCA2 and CDKN1A-interacting protein	1,8	0,006	PRDX1
O00483	NDUFA4	Cytochrome c oxidase subunit NDUFA4	1,8	0,006	PRDX1
Doman (	CAPN1	Calpain-1 catalytic subunit	1.8	0,006	PRDX1
P0/384	Chinter			· · · · ·	
Q13951	CBFB	Core-binding factor subunit beta	1,8	0,007	PRDX1
Q13951 G3V1C3	CBFB API5	Core-binding factor subunit beta Apoptosis inhibitor 5	1,8 1,8	0,007 0,007	PRDX1 PRDX1

Q9HB07	MYG1	MYG1 exonuclease	1,8	0,008	PRDX1
P46940	IOGAP1	Ras GTPase-activating-like protein IOGAP1	1,8	0,009	PRDX1
H0Y5L2	ECHDC1	Ethylmalonyl-CoA decarboxylase	1,8	0.011	PRDX1
P56962	STX17	Svntaxin-17	1,8	0.014	PRDX1
O60502	OGA	Protein O-GlcNAcase	1,8	0.014	PRDX1
O8NF37	LPCAT1	Lysophosphatidylcholine acyltransferase 1	1,8	0.018	PRDX1
O9Y657	SPIN1	Spindlin-1	1,8	0.028	PRDX1
A0A0B4I1Z1	SR SF7	Serine/arginine-rich-splicing factor 7	1.8	0.034	PR DX1
095376	ARIH2	E3 ubiquitin-protein ligase ARIH2	1.7	0	PR DX1
P11387	TOP1	DNA topoisomerase 1	1.7	0	PR DX1
043707	ACTN4	Alpha-actinin-4	1.7	0	PR DX1
014232	EIF2B1	Translation initiation factor eIF-2B subunit alpha	1.7	0	PR DX1
P53618	COPB1	Coatomer subunit beta	1.7	0	PRDX1
C9I4Z3	R PL 37A	60S ribosomal protein L37a	1.7	0	PR DX1
P38117	ETFB	Electron transfer flavoprotein subunit beta	1.7	0	PR DX1
095573	ACSL3	Long-chain-fatty-acidCoA ligase 3	1.7	0	PR DX1
015691	MAPRE1	Microtubule-associated protein R P/EB family member 1	1.7	0	PR DX1
09NV70	EXOC1	Exocyst complex component 1	1.7	0	PR DX1
P15121	AKR1B1	Aldo-keto reductase family 1 member B1	1.7	0	PR DX1
O9UKG1	APPL1	DCC-interacting protein 13-alpha	1.7	0	PR DX1
095292	VAPB	Vesicle-associated membrane protein-associated protein B/C	1.7	0	PR DX1
016531	DDB1	DNA damage-binding protein 1	1.7	0.001	PR DX1
P42224	STAT1	Signal transducer and activator of transcription 1-alpha/beta	17	0.002	PR DX1
G3V529	DDX24	R NA helicase	17	0.003	PR DX1
098X19	NAA15	N-alpha-acetyltransferase 15 Nat A auxiliary subunit	1.7	0.006	PR DX1
P22830	FFCH	Ferrochelatase mitochondrial	1.7	0.007	PR DX1
09Y262	FIF3I	Fukarvotic translation initiation factor 3 subunit I	1.7	0.007	PR DX1
P04844	R PN2	Dalichyl-dinhosphoaligosaccharideprotein glycosyltransferase subunit 2	1.7	0.01	PR DX1
D68 B59	FYOC3	Exocust complex component 3	1,7	0.013	DR DX1
09N732	ACTR 10	Actin-related protein 10	1,7	0.014	DR DX1
015717	FLAVI 1	FLAV-like protein 1	1,7	0.014	DR DX1
Q1)/1/ O9NWB6	ARGUUI	Arginine and glutamate rich protein 1	1,7	0.015	DR DX1
0961114	A RHD1/B	Protein A BHD1/B	1,7	0.016	DR DX1
01/789	COL CB1	Colorin subfamily B member 1	1,7	0.016	DR DX1
D35579	МУН9	Mussin 9	1,7	0.026	DR DX1
08N573	OYR1	Oxidation registance protein 1	1,7	0.031	DR DX1
I3KDC2	TDT1	Translationally controlled tumor protein	1,7	0.037	DR DX1
09V373	SAMHD1	Decomputer control et anno protein	1,7	0	DR DX1
Q)1525 D05455	SSR	Lupus La protein	1,0	0	DR DX1
C5F A 31	SEC24C	Protein transport protein Sec24C	1,0	0	DR DX1
D23921	R R M1	R ibonucleoside dinhosphate reductase large subunit	1,0	0	DR DX1
D0/181	OAT	Ornithine aminotransferase mitochondrial	1,0	0.001	DR DX1
015054	POLD3	DNA polymerase delta subunit 3	1,0	0.001	DR DX1
Q13034 D55769	SNU12	NHD2 like protein 1	1,6	0,001	DP DV1
002701	CERDZ	CCAAT/ophanear hinding protain gata	1,0	0.002	DP DV1
Q03/01 Q0V2T9	NOCI	Nuclealer complex protein 2 homolog	1,6	0,002	DP DV1
D22992	MCM5	DNA raplication licencing factor MCM5	1,6	0,002	DP DV1
D18031	DTDN1	Twosine-protein phosphatase non-recentor type 1	1,0	0.004	DR DX1
D22214	LIBA1	Ubiguitin like medifier estivating engume 1	1,6	0,004	DP DV1
08WTT2	NOC3I	Nucleolar complex protein 3 homolog	1,0	0,005	DR DX1
Q8W112	R SF1	Remodeling and enacing factor 1	1,0	0.007	DR DX1
015397	IPO8	Importin-8	1,6	0.012	PR DX1
05T307	HEATR1	HEAT repeat-containing protein 1	1,6	0.013	PR DY1
X6R M00	FRC1	FLKS/Rab6_interacting/CAST family member 1	1,0	0.013	DR DX1
I3OR D1	ALDH3A2	Aldebyde debydrogenase family 3 member 4 2	1,6	0.014	PR DY1
O9NYB0	TER F2IP	Telomeric repeat-binding factor 2-interacting protein 1	1,6	0.014	PR DX1
H3BV80	R NPS1	R NA-binding protein with serine-rich domain 1	1.6	0.015	PR DX1
098680	IVNS1 A BD	Influenza virus NS14 binding protein	1,6	0.016	PR DY1
014204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	1.6	0.017	PR DX1
Q11201	FANCI	Fanconi anemia group I protein	1.6	0.018	PR DX1
O9NP72	R A R18	R as related protein R ab. 18	1,0	0.024	DR DX1
001082	SPTBN1	Spectrin heta chain non-erythrocytic 1	1.6	0.024	PR DX1
P52565	ARHGDIA	R ho GDP-dissociation inhibitor 1	1.5	0	PR DX1
P53004	BLVR A	Biliverdin reductase A	15	0	PR DX1
075165	DNAIC13	Dnal homolog subfamily C member 13	15	0	PR DX1
P08240	SR PR A	Signal recognition particle receptor subunit alpha	15	0	PR DX1
007020	R PL 18	60S ribosomal protein L18	15	0	PR DX1
Q9BT78	COPS4	COP9 signalosome complex subunit 4	15	0	PR DX1
09U080	PA 2G4	Proliferation-associated protein 2G4	15	0	PR DX1
~~~~		romenation associated protein 201	-, <i>)</i>	5	. 1(1/211

D78247	CTE2I	Constal transcription factor II I	1.4	0.046	DP DV1
D2170/	UDAC1	When have been a been a set of the set of th	1,4	0,040	PRDA1
P21/96	V DACI		1,4	0,048	PRDAI
Q91580	RBM7	KNA-binding protein /	1,4	0,049	PRDXI
Q6WCQ1	MPRIP	Myosin phosphatase Rho-interacting protein	1,3	0	PRDX1
Q15029	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	1,3	0	PRDX1
Q9BRA2	TXNDC17	Thioredoxin domain-containing protein 17	1,3	0	PRDX1
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	1,3	0	PRDX1
P34949	MPI	Mannose-6-phosphate isomerase	1,3	0	PRDX1
P17987	TCP1	T-complex protein 1 subunit alpha	1.3	0	PR DX1
ACNERS	PNDED	Aminonentidasa B	1,3	0	DP DV1
120150	KNFLF SCO1	Provide SCO1 have been been been been been been been be	1,5	0	PRDA1
<u>J3QL56</u>	SCOI	Protein SCOI homolog, mitochondrial	1,3	0	PRDXI
P61247	RP\$3A	40S ribosomal protein S3a	1,3	0	PRDX1
P23396	RPS3	40S ribosomal protein S3	1,3	0	PRDX1
Q00325	SLC25A3	Phosphate carrier protein, mitochondrial	1,3	0	PRDX1
Q12788	TBL3	Transducin beta-like protein 3	1,3	0,001	PRDX1
P43246	MSH2	DNA mismatch repair protein Msh2	1,3	0,001	PRDX1
P60228	EIF3E	Eukarvotic translation initiation factor 3 subunit E	1.3	0.001	PR DX1
060934	NBN	Nibrin	1.3	0.001	DR DY1
OOUTA	NDO7	Function 7	1,5	0,001	DD DV1
Q90IA9	APO/		1,5	0,005	PRDAI
P180/7	RPL35A	608 ribosomal protein L35a	1,3	0,004	PRDXI
Q9UI12	ATP6V1H	V-type proton ATPase subunit H	1,3	0,005	PRDX1
E9PKP7	UBTF	Nucleolar transcription factor 1	1,3	0,005	PRDX1
Q12996	CSTF3	Cleavage stimulation factor subunit 3	1,3	0,005	PRDX1
Q9Y5J1	UTP18	U3 small nucleolar RNA-associated protein 18 homolog	1,3	0,005	PRDX1
09Y2O3	GSTK1	Glutathione S-transferase kappa 1	1.3	0.006	PR DX1
000610	CLTC	Clathrin heavy chain 1	13	0.008	PR DX1
0058(1	DDNT1		1,5	0,000	DD DV1
093861	DPINII	5 (2 ), 5 -bisphosphate nucleotidase 1	1,5	0,009	PRDAI
095202	LEIMI	Mitochondrial proton/calcium exchanger protein	1,3	0,013	PRDXI
O15042	U2SURP	U2 snRNP-associated SURP motif-containing protein	1,3	0,015	PRDX1
P47897	QARS1	GlutaminetRNA ligase	1,3	0,018	PRDX1
Q9Y6Y8	SEC23IP	SEC23-interacting protein	1,3	0,018	PRDX1
O00629	KPNA4	Importin subunit alpha-3	1,3	0,022	PRDX1
O9UG63	ABCF2	ATP-binding cassette sub-family F member 2	1.3	0.023	PRDX1
09Y2H1	STK38L	Serine/threonine-protein kinase 38-like	13	0.033	PR DX1
09/789	ULUP E1	F2 ubiquitin protoin ligan LIUP F1	1,3	0.045	DP DV1
Q70188	VTUDE	ES ubiquitili-proteining ase Official	1,5	0,043	PRDAI
Qabila	YIHDFI	I H domain-containing family protein 1	1,3	0,046	PRDXI
075367	MACROH2A1	Core histone macro-H2A.1	1,3	0,046	PRDX1
Q8NBY1	STK26	Serine/threonine-protein kinase 26	1,3	0,046	PRDX1
P08572	COL4A2	Collagen alpha-2(IV) chain [Cleaved into: Canstatin]	1,3	0,046	PRDX1
Q86TI2	DPP9	Dipeptidyl peptidase 9	1,3	0,047	PRDX1
Q13439	GOLGA4	Golgin subfamily A member 4	1,3	0,049	PRDX1
P56537	EIF6	Eukarvotic translation initiation factor 6	1.2	0	PR DX1
D0/899	CNA12	Guanine nucleotide binding protein G(i) subunit alpha 2	1.2	0	DR DY1
DC1140	D A D7A	Du sale a la serie D. l. 7.	1,2	0	DDDV1
1 31147	KAD/A	Ras-related protein Rab-/a	1,2	0	PRDAI
075396	SEC22B	Vesicle-trafficking protein SEC22b	1,2	0,001	PRDX1
Q99613	EIF3C	Eukaryotic translation initiation factor 3 subunit C	1,2	0,001	PRDX1
Q99567	NUP88	Nuclear pore complex protein Nup88	1,2	0,003	PRDX1
Q5JY65	CRNKL1	Crooked neck-like protein 1	1,2	0,003	PRDX1
P06744	GPI	Glucose-6-phosphate isomerase	1,2	0,003	PRDX1
P31943	HNR NPH1	Heterogeneous nuclear ribonucleoprotein H	1.2	0.004	PR DX1
O5T760	SR SF11	Serine/arginine-rich-splicing factor 11	1.2	0.005	PR DX1
Q)1700	TWE2		1,2	0,000	DD DV1
Q61B30	1 WF2		1,2	0,006	PRDAI
0949/3	AP2A2	AP-2 complex subunit alpha-2	1,2	0,007	PRDXI
P43897	TSFM	Elongation factor Ts, mitochondrial	1,2	0,008	PRDX1
O60678	PRMT3	Protein arginine N-methyltransferase 3	1,2	0,009	PRDX1
P56192	MARS1	MethioninetRNA ligase, cytoplasmic	1,2	0,009	PRDX1
P46199	MTIF2	Translation initiation factor IF-2, mitochondrial	1,2	0,01	PRDX1
Q9H8H0	NOL11	Nucleolar protein 11	1,2	0,01	PRDX1
O9H0E2	TOLLIP	Toll-interacting protein	1.2	0.013	PR DX1
PODPB6	POLR 1D	DNA-directed RNA polymerases Land III subunit R PAC2	1.2	0.013	PR DX1
053H12	ACK	Acylglycerol kinase mitochondrial	1.2	0.015	DR DV1
0(020(	AOD	D XA Laliance minimumana	1,2	0,015	DDDDV1
060306	AQK	KINA nencase aquarius	1,2	0,016	PRDAI
Q9Y5L0	TNPO3	Iransportin-3	1,2	0,019	PRDX1
P35659	DEK	Protein DEK	1,2	0,019	PRDX1
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	1,2	0,022	PRDX1
O75688	PPM1B	Protein phosphatase 1B	1,2	0,025	PRDX1
O9NOG5	RPRD1B	Regulation of nuclear pre-mRNA domain-containing protein 1B	1,2	0,025	PRDX1
P23284	PPIB	Pentidyl-prolyl cis-trans isomerase B	1.2	0.026	PR DX1
D20740	SED DINID1	Laukoauto alastasa indibitar	1.2	0.027	DP DV1
1 JU/10	JERTINDI	LEUROCYTE CLASTASE IIIIIDITOL	1,2	0,02/	I KDA1

P27824	CANX	Calnexin	1,2	0,032	PRDX1
Q9Y2X3	NOP58	Nucleolar protein 58	1,2	0,036	PRDX1
Q9BTT0	ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family member E	1,2	0,038	PRDX1
E7EVH7	E7EVH7	Kinesin light chain	1.2	0,045	PRDX1
M0R 026	II VBL	2-hydroxyacyl-CoA lyase 2	11	0	PR DX1
099733	NAP1L4	Nucleosome assembly protein 1-like 4	11	0	PR DX1
D09960	LTA/U	Laukotrione A / hydrolese	1 1	0	DP DV1
P07760	CI COS A S	ADD/ATD	1,1	0	DR DV1
P05141	SLC25A5	ADP/ATP transiocase 2	1,1	0	PRDAI
Q9B1X1	NDCI	Nucleoporin NDCI	1,1	0	PRDXI
Q7Z4H7	HAUS6	HAUS augmin-like complex subunit 6	1,1	0,001	PRDX1
J3QLD9	FLOT2	Flotillin	1,1	0,001	PRDX1
Q96A33	CCDC47	Coiled-coil domain-containing protein 47	1,1	0,001	PRDX1
C9J8Q5	ALDH5A1	Succinate-semialdehyde dehydrogenase	1,1	0,001	PRDX1
P49327	FASN	Fatty acid synthase	1,1	0,001	PRDX1
P07814	EPRS1	Bifunctional glutamate/prolinetRNA ligase	1,1	0,002	PRDX1
O9NO88	TIGAR	Fructose-2,6-bisphosphatase TIGAR	1,1	0,002	PRDX1
P31942	HNRNPH3	Heterogeneous nuclear ribonucleoprotein H3	11	0.004	PR DX1
F9PIF2	DDX10	R NA helicase	11	0.005	PR DX1
D25572	ACI	Chargen debauerbing ensure	1,1	0,005	DR DV1
P 333/ 3	AD2A1	A D 2 secolo subscript local	1,1	0,006	PRDA1
095/82	APZAI	AP-2 complex subunit alpha-1	1,1	0,006	PRDXI
075874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	1,1	0,006	PRDX1
A0A024R4M0	RPS9	40S ribosomal protein S9	1,1	0,006	PRDX1
Q9UNM6	PSMD13	26S proteasome non-ATPase regulatory subunit 13	1,1	0,007	PRDX1
P52948	NUP98	Nuclear pore complex protein Nup98-Nup96	1,1	0,008	PRDX1
Q5T3I0	GPATCH4	G patch domain-containing protein 4	1,1	0,008	PRDX1
P46087	NOP2	Probable 28S rRNA	1,1	0,01	PRDX1
Q13085	ACACA	Acetyl-CoA carboxylase 1	1,1	0,011	PRDX1
O9Y4E8	USP15	Ubiquitin carboxyl-terminal hydrolase 15	1.1	0.014	PR DX1
A0A 2R 8Y566	RFLCH	R A R11-binding protein R FL CH	11	0.015	PR DX1
015226	NEDE	NE kappa B represeing factor	1,1	0.015	DR DV1
013226	D DC27I	(OC il constanti	1,1	0,015	PRDA1
Q/10M5	KP52/L	405 ribosomai protein 52/-like	1,1	0,015	PRDAI
095433	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1	1,1	0,017	PRDX1
Q9Y371	SH3GLB1	Endophilin-B1	1,1	0,018	PRDX1
Q9BYG3	NIFK	MKI67 FHA domain-interacting nucleolar phosphoprotein	1,1	0,019	PRDX1
O14776	TCERG1	Transcription elongation regulator 1	1,1	0,02	PRDX1
P08670	VIM	Vimentin	1,1	0,023	PRDX1
P39687	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A	1,1	0,024	PRDX1
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating	1,1	0,025	PRDX1
099426	TBCB	Tubulin-folding cofactor B	1.1	0.025	PR DX1
P26583	HMGB2	High mobility group protein B2	11	0.025	PR DX1
096TC7	R MDN3	Regulator of microtubule dynamics protein 3	1 1	0.032	DR DY1
000045	COD D1	EACT complex suburit SSD D1	1,1	0,032	DR DV1
Q08745	DDD/D 24		1,1	0,035	PRDAI
Q61N85	PPP4K3A	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	1,1	0,034	PRDXI
Q9H0U4	RAB1B	Ras-related protein Rab-1B	1,1	0,034	PRDX1
P62258	YWHAE	14-3-3 protein epsilon	1,1	0,034	PRDX1
F8W0J6	NAP1L1	Nucleosome assembly protein 1-like 1	1,1	0,034	PRDX1
Q9C0B0	UNK	RING finger protein unkempt homolog	1,1	0,034	PRDX1
Q8IZ73	RPUSD2	RNA pseudouridylate synthase domain-containing protein 2	1,1	0,036	PRDX1
O43776	NARS1	AsparaginetRNA ligase, cytoplasmic	1	0	PRDX1
P23528	CFL1	Cofilin-1	1	0	PRDX1
O5H928	HSD17B10	3-hvdroxvacvl-CoA dehvdrogenase type-2	1	0	PRDX1
095168	NDUFR4	NADH dehydrogenase [ubiguinone] 1 beta subcomplex subunit 4	- 1	0.001	PR DX1
D62136	DDD1C A	Serine/threenine-protein phoephotace DD1 alpha catalutic subunit	1	0.001	DR DV1
D(910/	FFFICA FFF1A1	Flopgetion factor 1 alpha 1	1	0,001	DD DV1
100104	LEFIAI	Elongation factor 1-april 1	1	0,002	PRDAI
AUAU8/WXC5	NDUFA10	NADH dehydrogenase [ubiquinone] I alpha subcomplex subunit 10, mitochondrial	1	0,002	PKDXI
075083	WDR1	WD repeat-containing protein 1	1	0,004	PRDX1
P31040	SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	1	0,005	PRDX1
Q9BV20	MRI1	Methylthioribose-1-phosphate isomerase	1	0,007	PRDX1
P60953	CDC42	Cell division control protein 42 homolog	1	0,008	PRDX1
P55060	CSE1L	Exportin-2	1	0,011	PRDX1
Q09161	NCBP1	Nuclear cap-binding protein subunit 1	1	0,024	PRDX1
P15927	RPA2	Replication protein A 32 kDa subunit	1	0.027	PRDX1
O00273	DFFA	DNA fragmentation factor subunit alpha	1	0.027	PR DX1
09NVV2	NI E1	Notchless protein homolog 1	1	0.02 /	DR DV1
07(002	CLDV2	Characteria 2	1	0,034	DDDV1
0/6003	GLKAJ		1	0,036	PRDAI
060885	BRD4	Bromodomain-containing protein 4	1	0,046	PRDX1
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	8,9	0	PRDX2
Q15388	TOMM20	Mitochondrial import receptor subunit TOM20 homolog	3,6	0,001	PRDX2
P78417	GSTO1	Glutathione S-transferase omega-1	2,8	0	PRDX2

ONIZKO	ABUD12	Lycophoenhatidylcoring linges A RUD12	2.8	0.003	DP DV2
Q01V2K0	ADIID12		2,0	0,003	PRDA2
P30519	HMOA2	PNA Li	2,/	0,007	PRDA2
P981/5	KBM10	KNA-binding protein 10	2,6	0	PRDX2
Q8N5K1	CISD2	CDGSH iron-sulfur domain-containing protein 2	2,6	0,007	PRDX2
Q07820	MCL1	Induced myeloid leukemia cell differentiation protein Mcl-1	2,5	0	PRDX2
B3KUS5	USP30	Ubiquitin carboxyl-terminal hydrolase	2,5	0	PRDX2
A0A3B3ITJ4	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	2,5	0,001	PRDX2
Q16352	INA	Alpha-internexin	2,3	0	PRDX2
Q8N6T3	ARFGAP1	ADP-ribosylation factor GTPase-activating protein 1	2,3	0,001	PRDX2
Q8N4V1	MMGT1	Membrane magnesium transporter 1	2,3	0,002	PRDX2
A0A0A0MS29	MFF	Mitochondrial fission factor	2.3	0.003	PRDX2
A0A0A0MR02	VDAC2	Quiter mitochondrial membrane protein porin?	2,5	0	PR DY2
01/257	PCN2	Patienda aultria 2	2,2	0.001	DR DV2
Q1423/	RCIN2		2,2	0,001	PRDA2
Q9Y2H1	S1K38L	Serine/threonine-protein kinase 38-like	2,2	0,008	PRDX2
096008	TOMM40	Mitochondrial import receptor subunit TOM40 homolog	2,2	0,021	PRDX2
Q13464	ROCK1	Rho-associated protein kinase 1	2,1	0	PRDX2
Q9NQG6	MIEF1	Mitochondrial dynamics protein MID51	2,1	0,01	PRDX2
Q15075	EEA1	Early endosome antigen 1	2	0	PRDX2
O75688	PPM1B	Protein phosphatase 1B	2	0,001	PRDX2
H0Y5L2	ECHDC1	Ethylmalonyl-CoA decarboxylase	2	0,008	PRDX2
P56962	STX17	Syntaxin-17	2	0.01	PRDX2
014789	GOLGB1	Golgin subfamily B member 1	2	0.011	PR DX2
097(57	SDIN1		2	0.021	DR DV2
Q9163/	DADGO	Spindin-1	2	0,021	PRDA2
P51148	KABSC	Ras-related protein Rab-5C	2	0,021	PRDX2
Q5SZR4	TDRKH	Tudor and KH domain containing, isoform CRA_a	2	0,04	PRDX2
O00268	TAF4	Transcription initiation factor TFIID subunit 4	1,9	0	PRDX2
Q9Y679	AUP1	Lipid droplet-regulating VLDL assembly factor AUP1	1,9	0,002	PRDX2
O00629	KPNA4	Importin subunit alpha-3	1,9	0,002	PRDX2
H3BPE1	MACF1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	1,9	0,003	PRDX2
Q8N6R0	EEF1AKNMT	eEF1A lysine and N-terminal methyltransferase	1,9	0,007	PRDX2
P57076	CFAP298	Cilia- and flagella-associated protein 298	19	0.01	PR DX2
09V371	SH3CLB1	Endophilin.B1	1.8	0	PR DY2
Q713/1 Q8W/TT2	NOC2L	Nuclealer complex protein 2 homolog	1,0	0.002	DR DV2
Q8W112	NUCSL	Nucleolar complex protein 5 homolog	1,0	0,002	PRDA2
Q92667	AKAPI	A-kinase anchor protein 1, mitochondrial	1,8	0,005	PRDX2
J3QRD1	ALDH3A2	Aldehyde dehydrogenase family 3 member A2	1,8	0,009	PRDX2
Q6ZVM7	TOM1L2	TOM1-like protein 2	1,8	0,011	PRDX2
Q8TB36	GDAP1	Ganglioside-induced differentiation-associated protein 1	1,8	0,013	PRDX2
O60566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	1,8	0,024	PRDX2
Q7Z3C6	ATG9A	Autophagy-related protein 9A	1,8	0,033	PRDX2
O8TCG1	CIP2A	Protein CIP2A	1.7	0	PRDX2
O5T3I0	GPATCH4	G patch domain-containing protein 4	17	0	PR DX2
013/51	EK BD5	Dentidul prolyl cis trans isomerase FK RDS	17	0	PR DY2
042822		A him one and an analysis of the second seco	1,7	0.002	DR DV2
043825	AKAPo	A-kinase anchor protein 8	1,7	0,002	PRDAZ
P18031	PIPNI	Tyrosine-protein phosphatase non-receptor type 1	1,/	0,002	PRDX2
F5H008	VPS33B	Vacuolar protein sorting-associated protein 33B	1,7	0,033	PRDX2
P35580	MYH10	Myosin-10	1,6	0	PRDX2
P56182	RRP1	Ribosomal RNA processing protein 1 homolog A	1,6	0	PRDX2
Q8TC07	TBC1D15	TBC1 domain family member 15	1,6	0	PRDX2
Q4J6C6	PREPL	Prolyl endopeptidase-like	1,6	0	PRDX2
Q9UBB4	ATXN10	Ataxin-10	1,6	0	PRDX2
Q96CS3	FAF2	FAS-associated factor 2	1.6	0.001	PRDX2
K7FSF9	BCAS3	Breast carcinoma.amplified sequence 3	1.6	0.002	PR DX2
E7ESD9	NEEM	160kDa neurofilament protein	1,0	0.006	DP DY2
CORVER	CNU 2	Consistent of the line protection life 2	1,0	0,006	PRDA2
Q9BVP2	GNL3	Guanine nucleotide-binding protein-like 5	1,6	0,006	PRDAZ
A0A2Q21H//	A0A2Q21H//	>tr A0A2Q21H// A0A2Q21H//_HUMAN Golgin subfamily A member 2	1,6	0,026	PRDX2
		OS=Homo sapiens OX=9606 GN=GOLGA2 PE=1 SV=1;>sp[Q083/9]GOGA2_			
		HUMAN Golgin subramily A member 2 US=Homo sapiens UA=9606 GN=GULGA2			
		PE=15v=5;>tr A0A1w2PQ15 A0A1w2PQ15_HUMAN Goigin subramily A member			
P23284	PPIB	Peptidyl-prolyl cis-trans isomerase B	1,6	0,028	PRDX2
Q96T88	UHRF1	E3 ubiquitin-protein ligase UHRF1	1,6	0,029	PRDX2
P48449	LSS	Lanosterol synthase	1,6	0,036	PRDX2
Q8ND04	SMG8	Protein SMG8	1,6	0,038	PRDX2
Q9BZG1	RAB34	Ras-related protein Rab-34	1,6	0,049	PRDX2
P42166	ТМРО	Lamina-associated polypeptide 2, isoform alpha	1,5	0	PRDX2
06WC01	MPRIP	Myosin phosphatase R ho-interacting protein	15	0	PR DX2
095373	IPO7	Importin.7	15	0.001	DR DY2
07373	ETCI2	mportury	1,5	0,001	DD DV2
Q81181	r 1 5J3	pre-rk/NA 2-O-ribose K/NA methyltransterase F 15J3	1,5	0,001	PKDX2
Q9N Y61	AAIF	Protein AA1F	1,5	0,001	PKDX2
014579	COPE	Coatomer subunit epsilon	1,5	0,001	PRDX2
O00505	KPNA3	Importin subunit alpha-4	1,5	0,002	PRDX2

OVTO         MTARCA         Mice-bandral anisotion-scheming component         1.5         0.002           OVD0261         MARCAS         WINN Predices main: associated scine dependent regulator of chronic nubrkamily         1.5         0.009           PRINP         Marched S         Marched S         0.009         1.5         0.009           PRINP         Marched S         0.009         1.5         0.001           PRINP         Marched SK (KR) based         0.001         0.002         1.5         0.002           QVM00         POCTID         Detates (KR) based         0.5         0.004         1.5         0.004           QVM01         LASIL         Rubancing population (TASIL)         1.6         0.014         1.4         0.01         1.9           QVM02         LASIL         Rubancing population (TASIL)         1.4         0.001         1.0         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         1.0         0.001         0.001         0.0         0.001         0.001						
Odd2A         SMARAS         SWIANF-scient matrix-associal actiniz-gendent regulator of thematin authenal J.         1.5         4.007           QPNOYA         SIG23M         SIG23M contrastruing partial         1.5         0.001         1           AdAGAS         DCTNID         Drankenin submits         1.5         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         1         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         0.001         <	Q5VT66	MTARC1	Mitochondrial amidoxime-reducing component 1	1,5	0,002	PRDX2
Anombre 5           PRIV3 CC3.JBrezzing protein         1.5         0.049           PRIV4 ATP2.0         Calcium ransporting ATPser type C member 1         1.5         0.041           QMSKS         DVCTNS         Dreatin submits         1.5         0.042           QMSW         PDCD1         Present RAP: benolog.         1.5         0.042           QMSM         DVCTNS         Dreatin RAP: benolog.         0.042         0.042           QMSM2         LASII         Belowing interpretation of the interpretat	O60264	SMARCA5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily	1,5	0,007	PRDX2
QPUP18         SIC2.310P         S			A member 5			
PM194         ATTPSC1         Calclustromsporting ATDex type 2C needed 1         1,5         0.014           QH-600         PDCCD11         Potentin RAPS homolog.         1,5         0.032           QH-600         PDCCD11         Potentin RAPS homolog.         1,5         0.032           P4013         MLK0         Polifistion marker protein RA-16.         1,3         0.047           QP1902         LASLL         Albosomal longering protein RA-16.         1,4         0           QP19142         TXNDC/T         Threedomic containing protein 17         1,4         0           QP19142         TXNDC/T         Threedomic containing protein 1         1,4         0           QP19143         USP15         Use protein containing protein 1         1,4         0.001           QP19140         SLC274.         Lange-during protein 4         1,4         0.003           QV1100         RF11         Telemond during protein 1         1,4         0.004           QV1004         RF11         Telemond during protein 4         1,4         0.004           QV1004         RF11         Telemond during protein 4         1,4         0.004           QV1004         RF11         Telemond during protein 4         1,4         0.001	Q9Y6Y8	SEC23IP	SEC23-interacting protein	1,5	0,009	PRDX2
X4RCB3         DC1N3         Dyractin subanis         1.5         0.021           QP447         PCCD11         Francischine-phosphare crythylfranderase         1.5         0.042           QP447         PCCD12         Francischine-phosphare crythylfranderase         1.5         0.042           QP4472         LASIL         Rebound Isogenes protein LASIL         1.5         0.042           QP4472         LASIL         Rebound Isogenes protein 1         1.4         0           QP1612         RED11         Enclude Mydrogenes 1         1.4         0           QP1612         RED14         Enclude Mydrogenes 1         1.4         0           QP1614         US9154         Use chart system receptor subant TOM 34         1.4         0.003           QP1016         TMMA4         Methode Mydrogenes receptor subant TOM 34         1.4         0.003           QP1016         Methode Mydrogenes receptor subant TOM 34         1.4         0.004           QP1016         Methode Mydrogenes receptor subant TOM 34         1.4         0.004           QP1016         Methode Mydrogenes receptor subant TOM 34         1.4         0.004           QP1016         MACM 222         Carchiteres merce-HZA2         1.4         0.004           QP1021	P98194	ATP2C1	Calcium-transporting ATPase type 2C member 1	1,5	0,014	PRDX2
Q4690         PICVT1         Preterin RAPS homolog         1,5         0.032           P4003         MKio         Polification muck protein K-62         1,5         0.047           Q7092         LASLE         RAbboard longerest protein LASL         1,3         0.048           Q7082         LPI         Designation domain containing protein 17         1,4         0           Q7082         LPI         Designation domain containing protein 17         1,4         0           Q7083         USP13         Designation domain containing protein 17         1,4         0           Q7084         USP13         Designation domain containing protein 17         1,4         0,001           Q7094         USP13         Designation domain containing protein 27         1,4         0,003           Q41700         SLC27A         Long chain frant call arrange trappoint TM44         1,4         0,003           Q41700         RF14         Telencontex-RAL         1,4         0,004         1           Q47904         MACQ0422.         Conchinos muccontex-RAL         1,4         0,004         1           Q47904         RM4C RALA         Conchinos muccontex-RAL         1,4         0,004         1           Q47904         RM110         Laccontex-RA	X6RCK5	DCTN3	Dynactin subunit 3	1,5	0,024	PRDX2
QP147         PCVT2         Enhansmine phashes cytridyfitzenterase         1,5         0,402           QP1692         LASIL         Robered is specification containing protein 17         1,4         0           QP1692         LASIL         Robered is specification containing protein 17         1,4         0           QP1613         ELP1         Element containing protein 17         1,4         0           QP1614         LSP15         Ubication containing protein 1         1,4         0           QP1712         RADINA         Lage contain containing protein 2         1,4         0,002           QP1783         US915         Ubication containing protein 2         1,4         0,002           QP1793         Matchedonial Contain term contain containing contain 100454         1,4         0,003           QP1794         Matchedonial Contain term contain containing contain 2         1,4         0,004           QP1795         ILP         Imminion phalophysic requires usand TDATS4         1,4         0,004           QP1795         ILP         Imminion phalophysic requires usand TDATS4         1,4         0,005           QP1794         ILATR1         IELA         Contains contain protein 4         1,4         0,015           QP1794         ILATR1         IELA <td>Q14690</td> <td>PDCD11</td> <td>Protein RRP5 homolog</td> <td>1,5</td> <td>0,032</td> <td>PRDX2</td>	Q14690	PDCD11	Protein RRP5 homolog	1,5	0,032	PRDX2
P4013         ML12         Penditrian marker protein k.67         1,5         0,448           QPRV202         LASIL         K.Booumil biogroups protein 17         1,4         0           QPRA24         TXNDC17         Therefore protein 17         1,4         0           QPRA24         TXNDC17         Therefore protein 17         1,4         0           QPT1618         LUP1         Enhance to protein 17         1,4         0           QPT1628         US131         1,4         0,0011         1,4         0,0011           QPT1648         US131         1,4         0,0012         1,4         0,0012           QPT1648         US131         1,4         0,0013         1,4         0,0033           QPU100         RT11         Teleformer structure protein RT12         1,4         0,0046           QPU104         MC124         Carc hintere machine protein LaC <sup>1</sup> like 1         1,4         0,0046           QPU102         LUC1         Paratext RAA binding protein LaC <sup>1</sup> like 1         1,4         0,001           QPU645         RTM12         Like 2         Like 4         0,011         1,2         0,011           QPU645         RTM12         Like 4         0,011         0,011         0,011 </td <td>Q99447</td> <td>PCYT2</td> <td>Ethanolamine-phosphate cytidylyltransferase</td> <td>1,5</td> <td>0,032</td> <td>PRDX2</td>	Q99447	PCYT2	Ethanolamine-phosphate cytidylyltransferase	1,5	0,032	PRDX2
QP14V2         LASIL         K Boesend Issgeries protein 1 (A)         1.4         0           QP18L2         TXNDCCT         TNDCCT         1.4         0           QP142         ELP1         Ebergare complex protein 1         1.4         0           QP1412         RDP11         Eledits of Marchand State 13         1.4         0           QP148         USP15         Usage complex protein 4         1.4         0.001           QP148         USP15         Usage complex protein 4         1.4         0.002           QP1400         SLC27A         Long-Child Transform remote marchand transformer marchand	P46013	MKI67	Proliferation marker protein Ki-67	1,5	0,047	PRDX2
QPBRA2         1 ANDL/         Instruction down occurs in protein 1/         1,4         0           QPTR163         ELP1         Reingstee organization growth in 1         1,4         0           QPTR164         DNP15         IDinguitric down-opterminal hypotrate 15         1,4         0,001           QPTR163         DNP15         TOMM34         Monobardial import receptor subunit TOM34         1,4         0,002           QPTR163         DNM54         Monobardial import temports and the temport accuration accu	Q9Y4W2	LASIL	Ribosomal biogenesis protein LAS1L	1,5	0,048	PRDX2
D29163         LDP         Lingster compare protein 1         1.4         0           Q297612         KDP111         Renind delytopagess 11         1.4         0           Q297628         USP15         Ubagatini carboxy-terminal hydrolau 15         1.4         0.001           Q297685         TOMM14         Mitochondrial incert resport subanit TOM34         1.4         0.003           Q297100         REF1         Tedmostroper subanit Tomatic resport subanit TOM34         1.4         0.003           Q201100         REF1         Tedmostroper subanit Tomatic resport subanit TOM34         1.4         0.004           Q20100         RELIN2         Careb biasom ancore 12A.2         1.4         0.006           Q20120         RBM6         RNA-biading protein fac721kc 1         1.4         0.006           Q20120         RBM6         RNA-biading protein fac721kc 1         1.4         0.01           Q20120         RLM6         RNA-biading protein fac721kc 1         1.4         0.01           Q20122         PUPR33         Senici Athenian protein fac721kc 1         1.4         0.01           Q20130         RLM6         RNA-biading protein fac721kc 1         1.4         0.04           Q20132         PUPR33         Senici Athenia fac721kc 1	Q9BRA2	TXNDC1/	I hioredoxin domain-containing protein 1/	1,4	0	PRDX2
QB10.12         KUP11         Netlini Ketting Sector subanit TOM34         1.4         0.001           QB7828         TOMM04         Micebondral import receptor subanit TOM34         1.4         0.003           QB7848         TOMM04         Micebondral import receptor subanit TOM34         1.4         0.003           QB7848         TIMM44         Micebondral import incer methrane transforces subanit TDM44         1.4         0.003           QB7904         MiceBondral import incer methrane transforces subanit TDM44         1.4         0.004           QP1040         MiceBondral import incer H2A.2         1.4         0.004           QP1923         IUP         junction placoglobin         1.4         0.006           QP1924         IUC7.         Partner RNA binding protein in Lar-Tike 1         1.4         0.006           QP1024         IUTA         ITTA repear comarining protein in Lar-Tike 1         1.4         0.015           QP1350         REM6         RNA binding protein face Tike 1         1.4         0.021           QP1352         ILF48         Interview RNA binding protein face Tike 1         1.4         0.041           QP1352         ILF48         Interview RNA binding protein face Tike 1         1.4         0.042           QP1354         ITTG11         A	095163	ELPI	Elongator complex protein 1	1,4	0	PRDX2
CPT1E3         Constrain Category emmining Parsake 70         1.4         0.001           QPT1M0         SLC.27A4         Lang chain firty acid transport protein 4         1.4         0.003           QPT1M0         SLC.27A4         Lang chain firty acid transport protein 4         1.4         0.003           QPU100         RTF1         Tobuscoper acid transport protein 70         1.4         0.004           QPU104         MACROPL20         Core bisoon more PEA.2         1.4         0.004           QPU046         MACROPL20         Core bisoon more PEA.2         1.4         0.005           QPU052         RBM6         RNAbiding protein 6.         1.4         0.006           QPU202         LUC7L         Patrick RNA-biding protein 6.         1.4         0.006           QPU304         OTU204         OTU domain comarining protein 1         1.4         0.01           P23272         MPG         DNA-3-metribulation factory abunt 3         1.4         0.048           QPU304         OTU204         OTU30-metribulation factory abunt 3         1.4         0.048           P23272         MPG         DNA-3-metribulation factory abunt 3         1.4         0.048           P4179         MT12         Transdabun inininin factory abunt 3         1.4         <	Q81C12	KDHII	Ketinol dehydrogenase 11	1,4	0	PRDX2
Q27:53         1.00x131         2.00x133         2.00x133         2.00x133           Q4P1M0         SLG27A4         Long-chain frequency sectors         1.4         0.003         1           Q45015         T1MM44         Micochondrial importing motion and sectors         1.4         0.003         1           Q49016         MACRO112A2         Constitution marces 112A.2         1.4         0.004         1           Q49046         MACRO112A2         Constitution marces 112A.2         1.4         0.004         1           Q49055         FRLINZ         Linit-2         1.4         0.006         1           Q49050         RMA         Number constraining protein factors         1.4         0.006         1           Q49052         LUC7L         Putative RNA-sheading protein factors         1.4         0.011         1           Q57320         HEATRI         HEAT repeat-constaining protein factors         1.4         0.022         1           Q57452         MFG         DNA-smechyladenic glycosylase         1.4         0.044         1           Q57453         ATGI6L1         Aurophage-related protein factor 4         1.4         0.048         1           Q45045         ATGI6L1         Aurophage-related protein factor 4	Q914E8	USP15	Ubiquitin carboxyl-terminal hydrolase 15	1,4	0,001	PRDX2
Qer Low         3.6.2.74         Lönge until hör könd möngör fjörkörn –         1,4         0.003           QVUIP0         R1P1         Telomer-associared protein R1P1         1,4         0.003           QVUIP0         R1P1         Telomer-associared protein R1P1         1,4         0.004           QVUIP0         R1P1         Jure interine pikagelsin         1,4         0.004           QV0295         R1MA         RNA         0.005         1,4         0.005           QV0295         R1MA         RNA         0.005         1,4         0.006           QV0295         LUC7L         Purative RNA-binding protein fac?tike 1         1,4         0.01         1           QV1804         OTUD4         OTU domain-containing protein 1         1,4         0.01         1           P23325         EIF4B         Eldaryoric tranalation initation factor 61         1,4         0.01         1           P23325         MFG         DNA-4-methyladening phycospitase 6 regulatory ubenit 3         1,4         0.04         1           P46929         MTTE2         Tranalation initiation factor IF2, minochondrial         1,4         0.04         1           P6452         PEX5         Perosithomalogy ubenology ubenology ubenology         1,3         0.01	Q15/85	SL C274.4	L and a height for the contract protocol and the contract of t	1,4	0,002	PRDA2
Organ         1100000         11000000         1.1         1.1         0.003           QPUID0         NIF1         1.4         0.003         1           QPU0M6         MACROH12A2         Consisteme marces 712A.2         1.4         0.004         1           QPU0M6         MACROH12A2         Consisteme marces 712A.2         1.4         0.004         1           QPU0M6         MACROH12A2         Enhance         1.4         0.004         1           QPU0M6         RNA binding protein fac         1.4         0.006         1           QPU0M2         LUC7L         Putative RNA-binding protein fac?1ike 1         1.4         0.001         1           QPU0M2         HEATRI         HEAT repeacementation initiation factor 614         1.4         0.011         1           QPUSM2         HEG         DNA-3-methyladenite ghossylase focus republics (focus factor)         1.4         0.048         1           QPUSM2         ATGIAL         Amophage related protein factor factor)         1.4         0.048         1           QPUSM2         ATGIAL         Amophage related protein factor         1.3         0         1           QPUSM2         TETEL         Transistion factor fBe2, mitochoatration factor factor         1.3	Q6P1M0	TIMM44	Mitochandrial import inner membrane translocase subunit TIM//	1,4	0,003	PRDA2
QC/010         IAI         0.001           QP00M6         MACROH2A2         Corchistone maco-H2A.2         1.4         0.004           P14923         JUP         Junction plakeglobin         1.4         0.004           QP0056         ERLIN2         1.4         0.006         1           QP02905         ERLIN2         1.4         0.006         1           QP02905         UC/T.L         Putarits RNA binding protein fac?tike 1         1.4         0.006           QP0292         UU/T.L         Putarits RNA binding protein fac?tike 1         1.4         0.01           QP1302         HEATRI         HEATRI         HEATRI         HEATRI         HEATRI           QP1302         HEATRI         HEATRIC         Autoplage reconstraintig protein 1         1.4         0.01           QP352         DNAmethylasking reconstraintig protein 1         1.4         0.048         1           P4592         MT172         Translation initiation factor 16 a         1.4         0.048         1           P6542         PEX5         Peroxinonal targeting iqual 1 receptor         1.3         0         1           OP14W7         GRP111         Craft protein flags 1         1.3         0.001         1	OSUIDO	D IE1	Telemere accogisted protein P IE1	1,4	0,003	PRDA2
Culture         Display         Data         Description         Description           04905         FRLIN2         Ethna2         1.4         0.004           02920         RBM6         RNA-binding protein fac?like1         1.4         0.006           QRNQ2         LUC7L         Purstrive RNA-binding protein fac?like1         1.4         0.006           QRNQ2         LUC7L         Purstrive RNA-binding protein fac?like1         1.4         0.01           QRNQ2         HEATRI         HEAT repeat-constaining protein fac?like1         1.4         0.02           QRNQ2         HEATRI         HEAT repeat-constaining protein fac?like1         1.4         0.048           P29372         MPG         DNA-smchyladenie dysooylase         1.4         0.048           P20453         Atroich.         Atroichyladenie dysooylase         1.4         0.048           P40499         MTH2         Translotenin inition factore F12, imbechandrial         1.4         0.048           P40499         MTH2         Translotenin inition factore F12, imbechandrial         1.3         0         1           QR0136         PBRM1         Protein dyshome1         1.3         0         1         3         0.002         1           QPHAV7	0920146	MACROH2A2	Core histone macro. H2A 2	1,4	0,003	PR DY2
112.2.         101.         101.000 protogram         1.9         0.004           C)250         R.BM6         RNA-binding protein 6         1.4         0.006           C)250         R.BM6         RNA-binding protein 46         1.4         0.006           Q01804         OTUD4         OTU domain-containing protein 14.7-like 1         1.4         0.01           Q13804         OTUD4         OTU domain-containing protein 14.7-like 1         1.4         0.01           P23588         E1F181         Eakaryotic translation initiation factor 48         1.4         0.045           HOYEN2         PP07033         Scrinc/Arconine-protein phospharas 6 regularry subuni 3         1.4         0.048           P46199         MTE2         Translation initiation factor 1F2, mitochondrial         1.4         0.048           P64591         MTE2         Translation initiation factor 1F2, mitochondrial         1.3         0         1           P64592         PEX5         PEX5         PEX5         PEX5         0         0           P54542         PEX5         PEX5         Perosional targeting ispal 1 receptor         1.3         0         0           Q46046         PER141         Perosional targeting ispal 1         1.3         0.002         1	D1/923	II ID	Junction plakoglobin	1,4	0,004	PR DY2
07.00         LN112         LN122         1,4         0.000         1           QPNQ2         LLC7L         Putative RNA-binding protein Luc7like1         1,4         0.006         1           QN122         LLC7L         Putative RNA-binding protein 1         1,4         0.01         1           QT120         HEATR1         HEATR1 exploring protein 1         1,4         0.01         1           QT120         HEATR1         HEATR2 croating protein factor 43         1,4         0.01         1           P23372         MPG         DNA-3-mechyladening foctor 16,20         1,4         0.048         1           P10712         Tanadation initiation factor 16,2         1,3         0         1         1,4         0.048           P46199         MT112         Tanadation initiation factor 16,2         1,3         0         1         3         0         1           P46199         MT12         Tanadation initiation factor 17,2         1,3         0         1         3         0         1           P46199         MT12         Tanadation initiation factor 13         1,3         0         1         3         0         1         3         0         1         3         0         1 <t< td=""><td>09/905</td><td>EP LIN2</td><td>Felin 2</td><td>1,4</td><td>0,004</td><td>DP DV2</td></t<>	09/905	EP LIN2	Felin 2	1,4	0,004	DP DV2
CALM         Extension         1-3         0.0006           QMRQ2         LLCCL         Paratrike RAshinding protein Lut-Zitke 1         1.4         0.016           QMRQ4         OTUD4         OTU domain-containing protein 1         1.4         0.01           QTSQ7         HFATR         HEAT repare-containing protein 1         1.4         0.01           P2558         EFF4B         Enkaryotic translation initiation factor 4B         1.4         0.022           HOYEN2         PP0703         Scienc/Atrenoine-protein phosphazes 6 equalatory subunit 3         1.4         0.048           P40192         MTI2         Translation initiation factor 1E2, mitochondrial         1.4         0.048           P40192         MTI2         Translation initiation factor 1E2, mitochondrial         1.3         0           P40492         MTI2         Translation initiation factor 1E2, mitochondrial         1.3         0           P40404         MVCT         Graph protein phoreanial 1         1.3         0         1           QMLA04         PEX5         Peroxitam homolog 1, mitochondrial         1.3         0.001         1           QMLA04         MVG         Uncoversition globrismic 6         1.3         0.002         1           QMLA04         MVG1	C91250	D RMC	DNA hinding protein 6	1,4	0,005	DP DV2
Context         Difference         Difference         Difference         Difference           QUIS04         OTUD domain-containing protein 1         1.4         0.01         J           QUIS04         OTUD domain-containing protein 1         1.4         0.01         J           P2372         MPG         DNA-3-methyladening glycosylase         1.4         0.02           P19752         MPG         DNA-3-methyladening glycosylase         1.4         0.04           Qe76US         ATG16L1         Autophagr-related protein 16-1         1.4         0.048           Qe76US         ATG16L1         Autophagr-related protein 16-1         1.3         0         1           P46199         MTIF2         Translation initiation factore 172, mitochondrial         1.3         0         1           Qe6U86         PBRML         Protein onlybormon-1         1.3         0         1         3         0         1           QPHAYT         GRPE Protein homolog a luminly Chemebra 13         1.3         0.002         1         AuAuAuMKM&         MYO6         Unconventional myosin 6         1.3         0.002         1           QPHAYT         RCRE11         Greg Protein homolog a luminly Chemebra 13         1.3         0.002         1	09N029	LUC7I	Putative R NA-binding protein Luc7-like 1	1.4	0,006	PR DX2
QCTQC         D10 Common protein         11         0.01           QCTQC         HEATRI         HEATRI         14         0.01           P2358         EIF4B         Eukaryoti translution initiation factor 4B         1.4         0.022           P23572         MPG         DNA-3-methyladining gyocylase         1.4         0.048           P23572         MPG         DNA-3-methyladining gyocylase         1.4         0.048           P3619         MTTF2         Translation initiation factor IF2, mitochondrial         1.4         0.048           P4619         MTTF2         Translation initiation factor IF2, mitochondrial         1.3         0         1           P3642         PEX         Protein bolog subfamily C member 13         1.3         0         1           Q86086         PBRM1         Protein homolog subfamily C member 13         1.3         0,001         1           QMA0A0MKMK         MYGO         Uncorrection homolog 1. mitochondrial         1.3         0,002         1           QPUIG3         HOOK1         Protein Hook homolog 1         1.3         0,002         1           QPUIG3         HOOK1         Protein Homolog 1.         1.3         0,002         1           QPUIG3         HOOK1	001804	OTUD4	OTU domain_containing protein 4	1.4	0.01	PR DX2
Sec.         EIF48         Eukaroptic translation inflation factor 4B         1.4         0.015         1           P29572         MPG         DNA-3-methyladining glycoylass         1.4         0.029         1           P197272         MPG         DNA-3-methyladining glycoylass         1.4         0.048         1           Qc76U5         ATG16L1         Autophagy-related protein 16-1         1.4         0.048         1           QeV055         MTIF2         Translation inflation factor 16-2, mitchcondrial         1.3         0         1           QeV056         PRM1         Prest         Proxisional targeting signal 1 receptor         1.3         0         1           Q6V056         DRAJC13         Dnaj homolog subfamily Cnember 13         1.3         0.001         1           QMA0MRM8         MYO6         Unconventional myosin 6         1.3         0.002         1           QMA0MRM8         MYO6         Unconventional myosin 6         1.3         0.002         1           QV1C3         HOOK1         Protein homolog 1         1.3         0.002         1           QV1C3         HOOK1         Protein homolog 1         1.3         0.005         1           QV1F07         UBTF         Nuclear valosin	05T307	HEATR1	HEAT repeat-containing protein 1	1,1	0.01	PR DX2
P3972         MPG         DNA.3-methyladenine glycoxylase         1.4         0.029         1           H0TEN2         PPPRA3         Serine/threeonine protein phospharase forgulatory subunit 3         1.4         0.04           H0TEN2         PTPRA3         Serine/threeonine protein phospharase forgulatory subunit 3         1.4         0.048           P46192         MTTE2         Tranalation initiation factor IF-2, nitochondrial         1.4         0.048           P46192         MTTE2         Tranalation initiation factor IF-2, nitochondrial         1.3         0           P098542         PEX5         Perovisional targeting signal 1 receptor         1.3         0         1           Q960486         DBRMI1         Dratein polybromo-1         1.3         0.001         1           Q91LQ7         GRPEL1         Gr.pF protein homolog ubfamily C member 13         1.3         0.002         1           Q91LQ3         HOOK1         Putein howholog 1         1.3         0.002         1           Q91LQ3         HOOK1         Nucleal transcription factor 1         1.3         0.002         1           Q91LQ3         NDLD8         NEDD8         1.3         0.004         1           Q91B07         MYC1         MYG1 econuclease         1.3	P23588	EIF4B	Fukarvotic translation initiation factor 4B	1,1	0.015	PR DX2
HYEN2         PPP6R3         Serinc/threenine-protein phosphatase 6 regulatory subunit 3         1,4         0,04           Qc7cUS         ATGIGL1         Autophage-related protein 16-1         1,4         0,048         1           Qv6457         UFL1         E3 UFM1 protein ligase 1         1,3         0         1           Qv6467         UFL1         E3 UFM1 protein ligase 1         1,3         0         1           Qv6486         PBRM1         Protein polybrome 1         1,3         0         1           Qv6487         DRAJCI3         Du1 homolog ub/maily cmember 13         1,3         0,001         1           Qv64184         MYO6         Unconventional myosin-6         1,3         0,002         1           Qv11C3         HOOK1         Protein homolog 1, mitochondrial         1,3         0,002         1           Qv11C3         HOOK1         Protein homolog 1         1,3         0,002         1           Qv11C3         HOOK1         Protein homolog 1         1,3         0,003         1           Qv11C3         HOOK1         Protein homolog 1         1,3         0,005         1           Qv11C3         HOOK1         Protein homolog 1         1,3         0,005         1	P29372	MPG	DNA-3-methyladenine glycosylase	1,1	0.029	PR DX2
Qe76U5         ATG16L1         Autophagy-related protein 16-1         1.4         0.048           P46199         MTTP2         Translation initiation factor IF-2, mitochondrial         1.4         0.048           P46199         MTTP2         Translation initiation factor IF-2, mitochondrial         1.3         0         1           P50542         PEXS         Peroxisomal targeting signal 1 receptor         1.3         0         1           P50542         DNAJC13         Dnal homolog subfamily C member 13         1.3         0         1           Qe8U86         DNAJC13         Dnal homolog subfamily C member 13         1.3         0,002         1           QPUIC3         HOOK1         Protein hook pmolog 1         1.3         0,002         1           QPUIC3         HOOK1         Protein Hook bomolog 1         1.3         0,002         1           QVID3         HOOK1         Nuclealer tasks in took pmolog 1         1.3         0,003         1           QVID3         HOOK1         Nuclealer tasks in took pmolog 1         1.3         0,004         1           QVID3         MOC1         MyG1 exonuclease         1.3         0,005         1           QVID3         MOC2L         Muclealar complex protein 2 homolog <t< td=""><td>H0YEN2</td><td>PPP6R3</td><td>Serine/threonine-protein phosphatase 6 regulatory subunit 3</td><td>1,4</td><td>0,04</td><td>PRDX2</td></t<>	H0YEN2	PPP6R3	Serine/threonine-protein phosphatase 6 regulatory subunit 3	1,4	0,04	PRDX2
P46199         MTIF2         Translation initiation factor IF-2, mitochondrial         1,4         0,048           OP4874         UFL1         E3 UFM4 protein ligare 1         1,3         0         1           OP4874         UFL1         E3 UFM4 protein ligare 1         1,3         0         1           Q86U86         PBKM1         Protein polybromo-1         1,3         0         1           Q84U86         DBA(C13         Dnaj homolog subfamily Cemebr 13         1,3         0,002         1           Q9H4V7         GRPEL1         GrpE protein homolog 1         1,3         0,002         1           A0A0A0MRM8         MYO6         Unconventional myosin-6         1,3         0,002         1           Q101C3         H0OK1         Protein Hook homolog 1         1,3         0,004         1           QVUC3         HOOK1         Protein Hook homolog 1         1,3         0,005         1           Q15381         NEDD8         NEDD8         NED08         1,3         0,005         1           Q9HB07         MYG1         MYG1 consultargering protein 21,0 molog         1,3         0,005         1           Q91804         MRPS26         2887 itoosomal protein 526, niticochondrial         1,3         0	O676U5	ATG16L1	Autophagy-related protein 16-1	1,4	0,048	PRDX2
094874         UFL1         E3 UFM1-protein ligue 1         1,3         0           P50542         PFX5         Peroxisomal trageting signal 1 receptor         1,3         0         1           P50542         PFX5         Drad homolog subfimily C member 13         1,3         0         1           075165         DNAJC13         Dagl homolog subfimily C member 13         1,3         0,001         1           0A0A0MRM8         MYO6         Unconventional myssin-6         1,3         0,002         1           197KP7         UBTF         Nucleolar transcription factor 1         1,3         0,002         1           0J1581         NVL         Nucleolar transcription factor 1         1,3         0,004         1           0J1833         NEDD8         NEDD8         1,3         0,004         1           0J1843         NEDA         MVC1         Nucleolar complex protein 2 homolog         1,3         0,005         1           0J1850         TRLP4         MxG1 and contragrator 1         1,3         0,005         1           0J1800         TRLP4         Activating galaci ointegrator 1         1,3         0,007         1           0J2650         TRLP4         Activating galaci ointegrator 1         1,3	P46199	MTIF2	Translation initiation factor IF-2, mitochondrial	1,4	0,048	PRDX2
P50542         PEXS         Peroxioomal targeting signal 1 receptor         1,3         0           Q66U86         PBRM1         Protein polybrome-1         1,3         0         1           Q9H4W7         GRPEL1         GrpE protein homolog 1, mitochondrial         1,3         0,001         1           A0A0A0MRM8         MYO6         Unconventional myosin-6         1,3         0,002         1           PMFN7         UBTF         Nucleolar transcription factor 1         1,3         0,002         1           Q9U1C3         HOOK1         Protein Hook homolog 1         1,3         0,003         1           Q9U1C3         NUL         Nucleolar transcription factor 1         1,3         0,004         1           Q9U1C3         HOOK1         Protein Hook homolog 1         1,3         0,004         1           Q9T180         NEDD8         NEDD8         NEDD8         1,3         0,005         1           Q9T317         NCC12         Nucleolar complex protein 25c, mitochondrial         1,3         0,007         1           Q9ST01         CEBT2         CCAAT/enhancer-binding protein zta         1,3         0,007         1           Q9GOK1         VP35         Vacualar protein sortin-gasocactacd protein asortin-ga s	O94874	UFL1	E3 UFM1-protein ligase 1	1,3	0	PRDX2
Q86U86         PBRM1         Protein polybrome-1         1,3         0           O7S165         DNAJC13         Dnal homolog subfamily C member 13         1,3         0           QPHAY7         GRPELI         GrpE protein homolog I, mitochondrial         1,3         0,001         1           A0A0A0MRM8         MYO6         Unconventional myosin-6         1,3         0,002         1           DPMP7         UBTF         Nuclear transcription factor 1         1,3         0,002         1           O15581         NVL         Nuclear transcription factor 1         1,3         0,004         1           Q15543         NEDD8         NEEDD8         1,3         0,004         1           Q91807         MYG1         MYG1 esonaclease         1,3         0,005         1           Q918179         NOC2L         Nucleolar complex protein 24molog         1,3         0,005         1           Q9501         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q95701         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,017         1           Q9502         ST13         Hsc?0-intracting protein sociated protein 35         1,3         0,016         1	P50542	PEX5	Peroxisomal targeting signal 1 receptor	1,3	0	PRDX2
O'7516'         DNAJC13         DnaJ homolog subfamily C member 13         1,3         0           QPHAV7         GRPE11         GrpE protein homolog 1, nincohondrial         1,3         0,001         1           ADAQAMMRM         MYO6         Unconventional myosin-6         1,3         0,002         1           EPPKP7         UBTF         Nuclear transcription factor 1         1,3         0,002         1           QUJC3         HOOK1         Protein Hook homolog 1         1,3         0,004         1           Q1584         NVL         Nuclear valosin-containing protein-like         1,3         0,004         1           Q1584         NEDD8         NEDD8         1,3         0,005         1           Q1584         NED2         Nuclear complex protein 24 nomolog         1,3         0,005         1           Q16604         KPNA6         Importin subunit alpha-7         1,3         0,006         1           Q1550         TRIP4         Activating signal cointegrator 1         1,3         0,007         1           Q60CR1         VPS52         VacuAl protein storing associated protein 35         1,3         0,016         1           Q9502         ST13         HsC7O- interacting protein store1         1,3	Q86U86	PBRM1	Protein polybromo-1	1,3	0	PRDX2
QPHAV7         GRPEL1         GrpE protein homolog 1, mitochondrial         1,3         0,001         1           A0A0A0MRM8         MYO6         Unconventional myosin-6         1,3         0,002         1           A0A0A0MRM8         MYO6         Unconventional myosin-6         1,3         0,002         1           QPUIC3         HOOK1         Protein Hook homolog 1         1,3         0,002         1           QUIS48         NEDD8         NEDD8         1,3         0,004         1           QPHB07         MYG1         MYG1 exonalcase         1,3         0,004         1           QP1507         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           QP1507         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           QP3717         NOC2L         Nucleolar consplex protein 2 homolog         1,3         0,005         1           QP80K1         TRIP4         Activating signal cointegrator 1         1,3         0,007         1           Q9501         TRIP4         Activating gingal cointegrator 1         1,3         0,017         1           Q96QK1         VP535         Vacuolar protein sorting associated protein 35	075165	DNAJC13	DnaJ homolog subfamily C member 13	1,3	0	PRDX2
A0A0A0MRM8         MYO6         Unconventional myosine 6         1,3         0,002         1           EPPKP7         UBTF         Nucleolar transcription factor 1         1,3         0,002         1           QVUC3         HOOK1         Protein Hook homolog 1         1,3         0,003         1           Q15381         NVL         Nuclear valosin-containing protein-like         1,3         0,004         1           Q15383         NEDD8         NEDD8         1,3         0,004         1           Q9HB07         MYG1         MYG1 econuclease         1,3         0,005         1           Q91719         NOC2L         Nucleolar complex protein 20,6mitochondrial         1,3         0,005         1           Q9181N8         MRPS26         285 ribosomal protein 526, mitochondrial         1,3         0,007         1           Q03701         CEBPT         CCAAT/rehancer-binding protein zta         1,3         0,007         1           Q03701         CEBPT         CCAAT/rehancer-binding protein zta         1,3         0,011         1           Q03701         CEBPT         CCAAT/rehancer protein stat         1,3         0,011         1           Q046K1         VPS35         Vacuolar protein staton its StRP1	Q9HAV7	GRPEL1	GrpE protein homolog 1, mitochondrial	1,3	0,001	PRDX2
E9PR/P7         UBTF         Nucleolar transcription factor 1         1,3         0,002         1           QPUIC3         HOOK1         Protein Hook homolog 1         1,3         0,003         1           015381         NVL         Nucleolar transcription training protein-like         1,3         0,004         1           QPHB07         MYG1         MYG1 consulcase         1,3         0,004         1           QPHB07         MYG1         MYG1 consulcase         1,3         0,005         1           QPHB07         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           QPST97         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           QPST94         MRPS26         285 ribssomal protein 52,6, mitochonfrial         1,3         0,006         1           Q0500         TR1P4         Activating signal cointegrator 1         1,3         0,007         1           Q96QK1         VPS55         Vacuolar protein sorting associated protein 35         1,3         0,001         1           Q0502         ST13         HsC70-interacting protein 24         1,3         0,015         1           Q9426         TBCB         Tubulin-folding coffo	A0A0A0MRM8	MYO6	Unconventional myosin-6	1,3	0,002	PRDX2
QPU[C3         HOOK1         Protein Hook homolog 1         1,3         0,002         1           01581         NVL         Nuclear valosin-containing protein-like         1,3         0,003         1           Q15843         NEDD8         NEDD8         NEDD8         1,3         0,004         1           Q9HB07         MYG1         MYG1 exonuclease         1,3         0,005         1           Q9Y379         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           Q9BYN8         MRPS26         285 ribosomal protein 326, mitochondrial         1,3         0,006         1           Q96QK1         VPS35         Vacuolar protein sorting associated protein 35         1,3         0,007         1           Q06QK1         VPS35         Vacuolar protein sorting associated protein 35         1,3         0,017         1           P07196         NEFL         Neurofilament light polypeptide         1,3         0,015         1           Q08945         SRP1         FACT complex subunit SRP1         1,3         0,015         1           Q02665         MRPS31         285 ribosomal protein S31, mitochondrial         1,3         0,015         1           Q72406         MYH4	E9PKP7	UBTF	Nucleolar transcription factor 1	1,3	0,002	PRDX2
O15381         NVL         Naclear valosin containing protein-like         1,3         0,003         1           Q15843         NEDD8         NEDD8         NEDD8         1,3         0,004         1           Q15843         NEDD8         NEDD8         NGC         1,3         0,004         1           Q9HB07         MYG1         MYG1 exonuclease         1,3         0,005         1           Q981X8         MRPS26         285 ribosonal protein 326, mitochondrial         1,3         0,006         1           Q0560         TRIP4         Activating signal cointegrator 1         1,3         0,006         1           Q05701         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q96QK1         VPS55         Vacuolar protein sorting-associated protein 35         1,3         0,01         1           P5050         ST13         Hsc70-interacting protein         1,3         0,01         1           Q96QK1         VPS55         Vacuolar protein subunit SSRP1         1,3         0,01         1           Q98945         SSRP1         FACT complex subunit SGNP1         1,3         0,015         1           Q98945         SSRP1         FACT complex subunit sof	Q9UJC3	HOOK1	Protein Hook homolog 1	1,3	0,002	PRDX2
Q15843         NEDD8         1,3         0,004         1           Q9HB07         MYG1         MYG1 exonuclease         1,3         0,005         1           Q9HB07         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           Q9BX79         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           Q9BX78         MRPS26         285 ribosomal protein 526, mitochondrial         1,3         0,006         1           Q05701         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q9504         VP535         Vacuolar protein sorting-associated protein 35         1,3         0,007         1           Q96QK1         VP535         Vacuolar protein sorting-associated protein 35         1,3         0,01         1           Q96945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q92665         MRPS31         285 ribosomal protein 31, mitochondrial         1,3         0,016         1           Q92665         MRPS1         ASB ribosomal protein 51, mitochondrial         1,2         0         1           Q92656         MRPS1         285 ribosomal protein 51,	O15381	NVL	Nuclear valosin-containing protein-like	1,3	0,003	PRDX2
QPHB07         MYG1         MYG1 conuclease         1,3         0,004         1           QPY3T9         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           QPY3T9         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           Q9BYN8         MRPS26         28S ribosomal protein 526, mitochondrial         1,3         0,006         1           Q9505         TRIP4         Activating signal cointegrator 1         1,3         0,007         1           Q96QK1         VPS35         Vacuolar protein sorting associated protein 35         1,3         0,007         1           Q96QK1         VPS35         Vacuolar protein sorting associated protein 35         1,3         0,001         1           Q97196         NEFL         Neurofilament light polypeptide         1,3         0,015         1           Q99426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q272406         MRPS1         28S ribosomal protein S31, mitochondrial         1,3         0,016         1           Q72406         MRP14         Myosin-14         1,3         0,022         1           Q72406         MRP14         Myosin	Q15843	NEDD8	NEDD8	1,3	0,004	PRDX2
QPY379         NOC2L         Nucleolar complex protein 2 homolog         1,3         0,005         1           060684         KPNA6         Importin subunit alpha-7         1,3         0,005         1           QB9TN8         MRPS26         28S ribosomal protein 526, mitochondrial         1,3         0,006         1           Q15650         TRIP4         Activating signal cointegrator 1         1,3         0,007         1           Q3701         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q96QK1         VP835         Vacuolar protein sorting-associated protein 35         1,3         0,007         1           P07196         NEFL         Neurofilament light polypeptide         1,3         0,01         1           Q96QK1         VP835         Sacuolar protein S31, mitochondrial         1,3         0,015         1           Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,016         1           Q99426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q92665         MRPS31         28S ribosomal protein S31, mitochondrial         1,2         0         1           Q7Z406         MYH4	Q9HB07	MYG1	MYG1 exonuclease	1,3	0,004	PRDX2
O60684         KPNA6         Importin subunit alpha-7         1,3         0,005         1           Q9BYN8         MRPS26         28S ribosonal protein S26, mitochondrial         1,3         0,005         1           Q15650         TRIP4         Activating signal cointegrator 1         1,3         0,007         1           Q96QK1         VPS35         Vacuolar protein sorting-associated protein 35         1,3         0,007         1           Q0710         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q96QK1         VPS35         Vacuolar protein sorting-associated protein 35         1,3         0,007         1           P07196         NEFL         Neurofilament light polypeptide         1,3         0,01         1           Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q92426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q92461         ARPS31         285 ribosonal protein S31, mitochondrial         1,2         0         1           Q72406         MYH14         Myosin-14         1,3         0,032         1           Q72417         HAUS6         HAUS augmi	Q9Y3T9	NOC2L	Nucleolar complex protein 2 homolog	1,3	0,005	PRDX2
Q2BYN8         MRP526         288 ribosomal protein S26, mitochondrial         1,3         0,005         1           Q15650         TRIP4         Activating signal cointegrator 1         1,3         0,006         1           Q03701         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q96QK1         VPS55         Vacuolar protein sorting-associated protein 35         1,3         0,001         1           Q96QK1         VPS55         Vacuolar protein sorting-associated protein 35         1,3         0,01         1           Q96QK1         VPS55         Vacuolar protein sorting-associated protein 35         1,3         0,01         1           Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q99426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q92665         MRPS31         285 ribosomal protein \$31, mitochondrial         1,3         0,026         1           Q72406         MYH14         Myosin-14         G         1         0         1           Q72406         MYH14         Myosin-14         1,2         0         1         1         2         0         1 <td>O60684</td> <td>KPNA6</td> <td>Importin subunit alpha-7</td> <td>1,3</td> <td>0,005</td> <td>PRDX2</td>	O60684	KPNA6	Importin subunit alpha-7	1,3	0,005	PRDX2
Q15650         TRIP4         Activating signal cointegrator 1         1,3         0,006         1           Q03701         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q96QK1         VP535         Vacualar protein sorting-associated protein 35         1,3         0,007         1           P07196         NEFL         Neurofilament light polypeptide         1,3         0,01         1           Q089QK1         VP535         Start protein sorting-associated protein 35         1,3         0,01         1           Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q99426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q2665         MRP531         285 ribosomal protein is 31, mitochondrial         1,3         0,026         1           P40616         ARL1         ADP-ribosylation factor-like protein 1         1,3         0,032         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z417         HAUS6         HAUS augnin-like complex subunit clpX-like, mitochondrial         1,2         0         1           Q46555         WRNIP	Q9BYN8	MRPS26	28S ribosomal protein S26, mitochondrial	1,3	0,005	PRDX2
Q03701         CEBPZ         CCAAT/enhancer-binding protein zeta         1,3         0,007         1           Q96QK1         VPS35         Vacuolar protein sorting-associated protein 35         1,3         0,007         1           P07196         NEFL         Neurofilament light polypeptide         1,3         0,01         1           P0502         ST13         Hsc70-interacting protein         1,3         0,01         1           Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q99426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q92665         MRPS31         288 ribosomal protein S31, mitochondrial         1,3         0,026         1           Q72406         MYH14         Myosin-14         1,3         0,032         1           Q72407         HAUS6         HAUS augmin-like complex subunit 6         1,2         0         1           Q9655         WRNIP1         ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial         1,2         0         1           Q96555         WRNIP1         ATPase WRNIP1         1,2         0         1         Q           Q9NX63         CHCHD3 <td< td=""><td>Q15650</td><td>TRIP4</td><td>Activating signal cointegrator 1</td><td>1,3</td><td>0,006</td><td>PRDX2</td></td<>	Q15650	TRIP4	Activating signal cointegrator 1	1,3	0,006	PRDX2
Q96QK1         VPS3         Vacuolar protein sorting-associated protein 35         1,3         0,007         1           P07196         NEFL         Neurofilament light polypeptide         1,3         0,01         1           P07196         NEFL         Neurofilament light polypeptide         1,3         0,01         1           Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q99426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q92466         MRP531         285 ribosonal protein S31, mitochondrial         1,3         0,026         1           P40616         ARL1         ADP-ribosylation factor-like protein 1         1,3         0,032         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z4H7         HAUS6         HAUS augmin-like complex subunit 6         1,2         0         1           J3QLD9         FLOT2         Flortlin         1,2         0         1           Q98555         WRNIP1         ATPase WRNIP1         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,0	Q03701	CEBPZ	CCAAT/enhancer-binding protein zeta	1,3	0,007	PRDX2
P07196         NEL         Neurofilament light polypeptide         1,3         0,01         1           P50502         ST13         Hsc70-interacting protein         1,3         0,01         1           Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q09426         TBCB         Tubulin-folding cofactor B         1,3         0,016         1           Q2665         MRP831         28S ribosomal protein \$31, mitochondrial         1,3         0,026         1           P40616         ARL1         ADP-ribosylation factor-like protein 1         1,3         0,032         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z407         HAUS6         HAUS augmin-like complex subunit 6         1,2         0         1           Q76031         CLPX         ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial         1,2         0         1           Q9855         WRNIP1         ATP-ase WRNIP1         1,2         0         1         2         0         1           Q98X63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1         2         0,002         1 <td>Q96QK1</td> <td>VPS35</td> <td>Vacuolar protein sorting-associated protein 35</td> <td>1,3</td> <td>0,007</td> <td>PRDX2</td>	Q96QK1	VPS35	Vacuolar protein sorting-associated protein 35	1,3	0,007	PRDX2
P50502       ST13       Hsc70-interacting protein       1,3       0,01       1         Q08945       SSRP1       FACT complex subunit SSRP1       1,3       0,015       1         Q99426       TBCB       Tubulin-folding cofactor B       1,3       0,016       1         Q92665       MRPS31       285 ribosomal protein S31, mitochondrial       1,3       0,016       1         Q92664       ARL1       ADP-ribosylation factor-like protein 1       1,3       0,026       1         Q7Z406       MYH14       Myosin-14       1,3       0,032       1         Q7Z406       MYH14       Myosin-14       1,2       0       1         Q7Z406       MYH14       Myosin-14       1,2       0       1         Q7Z406       MYH14       Myosin-14       1,2       0       1         Q7Z406       HAUS augmin-like complex subunit 6       1,2       0       1         Q7Z407       HAUS6       HAUS augmin-like complex subunit clpX-like, mitochondrial       1,2       0       1         Q8055       WRNIP1       ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial       1,2       0       1         Q98056       WRNIP1       ATP-ase WRNIP1       1,2       <	P07196	NEFL	Neurofilament light polypeptide	1,3	0,01	PRDX2
Q08945         SSRP1         FACT complex subunit SSRP1         1,3         0,015         1           Q99426         TBCB         Tubulin-folding cofactor B         1,3         0,015         1           Q92665         MRPS31         28S ribosomal protein S31, mitochondrial         1,3         0,016         1           Q92665         MRPS31         28S ribosomal protein S31, mitochondrial         1,3         0,026         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z417         HAUS6         HAUS augmin-like complex subunit 6         1,2         0         1           Q76031         CLPX         ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial         1,2         0         1           Q98S55         WRNIP1         ATPase WRNIP1         1,2         0         1         2         0         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NX84         Focntrin         1,2         0,002         1           Q9NZ82         FAM120A         Constitutive coactivator of PP	P50502	ST13	Hsc70-interacting protein	1,3	0,01	PRDX2
Q29426         TBCB         Tubulin-folding cofactor B         1,3         0,015         1           Q2665         MRPS31         288 ribosomal protein \$31, mitochondrial         1,3         0,016         1           P40616         ARL1         ADP-ribosylation factor-like protein 1         1,3         0,026         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z406         MYH14         Myosin-14         1,2         0         1           Q7Z406         MYH14         Myosin-14         1,2         0         1           Q7Z407         HAUS6         HAUS augmin-like complex subunit 6         1,2         0         1           Q7Z417         HAUS6         HAUS augmin-like complex subunit clpX-like, mitochondrial         1,2         0         1           Q9C555         WRNIP1         ATP-set WRNIP1         1,2         0         1         1         2         0         1         2         0         1         2         0         1         2         0,001         1         2         0,001         1         2         0,001         1         2         0,001         1         2         0,002         1         2	Q08945	SSRP1	FACT complex subunit SSRP1	1,3	0,015	PRDX2
Q92665         MRP531         28S ribosomal protein S31, mitochondrial         1,3         0,016         1           P40616         AR L1         ADP-ribosylation factor-like protein 1         1,3         0,026         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z406         MYH14         Myosin-14         1,3         0,032         1           Q7Z4H7         HAUS6         HAUS augmin-like complex subunit 6         1,2         0         1           Q76031         CLPX         ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial         1,2         0         1           Q96555         WRNIP1         ATPase WRNIP1         1,2         0         1         2         0         1           Q96555         WRNIP1         ATPase WRNIP1         1,2         0,001         1         2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q94826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002	Q99426	TBCB	Tubulin-folding cofactor B	1,3	0,015	PRDX2
P40616       ARL1       ADP-ribosylation factor-like protein 1       1,3       0,026       1         Q7Z406       MYH14       Myosin-14       1,3       0,032       1         Q7Z406       MYH14       Myosin-14       1,2       0       1         Q7Z4H7       HAUS6       HAUS augmin-like complex subunit 6       1,2       0       1         O76031       CLPX       ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial       1,2       0       1         Q96555       WRNIP1       ATP-ase WRNIP1       1,2       0       1         Q96555       WRNIP1       ATPase WRNIP1       1,2       0,001       1         Q98X63       CHCHD3       MICOS complex subunit MIC19       1,2       0,001       1         Q9NZB2       FAM120A       Constitutive coactivator of PPAR-gamma-like protein 1       1,2       0,002       1         Q94826       TOMM70       Mitochondrial import receptor subunit TOM70       1,2       0,002       1         Q94826       TOMM70       Mitochondrial import receptor subunit TOM70       1,2       0,002       1         Q5214       SNRPD1       Small nuclear ribonucleoprotein Sm D1       1,2       0,002       1         Q65236	Q92665	MRPS31	28S ribosomal protein S31, mitochondrial	1,3	0,016	PRDX2
Q/Z406         MTH14         Myosin-14         1,3         0,052         1           Q7Z4H7         HAUS6         HAUS augmin-like complex subunit 6         1,2         0         1           Q76031         CLPX         ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial         1,2         0         1           J3QLD9         FLOT2         Flotillin         1,2         0         1           Q96555         WRNIP1         ATP-ase WRNIP1         1,2         0         1           Q98XC45         FAM98A         Protein FAM98A         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9X866         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           Q52314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           Q4126         DC27         Cell	P40616	ARL1	ADP-ribosylation factor-like protein 1	1,3	0,026	PRDX2
Q/Z4H/         HAUS6         HAUS6 augmin-like complex subunit 6         1,2         0         1           O76031         CLPX         ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial         1,2         0         1           J3QLD9         FLOT2         Flotillin         1,2         0         1           Q96555         WRNIP1         ATP-ase WRNIP1         1,2         0         1           Q96X55         FAM98A         Protein FAM98A         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9NX86         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           Q94826         TOMM70         Mitochondrial receptor subunit TOM70         1,2         0,002         1           Q52314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           Q6436         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,003         1           Q14126         DSG2	Q7Z406	MYH14	Myosin-14	1,3	0,032	PRDX2
O/6031         CLPX         ATP-dependent Clp protease ATP-binding subunit clpA-like, mitochondrial         1,2         0         1           J3QLD9         FLOT2         Flotillin         1,2         0         1           Q96S55         WRNIP1         ATP-ase WRNIP1         1,2         0         1           Q8NCA5         FAM98A         Protein FAM98A         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q94826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,002         1           Q4126         DSG2         Desmoglein-2         1,2         0,003         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4 </td <td>Q/Z4H/</td> <td>HAUS6</td> <td>HAUS augmin-like complex subunit 6</td> <td>1,2</td> <td>0</td> <td>PRDX2</td>	Q/Z4H/	HAUS6	HAUS augmin-like complex subunit 6	1,2	0	PRDX2
JSQLD9         FLOT2         FlotTin         1,2         0         1           Q96S55         WRNIP1         ATPase WRNIP1         1,2         0         1           Q8NCA5         FAM98A         Protein FAM98A         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9X826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           G62314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,002         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P58546         MTPN         Myotrophin         1,2	0/6031	CLPX FLOT2	A I P-dependent Clp protease A I P-binding subunit clpX-like, mitochondrial	1,2	0	PRDX2
WENNET         AT rase WENTF1         1,2         0         1           Q8NCA5         FAM98A         Protein FAM98A         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           Q9NXB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q94826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           P62314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,003         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P58546         MTPN         Myotrophin         1,2         0,005         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2	13QLD7	TLUIZ WD NID1	FIOLIHIH ATDaca W/D NID1	1,2	0	PKDA2
QaNCAS         FAM5A         Flotein FAM5A         1,2         0,001         1           Q9NX63         CHCHD3         MICOS complex subunit MIC19         1,2         0,001         1           O95613         PCNT         Pericentrin         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9XZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9XZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9X2B2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9X826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           P62314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,003         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P5854	Q96355	EA MORA	A I Pase W KINIPI	1,2	0 001	PRDA2
QNX65         CHCHDS         MICOS complex shuft MIC19         1,2         0,001         1           O95613         PCNT         Pericentrin         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           Q9NZB2         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           Q94826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           P62314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,003         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P58546         MTPN         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	QONUX(2	CUCUD2	MICOS complex subunit MIC19	1,2	0,001	PRDA2
OPAC         FORT         Function         1,2         0,001         1           Q9NZB2         FAM120A         Constitutive coactivator of PPAR-gamma-like protein 1         1,2         0,002         1           O94826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           P62314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,002         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P58546         MTPN         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	095613	PCNT	Pericentrin	1.2	0,001	PR DY2
QNE22         Tright of the Constructive conclusion of r1 meganing interpretent 1         1,2         0,002         1           O94826         TOMM70         Mitochondrial import receptor subunit TOM70         1,2         0,002         1           P62314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,002         1           Q040D9SF70         ARFGAP2         ADP-ribosylation factor GTPase-activating protein 2         1,2         0,003         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P58546         MTPN         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	09N7B2	FAM120A	Constitutive coactivator of PDAR gamma-like protein 1	1.2	0,001	PR DY2
OPAGE         FORMAT/V         Mitocholdrata import receptor submit 10M/V         1,2         0,002         1           P62314         SNRPD1         Small nuclear ribonucleoprotein Sm D1         1,2         0,002         1           G5EA36         CDC27         Cell division cycle 27, isoform CRA_c         1,2         0,002         1           A0A0D9SF70         ARFGAP2         ADP-ribosylation factor GTPase-activating protein 2         1,2         0,003         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P88546         MTPN         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	09/826	TOMM70	Mitochondrial import receptor subunit TOM70	1.2	0,002	PRDA2
ACCAT         OTCL P         Shart indexta filtering indexta	P62314	SNR DD1	Small nuclear ribonucleonrotein Sm D1	1.2	0,002	PR DY2
OAADD9SF70         ARFGAP2         ADP-ribosylation factor GTPase-activating protein 2         1,2         0,002         1           Q14126         DSG2         Desmoglein-2         1,2         0,004         1           P\$8546         MTPN         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	C5FA36	CDC27	Cell division cycle 27 isoform CR A c	1.2	0,002	PR DV2
Q14126         DSG2         Desmoglein-2         1,2         0,005         1           P58546         MTPN         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	A0A0D995F70	ARFCAD2	ADP_ribosylation factor GTPase_activating protein 2	1.2	0,002	PR DY2
P352         Dissingening         1,2         0,004         1           P58546         MTPN         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	01/12/	DSC2	Desmorlein 2	1.2	0,005	DR DV2
x 30340         M 17 M         Myotrophin         1,2         0,004         1           Q9NSK0         KLC4         Kinesin light chain 4         1,2         0,005         1	Q14120	MTDN	Desmogletti-2	1,2	0,004	PRDA2
V/NJRU RLC4 Kilesin igit châlî 4 1,2 0,005	CONSK0	WIPN KLC4	Wyottophin Kinggin light chain 4	1,2	0,004	PRDA2
	Q9N5K0	KLC4	Kinesin light chain 4	1,2	0,005	PKDX2

012996	CSTF3	Cleavage stimulation factor subunit 3	1.2	0.006	PRDX2
043707	ACTN4	Alphaactinin-4	1,2	0.006	PR DX2
015305	PMM2	Phosphomannomutase 2	1,2	0.006	DR DY2
099567	NILID88	Nuclear pore complex protein Nup88	1,2	0.006	DR DY2
Q77387	ALCS	Delichyl phoephata hata glucocyltransforace	1,2	0,008	DP DV2
Q916/5	CNAS	Coursing and estimation of the second s	1,2	0,007	PRDA2
P63092	GNAS	Guanine nucleotide-binding protein G(s) subunit alpha isoforms snort	1,2	0,007	PRDA2
Q961C/	RMDN3	Regulator of microtubule dynamics protein 3	1,2	0,007	PRDX2
P42696	RBM34	RNA-binding protein 34	1,2	0,007	PRDX2
015226	NKRF	NF-kappa-B-repressing factor	1,2	0,009	PRDX2
P19022	CDH2	Cadherin-2	1,2	0,011	PRDX2
095376	ARIH2	E3 ubiquitin-protein ligase ARIH2	1,2	0,011	PRDX2
A0A2R8Y566	RELCH	RAB11-binding protein RELCH	1,2	0,011	PRDX2
O00291	HIP1	Huntingtin-interacting protein 1	1,2	0,011	PRDX2
O00170	AIP	AH receptor-interacting protein	1,2	0,011	PRDX2
Q15042	RAB3GAP1	Rab3 GTPase-activating protein catalytic subunit	1,2	0,011	PRDX2
P52701	MSH6	DNA mismatch repair protein Msh6	1,2	0,015	PRDX2
O75146	HIP1R	Huntingtin-interacting protein 1-related protein	1,2	0,019	PRDX2
P20042	EIF2S2	Eukaryotic translation initiation factor 2 subunit 2	1,2	0,023	PRDX2
P07947	YES1	Tyrosine-protein kinase Yes	1,2	0,023	PRDX2
014828	SCAMP3	Secretory carrier-associated membrane protein 3	1.2	0.025	PRDX2
F8W0I6	NAP1L1	Nucleosome assembly protein 1-like 1	1.2	0.025	PR DX2
OPRTTO	AND32E	Acidic leucine, rich nuclear phosphoprotein 32 family member F	1,2	0.026	DR DY2
01/46/46	CHD1	Chromodomain helicase DNA binding protein 1	1,2	0.027	DR DY2
EQDNIWO	EAD1	Enternand Ca Andrease	1,2	0,027	DR DV2
CONUW12	P.D.(20	PNIA Line line martin 20	1,2	0,028	PRDA2
Q9N W15	RDM28	RINA-binding protein 28	1,2	0,032	PRDX2
Q96151	RCCIL	RCC1-like G exchanging factor-like protein	1,2	0,033	PRDX2
Q/10M5	RPS2/L	408 ribosomal protein S2/-like	1,2	0,035	PRDX2
015160	POLR1C	DNA-directed RNA polymerases I and III subunit RPAC1	1,2	0,04	PRDX2
Q9Y3B7	MRPL11	39S ribosomal protein L11, mitochondrial	1,2	0,046	PRDX2
P35251	RFC1	Replication factor C subunit 1	1,1	0	PRDX2
O43396	TXNL1	Thioredoxin-like protein 1	1,1	0	PRDX2
Q8IYB8	SUPV3L1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	1,1	0	PRDX2
Q9UPT5	EXOC7	Exocyst complex component 7	1,1	0	PRDX2
B8ZZC5	GLS	Glutaminase	1,1	0,001	PRDX2
P60983	GMFB	Glia maturation factor beta	1,1	0,001	PRDX2
Q14974	KPNB1	Importin subunit beta-1	1,1	0,001	PRDX2
Q9NV70	EXOC1	Exocyst complex component 1	1,1	0,001	PRDX2
Q8N122	RPTOR	Regulatory-associated protein of mTOR	1,1	0,002	PRDX2
075116	ROCK2	Rho-associated protein kinase 2	1,1	0,002	PRDX2
O96EY7	PTCD3	Pentatricopeptide repeat domain-containing protein 3. mitochondrial	1.1	0.002	PRDX2
O9UKG1	A PPI 1	DCC einteracting protein 13-alpha	1.1	0.002	PR DX2
096433	CCDC/7	Coiled-coil domain-containing protein /7	1,1	0.002	DR DY2
094207	ACBD2	Coldination COP(0	1,1	0.002	DP DY2
012907	IDU	January disk and sta Dalta isomerces 1	1,1	0,005	DR DV2
Q1390/	IDII	Tsopentenyi-dipriosphate Delta-Isomerase 1	1,1	0,004	PRDA2
Q86V58	HOOK3	Protein Hook homolog 3	1,1	0,005	PRDX2
Q96P70	IPO9	Importin-9	1,1	0,005	PRDX2
Q13085	ACACA	Acetyl-CoA carboxylase 1	1,1	0,006	PRDX2
Q7Z7K6	CENPV	Centromere protein V	1,1	0,006	PRDX2
O00410	IPO5	Importin-5	1,1	0,006	PRDX2
Q5QJE6	DNTTIP2	Deoxynucleotidyltransferase terminal-interacting protein 2	1,1	0,006	PRDX2
P16435	POR	NADPHcytochrome P450 reductase	1,1	0,007	PRDX2
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	1,1	0,009	PRDX2
Q04837	SSBP1	Single-stranded DNA-binding protein, mitochondrial	1,1	0,011	PRDX2
P57740	NUP107	Nuclear pore complex protein Nup107	1,1	0,013	PRDX2
Q6P996	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing protein 1	1,1	0,013	PRDX2
075691	UTP20	Small subunit processome component 20 homolog	1,1	0,017	PRDX2
O5T4S7	UBR4	E3 ubiquitin-protein ligase UBR4	1,1	0,018	PRDX2
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1.1	0.021	PRDX2
D6R B59	EXOC3	Exocyst complex component 3	11	0.024	PR DX2
P62879	GNB2	Guanine nucleotide binding protein G(I)/G(S)/G(T) subunit beta-2	1,1	0.025	PR DX2
01/218	EV BDS	Deptidul prolul die trane isomersee EKBD8	1,1	0,023	DP DY2
D50995	ANVA11	Apperin A11	1 1	0,033	DDDD
1 30773	EVOSC2		1,1	0,035	PRDA2
	EAUSU3	Exosonie complex component KKP40	1,1	0,036	PRDAZ
Q9HUE2	TULLIP	1011-Interacting protein	1,1	0,036	PKDX2
Q9H650	YTHDC2	5-5 KNA helicase Y I HDC2	1,1	0,041	PKDX2
Q9U130	1 RM1112	Multifunctional methyltransferase subunit TRM112-like protein	1,1	0,042	PRDX2
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	1,1	0,047	PRDX2
O43719	HTATSF1	HIV Tat-specific factor 1	1,1	0,048	PRDX2
Q8ND24	RNF214	RING finger protein 214	1	0,001	PRDX2

Q6UWP7	LCLAT1	Lysocardiolipin acyltransferase 1	1	0,001	PRDX2
Q86UP2	KTN1	Kinectin	1	0,002	PRDX2
Q9NY93	DDX56	Probable ATP-dependent RNA helicase DDX56	1	0,002	PRDX2
P56537	EIF6	Eukaryotic translation initiation factor 6	1	0,002	PRDX2
Q15555	MAPRE2	Microtubule-associated protein RP/EB family member 2	1	0,003	PRDX2
P58107	EPPK1	Epiplakin	1	0,007	PRDX2
A0A1B0GV47	KIF21A	Kinesin-like protein KIF21A	1	0,007	PRDX2
013951	CBFB	Core-binding factor subunit beta		0.011	PR DX2
O8IWS0	PHF6	PHD finger protein 6	1	0.011	PR DX2
D5338/	NURD1	Cutosolic Fe S cluster assembly factor NUBD1	1	0.013	PR DY2
09303/	CUIS	Cullin 5	1	0.014	PR DY2
Q73034 071PC2	LAPD4	La related protein 4	1	0,014	DR DY2
Q/1RC2	CLMN	Clamplin	1	0,017	PRDA2
Q92990	GLMN		1	0,017	PRDA2
043149	ZZEFI	Zinc finger ZZ-type and EF-hand domain-containing protein 1	1	0,018	PRDX2
F8VYE8	PPPICC	Serine/threonine-protein phosphatase	1	0,022	PRDX2
P4156/	EIFI	Eukaryotic translation initiation factor 1	1	0,033	PRDX2
P08670	VIM	Vimentin	1	0,038	PRDX2
Q9BZE4	GTPBP4	Nucleolar GTP-binding protein 1	1	0,038	PRDX2
O60502	OGA	Protein O-GlcNAcase	1	0,044	PRDX2
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating	1	0,048	PRDX2
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	5,4	0	PRDX4
P61106	RAB14	Ras-related protein Rab-14	3,1	0	PRDX4
O00629	KPNA4	Importin subunit alpha-3	3,1	0	PRDX4
Q9Y679	AUP1	Lipid droplet-regulating VLDL assembly factor AUP1	3,1	0	PRDX4
Q8N5K1	CISD2	CDGSH iron-sulfur domain-containing protein 2	3,1	0,003	PRDX4
Q07820	MCL1	Induced myeloid leukemia cell differentiation protein Mcl-1	2,8	0,001	PRDX4
P51148	RAB5C	Ras-related protein Rab-5C	2,8	0,004	PRDX4
Q5SZR4	TDRKH	Tudor and KH domain containing, isoform CRA a	2,8	0,007	PRDX4
P19022	CDH2	Cadherin-2	2.7	0	PRDX4
095373	IPO7	Importin-7	2.7	0	PR DX4
O96008	TOMM40	Mitochondrial import receptor subunit TOM40 homolog	2.7	0.005	PR DX4
015388	TOMM20	Mitochondrial import receptor subunit TOM20 homolog	2.7	0.007	PR DX4
D30519	HMOX2	Heme oxygenase 2	2,7	0,007	DR DY/
C5EA0(	MP DS27	285 ribosomal protein \$27 mitoshondrial	2,7	0,007	DP DY/
OPLIADO	DDU5	Diskt is a masked aster surth as	2,6	0,001	DR DX4
Q7H2P7	UROD	Dipititime methyl ester synthase	2,6	0,001	PRDA4
P06132	UROD		2,6	0,002	PRDA4
Q8N613	AKFGAPI	ADP-ribosylation factor G I Pase-activating protein 1	2,5	0	PRDX4
P98194	ATP2CI	Calcium-transporting A I Pase type 2C member 1	2,5	0	PRDX4
H/BXII	ESY12	Extended synaptotagmin-2	2,4	0	PRDX4
Q81EX9	IPO4	Importin-4	2,4	0	PRDX4
Q9BSJ8	ESYT1	Extended synaptotagmin-1	2,4	0,001	PRDX4
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	2,4	0,006	PRDX4
Q8N4V1	MMGT1	Membrane magnesium transporter 1	2,3	0,001	PRDX4
P42574	CASP3	Caspase-3	2,3	0,003	PRDX4
A0A0A0MS29	MFF	Mitochondrial fission factor	2,3	0,003	PRDX4
A0A2R8YFH5	SEC23B	Protein transport protein SEC23	2,3	0,004	PRDX4
Q7Z3C6	ATG9A	Autophagy-related protein 9A	2,3	0,015	PRDX4
O00505	KPNA3	Importin subunit alpha-4	2,2	0	PRDX4
Q9BTE1	DCTN5	Dynactin subunit 5	2,2	0,002	PRDX4
P51809	VAMP7	Vesicle-associated membrane protein 7	2,2	0,011	PRDX4
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	2,1	0	PRDX4
O5VT66	MTARC1	Mitochondrial amidoxime-reducing component 1	2,1	0	PRDX4
P50542	PEX5	Peroxisomal targeting signal 1 receptor	2.1	0	PR DX4
0%DH6	MSI2	R NA-binding protein Musashi homolog 2	2,1	0.002	PR DX4
092667	AKAP1	A kinase anchor protein 1 mitochondrial	2,1	0.002	PR DX4
012190	STV5	Suntavin S	2,1	0,002	DP DY/
Q15170	ADEC	ADD sile substant factor f	2,1	0,003	DR DX4
P84083	AKI)	ADF-fibosylation factor 5	2,1	0,007	PRDA4
Q9NQG6	MIEFI		2,1	0,009	PRDA4
Q96EA4	SPDLI	Protein Spindly	2,1	0,014	PRDX4
P0/384	CAPNI	Calpain-1 catalytic subunit	2	0,003	PRDX4
E9PHS0	LANCL1	Glutathione S-transferase LANCL1	2	0,006	PRDX4
P56962	STX17	Syntaxin-17	2	0,009	PRDX4
Q8WVC2	RPS21	40S ribosomal protein S21	2	0,009	PRDX4
P49642	PRIM1	DNA primase small subunit	1,9	0	PRDX4
Q9H0E2	TOLLIP	Toll-interacting protein	1,9	0,001	PRDX4
P18031	PTPN1	Tyrosine-protein phosphatase non-receptor type 1	1,9	0,001	PRDX4
B3KUS5	USP30	Ubiquitin carboxyl-terminal hydrolase	1,9	0,002	PRDX4
P40616	ARL1	ADP-ribosylation factor-like protein 1	1,9	0,003	PRDX4
Q9BPW8	NIPSNAP1	Protein NipSnap homolog 1	1,9	0,005	PRDX4
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Q9NZ32	ACTR10	Actin-related protein 10	1,9	0,009	PRDX4
Q14789	GOLGB1	Golgin subfamily B member 1	1,9	0,01	PRDX4
Q6FI81	CIAPIN1	Anamorsin	1,9	0,013	PRDX4
A0A0A0MR09	PTPN9	Tyrosine-protein phosphatase non-receptor type 9	1,9	0,015	PRDX4
P12236	SLC25A6	ADP/ATP translocase 3	1,8	0	PRDX4
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	1,8	0,007	PRDX4
Q6ZVM7	TOM1L2	TOM1-like protein 2	1,8	0,009	PRDX4
P49458	SRP9	Signal recognition particle 9 kDa protein	1,8	0,012	PRDX4
Q9NP72	RAB18	Ras-related protein Rab-18	1,8	0,015	PRDX4
095163	ELPI	Elongator complex protein 1	1,7	0	PRDX4
Q14318	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8	1,/	0,001	PRDX4
P31689	TOMM22	Diaj nomolog subramily A member 1 Mise share driel imment accenter where it TOM22 here also	1,/	0,004	PRDA4
Q91N369 Q14828	SCAMD2	Secretory carrier associated membrane protein 3	1,7	0,007	PRDA4
U14626	WDP 18	WD repeat containing protein 18	1,7	0,008	PRDA4
4043B3ITI/	HNRNDI	Heterogeneous nuclear ribonucleonrotein I	1,7	0.01	PRDX4
P42025	ACTR 1B	Beta-centractin	1.7	0.011	PR DX4
000291	HIP1	Huntingtin-interacting protein 1	1,7	0.012	PR DX4
O8NI60	COO8A	Atypical kinase COO8A, mitochondrial	1,7	0,014	PRDX4
Q16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	1,7	0,014	PRDX4
Q9Y4P1	ATG4B	Cysteine protease ATG4B	1,7	0,014	PRDX4
Q9NP97	DYNLRB1	Dynein light chain roadblock-type 1	1,7	0,015	PRDX4
P30740	SERPINB1	Leukocyte elastase inhibitor	1,7	0,017	PRDX4
Q5JRI1	SRSF10	Serine/arginine-rich-splicing factor 10	1,7	0,021	PRDX4
O60566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	1,7	0,023	PRDX4
Q7L5D6	GET4	Golgi to ER traffic protein 4 homolog	1,7	0,027	PRDX4
Q9NVJ2	ARL8B	ADP-ribosylation factor-like protein 8B	1,7	0,027	PRDX4
P48449	LSS	Lanosterol synthase	1,7	0,032	PRDX4
P08243	ASNS	Asparagine synthetase [glutamine-hydrolyzing]	1,6	0	PRDX4
P16435	POR	NADPHcytochrome P450 reductase	1,6	0	PRDX4
Q8TC07	TBC1D15	TBC1 domain family member 15	1,6	0	PRDX4
Q9UBB4	ATXN10	Ataxin-10	1,6	0	PRDX4
P21964	COMT	Catechol O-methyltransferase	1,6	0,001	PRDX4
Q8TCG1	CIP2A	Protein CIP2A	1,6	0,001	PRDX4
014964	HGS	Hepatocyte growth factor-regulated tyrosine kinase substrate	1,6	0,002	PRDX4
P04843	RPNI	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 1	1,6	0,004	PRDX4
Q53H96	PICR3	Pyrroline-5-carboxylate reductase 3	1,6	0,012	PRDX4
U95295	DARCCTA	SNAR E-associated protein Snapin	1,6	0,012	PRDA4
O8NE37	LDCAT1	Lysophosphatidylcholine acyltransferase 1	1,6	0,012	PRDX4
Q811137 Q9H840	GFMIN7	Gem-associated protein 7	1,0	0.033	PR DX4
Q8N573	OXR1	Oxidation resistance protein 1	1,0	0.043	PR DX4
Q9Y371	SH3GLB1	Endophilin-B1	1,5	0	PRDX4
P35232	PHB	Prohibitin	1,5	0	PRDX4
Q9Y262	EIF3L	Eukaryotic translation initiation factor 3 subunit L	1,5	0,01	PRDX4
Q9Y6Y8	SEC23IP	SEC23-interacting protein	1,5	0,013	PRDX4
Q6DKI1	RPL7L1	60S ribosomal protein L7-like 1	1,5	0,015	PRDX4
Q9BZE1	MRPL37	39S ribosomal protein L37, mitochondrial	1,5	0,019	PRDX4
Q86W42	THOC6	THO complex subunit 6 homolog	1,5	0,027	PRDX4
Q9Y580	RBM7	RNA-binding protein 7	1,5	0,031	PRDX4
Q9NUY8	TBC1D23	TBC1 domain family member 23	1,5	0,037	PRDX4
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	1,5	0,038	PRDX4
O95573	ACSL3	Long-chain-fatty-acidCoA ligase 3	1,4	0	PRDX4
Q9UKG1	APPL1	DCC-interacting protein 13-alpha	1,4	0	PRDX4
O95292	VAPB	Vesicle-associated membrane protein-associated protein B/C	1,4	0	PRDX4
P35573	AGL	Glycogen debranching enzyme	1,4	0,001	PRDX4
Q9Y4E8	USP15	Ubiquitin carboxyl-terminal hydrolase 15	1,4	0,001	PRDX4
Q6P1M0	SLC27A4	Long-chain fatty acid transport protein 4	1,4	0,002	PRDX4
A0A0C4DGQ6	RPRDIA	Regulation of nuclear pre-mRNA domain-containing protein IA	1,4	0,002	PRDX4
<u>r14723</u>	JUP EAE2	Junction piakogiotin	1,4	0.004	PKDX4
D35237	SER DINIRC	Servin B4	1,4	0.004	DR DV/
<u>r 3323/</u> OS3EL 6	PDCD4	Drogrammed cell death protein (	1,4	0.005	PRDX4
P42771	CDKN24	Cyclin.dependent kinase inhibitor 2 A	1,4	0.005	PR DY/
A0A3B3IUD2	MSTO1	Protein misato homolog 1	1 4	0.008	PR DX4
O9BTT0	ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family member E	1.4	0.008	PRDX4
A0A0D9SF70	ARFGAP2	ADP-ribosylation factor GTPase-activating protein 2	1.4	0.009	PRDX4
P63167	DYNLL1	Dynein light chain 1, cytoplasmic	1,4	0,021	PRDX4
Q5QNY5	PEX19	Peroxin-19	1,4	0,027	PRDX4

D/1050	04004				DD DVI (
P41250	GARS1	GlycinetRNA ligase	1,4	0,03	PRDX4
AUAU8/X2D5	MKPL45	395 ribosomal protein L45, mitochondrial	1,4	0,039	PRDX4
Q6PGP/	07072	Detratricopeptide repeat protein 3/	1,4	0,044	PRDX4
Q9H9/4	QIRIZ	Queuine tRNA-ribosyltransferase accessory subunit 2	1,4	0,045	PRDX4
Q916/3	ALGS	Dolichyl-phosphate beta-glucosyltransferase	1,4	0,04/	PRDX4
GSEA36	CDC2/	Cell division cycle 2/, isoform CRA_c	1,3	0	PRDX4
Q4J6C6	PREPL	Prolyl endopeptidase-like	1,3	0	PRDX4
E/E1Z4	BZW2	Basic leucine zipper and W2 domain-containing protein 2	1,3	0,001	PRDX4
Q51310	GPATCH4	G patch domain-containing protein 4	1,3	0,001	PRDX4
D6K938	CAMK2D	Calcium/calmodulin-dependent protein kinase	1,3	0,002	PRDX4
P31930	UQCRCI	Cytochrome b-c1 complex subunit 1, mitochondrial	1,3	0,003	PRDX4
P3489/	SHM12	Serine hydroxymethyltransferase, mitochondrial	1,3	0,003	PRDX4
P51452	DUSP3	Dual specificity protein phosphatase 3	1,3	0,003	PRDX4
K/ESE9	BCAS3	Breast carcinoma-amplified sequence 3	1,3	0,003	PRDX4
AUA2Q21H//	AUA2Q21H//	>tr[A0A2Q21 H//[A0A2Q21 H//_HOMAN Golgin subtamily A member 2 OS=Homo sapiens OX=9606 GN=GOLGA2 PE=1 SV=1;>sp]Q08379]GOGA2_ HUMAN Golgin subfamily A member 2 OS=Homo sapiens OX=9606 GN=GOLGA2 PE=1 SV=3;>tr[A0A1W2PQY5]A0A1W2PQY5_HUMAN Golgin subfamily A member		0,004	PKDX4
Q15276	RABEP1	Rab GTPase-binding effector protein 1	1,3	0,004	PRDX4
Q6UWP7	LCLAT1	Lysocardiolipin acyltransferase 1	1,3	0,004	PRDX4
O60678	PRMT3	Protein arginine N-methyltransferase 3	1,3	0,004	PRDX4
Q9NQG5	RPRD1B	Regulation of nuclear pre-mRNA domain-containing protein 1B	1,3	0,01	PRDX4
F8W0J6	NAP1L1	Nucleosome assembly protein 1-like 1	1,3	0,014	PRDX4
P19367	HK1	Hexokinase-1	1,3	0,018	PRDX4
Q9Y394	DHRS7	Dehydrogenase/reductase SDR family member 7	1,3	0,022	PRDX4
F5H008	VPS33B	Vacuolar protein sorting-associated protein 33B	1,3	0,028	PRDX4
P35606	COPB2	Coatomer subunit beta'	1,3	0,028	PRDX4
P25705	ATP5F1A	ATP synthase subunit alpha, mitochondrial	1,2	0	PRDX4
P04899	GNAI2	Guanine nucleotide-binding protein G(i) subunit alpha-2	1,2	0	PRDX4
P36542	ATP5F1C	ATP synthase subunit gamma, mitochondrial	1,2	0	PRDX4
P68104	EEF1A1	Elongation factor 1-alpha 1	1,2	0,001	PRDX4
O96A33	CCDC47	Coiled-coil domain-containing protein 47	1,2	0,001	PRDX4
O9BVG4	PBDC1	Protein PBDC1	1.2	0.002	PR DX4
095168	NDUFB4	NADH debydrogenase [ubiquinone] 1 beta subcomplex subunit 4	1.2	0.002	PR DX4
08IXI1	RHOT2	Mitochondrial R ho GTPase 2	1.2	0.002	PR DX4
P31040	SDHA	Succinate debydrogenase [ubiguinone] flavoprotein subunit mitochondria]	1.2	0.002	PR DX4
09UNM6	PSMD13	26S protessome non-ATPase regulatory subunit 13	1.2	0.003	PR DX4
092769	HDAC2	Histope deacetylase ?	1.2	0.003	PR DY/
01/579	COPE	Contomer subunit ensilon	1.2	0.004	PR DY/
01/126	DSG2	Desmonlein 2	1.2	0,001	PR DY/
F9PKG1	PR MT1	Protein arginine N-methyltransferase 1	1.2	0.007	PR DX4
05T760	SR SF11	Serine/arginine-rich-splicing factor 11	1.2	0.009	PR DX4
Q91700	HAUS8	HAUS augmin-like complex subunit 8	1.2	0.014	PR DX4
P63244	R ACK1	Recentor of activated protein C kinase 1	1,2	0.016	PR DX4
013/6/	ROCK1	Receptor of activated protein C kinase 1	1,2	0.021	PR DY/
D(2000	P AC1	Rito-associated protein kinase 1	1,2	0,021	DP DV4
DCREAD	CATR	Chatemarker C S bottimitum toxin substrate 1	1,2	0,022	DR DX4
07529(	GAID	Vasiala tar Calcing annual SEC22h	1,2	0,039	PRDA4
D28288	APCD2	ATD Lin line security of family Dependent 2	1,1	0,001	PRDA4
P28288	ALDUCA1	A I P-binding cassette sub-ramily D member 5	1,1	0,002	PRDA4
015207	ALDHSAI	Succinate-semialdenyde denydrogenase	1,1	0,002	PRDA4
01539/	IPO8	Importin-8	1,1	0,002	PRDX4
P56545	CT BP2	C-terminal-binding protein 2	1,1	0,002	PRDX4
Q9HAV7	GRPELI	GrpE protein homolog I, mitochondrial	1,1	0,002	PRDX4
Q8N122	RPIOR	Regulatory-associated protein of mTOR	1,1	0,003	PRDX4
Q/Z4Q2	HEATR3	HEA1 repeat-containing protein 3	1,1	0,003	PRDX4
P23526	AHCY	Adenosylhomocysteinase	1,1	0,003	PRDX4
Q9BRA2	TXNDC17	Thioredoxin domain-containing protein 17	1,1	0,004	PRDX4
Q96P70	IPO9	Importin-9	1,1	0,004	PRDX4
Q96TC7	RMDN3	Regulator of microtubule dynamics protein 3	1,1	0,006	PRDX4
Q8WUM0	NUP133	Nuclear pore complex protein Nup133	1,1	0,008	PRDX4
P63092	GNAS	Guanne nucleotide-binding protein G(s) subunit alpha isoforms short	1,1	0,01	PRDX4
Q15738	NSDHL	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	1,1	0,015	PRDX4
Q9HAV4	XPO5	Exportin-5	1,1	0,024	PRDX4
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1,1	0,024	PRDX4
Q16352	INA	Alpha-internexin	1,1	0,025	PRDX4
-	EEA1	Early endosome antigen 1	1.1	0,03	PRDX4
Q15075	EEAI		,		
Q15075 Q9Y619	TEX264	Testis-expressed protein 264	1,1	0,033	PRDX4
Q15075 Q9Y6I9 Q9H0U4	TEX264 RAB1B	Testis-expressed protein 264 Ras-related protein Rab-1B	1,1 1,1	0,033 0,036	PRDX4 PRDX4
Q15075 Q9Y6I9 Q9H0U4 P62879	TEX264 RAB1B GNB2	Testis-expressed protein 264 Ras-related protein Rab-1B Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	1,1 1,1 1,1	0,033 0,036 0,036	PRDX4 PRDX4 PRDX4

O9U130	TR MT112	Multifunctional methyltransferase subunit TR M112-like protein	11	0.04	PR DX4
Q60306	AOR	R NA belicase aquarius	1,1	0.044	PR DX4
D/7755	CAPZA2	Factin capping protein subunit alpha 2	1,1	0.047	DP DV4
01/02/	CAPUD1	CTDess estimation protein and VDS9 domain containing protein 1	1,1	0,047	PRDA4
Q14C86	ADSS2	G I Pase-activating protein and v P39 domain-containing protein 1	1,1	0,049	PRDA4
P30520	AD552	Adenylosuccinate synthetase isozyme 2	1,1	0,049	PRDA4
P19525	EIFZAKZ	Interferon-induced, double-stranded KNA-activated protein kinase	1	0,001	PRDX4
Q92973	TNPO1	Iransportin-1	1	0,002	PRDX4
P60983	GMFB	Glia maturation factor beta	1	0,003	PRDX4
Q96EY7	PTCD3	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	1	0,003	PRDX4
Q6P996	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing protein 1	1	0,003	PRDX4
P41240	CSK	Tyrosine-protein kinase CSK	1	0,003	PRDX4
Q8NCA5	FAM98A	Protein FAM98A	1	0,004	PRDX4
H3BTA2	PPP4C	Serine/threonine-protein phosphatase	1	0,006	PRDX4
013951	CBFB	Core-binding factor subunit beta	1	0.012	PRDX4
016718	NDUFA5	NA DH debudrogenase [ubiquinone] 1 alpha subcomplex subunit 5	1	0.012	PR DY/
0427(5	SCTA		1	0.012	DR DX4
043/63 Forward	JUDTE	Sman glutamme-rich tetratricopeptide repeat-contaming protein alpha	1	0,013	PRDA4
E9PKP/	UDIF		1	0,021	PRDX4
Q90JS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	1	0,025	PRDX4
015144	ARPC2	Actin-related protein 2/3 complex subunit 2	1	0,03	PRDX4
P61353	RPL27	60S ribosomal protein L27	1	0,031	PRDX4
Q03701	CEBPZ	CCAAT/enhancer-binding protein zeta	1	0,035	PRDX4
O60684	KPNA6	Importin subunit alpha-7	1	0,035	PRDX4
P15374	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	1	0,036	PRDX4
O95373	IPO7	Importin-7	3,5	0	PRDX5
000629	KPNA4	Importin subunit alpha-3	3.3	0	PR DX5
09Y224	RTRAF	R NA transcription translation and transport factor protein	3.2	0	PR DX5
0964.01	EEP MT2	Formitin family homolog 2	2	0	DP DV5
Q76AC1	PLRM12	Plants	3.0	0 001	PRDA)
Q15149	PLEC	Plectin	2,9	0,001	PRDAS
Q81CGI	CIP2A	Protein CIP2A	2,8	0	PRDX5
E9PHS0	LANCL1	Glutathione S-transferase LANCL1	2,7	0	PRDX5
P61106	RAB14	Ras-related protein Rab-14	2,7	0	PRDX5
Q07820	MCL1	Induced myeloid leukemia cell differentiation protein Mcl-1	2,7	0	PRDX5
Q8N2K0	ABHD12	Lysophosphatidylserine lipase ABHD12	2,7	0,002	PRDX5
P30519	HMOX2	Heme oxygenase 2	2,6	0,005	PRDX5
P19105	MYL12A	Myosin regulatory light chain 12A	2,5	0	PRDX5
P19022	CDH2	Cadherin-2	2,5	0	PRDX5
P06132	UROD	Uroporphyrinogen decarboxylase	2.5	0.001	PR DX5
OSTEX9	IPO/	Importin_4	2,5	0	DR DY5
U2PDE1	MACEI	Minnerschule antie mens liebing faster 1 insferme 1/2/2/5	2,1	0	DDDV5
H3BPEI	MACFI	Microtubule-actili cross-linking factor 1, isoformis 1/2/3/3	2,5	0	PRDAS
Q/Z406	MIHI4	Myosin-14	2,5	0	PRDAS
Q13464	ROCKI	Rho-associated protein kinase 1	2,3	0	PRDX5
B3KUS5	USP30	Ubiquitin carboxyl-terminal hydrolase	2,2	0	PRDX5
Q9Y679	AUP1	Lipid droplet-regulating VLDL assembly factor AUP1	2,2	0	PRDX5
O00505	KPNA3	Importin subunit alpha-4	2,2	0	PRDX5
P62879	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	2,2	0	PRDX5
Q16352	INA	Alpha-internexin	2,2	0	PRDX5
Q8N4V1	MMGT1	Membrane magnesium transporter 1	2,2	0,001	PRDX5
015477	SKIV2L	Helicase SK12W	2.2	0.001	PR DX5
P98194	ATP2C1	Calcium-transporting ATPase type 2C member 1	2.2	0.001	PR DX5
0%DH6	MSI2	R NA binding protein Mussibi homolog 2	2,2	0.001	DR DY5
Q70D110	IIADUR	Trifun ational annume subunit hate mite aban driel	2,2	0,004	DDDV5
077/2/	MAVE	Ministry and the set of the set of the second se	2,2	0,004	PRDA)
Q/Z434	MAVS		2,2	0,004	PRDAS
Q9BVP2	GNL3	Guanine nucleotide-binding protein-like 3	2,1	0	PRDX5
P40616	ARL1	ADP-ribosylation factor-like protein 1	2,1	0	PRDX5
Q9BTT0	ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family member E	2,1	0	PRDX5
O95861	BPNT1	3'(2'),5'-bisphosphate nucleotidase 1	2,1	0	PRDX5
Q9UBB4	ATXN10	Ataxin-10	2,1	0	PRDX5
P63167	DYNLL1	Dynein light chain 1, cytoplasmic	2,1	0,001	PRDX5
A0A0A0MR09	PTPN9	Tyrosine-protein phosphatase non-receptor type 9	2,1	0,001	PRDX5
O9BTE1	DCTN5	Dynactin subunit 5	2.1	0.002	PR DX5
A0A0A0M\$29	MFF	Mitochondrial fission factor	2.1	0.003	PR DX5
P51809	VAMP7	Vesicle-associated membrane protein 7	2.1	0.009	PR DYS
057207	LIEATD 1	UEAT associated memorane protein /	2,1	0,007	DDDVC
<u>V)13U/</u>			2	0	PRDAS
Q13085	ACACA	Acetyi-CoA carboxylase 1	2	0	PKDX5
G5EA31	SEC24C	Protein transport protein Sec24C	2	0	PRDX5
Q9NY93	DDX56	Probable ATP-dependent RNA helicase DDX56	2	0	PRDX5
O95163	ELP1	Elongator complex protein 1	2	0	PRDX5
Q6P2E9	EDC4	Enhancer of mRNA-decapping protein 4	2	0,001	PRDX5
Q9BZE1	MRPL37	39S ribosomal protein L37, mitochondrial	2	0,002	PRDX5

OSTITUTAA					
Q5VW32	BROX	BRO1 domain-containing protein BROX	2	0,003	PRDX5
H0YMZ1	PSMA4	Proteasome subunit alpha type	2	0,004	PRDX5
Q8IZ07	ANKRD13A	Ankyrin repeat domain-containing protein 13A	2	0,025	PRDX5
Q15388	TOMM20	Mitochondrial import receptor subunit TOM20 homolog	2	0,025	PRDX5
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	11,1	0	PRDX5
Q9P0M6	MACROH2A2	Core histone macro-H2A.2	1,9	0	PRDX5
P08670	VIM	Vimentin	1,9	0	PRDX5
O94925	GLS	Glutaminase kidney isoform, mitochondrial	1,9	0	PRDX5
Q9HAV4	XPO5	Exportin-5	1,9	0	PRDX5
P35580	MYH10	Myosin-10	1,9	0	PRDX5
E9PKP7	UBTF	Nucleolar transcription factor 1	1,9	0	PRDX5
O14579	COPE	Coatomer subunit epsilon	1,9	0	PRDX5
P35606	COPB2	Coatomer subunit beta'	1,9	0,001	PRDX5
P51570	GALK1	Galactokinase	1,9	0,001	PRDX5
P42345	MTOR	Serine/threonine-protein kinase mTOR	1,9	0,003	PRDX5
Q16762	TST	Thiosulfate sulfurtransferase	1,9	0,003	PRDX5
P46940	IQGAP1	Ras GTPase-activating-like protein IQGAP1	1,9	0,004	PRDX5
O60678	PRMT3	Protein arginine N-methyltransferase 3	1,9	0,004	PRDX5
P11388	TOP2A	DNA topoisomerase 2-alpha	1,9	0,005	PRDX5
Q14690	PDCD11	Protein RRP5 homolog	1,9	0,005	PRDX5
Q86WA6	BPHL	Valacyclovir hydrolase	1,9	0,006	PRDX5
Q6DKI1	RPL7L1	60S ribosomal protein L7-like 1	1,9	0,006	PRDX5
P84085	ARF5	ADP-ribosylation factor 5	1,9	0,007	PRDX5
P46013	MKI67	Proliferation marker protein Ki-67	1,9	0,008	PRDX5
Q9NQG6	MIEF1	Mitochondrial dynamics protein MID51	1,9	0,009	PRDX5
P56962	STX17	Syntaxin-17	1,9	0,009	PRDX5
Q7Z3C6	ATG9A	Autophagy-related protein 9A	1,9	0,014	PRDX5
Q5VT66	MTARC1	Mitochondrial amidoxime-reducing component 1	1,8	0	PRDX5
O94905	ERLIN2	Erlin-2	1,8	0	PRDX5
P08240	SRPRA	Signal recognition particle receptor subunit alpha	1,8	0	PRDX5
O95168	NDUFB4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	1,8	0	PRDX5
O6WCO1	MPRIP	Myosin phosphatase Rho-interacting protein	1.8	0	PRDX5
O9NW13	RBM28	RNA-binding protein 28	1.8	0,001	PRDX5
O02880	TOP2B	DNA topoisomerase 2-beta	1.8	0,002	PRDX5
O96RP9	GFM1	Elongation factor G, mitochondrial	1.8	0,002	PRDX5
097678	SEC23ID	SEC23-interacting protein	1.8	0.002	DR DYS
			1.0	V.V.V.Z.	
K7ESE9	BCAS3	Breast carcinoma-amplified sequence 3	1,8	0.002	PR DX5
K7ESE9 E7EVH7	BCAS3 E7EVH7	Breast carcinoma-amplified sequence 3 Kinesin light chain	1,8 1,8	0,002	PRDX5 PRDX5
K7ESE9 E7EVH7 Q4VCS5	BCAS3 E7EVH7 AMOT	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin	1,8 1,8 1,8 1.8	0,002 0,002 0,003 0,003	PRDX5 PRDX5 PRDX5 PRDX5
K7ESE9 E7EVH7 Q4VCS5 P07384	BCAS3 E7EVH7 AMOT CAPN1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calvain-1 catalytic subunit	1,8 1,8 1,8 1,8 1,8	0,002 0,002 0,003 0,003 0,004	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
K7ESE9 E7EVH7 Q4VCS5 P07384 O13951	BCAS3 E7EVH7 AMOT CAPN1 CBFB	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-bindine factor subunit beta	1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,002 0,003 0,003 0,004 0,005	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q1010           K7ESE9           E7EVH7           Q4VCS5           P07384           Q13951           O9BPW8	BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NioSnap homolog 1	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,002 0,003 0,003 0,004 0,005 0,006	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q17010           K7ESE9           E7EVH7           Q4VCS5           P07384           Q13951           Q9BPW8           P42704	BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q17010           K7ESE9           E7EVH7           Q4VCS5           P07384           Q13951           Q9BPW8           P42704           G5EA06	BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MR PS27	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 285 ribosomal protein \$27. mitochondrial	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,002 0,003 0,003 0,004 0,005 0,006 0,006	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q17010           K7ESE9           E7EVH7           Q4VCS5           P07384           Q13951           Q9BPW8           P42704           G5EA06           O60502	BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q71010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 O8WVC2	BCAS3 BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA R PS21	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein \$27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein \$21	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q1010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 O14789	BCAS3 BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28\$ ribosomal protein \$27, mitochondrial Protein O-GlcNAcase 40\$ ribosomal protein \$21 Coldrin subfamile B member 1	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,006 0,009 0,009 0,009	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q1010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133	BCAS3 BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin a Juba skeletal muscle	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,006 0,009 0,009 0,009 0,010	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q1010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008	BCAS3 BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein \$27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein \$21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import recentor subunit TOM40 homolog	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,006 0,009 0,009 0,009 0,010 0,019 0,033	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q14755 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 O98WN0	BCAS3 BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SR XN1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein \$27, mitochondrial Protein O-GIcNAcase 40S ribosomal protein \$21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfizedovin_1	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,006 0,009 0,009 0,01 0,019 0,038	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q1475 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 O15075	BCAS3 BCAS3 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 FFA1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,006 0,009 0,009 0,009 0,01 0,019 0,033 0,038 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q13010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973	BCA53 BCA53 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,019 0,033 0,038 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q13010           K7ESE9           E7EVH7           Q4VCS5           P07384           Q13951           Q9BPW8           P42704           G5EA06           O60502           Q8WVC2           Q14789           P68133           O96008           Q9BYN0           Q15075           O94973           O92G7T3	BCA53 BCA53 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIR P	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SR A stem-loop interacting R NA-binding protein, mitochondrial	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,019 0,033 0,038 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q13010           K7ESE9           E7EVH7           Q4VCS5           P07384           Q13951           Q9BPW8           P42704           G5EA06           O60502           Q8WVC2           Q14789           P68133           O96008           Q9BYN0           Q15075           O94973           Q9GZT3           O15381	BCA231 BCA33 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVI	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valonin-containing protein, Mitochondrial	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,019 0,033 0,038 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q71010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q4789 P68133 O96008 Q15075 O94973 Q9GZT3 O15381 O6E996	BCA53 BCA53 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q71616 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 D58107	BCA231 BCA33 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EEDK1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyrtidoxal-dependent decarboxylase domain-containing protein 1 Enipleki in	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,010 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q1515 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899	BCA231 BCA33 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 CNA12	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Cuaning protein G(i) cubunit alpha-2	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,010 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q15010 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 D56545	BCA231 BCA233 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 GNAI2 CTBP2	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C. termingl binding protein 2	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5
Q15015 Q4VCS5 P07384 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56955 D50995	BCA231           BCAS3           E7EVH7           AMOT           CAPN1           CBFB           NIPSNAP1           LRPPRC           MRPS27           OGA           RPS21           GOLGB1           ACTA1           TOMM40           SRXN1           EEA1           AP2A2           SLIRP           NVL           PDXDC1           EPPK1           GNAI2           CTBP2           ANY 411	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
Q15015 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597	BCA33           BCA53           E7EVH7           AMOT           CAPN1           CBFB           NIPSNAP1           LRPPRC           MRPS27           OGA           RPS21           GOLGB1           ACTA1           TOMM40           SRXN1           EEA1           AP2A2           SLIRP           NVL           PDXDC1           EPPK1           GNA12           CTBP2           ANXA11           SUICI G1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 Succinese CoAl image IADP/GDP.forminal subunit alpha mitochondrial	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,010 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5
Q13010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597 P18031	BCA231           BCAS3           E7EVH7           AMOT           CAPN1           CBFB           NIPSNAP1           LRPPRC           MRPS27           OGA           RPS21           GOLGB1           ACTA1           TOMM40           SRXN1           EEA1           AP2A2           SLIRP           NVL           PDXDC1           EPPK1           GNA12           CTBP2           ANXA11           SUCLG1           PTDN1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,003 0,033 0,033 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td
Q1810 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597 P18031 OSWTT2	BCA33           BCA53           E7EVH7           AMOT           CAPN1           CBFB           NIPSNAP1           LRPPRC           MRPS27           OGA           RPS21           GOLGB1           ACTA1           TOMM40           SRXN1           EEA1           AP2A2           SLIRP           NVL           PDXDC1           EPPK1           GNAI2           CTBP2           ANXA11           SUCLG1           PTPN1           NOC31	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 285 ribosomal protein S27, mitochondrial Protein O-GlcNAcase 405 ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tyrosine-protein phosphatase non-receptor type 1	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5
Q1010 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597 P18031 Q8WTT2 P09110	BCA33           BCA53           E7EVH7           AMOT           CAPN1           CBFB           NIPSNAP1           LRPPRC           MRPS27           OGA           RP521           GOLGB1           ACTA1           TOMM40           SRXN1           EEA1           AP2A2           SLIRP           NVL           PDXDC1           EPPK1           GNAI2           CTBP2           ANXA11           SUCLG1           PTPN1           NOC3L	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tyrosine-protein phosphatase non-receptor type 1 Nucleolar complex protein 3 homolog	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td
Q147030 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597 P18031 Q8WTT2 P09110 D68047	BCA231 BCA233 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 GNA12 CTBP2 ANXA11 SUCLG1 PTPN1 NOC3L ACAA1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit Core-binding factor subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tytosine-protein phosphatase non-receptor type 1 Nucleolar complex protein 3 homolog 3-ketoacyl-CoA thiolase, peroxisomal	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,019 0,033 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td
Q71010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P5995 P58597 P18031 Q8WTT2 P09110 P48047 O534194	BCA231 BCA233 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 GNA12 CTBP2 ANXA11 SUCLG1 PTPN1 NOC3L ACAA1 ATP5PO DVCP 2	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tyrosine-protein phosphatase non-receptor type 1 Nucleolar complex protein 3 homolog 3-ketoacyl-CoA thiolase, peroxisomal ATP synthase subunit, reductive 2	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,010 0,019 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td
Q1010 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P563597 P18031 Q8WTT2 P09110 P48047 Q53H26 Colt2P 2	BCA33 BCA33 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 GNAI2 CTBP2 ANXA11 SUCLG1 PTPN1 NOC3L ACAA1 ATP5PO PYCR3 CTNINY	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tyrosine-protein phosphatase non-receptor type 1 Nucleolar complex protein 3 homolog 3-ketoacyl-CoA thiolase, peroxisomal ATP synthase subunit O, mitochondrial Pyroline-5-carboxylate reductase 3 C-terminal-binding proteins 2 Carvenia data 1	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,003 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td
Q71010 K7ESE9 E7EVH7 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597 P18031 Q8WTT2 P09110 P48047 Q3H96 C9JZR2 D78216	BCA231 BCA33 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 GNA12 CTBP2 ANXA11 SUCLG1 PTPN1 NOC3L ACAA1 ATP5PO PYCR3 CTNND1	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tyrosine-protein phosphatase non-receptor type 1 Nucleolar complex protein 3 homolog 3-ketoacyl-CoA thiolase, peroxisomal ATP synthase subunit O, mitochondrial Pyrtoline-5-carboxylate reductase 3 Catenin delta-1 Nucleonare in 16	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,003 0,004 0,005 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,009 0,003 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td
Q1010 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597 P18031 Q8WTT2 P09110 P48047 Q53H96 C9JZR2 P78316 O42747	BCA231 BCA33 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 GNAI2 CTBP2 ANXA11 SUCLG1 PTPN1 NOC3L ACAA1 ATP5PO PYCR3 CTNND1 NOP14 TOWW 2	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyridoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tyrosine-protein phosphatase non-receptor type 1 Nucleolar complex protein 3 homolog 3-ketoacyl-CoA thiolase, peroxisomal ATP synthase subunit O, mitochondrial Pyrtoline-5-carboxylate reductase 3 Catenin delta-1 Nucleolar protein 14 TCOML 11 constri c 2	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,003 0,004 0,005 0,006 0,006 0,009 0,009 0,009 0,009 0,009 0,009 0,010 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td
Q1010 Q4VCS5 P07384 Q4VCS5 P07384 Q13951 Q9BPW8 P42704 G5EA06 O60502 Q8WVC2 Q14789 P68133 O96008 Q9BYN0 Q15075 O94973 Q9GZT3 O15381 Q6P996 P58107 P04899 P56545 P50995 P53597 P18031 Q8WTT2 P09110 P48047 Q53H96 C9JZR2 P78316 Q62VM7	BCA33 BCA33 E7EVH7 AMOT CAPN1 CBFB NIPSNAP1 LRPPRC MRPS27 OGA RPS21 GOLGB1 ACTA1 TOMM40 SRXN1 EEA1 AP2A2 SLIRP NVL PDXDC1 EPPK1 GNA12 CTBP2 ANXA11 SUCLG1 PTPN1 NOC3L ACAA1 ATP5PO PYCR3 CTNND1 NOP14 TOM12 CTND1 NOP14	Breast carcinoma-amplified sequence 3 Kinesin light chain Angiomotin Calpain-1 catalytic subunit beta Protein NipSnap homolog 1 Leucine-rich PPR motif-containing protein, mitochondrial 28S ribosomal protein S27, mitochondrial Protein O-GlcNAcase 40S ribosomal protein S21 Golgin subfamily B member 1 Actin, alpha skeletal muscle Mitochondrial import receptor subunit TOM40 homolog Sulfiredoxin-1 Early endosome antigen 1 AP-2 complex subunit alpha-2 SRA stem-loop-interacting RNA-binding protein, mitochondrial Nuclear valosin-containing protein-like Pyrtidoxal-dependent decarboxylase domain-containing protein 1 Epiplakin Guanine nucleotide-binding protein G(i) subunit alpha-2 C-terminal-binding protein 2 Annexin A11 SuccinateCoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial Tyrosine-protein hosphatase non-receptor type 1 Nucleolar complex protein 3 homolog 3-ketoacyl-CoA thiolase, peroxisomal ATP synthase subunit O, mitochondrial Pyrroline-5-carboxylate reductase 3 Catenin delta-1 Nucleolar protein 14 TOM1-like protein 2 Purcland-public protein 2 Purcland-public protein 2 Purcleolar protein 14 TOM1-like protein 14 TOM1-like protein 2 Purcleolar protein 14 TOM1-like protein 2 Purcleolar protein 14 TOM1-like protein 2 Purcleolar protein 14 TOM1-like protein 2 Purcleolar protein 14 TOM1-like protein 14 TOM1-like protein 2 Purcleolar protein 14 TOM1-like protein 14	1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8 1,8	0,002 0,003 0,003 0,004 0,005 0,006 0,006 0,006 0,009 0,009 0,009 0,009 0,010 0,013 0,033 0,038 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX5           PRDX5 </td

O AVI (D A	DUIMAA			0.044	DD DV/
Q9H6R0	DHX33	ATP-dependent RNA helicase DHX33	1,7	0,015	PRDX5
P15924	DSP	Desmoplakin	1,7	0,016	PRDX5
Q9NZ45	CISD1	CDGSH iron-sulfur domain-containing protein 1	1,7	0,04	PRDX5
O8N5K1	CISD2	CDGSH iron-sulfur domain-containing protein 2	1.7	0.047	PRDX5
D529/8	NUIDAS	Nuclear para complex protein Nup98 Nup96	1.6	0	DP DV5
F 32/48	NUF 78	The second protection is a second protection of the second protection o	1,0	0	PRDAS
QSUIPO	KIFI	Telomere-associated protein RTF1	1,6	0	PRDX5
Q5T3I0	GPATCH4	G patch domain-containing protein 4	1,6	0	PRDX5
Q86U42	PABPN1	Polyadenylate-binding protein 2	1,6	0	PRDX5
075439	PMPCB	Mitochondrial-processing peptidase subunit beta	16	0	PR DX5
D/2807	TEFM		1,0	0	DDDV5
P4389/	1 SF M		1,6	0	PKDA5
A0A0D9SF70	ARFGAP2	ADP-ribosylation factor GTPase-activating protein 2	1,6	0	PRDX5
B8ZZC5	GLS	Glutaminase	1,6	0	PRDX5
O00410	IPO5	Importin-5	1,6	0	PRDX5
O9Y2R 9	MR PS7	28S ribosomal protein S7 mitochondrial	1.6	0	PR DX5
Q/121()	DOD	NADDIL	1,0	0	DDDV
P16435	POK	NADPHcytochrome P450 reductase	1,6	0	PKDA5
E9PFR3	PPP2R5D	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit	1,6	0	PRDX5
095573	ACSL3	Long-chain-fatty-acidCoA ligase 3	1,6	0	PRDX5
Q8TC07	TBC1D15	TBC1 domain family member 15	1,6	0	PRDX5
09N088	TIGAR	Fructose 2 6 hisphosphatase TIGAR	1.6	0	PR DX5
A0A007V1A5	CTALI	De la constructione de la DNA la disconstructione de la constructione de la DNA la disconstructione de la constructione de la	1,0	0	DDDVC
A0A08/X1A5	STAUL	Double-stranded KNA-binding protein Staufen homolog I	1,6	0	PRDX5
D6RB59	EXOC3	Exocyst complex component 3	1,6	0,001	PRDX5
E9PF10	NUP155	Nuclear pore complex protein Nup155	1,6	0,001	PRDX5
Q03701	CEBPZ	CCAAT/enhancer-binding protein zeta	1,6	0,001	PRDX5
D63244	RACK1	Receptor of activated protein C kinase 1	1.6	0.001	DR DY5
0/2/17	TDOU		1,0	0,001	DDDVC
043615	IIMM44	Mitochondrial import inner membrane translocase subunit 11M44	1,6	0,001	PRDX5
075691	UTP20	Small subunit processome component 20 homolog	1,6	0,001	PRDX5
P14923	JUP	Junction plakoglobin	1,6	0,001	PRDX5
P61353	RPL27	60S ribosomal protein L27	1.6	0,002	PRDX5
E511008	VDS22B	Vacualar protein corting accordiated protein 22B	1.6	0.003	DP DV5
0.000	VISSO		1,0	0,003	PRDAJ
Q9BW92	TARS2	I hreoninetKNA ligase, mitochondrial	1,6	0,003	PRDX5
Q9H3U1	UNC45A	Protein unc-45 homolog A	1,6	0,003	PRDX5
Q9NTJ5	SACM1L	Phosphatidylinositol-3-phosphatase SAC1	1,6	0,003	PRDX5
O9UHI6	DDX20	Probable ATP-dependent R NA helicase DDX 20	1.6	0.004	PRDX5
071.253	DUV20	ATD dependent P NA belieses DHY20	1.6	0.007	DP DV5
Q/L2L3	DIIAJO	D D D D D D D D D D D D D D D D D D D	1,0	0,007	PRDAJ
Q5VYK3	ECPAS	Proteasome adapter and scaffold protein ECM29	1,6	0,008	PRDX5
Q9Y2R4	DDX52	Probable ATP-dependent RNA helicase DDX52	1,6	0,008	PRDX5
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	1,6	0,01	PRDX5
P08559	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	1.6	0.012	PRDX5
OSTB36	CDAP1	Ganglioside induced differentiation associated protein 1	1.6	0.013	DR DY5
Q01000	ODTINI		1,0	0,015	DDDVC
Q01082	SPIBNI	Spectrin beta chain, non-erythrocytic 1	1,6	0,016	PRDAS
Q16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	1,6	0,016	PRDX5
Q9Y4P1	ATG4B	Cysteine protease ATG4B	1,6	0,016	PRDX5
O13813	SPTAN1	Spectrin alpha chain, non-ervthrocytic 1	1.6	0.021	PRDX5
OSIR II	SR SE10	Serine/arginine_rich_splicing factor 10	1.6	0.022	DR DY5
2))((1)	DUDID		1,0	0,022	DD DV/
060566	BOBIB	Mitotic checkpoint serine/threonine-protein kinase BUBI beta	1,6	0,024	PRDAS
K7ELV2	SEH1L	Nucleoporin SEH1	1,6	0,025	PRDX5
H3BRY6	INTS14	Integrator complex subunit 14	1,6	0,027	PRDX5
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	1,5	0	PRDX5
P08243	ASNS	A sparagine synthetase [glutamine-bydrolyzing]	15	0	PR DX5
0011127	VDC ( A	We well as we the second	1,5	0	DDDV5
Q901N37	VP34A	vacuolar protein sorting-associated protein 4A	1,5	0	PKDA5
A0A0A0MRM8	MYO6	Unconventional myosin-6	1,5	0	PRDX5
Q9Y2Q3	GSTK1	Glutathione S-transferase kappa 1	1,5	0	PRDX5
P49327	FASN	Fatty acid synthase	1,5	0	PRDX5
092973	TNPO1	Transportin-1	15	0	PR DX5
D10525	FIEDAKD	Interform induced double strended DNA conjusted methics in his con-	1.5	0	DDDV5
P17525	EIFZAKZ	niterreron-induced, double-stranded KINA-activated protein kinase	1,5	0	PRDAS
Q9Y371	SH3GLB1	Endophilin-B1	1,5	0,001	PRDX5
O15226	NKRF	NF-kappa-B-repressing factor	1,5	0,001	PRDX5
Q9Y4E8	USP15	Ubiquitin carboxyl-terminal hydrolase 15	1,5	0,003	PRDX5
P04181	OAT	Ornithine aminotransferase, mitochondrial	1,5	0,003	PRDX5
013363	CTBD1	C-terminal-binding protein 1	15	0.004	DRDVS
213303	CIDP1		1,)	0,004	ricDA)
060264	SMARCA5	5 W 1/SINF-related matrix-associated actin-dependent regulator of chromatin subfamily	1,5	0,004	PRDX5
		A member 5			
P82930	MRPS34	28S ribosomal protein \$34, mitochondrial	1,5	0,005	PRDX5
Q92616	GCN1	eIF-2-alpha kinase activator GCN1	1,5	0,006	PRDX5
Q9Y394	DHRS7	Dehydrogenase/reductase SDR family member 7	1,5	0,008	PRDX5
A0A3B3ILID2	MSTO1	Protein misato homolog 1	15	0.01	PR DX5
0011100	CVDcD1	NADIL and some 15 and some 1	1.5	0.012	DDDDV
Q9UHQ9	CIBSKI	NADH-cytochrome b) reductase 1	1,5	0,012	PKDX5
P07947	YES1	Tyrosine-protein kinase Yes	1,5	0,013	PRDX5
P42694	HELZ	Probable helicase with zinc finger domain	1,5	0,013	PRDX5

H0YLH3	RABGGTA	Geranylgeranyl transferase type-2 subunit alpha	1,5	0,014	PRDX5
Q13561	DCTN2	Dynactin subunit 2	1,5	0,015	PRDX5
Q8NI60	COQ8A	Atypical kinase COQ8A, mitochondrial	1,5	0,016	PRDX5
A0A0A0MRT6	ABI1	Abl interactor 1	1,5	0,016	PRDX5
P31327	CPS1	Carbamoyl-phosphate synthase [ammonia], mitochondrial	1,5	0,017	PRDX5
Q9NP97	DYNLRB1	Dynein light chain roadblock-type 1	1,5	0,018	PRDX5
O15143	ARPC1B	Actin-related protein 2/3 complex subunit 1B	1,5	0,019	PRDX5
Q14204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	1,5	0,021	PRDX5
A0A2R8YFH5	SEC23B	Protein transport protein SEC23	1,5	0,026	PRDX5
Q9NXH9	TRMT1	tRNA	1,5	0,028	PRDX5
Q7L5D6	GET4	Golgi to ER traffic protein 4 homolog	1,5	0,028	PRDX5
O43347	MSI1	RNA-binding protein Musashi homolog 1	1,5	0,029	PRDX5
Q9H840	GEMIN7	Gem-associated protein 7	1,5	0,034	PRDX5
Q99459	CDC5L	Cell division cycle 5-like protein	1,5	0,04	PRDX5
Q9NY61	AATF	Protein AATF	1,4	0	PRDX5
E7ETZ4	BZW2	Basic leucine zipper and W2 domain-containing protein 2	1,4	0	PRDX5
Q9HAV7	GRPEL1	GrpE protein homolog 1, mitochondrial	1,4	0	PRDX5
P50542	PEX5	Peroxisomal targeting signal 1 receptor	1,4	0	PRDX5
Q4J6C6	PREPL	Prolyl endopeptidase-like	1,4	0	PRDX5
Q99/98	ACO2	Aconitate hydratase, mitochondrial	1,4	0	PRDX5
0/6031	CLPX	A I P-dependent Clp protease A I P-binding subunit clpX-like, mitochondrial	1,4	0	PRDX5
A0A0UIKKM6	ENAH	Protein enabled homolog	1,4	0,001	PRDX5
Q9D3H4	KINIA	Iransiational activator of cytochrome c oxidase 1	1,4	0,001	PRDAS
D5 412 (	D A D S1	Appining a PNA linear system lasmin	1,4	0,001	PRDA5
P34136	KAK51 NUD122	ArgininetKINA ligase, cytoplasmic	1,4	0,001	PRDA5
Q8WVE1	DSDC1	Paraspackle component 1	1,4	0,002	PRDA3
C5F9W7	MR DS22	28S ribosomal protein \$22 mitochondrial	1,4	0,002	PR DY5
012849	GR SF1	G-rich sequence factor 1	1,4	0.002	PR DX5
015397	IPO8	Importin-8	1,4	0.002	PR DX5
093034	CUL5	Cullin-5	1,1	0.002	PR DX5
A0A0G2INZ2	SCRIB	Protein scribble homolog	1.4	0.002	PR DX5
092621	NUP205	Nuclear pore complex protein Nup205	1,1	0.002	PR DX5
P11172	UMPS	Uridine 5'-monophosphate synthase	1,4	0,003	PRDX5
Q7L1Q6	BZW1	Basic leucine zipper and W2 domain-containing protein 1	1,4	0,003	PRDX5
Q9Y678	COPG1	Coatomer subunit gamma-1	1,4	0,003	PRDX5
P84103	SRSF3	Serine/arginine-rich splicing factor 3	1,4	0,003	PRDX5
B7Z6D5	DDX27	RNA helicase	1,4	0,004	PRDX5
Q00610	CLTC	Clathrin heavy chain 1	1,4	0,004	PRDX5
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating	1,4	0,004	PRDX5
P04843	RPN1	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 1	1,4	0,004	PRDX5
D6R938	CAMK2D	Calcium/calmodulin-dependent protein kinase	1,4	0,005	PRDX5
O14980	XPO1	Exportin-1	1,4	0,006	PRDX5
P19367	HK1	Hexokinase-1	1,4	0,006	PRDX5
P33992	MCM5	DNA replication licensing factor MCM5	1,4	0,006	PRDX5
Q5JTH9	RRP12	RRP12-like protein	1,4	0,006	PRDX5
Q6P1M0	SLC27A4	Long-chain fatty acid transport protein 4	1,4	0,006	PRDX5
P07196	NEFL	Neurofilament light polypeptide	1,4	0,007	PRDX5
Q96IU4	ABHD14B	Protein ABHD14B	1,4	0,007	PRDX5
Q6P2Q9	PRPF8	Pre-mRNA-processing-splicing factor 8	1,4	0,007	PRDX5
Q9HB07	MYG1	MYG1 exonuclease	1,4	0,007	PRDX5
Q15061	WDR43	WD repeat-containing protein 43	1,4	0,009	PRDX5
Q7Z4Q2	HEATR3	HEAT repeat-containing protein 3	1,4	0,01	PRDX5
Q9Y262	EIF3L	Eukaryotic translation initiation factor 3 subunit L	1,4	0,012	PRDX5
Q5JRX3	PITRM1	Presequence protease, mitochondrial	1,4	0,012	PRDX5
Q14684	RRP1B	Ribosomal RNA processing protein 1 homolog B	1,4	0,018	PRDX5
Q9NWB6	ARGLU1	Arginine and glutamate-rich protein 1	1,4	0,021	PRDX5
O00411	POLRMT	DNA-directed RNA polymerase, mitochondrial	1,4	0,024	PRDX5
Q96KM6	ZNF512B	Zinc finger protein 512B	1,4	0,026	PRDX5
O60306	AQR	RNA helicase aquarius	1,4	0,029	PRDX5
P23284	PPIB	Peptidyl-prolyl cis-trans isomerase B	1,4	0,03	PRDX5
Q86W42	THOC6	THO complex subunit 6 homolog	1,4	0,031	PRDX5
Q9Y580	KBM7	KNA-binding protein 7	1,4	0,033	PRDX5
Q96L92	SNX27	Sorting nexin-27	1,4	0,034	PRDX5
075146	HIP1R	Huntingtin-interacting protein 1-related protein	1,4	0,039	PRDX5
Q6P1N0	CC2DIA	Colled-coll and C2 domain-containing protein 1A	1,3	0	PRDX5
Q8N335	GPD1L	Glycerol-3-phosphate dehydrogenase 1-like protein	1,3	0	PRDX5
000000000000000000000000000000000000000	T + 3 /	D I FINANA			DD DTT-
Q8NCA5	FAM98A	Protein FAM98A	1,3	0	PRDX5

A0A2R8Y855	SMARCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	1,3	0,001	PRDX5
Q14137	BOP1	Ribosome biogenesis protein BOP1	1,3	0,001	PRDX5
P55060	CSE1L	Exportin-2	1,3	0,001	PRDX5
J3QLD9	FLOT2	Flotillin	1,3	0,001	PRDX5
Q9NV70	EXOC1	Exocyst complex component 1	1,3	0,001	PRDX5
A1X283	SH3PXD2B	SH3 and PX domain-containing protein 2B	1,3	0,001	PRDX5
P35237	SERPINB6	Serpin B6	1,3	0,002	PRDX5
P62495	ETF1	Eukaryotic peptide chain release factor subunit 1	1,3	0,002	PRDX5
Q15785	TOMM34	Mitochondrial import receptor subunit TOM34	1,3	0,002	PRDX5
P50213	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	1,3	0,002	PRDX5
Q96EY7	PTCD3	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	1,3	0,002	PRDX5
Q8N122	RPTOR	Regulatory-associated protein of mTOR	1,3	0,002	PRDX5
P23258	TUBG1	Tubulin gamma-1 chain	1,3	0,003	PRDX5
Q9P0K7	RAI14	Ankycorbin	1,3	0,003	PRDX5
P82933	MRPS9	28S ribosomal protein S9, mitochondrial	1,3	0,003	PRDX5
Q02252	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	1,3	0,003	PRDX5
O00567	NOP56	Nucleolar protein 56	1,3	0,003	PRDX5
A5YKK6	CNOT1	CCR4-NOT transcription complex subunit 1	1,3	0,004	PRDX5
Q14258	TRIM25	E3 ubiquitin/ISG15 ligase TRIM25	1,3	0,004	PRDX5
Q9BYN8	MRPS26	28S ribosomal protein S26, mitochondrial	1,3	0,004	PRDX5
Q96N67	DOCK7	Dedicator of cytokinesis protein 7	1,3	0,006	PRDX5
P35659	DEK	Protein DEK	1,3	0,007	PRDX5
P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	1,3	0,007	PRDX5
Q02241	KIF23	Kinesin-like protein KIF23	1,3	0,007	PRDX5
Q8TEM1	NUP210	Nuclear pore membrane glycoprotein 210	1,3	0,007	PRDX5
Q13190	STX5	Syntaxin-5	1,3	0,009	PRDX5
O14964	HGS	Hepatocyte growth factor-regulated tyrosine kinase substrate	1,3	0,01	PRDX5
Q7KZ85	SUPT6H	Transcription elongation factor SPT6	1,3	0,012	PRDX5
E7ESP9	NEFM	160 kDa neurofilament protein	1,3	0,015	PRDX5
Q86XI2	NCAPG2	Condensin-2 complex subunit G2	1,3	0,017	PRDX5
A0A087WZ13	RAVER1	Ribonucleoprotein PTB-binding 1	1,3	0,02	PRDX5
Q96GD0	PDXP	Pyridoxal phosphate phosphatase	1,3	0,023	PRDX5
O14974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	1,3	0,024	PRDX5
Q9BXJ9	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	1,3	0,024	PRDX5
P62318	SNRPD3	Small nuclear ribonucleoprotein Sm D3	1,3	0,024	PRDX5
Q99959	PKP2	Plakophilin-2	1,3	0,027	PRDX5
Q9Y2R5	MRPS17	28S ribosomal protein S17, mitochondrial	1,3	0,03	PRDX5
F8W108	ARID2	AT-rich interactive domain-containing protein 2	1,3	0,031	PRDX5
Q92878	RAD50	DNA repair protein RAD50	1,3	0,034	PRDX5
Q15058	KIF14	Kinesin-like protein KIF14	1,3	0,037	PRDX5
P42025	ACTR1B	Beta-centractin	1,3	0,038	PRDX5
Q9Y5L0	TNPO3	Transportin-3	1,3	0,039	PRDX5
Q96MW1	CCDC43	Coiled-coil domain-containing protein 43	1.2	0.04	PRDX5
Q969Z0	TBRG4		1,5		
Q6PGP7		FAST kinase domain-containing protein 4	1,3	0,046	PRDX5
075643	TTC37	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37	1,3 1,3	0,046 0,047	PRDX5 PRDX5
	TTC37 SNRNP200	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase	1,5 1,3 1,3 1,3	0,046 0,047 0,048	PRDX5 PRDX5 PRDX5
P48449	TTC37 SNRNP200 LSS	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase	1,3 1,3 1,3 1,3 1,3	0,046 0,047 0,048 0,049	PRDX5 PRDX5 PRDX5 PRDX5
P48449 P60983	TTC37 SNRNP200 LSS GMFB	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta	1,3 1,3 1,3 1,3 1,3 1,2	0,046 0,047 0,048 0,049 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
P48449 P60983 Q9BSJ2	TTC37 SNRNP200 LSS GMFB TUBGCP2	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2	1,3 1,3 1,3 1,3 1,3 1,2 1,2	0,046 0,047 0,048 0,049 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
P48449 P60983 Q9BSJ2 Q9UPT5	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7	1,3 1,3 1,3 1,3 1,3 1,2 1,2 1,2 1,2	0,046 0,047 0,048 0,049 0 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2	1,3       1,3       1,3       1,3       1,3       1,2       1,2       1,2       1,2       1,2       1,2       1,2	0,046 0,047 0,048 0,049 0 0 0 0 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2 Pericentrin	1,3       1,3       1,3       1,3       1,3       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2	0,046 0,047 0,048 0,049 0 0 0 0 0 0 0 0 0	PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5 PRDX5
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2 Pericentrin 3-hydroxyacyl-CoA dehydrogenase type-2	1,3       1,3       1,3       1,3       1,3       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2	0,046 0,047 0,048 0,049 0 0 0 0 0 0 0 0 0 0 0	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928 Q9BTW9	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2 Pericentrin 3-hydroxyacyl-CoA dehydrogenase type-2 Tubulin-specific chaperone D	1,3       1,3       1,3       1,3       1,3       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928 Q9BTW9 Q9P2R3	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2 Pericentrin 3-hydroxyacyl-CoA dehydrogenase type-2 Tubulin-specific chaperone D Rabankyrin-5	1,3       1,3       1,3       1,3       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2       1,2	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928 Q9BTW9 Q9P2R3 P35249	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2 Pericentrin 3-hydroxyacyl-CoA dehydrogenase type-2 Tubulin-specific chaperone D Rabankyrin-5 Replication factor C subunit 4	1,3         1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928 Q9BTW9 Q9P2R3 P35249 A0A140T9R1	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2 Pericentrin 3-hydroxyacyl-CoA dehydrogenase type-2 Tubulin-specific chaperone D Rabankyrin-5 Replication factor C subunit 4 Flotillin	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928 Q9BTW9 Q9P2R3 P35249 A0A140T9R1 Q5QJE6	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2	FAST kinase domain-containing protein 4 Tetratricopeptide repeat protein 37 U5 small nuclear ribonucleoprotein 200 kDa helicase Lanosterol synthase Glia maturation factor beta Gamma-tubulin complex component 2 Exocyst complex component 7 Microtubule-associated protein RP/EB family member 2 Pericentrin 3-hydroxyacyl-CoA dehydrogenase type-2 Tubulin-specific chaperone D Rabankyrin-5 Replication factor C subunit 4 Flotillin Deoxynucleotidyltransferase terminal-interacting protein 2	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,001         0,001	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449         P60983         Q9BSJ2         Q9UPT5         Q15555         O95613         Q5H928         Q9P2R3         P35249         A0A140T9R1         Q5QJE6         P35573	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,001         0,002	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449         P60983         Q9BSJ2         Q9UPT5         Q15555         O95613         Q5H928         Q9P2R3         P35249         A0A140T9R1         Q5QJE6         P35573         P57740	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,001         0,001           0,002         0,002	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449         P60983         Q9BSJ2         Q9UPT5         Q15555         O95613         Q5H928         Q9P2R3         P35249         A0A140T9R1         Q5QJE6         P35573         P57740         P56182	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107 RRP1	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107         Ribosomal RNA processing protein 1 homolog A	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,001         0,001           0,002         0,002	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449         P60983         Q9BSJ2         Q9UPT5         Q15555         O95613         Q9BTW9         Q9P2R3         P35249         A0A140T9R1         Q5QJE6         P35573         P57740         P56182         Q5JTZ9	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107 RRP1 AARS2	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107         Ribosomal RNA processing protein 1 homolog A         AlaninetRNA ligase, mitochondrial	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,002         0,002           0,002         0,002           0,003         0	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449         P60983         Q9BSJ2         Q9UPT5         Q15555         O95613         Q9BTW9         Q9P2R3         P35249         A0A140T9R1         Q5QJE6         P35573         P57740         P56182         Q5JTZ9         Q8TEQ6	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107 RRP1 AARS2 GEMIN5	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107         Ribosomal RNA processing protein 1 homolog A         AlaninetRNA ligase, mitochondrial         Gem-associated protein 5	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,002         0,002           0,002         0,002           0,003         0,003	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449         P60983         Q9BSJ2         Q9UPT5         Q15555         O95613         Q5H928         Q9BTW9         Q9P2R3         P35249         A0A140T9R1         Q5[JE6         P5573         P57740         P56182         Q5JTZ9         Q8TEQ6         P63092	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107 RRP1 AARS2 GEMIN5 GNAS	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107         Ribosomal RNA processing protein 1 homolog A         AlaninetRNA ligase, mitochondrial         Gem-associated protein 5         Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0,040         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,002         0,002           0,002         0,002           0,003         0,003	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449         P60983         Q9BSJ2         Q9UPT5         Q15555         O95613         Q5H928         Q9BTW9         Q9P2R3         P35249         A0A140T9R1         Q5JE6         P35573         P56182         Q5JTZ9         Q8TEQ6         P63092         Q9Y2H6	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107 RRP1 AARS2 GEMIN5 GNAS FNDC3A	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flottilin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107         Ribosomal RNA processing protein 1 homolog A         AlaninetRNA ligase, mitochondrial         Gem-associated protein 5         Guanine nucleotide-binding protein G(s) subunit alpha isoforms short         Fibronectin type-III domain-containing protein 3A	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,002         0,002           0,002         0,002           0,003         0,003	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928 Q9BTW9 Q9P2R3 P35249 A0A140T9R1 Q5QJE6 P35573 P57740 P56182 Q5JTZ9 Q8TEQ6 P63092 Q9Y2H6 P51452	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107 RRP1 AARS2 GEMIN5 GNAS FNDC3A DUSP3	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107         Ribosomal RNA processing protein 1 homolog A         Alanine-:rRNA ligase, mitochondrial         Gem-associated protein 5         Guanine nucleotide-binding protein G(s) subunit alpha isoforms short         Fibronectin type-III domain-containing protein 3A         Dual specificity protein phosphatase 3	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,002         0,002           0,002         0,003           0,003         0,003           0,003         0,003	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS
P48449 P60983 Q9BSJ2 Q9UPT5 Q15555 O95613 Q5H928 Q9BTW9 Q9P2R3 P35249 A0A140T9R1 Q5QJE6 P35573 P57740 P56182 Q5JTZ9 Q8TEQ6 P63092 Q9Y2H6 P51452 Q9BSD7	TTC37 SNRNP200 LSS GMFB TUBGCP2 EXOC7 MAPRE2 PCNT HSD17B10 TBCD ANKFY1 RFC4 FLOT1 DNTTIP2 AGL NUP107 RRP1 AARS2 GEMIN5 GMAS FNDC3A DUSP3 NTPCR	FAST kinase domain-containing protein 4         Tetratricopeptide repeat protein 37         U5 small nuclear ribonucleoprotein 200 kDa helicase         Lanosterol synthase         Glia maturation factor beta         Gamma-tubulin complex component 2         Exocyst complex component 7         Microtubule-associated protein RP/EB family member 2         Pericentrin         3-hydroxyacyl-CoA dehydrogenase type-2         Tubulin-specific chaperone D         Rabankyrin-5         Replication factor C subunit 4         Flotillin         Deoxynucleotidyltransferase terminal-interacting protein 2         Glycogen debranching enzyme         Nuclear pore complex protein Nup107         Ribosomal RNA processing protein 1 homolog A         AlaninetRNA ligase, mitochondrial         Gem-associated protein 5         Guanine nucleotide-binding protein G(s) subunit alpha isoforms short         Fibronectin type-III domain-containing protein 3A         Dual specificity protein phosphatase 3         Cancer-related nucleoside-triphosphatase	1,3         1,3         1,3         1,3         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1	0,046         0,047           0,048         0,049           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0,001         0,001           0,002         0,002           0,002         0,003           0,003         0,003           0,003         0,003           0,003         0,003           0,003         0,003	PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS PRDXS

0/3795	MYO1B	Unconventional myosin. Ib	1.2	0.004	DR DX5
09279	NOCU	Nuclealer complex protein 2 homolog	1,2	0.004	DP DV5
015021	LADC2L	Duck the low in a PNA line with the data l	1,2	0,004	PRDA)
Q15031	LAR52	Probable leucinetKINA ligase, mitochondriai	1,2	0,004	PRDAS
Q00688	FKBP3	Peptidyl-prolyl cis-trans isomerase FKBP3	1,2	0,005	PRDX5
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	1,2	0,005	PRDX5
P09543	CNP	2',3'-cyclic-nucleotide 3'-phosphodiesterase	1,2	0,006	PRDX5
Q15042	RAB3GAP1	Rab3 GTPase-activating protein catalytic subunit	1,2	0,006	PRDX5
Q96QK1	VPS35	Vacuolar protein sorting-associated protein 35	1,2	0,006	PRDX5
P25685	DNAJB1	DnaJ homolog subfamily B member 1	1,2	0,006	PRDX5
O8WYP5	AHCTF1	Protein ELYS	1,2	0,008	PRDX5
092665	MR PS31	28S ribosomal protein \$31 mitochondrial	1.2	0.008	PR DX5
QJ200J	CHEDD	Calcium homoostacis and anlasmic raticulum protein	1.2	0,000	DP DV5
DOREAD	CATR	Chevron Le D NA (Che) and descend and the second se	1,2	0,007	DRDXS
D6KEA0	GAIB	Glutamyl-tKNA(GIn) amidotransferase subunit B, mitochondrial	1,2	0,009	PRDX5
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1,2	0,009	PRDX5
A0A0A0MRJ0	CDC42BPA	Non-specific serine/threonine protein kinase	1,2	0,01	PRDX5
P19338	NCL	Nucleolin	1,2	0,01	PRDX5
P30520	ADSS2	Adenylosuccinate synthetase isozyme 2	1,2	0,011	PRDX5
P52701	MSH6	DNA mismatch repair protein Msh6	1,2	0,013	PRDX5
Q8WVM8	SCFD1	Sec1 family domain-containing protein 1	1,2	0,018	PRDX5
014828	SCAMP3	Secretory carrier-associated membrane protein 3	1.2	0.018	PR DX5
09NIU22	MDN1	Midacin	1.2	0.019	DR DY5
Q1N022	MDINI		1,2	0,017	DRDX5
000566	MPHOSPH10	U3 small nucleolar ribonucleoprotein protein MPP10	1,2	0,021	PRDX5
A0A3B311J4	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	1,2	0,022	PRDX5
P49642	PRIM1	DNA primase small subunit	1,2	0,039	PRDX5
Q5TG40	DMAP1	DNA methyltransferase 1-associated protein 1	1,2	0,044	PRDX5
P46060	RANGAP1	Ran GTPase-activating protein 1	1,2	0,045	PRDX5
Q9H2M9	RAB3GAP2	Rab3 GTPase-activating protein non-catalytic subunit	1,1	0	PRDX5
094874	UFL1	E3 UFM1-protein ligase 1	1.1	0	PR DX5
095292	VAPR	Vesicle-associated membrane protein-associated protein B/C	11	0	PR DX5
O(LIWD7	LCLAT1	I vescerdialinin acultransforaça 1	1,1	0	DP DV5
Q60 WP7	LCLAII		1,1	0	PRDAS
Q6P3W/	SCYL2	SCY1-like protein 2	1,1	0	PRDX5
Q81C12	RDH11	Retinol dehydrogenase 11	1,1	0	PRDX5
075396	SEC22B	Vesicle-trafficking protein SEC22b	1,1	0,001	PRDX5
P35221	CTNNA1	Catenin alpha-1	1,1	0,001	PRDX5
P23919	DTYMK	Thymidylate kinase	1,1	0,001	PRDX5
O14530	TXNDC9	Thioredoxin domain-containing protein 9	1,1	0,001	PRDX5
C9IRI5	LIMD1	LIM domain-containing protein 1	1.1	0.001	PR DX5
06P9B6	MEAK7	MTOR associated protein MEAK7	11	0.001	DR DY5
00(122	CCDC/7	Cailed acil domain containing matching (7	1,1	0,001	DP DV5
Q76A33	CCDC4/	Coned-con domain-containing protein 4/	1,1	0,001	PRDAS
E9PS1/	SCILI	N-terminal kinase-like protein	1,1	0,001	PRDX5
Q14166	TTLL12	Tubulintyrosine ligase-like protein 12	1,1	0,002	PRDX5
Q6NVY1	HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	1,1	0,002	PRDX5
P68104	EEF1A1	Elongation factor 1-alpha 1	1,1	0,002	PRDX5
Q8IXI1	RHOT2	Mitochondrial Rho GTPase 2	1,1	0,003	PRDX5
Q96P70	IPO9	Importin-9	1,1	0,003	PRDX5
O4G0F5	VPS26B	Vacuolar protein sorting-associated protein 26B	1.1	0.004	PR DX5
D63010	4 P2B1	A D.2 complex subunit beta	11	0.004	DR DY5
CONTROL OF	AF2DI	A P-2 complex subulit beta	1,1	0,004	DRDXS
QalwCl	MAP/D5	MAP/ domain-containing protein 3	1,1	0,004	PRDAS
A0A3B3IS/1	KBI	Retinoblastoma-associated protein	1,1	0,004	PRDX5
A0A2R8YDQ9	SUCLA2	SuccinateCoA ligase [ADP-forming] subunit beta, mitochondrial	1,1	0,004	PRDX5
A0A1B0GV47	KIF21A	Kinesin-like protein KIF21A	1,1	0,004	PRDX5
Q01968	OCRL	Inositol polyphosphate 5-phosphatase OCRL	1,1	0,005	PRDX5
Q9NZL4	HSPBP1	Hsp70-binding protein 1	1,1	0,006	PRDX5
O10713	РМРСА	Mitochondrial-processing peptidase subunit alpha	1,1	0,006	PRDX5
P33993	MCM7	DNA replication licensing factor MCM7	11	0.006	PR DX5
09IV01	SUCD2	SUB D and C match domain containing metation 2	1,1	0,000	DR DVs
QolAUI	50GP2	SORP and G-patch domain-containing protein 2	1,1	0,007	PRDAS
Q81181	F18J3	pre-rRNA 2'-O-ribose RNA methyltransferase F 18J3	1,1	0,007	PRDX5
Q9BPX3	NCAPG	Condensin complex subunit 3	1,1	0,007	PRDX5
P53618	COPB1	Coatomer subunit beta	1,1	0,007	PRDX5
Q9Y237	PIN4	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	1,1	0,007	PRDX5
P46778	RPL21	60S ribosomal protein L21	1,1	0,007	PRDX5
O9BYG3	NIFK	MKI67 FHA domain-interacting nucleolar phosphoprotein	1.1	0.008	PR DX5
09BX Y0	MAK16	Drotein MAK16 homolog	11	0.008	DR DY5
D55725	SEC12	Dratain SEC12 homolog	1 1	0,000	DDDVC
r 33/ 33	SEC13		1,1	0,009	PRDAS
Q16512	PKN1	Serine/threonine-protein kinase N1	1,1	0,009	PKDX5
O76094	SRP72	Signal recognition particle subunit SRP72	1,1	0,01	PRDX5
Q7L0Y3	TRMT10C	tRNA methyltransferase 10 homolog C	1,1	0,011	PRDX5
Q9NSK0	KLC4	Kinesin light chain 4	1,1	0,012	PRDX5
Q8IYI6	EXOC8	Exocyst complex component 8	1,1	0,013	PRDX5
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014240	FIF4A2	Fukarvotic initiation factor 4A-II	11	0.014	PR DX5
Q11210	MACRODI	ADD riboss glyssbydralass MACP OD1	1,1	0.016	DP DV5
Q70Q67	FIE4C2	Full-mode given values in the store for store for the store of the sto	1,1	0,016	DDDV5
P/0344	EIF4G2	Eukaryotic translation initiation factor 4 gaining 2	1,1	0,016	PRDAS
Q14318	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8	1,1	0,017	PRDX5
Q8N3C0	ASCC3	Activating signal cointegrator 1 complex subunit 3	1,1	0,017	PRDX5
Q9UFC0	LRWD1	Leucine-rich repeat and WD repeat-containing protein 1	1,1	0,018	PRDX5
Q9ULX6	AKAP8L	A-kinase anchor protein 8-like	1,1	0,019	PRDX5
Q05655	PRKCD	Protein kinase C delta type	1,1	0,019	PRDX5
Q5T7U1	GTF3C5	General transcription factor 3C polypeptide 5	1,1	0,021	PRDX5
Q9BUF5	TUBB6	Tubulin beta-6 chain	1,1	0,021	PRDX5
P33176	KIF5B	Kinesin-1 heavy chain	1.1	0.022	PRDX5
08N9T8	KR I1	Protein KR I1 homolog	11	0.023	PR DX5
E7EVI4	TACCI	Transforming scidic coiled coil containing protein 1	11	0.024	DR DY5
DODECO	AVI	A developed in a second concerned to the second and the second se	1,1	0.024	DDDX5
P00368	AKI COD DI		1,1	0,024	PRDAS
Q08945	SSRPI	FAC I complex subunit SSRPI	1,1	0,024	PRDX5
P08754	GNA13	Guanine nucleotide-binding protein G(i) subunit alpha	1,1	0,025	PRDX5
Q5SY16	NOL9	Polynucleotide 5'-hydroxyl-kinase NOL9	1,1	0,026	PRDX5
075436	VPS26A	Vacuolar protein sorting-associated protein 26A	1,1	0,027	PRDX5
P48507	GCLM	Glutamatecysteine ligase regulatory subunit	1,1	0,029	PRDX5
F2Z388	RPL35	60S ribosomal protein L35	1,1	0,03	PRDX5
Q9H0E2	TOLLIP	Toll-interacting protein	1,1	0,03	PRDX5
O9NOT5	EXOSC3	Exosome complex component RRP40	1.1	0.031	PRDX5
099961	SH3GL1	Endophilin-A2	11	0.037	PR DX5
0911643	ABCE2	ATP. hinding cassette sub-family Emember 2	1,1	0.038	DR DY5
U2PTL2	RCVDV	Destain series /shasening binses	1,1	0,038	DDDX5
DIDIL2	CR DO		1,1	0,038	PRDAS
P49458	SKP9	Signal recognition particle 9 kDa protein	1,1	0,039	PRDX5
P47897	QARS1	GlutaminetRNA ligase	1,1	0,039	PRDX5
A0A087WU06	TUBGCP3	Gamma-tubulin complex component	1,1	0,039	PRDX5
Q9HCD5	NCOA5	Nuclear receptor coactivator 5	1,1	0,041	PRDX5
O60783	MRPS14	28S ribosomal protein S14, mitochondrial	1,1	0,047	PRDX5
G8JLH9	STAT3	Signal transducer and activator of transcription	1	0	PRDX5
P11498	PC	Pyruvate carboxylase, mitochondrial	1	0	PRDX5
Q6IAA8	LAMTOR1	Ragulator complex protein LAMTOR1	1	0	PRDX5
P41240	CSK	Tyrosine-protein kinase CSK	1	0.001	PRDX5
0965K2	TMFM209	Transmembrane protein 209	1	0.001	PR DX5
Q PR A 2	TVNDC17	Thinsdenin demain containing protein 17	1	0,001	DDDX5
QIBRAZ	A DOD1	A D 2 and a state of the state	1	0,002	PRDAS
000203	AP3B1	AP-3 complex subunit beta-1	1	0,002	PRDX5
Q86V\$8	HOOK3	Protein Hook homolog 3	1	0,002	PRDX5
Q13451	FKBP5	Peptidyl-prolyl cis-trans isomerase FKBP5	1	0,003	PRDX5
Q9H3P7	ACBD3	Golgi resident protein GCP60	1	0,003	PRDX5
Q9UPN9	TRIM33	E3 ubiquitin-protein ligase TRIM33	1	0,003	PRDX5
Q9NQT4	EXOSC5	Exosome complex component RRP46	1	0,004	PRDX5
Q15650	TRIP4	Activating signal cointegrator 1	1	0,005	PRDX5
Q12788	TBL3	Transducin beta-like protein 3	1	0,005	PRDX5
O8IWZ3	ANKHD1	Ankyrin repeat and KH domain-containing protein 1	1	0.006	PRDX5
012769	NUP160	Nuclear pore complex protein Nun160	1	0.006	PR DX5
01(527	CSP D2	Custoine and glucine rich protein 2	1	0.007	DP DV5
Q1032/	DDM1	Dilana da di da	1	0,007	DDDVC
P23921	CNOTO		1	0,007	PRDAS
Q92600	CN019	CCR4-NOT transcription complex subunit 9	1	0,009	PRDAS
<u>Малика</u>	3KP68	Signal recognition particle subunit SKP68	1	0,009	PKDX5
P21964	COMT	Catechol O-methyltransferase	1	0,012	PRDX5
P00519	ABL1	Tyrosine-protein kinase ABL1	1	0,014	PRDX5
Q8NI27	THOC2	THO complex subunit 2	1	0,015	PRDX5
P61163	ACTR1A	Alpha-centractin	1	0,015	PRDX5
Q9BQ39	DDX50	ATP-dependent RNA helicase DDX50	1	0,015	PRDX5
Q96RQ3	MCCC1	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	1	0,017	PRDX5
075150	RNF40	E3 ubiquitin-protein ligase BR E1B	1	0.024	PR DX5
O9UNX4	WDR 3	WD repeat-containing protein 3	1	0.025	PR DX5
01/232	FIE2B1	Translation initiation factor eIE-2B subunit alpha	1	0.027	DR DY5
	NADIT 1	Nucleosome assembly protein 1 like 1	1	0.029	DR DVS
0005(0	DVD4	Distantilia 4	1	0.020	DDDDVC
Q77567	rKr4		1	0,039	PRDAS
Q51760	5K5F11	Serine/arginine-rich-splicing factor 11	1	0,039	PKDX5
Q9Y5K6	CD2AP	CD2-associated protein	1	0,046	PRDX5
075131	CPNE3	Copine-3	1	0,047	PRDX5
P12277	CKB	Creatine kinase B-type	1	0,049	PRDX5
PRDX4 -specific intera	actors				
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	9,3	0	PRDX1
P13667	PDIA4	Protein disulfide-isomerase A4	6,7	0	PRDX1
Q15084	PDIA6	Protein disulfide-isomerase A6	5,1	0	PRDX1
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P2//9/	CALR	Calreticulin	5,1	0	PRDXI
P30101	PDIA3	Protein disulfide-isomerase A3	4,4	0	PRDX1
P62805	H4C1	Histone H4	4,1	0	PRDX1
O76094	SRP72	Signal recognition particle subunit SRP72	4	0	PRDX1
P02790	HPX	Hemopexin	3,9	0	PRDX1
012797	ASPH	A sparty / asparaginy beta-bydroxy lase	3.8	0	PR DX1
Q12/)/	LICCTI	LIDD down down index from 1	3,0	0	DD DV1
Q9N102	UGGII	ODP-giucose:giycoprotein giucosyltransferase 1	3,8	0	PKDAI
P07237	P4HB	Protein disulfide-isomerase	3,8	0	PRDX1
P27824	CANX	Calnexin	3,8	0	PRDX1
O60506	SYNCRIP	Heterogeneous nuclear ribonucleoprotein Q	3,7	0	PRDX1
P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	3,7	0	PRDX1
014257	RCN2	Reticulocalbin-2	3.6	0	PR DX1
A0A087¥054	LIVOU1	Hyporie up regulated protein 1	2.5	0	DP DV1
AUAU8/A034	H1001	Hypoxia up-regulated protein 1	5,5	0	PRDAI
P11047	LAMC1	Laminin subunit gamma-1	3,3	0	PRDX1
P05387	RPLP2	60S acidic ribosomal protein P2	3,3	0	PRDX1
P11021	HSPA5	Endoplasmic reticulum chaperone BiP	3,3	0	PRDX1
P35637	FUS	RNA-binding protein FUS	3,2	0	PRDX1
013217	DNAIC3	DnaI homolog subfamily C member 3	3.2	0	PR DX1
000469	DI OD2	Drag homolog subranny o memoer 5	3,2	0.001	DR DV1
000469	PLODZ	Procollagen-lysine,2-oxogiutarate 5-dioxygenase 2	3,2	0,001	PRDAT
Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	3,2	0,016	PRDX1
P40429	RPL13A	60S ribosomal protein L13a	3,1	0	PRDX1
P05386	RPLP1	60S acidic ribosomal protein P1	3	0	PRDX1
Q9UBS4	DNAJB11	DnaJ homolog subfamily B member 11	2,9	0	PRDX1
P98175	RBM10	RNA-binding protein 10	2.9	0	PR DX1
D78/17	CETOI	Clutathions & transformers are 1	2,7	0	DD DV1
r/841/	GSIUI	Giutatinone S-transferase omega-1	Z,/	-	PKDXI
C9J4Z3	RPL37A	60S ribosomal protein L37a	2,7	0	PRDX1
P14625	HSP90B1	Endoplasmin	2,7	0	PRDX1
B9A018	USP39	U4/U6.U5 tri-snRNP-associated protein 2	2,6	0	PRDX1
P23588	EIF4B	Eukarvotic translation initiation factor 4B	2,6	0	PRDX1
D19338	NCI	Nucleolin	2.6	0	DR DY 1
D50/5/	CED DIVIDI		2,0	0	DD DV1
P50454	SERPINHI	Serpin H1	2,6	0	PRDX1
Q9BZQ6	EDEM3	ER degradation-enhancing alpha-mannosidase-like protein 3	2,6	0,001	PRDX1
D6RBV2	LMAN2	Vesicular integral-membrane protein VIP36	2,6	0,002	PRDX1
P62314	SNRPD1	Small nuclear ribonucleoprotein Sm D1	2,5	0	PRDX1
P18077	R PL 35A	60\$ ribosomal protein 1.35a	2.5	0	PR DX1
000278	TAE4	Terrentiation initiation forten TEUD subunit (	2,5	0	DR DV1
000268	IAF4		2,5	0	PRDAI
P12109	COL6A1	Collagen alpha-1(VI) chain	2,5	0,002	PRDX1
Q9UBF2	COPG2	Coatomer subunit gamma-2	2,4	0	PRDX1
Q8TEM1	NUP210	Nuclear pore membrane glycoprotein 210	2,4	0,001	PRDX1
Q15293	RCN1	Reticulocalbin-1	2,4	0,001	PRDX1
O9Y680	FKBP7	Peptidyl-prolyl cis-trans isomerase FKBP7	2.4	0.003	PR DX1
015/59	SE2 A 1	Splicing factor 2 A subunit 1	2.4	0.049	DP DV1
Q1)+)/	31 341		2,4	0,047	PRDAT
P49257	LMANI	Protein ERGIC-53	2,3	0,001	PRDXI
P36957	DLST	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate	2,2	0	PRDX1
		dehydrogenase complex, mitochondrial			
Q02750	MAP2K1	Dual specificity mitogen-activated protein kinase kinase 1	2,1	0	PRDX1
Q9H8Y8	GORASP2	Golgi reassembly-stacking protein 2	2,1	0	PRDX1
P06730	FIF4F	Fukarvotic translation initiation factor 4F	2.1	0	PR DX1
OPLICO	DA 71D	Turning matrix Lines PA 71P	2,1	0	DR DV1
Q70100	DALID	Tyrosine-protein kinase DAZ1D	2,1	0	PRDAT
P31942	HNKNPH3	Heterogeneous nuclear ribonucleoprotein H3	2,1	0	PRDXI
P26196	DDX6	Probable ATP-dependent RNA helicase DDX6	2,1	0	PRDX1
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	2,1	0,001	PRDX1
Q8NI27	THOC2	THO complex subunit 2	2,1	0,001	PRDX1
O9BOG0	MYBBP1A	Myh-binding protein 1 A	2.1	0.001	PR DX1
QUVP1	DNAIC10	Dry Lhomalag whfemily Comments 10	2,1	0,002	DR DV1
Qoixbi	DINAJCIO		2,1	0,002	PRDAT
Q55116	NOL9	Polynucleotide 5-hydroxyl-kinase NOL9	2,1	0,002	PRDX1
P55268	LAMB2	Laminin subunit beta-2	2,1	0,003	PRDX1
P53350	PLK1	Serine/threonine-protein kinase PLK1	2,1	0,025	PRDX1
P09972	ALDOC	Fructose-bisphosphate aldolase C	2,1	0,048	PRDX1
P13674	P4HA1	Prolyl 4-hydroxylase subunit alpha-1	2	0	PRDX1
075821	FIF3C	Fukarvotic translation initiation factor 2 subunit C	2	0	DR DV1
0/3021	DD DD	Duckaryotic translation initiation factor 5 Subunit G	2	0.001	PRDA1
Q4J6C6	PKEPL	Protyl endopeptidase-like	2	0,001	PKDX1
D6RA00	ENOPH1	Enolase-phosphatase E1	2	0,003	PRDX1
P11388	TOP2A	DNA topoisomerase 2-alpha	2	0,003	PRDX1
Q13162	PRDX4	Peroxiredoxin-4	11,3	0	PRDX1
O9H0A0	NAT10	R NA cytidine acetyltransferase	1.9	0	PR DX1
DE0502	CT12	II-70 interesting protein	1.0	0	DD DV1
r 30302	3113	NUT Do Itle and a land	1,7	0	PRDAI
155/69	SNU13	NHP2-like protein 1	1,9	0	PKDX1
O75832	PSMD10	26S proteasome non-ATPase regulatory subunit 10	1,9	0	PRDX1

Q9Y3Z3	SAMHD1	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	1,9	0	PRDX1
O00203	AP3B1	AP-3 complex subunit beta-1	1,9	0	PRDX1
Q96H79	ZC3HAV1L	Zinc finger CCCH-type antiviral protein 1-like	1,9	0	PRDX1
P14324	FDPS	Farnesyl pyrophosphate synthase	1,9	0	PRDX1
G3V529	DDX24	RNA belicase	1.9	0.001	PR DX1
O9ULC3	R A B23	Ras-related protein Rah-23	19	0.003	PR DX1
D11182	DRT	Linoamide acultransferase component of branched chain alpha keto acid debudrogenase	1.9	0.004	PR DY1
111102	DDI	complex mitochondrial	1,7	0,004	IRDAI
09/925	CIS	Clutaminasa kidnawisafarm mitashandrial	1.0	0.006	DP DV1
D(21/7	OL3	Dencial links bein 1 a conformit	1,7	0,000	PRDA1
P6516/	DINLLI		1,9	0,019	PRDAI
A0A0B4J1Z1	SRSF/	Serine/arginine-rich-splicing factor /	1,9	0,028	PRDXI
P38159	RBMX	RNA-binding motif protein, X chromosome	1,9	0,029	PRDX1
P11387	TOP1	DNA topoisomerase 1	1,8	0	PRDX1
P49321	NASP	Nuclear autoantigenic sperm protein	1,8	0	PRDX1
P53985	SLC16A1	Monocarboxylate transporter 1	1,8	0	PRDX1
P40938	RFC3	Replication factor C subunit 3	1,8	0	PRDX1
075688	PPM1B	Protein phosphatase 1B	1,8	0,001	PRDX1
P52597	HNRNPF	Heterogeneous nuclear ribonucleoprotein F	1.8	0.001	PR DX1
092621	NUP205	Nuclear pore complex protein Nup205	1.8	0.002	PR DX1
092008	LISDAN	Drabable ubiquitin carboryl terminal hydrolase EA F Y	1,0	0.002	DP DV1
Q75008	COAF(		1,0	0,002	PRDAI
095104	SCAF4	SR-related and CTD-associated factor 4	1,8	0,006	PRDXI
C9J384	CMSS1	Protein CMSS1	1,8	0,009	PRDX1
Q9NQ29	LUC7L	Putative RNA-binding protein Luc7-like 1	1,8	0,009	PRDX1
P62750	RPL23A	60S ribosomal protein L23a	1,7	0	PRDX1
P52565	ARHGDIA	Rho GDP-dissociation inhibitor 1	1,7	0	PRDX1
E9PIF2	DDX10	RNA helicase	1,7	0	PRDX1
Q15691	MAPRE1	Microtubule-associated protein RP/EB family member 1	1,7	0	PRDX1
015393	SF3B3	Splicing factor 3B subunit 3	1.7	0,002	PRDX1
009028	R BBP4	Histone-binding protein R BBP4	17	0.002	PR DX1
D/1252	IADS1	Isolowing +PNA ligase systemic	1,7	0,002	DP DV1
D00750	ANYAS	Anna in AS	1,7	0,002	PRDA1
P00/30	ANAAS	Almexin AS	1,7	0,003	PRDAI
P2230/	SCP2	Non-specific lipid-transfer protein	1,/	0,003	PRDXI
Q01085	TIAL1	Nucleolysin TIAR	1,7	0,007	PRDX1
Q9Y2H1	STK38L	Serine/threonine-protein kinase 38-like	1,7	0,007	PRDX1
P63244	RACK1	Receptor of activated protein C kinase 1	1,7	0,01	PRDX1
P04844	RPN2	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 2	1,7	0,013	PRDX1
P61353	RPL27	60S ribosomal protein L27	1,7	0,016	PRDX1
E9PFZ2	CP	Ceruloplasmin	1,7	0,024	PRDX1
P35579	MYH9	Myosin-9	1.7	0.026	PR DX1
053G00	HSD17B12	Very long-chain 3-oxoacyl-CoA reductase	17	0.028	PR DX1
015291	P BBD5	Partiablestome binding protein 5	1,7	0	DP DV1
01/(07	CANAD	Neurolable and AD	1,0	0	PRDA1
Q1469/	GANAD	Neutral alpha-glucosidase AB	1,6	0	PRDAI
060934	NBN	Nibrin	1,6	0	PRDXI
P09211	GSTP1	Glutathione S-transferase P	1,6	0	PRDX1
P32969	RPL9	60S ribosomal protein L9	1,6	0	PRDX1
P43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB subunit beta	1,6	0	PRDX1
P34949	MPI	Mannose-6-phosphate isomerase	1,6	0	PRDX1
P62424	RPL7A	60S ribosomal protein L7a	1,6	0	PRDX1
P56192	MARS1	MethioninetRNA ligase, cytoplasmic	1,6	0,001	PRDX1
Q16531	DDB1	DNA damage-binding protein 1	1,6	0,001	PRDX1
043747	AP1G1	AP-1 complex subunit gamma-1	1.6	0.001	PR DX1
O01831	XPC	DNA repair protein complementing XP-C cells	16	0.001	PR DX1
0/3852	CALU	Columenin	1,6	0.002	PR DY1
043032 09(T22	D SE1	Dama delina and encering feature 1	1,0	0,002	DR DV1
Q76125	NJFI	Remodeling and spacing factor 1	1,6	0,008	PRDAI
Q5V W32	BRUX	BROI domain-containing protein BROX	1,6	0,008	PRDXI
P46821	MAP1B	Microtubule-associated protein 1B	1,6	0,013	PRDX1
075367	MACROH2A1	Core histone macro-H2A.1	1,6	0,015	PRDX1
Q9BZK7	TBL1XR1	F-box-like/WD repeat-containing protein TBL1XR1	1,6	0,016	PRDX1
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	1,6	0,026	PRDX1
P07942	LAMB1	Laminin subunit beta-1	1,6	0,027	PRDX1
Q9NVP1	DDX18	ATP-dependent RNA helicase DDX18	1,6	0,038	PRDX1
Q9BYN0	SRXN1	Sulfiredoxin-1	1,6	0,041	PRDX1
015372	EIF3H	Eukarvotic translation initiation factor 3 subunit H	1.5	0	PRDX1
P38117	ETFB	Electron transfer flavoprotein subunit beta	15	0	PR DX1
09/826	TOMM70	Mitochondrial import recentor subunit TOM70	1.5	0	DR DV1
0/9E01	INTS2	Internet a second and the suburnit 1 OMI/0	1,5	0	DD DV1
Q68EU1	11N 1 3 3	Integrator complex subunit 5	1,5	U	PKDXI
A0A2R8YD50	HSD17B4	Peroxisomal multifunctional enzyme type 2	1,5	0	PRDX1
O00299	CLIC1	Chloride intracellular channel protein 1	1,5	0	PRDX1
P61247	RP\$3A	40S ribosomal protein S3a	1,5	0	PRDX1

					DD DYY.
060763	USO1	General vesicular transport factor p115	1,5	0	PRDX1
095376	ARIH2	E3 ubiquitin-protein ligase ARIH2	1,5	0,001	PRDX1
Q15054	POLD3	DNA polymerase delta subunit 3	1,5	0,001	PRDX1
O9Y678	COPG1	Costomer subunit gamma-1	15	0.001	PR DX1
005 (22	A LIC A 1	A stimulation of the second se	1,5	0,001	DD DV1
095455	AH5A1	Activator of 90 kDa neat snock protein A I Pase nomolog I	1,5	0,002	PRDAT
Q9Y2X3	NOP58	Nucleolar protein 58	1,5	0,01	PRDX1
A0A3B3ISV3	COL4A1	Collagen alpha-1(IV) chain	1,5	0,019	PRDX1
096019	ACTL6A	Actin-like protein 6A	15	0.02	PR DX1
OONIVBO	TEPEND	Telemaric repeat hinding factor 2 interacting protein 1	15	0.021	DP DV1
Q9IN1B0	I EKF2IP	Telometric repeat-officing factor 2-interacting protein 1	1,5	0,021	PRDAT
P19174	PLCG1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	1,5	0,029	PRDX1
Q9UKN8	GTF3C4	General transcription factor 3C polypeptide 4	1,5	0,032	PRDX1
P11717	IGF2R	Cation-independent mannose-6-phosphate receptor	1,5	0,037	PRDX1
P27694	R PA 1	Replication protein A 70 kDa DNA-binding subunit	15	0.049	PR DX1
0274V7	CMU	WD (0 more to be been in C) (11	1,5	0,015	DD DV1
Q2IAY/	SMUI	WD40 repeat-containing protein SMU1	1,4	0	PRDXI
P42166	TMPO	Lamina-associated polypeptide 2, isoform alpha	1,4	0	PRDX1
J3QQW9	SUZ12	Polycomb protein SUZ12	1,4	0	PRDX1
O5T9A4	ATAD3B	ATPase family AAA domain-containing protein 3B	1,4	0	PRDX1
0511928	LISD17B10	2 hudrownery CoA debudrogeness tune 2	1.4	0	DP DV1
Q3H728	H3D1/B10	5-inydroxyacyi-CoA denydrogenase type-2	1,4	0	PRDAT
P53618	COPB1	Coatomer subunit beta	1,4	0,001	PRDX1
Q9Y5J1	UTP18	U3 small nucleolar RNA-associated protein 18 homolog	1,4	0,001	PRDX1
Q8IWB7	WDFY1	WD repeat and FYVE domain-containing protein 1	1,4	0,001	PRDX1
P62244	R PS15A	40S ribosomal protein \$15a	1.4	0.004	PR DX1
D1((15	ATTD2 4 2		1,4	0,004	DD DV1
P16615	ATPZAZ	Sarcoplasmic/endoplasmic reticulum calcium A I Pase 2	1,4	0,004	PRDX1
P26583	HMGB2	High mobility group protein B2	1,4	0,008	PRDX1
P33992	MCM5	DNA replication licensing factor MCM5	1,4	0,008	PRDX1
P20073	ANXA7	Annexin A7	1.4	0.008	PR DX1
D29022	P DI 2	(0S ribosomal protain I 2	1.4	0.01	DP DV1
F 37023	KrLJ		1,4	0,01	PRDAT
043719	HTATSF1	HIV Tat-specific factor 1	1,4	0,013	PRDX1
O14980	XPO1	Exportin-1	1,4	0,015	PRDX1
O00232	PSMD12	26S proteasome non-ATPase regulatory subunit 12	1,4	0,015	PRDX1
P35606	COPB2	Costomer subunit beta'	1.4	0.016	PR DX1
OSUVV2	ECDAC		1,1	0,027	DD DV1
Q5V1K3	ECPAS	Proteasome adapter and scaffold protein ECM29	1,4	0,02/	PRDXI
076021	RSL1D1	Ribosomal L1 domain-containing protein 1	1,4	0,03	PRDX1
P31327	CPS1	Carbamoyl-phosphate synthase [ammonia], mitochondrial	1,4	0,032	PRDX1
O8N335	GPD1L	Glycerol-3-phosphate dehydrogenase 1-like protein	1,4	0,035	PRDX1
D207/9	EEN1	Flap and an ucloses 1	1.4	0.042	DP DV1
P 37/40	FEINI	Fiap endonuclease 1	1,4	0,042	PRDAT
P78347	GTF2I	General transcription factor II-I	1,4	0,045	PRDX1
Q86TI2	DPP9	Dipeptidyl peptidase 9	1,4	0,046	PRDX1
Q9Y383	LUC7L2	Putative RNA-binding protein Luc7-like 2	1,3	0	PRDX1
09U080	PA2G4	Proliferation-associated protein 2G4	13	0	PR DX1
OWNELLS	NUID25	Neeleenein NUD25	1.2	0	DR DV1
Qainfith	NUP33	Nucleoponii NOF35	1,5	0	PKDAI
Q12788	TBL3	Transducin beta-like protein 3	1,3	0,001	PRDX1
P49916	LIG3	DNA ligase 3	1,3	0,001	PRDX1
Q9H3P7	ACBD3	Golgi resident protein GCP60	1,3	0,001	PRDX1
K7ED E1	EIE2V	Fulcarvotic translation initiation factor 2 subunit K	1.2	0.001	DP DV1
R/ERTI	LITJK	Eukaryotic translation initiation factor 5 subunit K	1,5	0,001	PRDAT
P29401	TKT	Transketolase	1,3	0,001	PRDX1
P62877	RBX1	E3 ubiquitin-protein ligase RBX1	1,3	0,001	PRDX1
P53004	BLVRA	Biliverdin reductase A	1,3	0,002	PRDX1
P61923	COP71	Coatomer subunit zeta-1	13	0.002	PR DX1
00(1104	DDLIME	DD7	1.2	0.002	DR DV1
Q96HC4	PDLIMS	PDZ and L1M domain protein 5	1,5	0,002	PKDAI
P62241	RPS8	40S ribosomal protein S8	1,3	0,003	PRDX1
O00116	AGPS	Alkyldihydroxyacetonephosphate synthase, peroxisomal	1,3	0,004	PRDX1
O92688	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B	1,3	0,004	PRDX1
I2KMV5	P DS12	40S ribosomal protain \$12	1.2	0.01	DP DV1
DOL(07)	LITI 1		1,5	0,01	DD DV1
0948/4	UFLI	E3 UFM1-protein ligase 1	1,3	0,01	PRDXI
P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	1,3	0,015	PRDX1
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	1,3	0,017	PRDX1
075131	CPNE3	Copine-3	1.3	0,018	PRDX1
092769	UDACO	Histope desectulars 2	1.2	0.027	DD DV1
Q92/69	HDAC2	Histone deacetylase 2	1,5	0,02/	PRDAT
095163	ELP1	Elongator complex protein 1	1,3	0,048	PRDX1
Q8ND82	ZNF280C	Zinc finger protein 280C	1,2	0	PRDX1
G8JLH9	STAT3	Signal transducer and activator of transcription	1.2	0	PRDX1
F5R HC9	FLOC	Flongin-C	1.2	0	DB DV 1
LJI(1100	LUC		1,2	0	r NDA1
P52594	AGFG1	Art-GAP domain and FG repeat-containing protein 1	1,2	0	PRDX1
Q5JXI8	FHL1	Four and a half LIM domains protein 1	1,2	0	PRDX1
	CHAF1B	Chromatin assembly factor 1 subunit B	1,2	0	PRDX1
Q13112					
Q13112 007020	R DI 18	60S ribosomal protein L18	1 2	0.001	PR DX1
Q13112 Q07020	RPL18	60S ribosomal protein L18	1,2	0,001	PRDX1
Q13112 Q07020 Q92600	RPL18 CNOT9	60S ribosomal protein L18 CCR4-NOT transcription complex subunit 9	1,2 1,2	0,001 0,001	PRDX1 PRDX1

E7ESY4	MTA1	Metastasis-associated protein MTA1	1.2	0.003	PR DX1
015008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	1.2	0.004	PR DX1
M00Y97	7C3H4	Zinc finger CCCH domain-containing protein 4	1,2	0.006	PR DX1
P55795	HNR NPH2	Heterogeneous nuclear ribonucleoprotein H?	1,2	0.006	PR DX1
0911KM9	RAIV	R N A binding protein R alv	1,2	0.007	DR DY1
Q)0KMI)	P DI C	60S ribecomal protein Kaly	1,2	0.01	DP DV1
Q028/8	NCDD1	Nu lucas lia lia anti i l	1,2	0,01	PRDA1
Q09161	NCBPI	Nuclear cap-binding protein subunit 1	1,2	0,01	PRDXI
P49/50	YLPMI	YLP motif-containing protein 1	1,2	0,01	PRDXI
095202	LETM1	Mitochondrial proton/calcium exchanger protein	1,2	0,019	PRDX1
Q86UP2	KTN1	Kinectin	1,2	0,022	PRDX1
P42224	STAT1	Signal transducer and activator of transcription 1-alpha/beta	1,2	0,026	PRDX1
Q9Y3T9	NOC2L	Nucleolar complex protein 2 homolog	1,2	0,028	PRDX1
Q9Y5V3	MAGED1	Melanoma-associated antigen D1	1,1	0,001	PRDX1
Q9UBU9	NXF1	Nuclear RNA export factor 1	1,1	0,002	PRDX1
Q9NTI5	PDS5B	Sister chromatid cohesion protein PDS5 homolog B	1,1	0,003	PRDX1
Q9BT78	COPS4	COP9 signalosome complex subunit 4	1,1	0,004	PRDX1
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	1,1	0,004	PRDX1
P23921	RRM1	Ribonucleoside-diphosphate reductase large subunit	1,1	0,006	PRDX1
P05455	SSB	Lupus La protein	1,1	0,006	PRDX1
P27144	AK4	Adenvlate kinase 4. mitochondrial	1,1	0,007	PRDX1
A0A024R4M0	R PS9	40S ribosomal protein S9	1.1	0.007	PRDX1
P31943	HNR NPH1	Heterogeneous nuclear ribonucleoprotein H	11	0.009	PR DX1
0/3390	HNRNDR	Heterogeneous nuclear ribonucleoprotein R	1.1	0.012	DR DY1
045570	EAE2	EAS associated factor 2	1,1	0.012	DP DV1
Q/6C33	DDI 14	(05 ribecomel motoria L 1/	1,1	0,012	DR DV1
P50914	CP D CO	605 ribosomai protein L14	1,1	0,015	PRDAI
Q9UHB9	SRP68	Signal recognition particle subunit SKP68	1,1	0,015	PRDXI
Q90112	AIP6VIH	V-type proton A I Pase subunit H	1,1	0,019	PRDXI
P08133	ANXA6	Annexin A6	1,1	0,022	PRDX1
Q71UM5	RPS27L	40S ribosomal protein S27-like	1,1	0,025	PRDX1
O76003	GLRX3	Glutaredoxin-3	1,1	0,026	PRDX1
P39687	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A	1,1	0,026	PRDX1
Q96SB4	SRPK1	SRSF protein kinase 1	1,1	0,029	PRDX1
P16435	POR	NADPHcytochrome P450 reductase	1,1	0,03	PRDX1
F8W6I7	HNRNPA1	Helix-destabilizing protein	1,1	0,031	PRDX1
O75381	PEX14	Peroxisomal membrane protein PEX14	1,1	0,037	PRDX1
P06748	NPM1	Nucleophosmin	1,1	0,039	PRDX1
Q99426	TBCB	Tubulin-folding cofactor B	1,1	0,045	PRDX1
Q9NW13	RBM28	RNA-binding protein 28	1,1	0,048	PRDX1
P78406	RAE1	mRNA export factor	1	0,001	PRDX1
014974	KPNB1	Importin subunit beta-1	1	0.002	PRDX1
086VM9	ZC3H18	Zinc finger CCCH domain-containing protein 18	1	0.005	PR DX1
Q9V5P6	GMPPR	Mannose-1-phosphate guanyltransferase beta	1	0.005	PR DX1
D/5972	CRV5	Chromobox protein homolog 5	1	0,009	DP DV1
000/10	UDOS		1	0,008	DR DV1
000410	IPO5	NTDDa literal and	1	0,008	PRDAI
<u>C9JR16</u>	NUBI	NEDD8 ultimate buster 1	1	0,009	PRDXI
P4389/	ISFM	Elongation factor 1s, mitochondrial	1	0,022	PRDXI
Q9Y2Q3	GSTK1	Glutathione S-transferase kappa 1	1	0,026	PRDX1
Q9BQ52	ELAC2	Zinc phosphodiesterase ELAC protein 2	1	0,031	PRDX1
P43490	NAMPT	Nicotinamide phosphoribosyltransferase	1	0,046	PRDX1
Q13162	PRDX4	Peroxiredoxin-4	9,7	0	PRDX2
P13667	PDIA4	Protein disulfide-isomerase A4	5,9	0	PRDX2
Q12797	ASPH	Aspartyl/asparaginyl beta-hydroxylase	4,2	0	PRDX2
Q9NYU2	UGGT1	UDP-glucose:glycoprotein glucosyltransferase 1	4	0	PRDX2
Q15084	PDIA6	Protein disulfide-isomerase A6	3,9	0	PRDX2
P07237	P4HB	Protein disulfide-isomerase	3,9	0	PRDX2
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	3,6	0	PRDX2
P98175	RBM10	RNA-binding protein 10	3,5	0	PRDX2
Q13217	DNAJC3	DnaJ homolog subfamily C member 3	3,4	0	PRDX2
P11021	HSPA5	Endoplasmic reticulum chaperone BiP	3,4	0	PRDX2
A0A087X054	HYOU1	Hypoxia up-regulated protein 1	3.3	0	PRDX2
000469	PLOD2	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 2	3.3	0.001	PR DX2
P11047	LAMC1	Laminin subunit gamma-1	31	0	PR DX2
	FR D/ 4	Endoplasmic raticulum resident protoin 4.4	3 1	0.02	DR DV2
D20101	DDIA 2	Drotoin digulfido icomoroso A 2	2.0	0,02	DD DV2
1 JUIUI D27707	CALP	Calculation	2,7	0	PRDA2
<u>F2//9/</u>	CALK		2,8	0	PKDX2
D6KBV2	LMAN2	vesicular integral-membrane protein V1P36	2,8	0,001	PKDX2
Q9BZQ6	EDEM3	EK degradation-enhancing alpha-mannosidase-like protein 3	2,8	0,001	PKDX2
P78417	GSTO1	Glutathione S-transferase omega-1	2,7	0	PRDX2
P12109	COL6A1	Collagen alpha-1(VI) chain	2,7	0,001	PRDX2

O75688	PPM1B	Protein phosphatase 1B	2,6	0	PRDX2
P50454	SERPINH1	Serpin H1	2,6	0	PRDX2
O00268	TAF4	Transcription initiation factor TFIID subunit 4	2,6	0	PRDX2
Q9Y2H1	STK38L	Serine/threonine-protein kinase 38-like	2,6	0,002	PRDX2
Q9Y680	FKBP7	Peptidyl-prolyl cis-trans isomerase FKBP7	2,6	0,002	PRDX2
Q14257	RCN2	Reticulocalbin-2	2,5	0	PRDX2
Q8TEM1	NUP210	Nuclear pore membrane glycoprotein 210	2,5	0	PRDX2
P49257	LMAN1	Protein ERGIC-53	2,5	0,001	PRDX2
P55268	LAMB2	Laminin subunit beta-2	2,3	0,002	PRDX2
P27824	CANX	Calnexin	2,2	0	PRDX2
P09972	ALDOC	Fructose-bisphosphate aldolase C	2,1	0,046	PRDX2
Q15424	SAFB	Scaffold attachment factor B1	2	0	PRDX2
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	2	0,002	PRDX2
P14625	HSP90B1	Endoplasmin	1,9	0	PRDX2
000399	DCTN6	Dynactin subunit 6	1,9	0,011	PRDX2
E9PFZ2	СР	Ceruloplasmin	1,9	0,013	PRDX2
Q12929	EPS8	Epidermal growth factor receptor kinase substrate 8	1,8	0,01	PRDX2
P57076	CFAP298	Cilia- and flagella-associated protein 298	1,8	0,011	PRDX2
P07942	LAMBI	Laminin subunit beta-1	1,8	0,015	PRDX2
P11/1/	IGF2R	Cation-independent mannose-6-phosphate receptor	1,8	0,021	PRDX2
043852	CALU		1,7	0,001	PRDX2
QSKKV6	EXUSC6	Exosome complex component M1R3	1,/	0,006	PRDX2
Q9UKN8	GIF3C4	General transcription factor 3C polypeptide 4	1,/	0,018	PRDX2
Q9HAU5	D4UA1	Regulator of honsense transcripts 2	1,/	0,019	PRDA2
022028	D2L1	Prolyl 4-hydroxylase subunit apria-1	1,6	0,003	PRDA2
Q32F28		2 katagarl CoA thiology patericomal	1,6	0,014	PRDA2
OSIYBI	DNAIC10	Drat homolog subfamily C member 10	1,0	0.002	PR DY2
D23588	EIE4B	Fukarwatic translation initiation factor /B	1,5	0,002	PR DY2
P67809	VBX1	V.box.binding protein 1	1,5	0.034	PR DX2
HOYEN2	PPP6R 3	Serine/threenine-protein phosphatase 6 regulatory subunit 3	1,5	0.036	PR DX2
O8N6R0	EEFIAKNMT	eEF1A lysine and N-terminal methyltransferase	1.5	0.037	PR DX2
P62314	SNR PD1	Small nuclear ribonucleoprotein Sm D1	1.4	0	PR DX2
O15020	SART3	Squamous cell carcinoma antigen recognized by T-cells 3	1,4	0,001	PRDX2
O99504	EYA3	Eves absent homolog 3	1,4	0,001	PRDX2
P56182	RRP1	Ribosomal RNA processing protein 1 homolog A	1,4	0,001	PRDX2
Q9H0H5	RACGAP1	Rac GTPase-activating protein 1	1,4	0,002	PRDX2
O00116	AGPS	Alkyldihydroxyacetonephosphate synthase, peroxisomal	1,4	0,004	PRDX2
O00170	AIP	AH receptor-interacting protein	1,4	0,005	PRDX2
E7ESP9	NEFM	160 kDa neurofilament protein	1,4	0,017	PRDX2
O60934	NBN	Nibrin	1,3	0	PRDX2
A6NHR9	SMCHD1	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	1,3	0	PRDX2
Q9UIG0	BAZ1B	Tyrosine-protein kinase BAZ1B	1,3	0,001	PRDX2
Q04837	SSBP1	Single-stranded DNA-binding protein, mitochondrial	1,3	0,002	PRDX2
Q01831	XPC	DNA repair protein complementing XP-C cells	1,3	0,003	PRDX2
P42696	RBM34	RNA-binding protein 34	1,3	0,005	PRDX2
Q9UBE0	SAE1	SUMO-activating enzyme subunit 1	1,3	0,012	PRDX2
P22307	SCP2	Non-specific lipid-transfer protein	1,3	0,014	PRDX2
Q14676	MDC1	Mediator of DNA damage checkpoint protein 1	1,3	0,034	PRDX2
P40938	RFC3	Replication factor C subunit 3	1,2	0	PRDX2
P25786	PSMA1	Proteasome subunit alpha type-1	1,2	0,001	PRDX2
B8ZZC5	GLS	Glutaminase	1,2	0,001	PRDX2
Q68E01	INT\$3	Integrator complex subunit 3	1,2	0,002	PRDX2
P49916	LIG3	DNA ligase 3	1,2	0,003	PRDX2
P31942	HNRNPH3	Heterogeneous nuclear ribonucleoprotein H3	1,2	0,004	PRDX2
Q9UBS4	DNAJB11	DnaJ homolog subfamily B member 11	1,2	0,004	PRDX2
P18583	SON	Protein SON	1,2	0,008	PRDX2
094906	PRPF6	Pre-mRNA-processing factor 6	1,2	0,009	PRDX2
M0QY97	ZC3H4	Zinc finger CCCH domain-containing protein 4	1,2	0,009	PRDX2
Q16352	INA	Alpha-internexin	1,2	0,012	PRDX2
Q9BZE4	GTPBP4	Nucleolar GTP-binding protein 1	1,2	0,013	PRDX2
Q02241	KIF23	Kinesin-like protein KIF23	1,2	0,015	PRDX2
PU5/83	KR118 TRCP	Keratin, type I cytoskeletal 18	1,2	0,021	PKDX2
014646	I BCB	Iubuin-roiding cotactor B Chammadamain baliana DNA Line line annuin 1	1,2	0,023	PKDX2
U14646	CHDI	Chromodomain-helicase-DNA-binding protein 1	1,2	0,027	PKDX2
OOV2DA	OTAGAD			13 13 13	PR DX 2
Q9Y3D0	CIAO2B	Cytosolic iron-sulfur assembly component 2B	1,2	0,031	DR DWG
Q9Y3D0 075152	CIAO2B ZC3H11A	Zinc finger CCCH domain-containing protein 11A	1,2	0,031	PRDX2
Q9Y3D0 075152 Q9NV17	CIAO2B ZC3H11A ATAD3A	Zinc finger CCCH domain-containing protein 11A ATPase family AAA domain-containing protein 3A	1,2 1,2 1,1	0,031 0,042 0	PRDX2 PRDX2 PRDX2

015785	TOMM34	Mitochondrial import receptor subunit TOM34	11	0.011	PR DX2
Q15/05	ETSI2	nto rP NA 2' O riboso P NA mothyltransforaso FTSI2	1,1	0,011	DP DY2
Q81181	CM661	Devide CMCC1	1,1	0,011	PRDA2
001000	CM331	Protein CM351	1,1	0,014	PRDA2
Q9NQ29	LUC/L	Putative RNA-binding protein Luc/-like I	1,1	0,01/	PRDX2
Q8N163	CCAR2	Cell cycle and apoptosis regulator protein 2	1,1	0,021	PRDX2
Q9Y2T2	AP3M1	AP-3 complex subunit mu-1	1,1	0,023	PRDX2
P52701	MSH6	DNA mismatch repair protein Msh6	1,1	0,027	PRDX2
P07196	NEFL	Neurofilament light polypeptide	1,1	0,03	PRDX2
C9J250	RBM6	RNA-binding protein 6	1,1	0,032	PRDX2
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	1,1	0,033	PRDX2
O71UM5	RPS27L	40S ribosomal protein S27-like	1,1	0.045	PRDX2
P04792	HSPB1	Heat shock protein beta-1	1	0	PR DX2
D02545	IMNA	Prolomin A /C [Closed into: Lamin A /C	1	0.001	DP DY2
	DTTO	Publication control for a 2	1	0,001	DD DV2
Q9D142	KIF2		1	0,004	PRDA2
Q13451	FKBP5	Peptidyl-prolyl cis-trans isomerase FKBP5	1	0,006	PRDX2
Q9NZB2	FAM120A	Constitutive coactivator of PPAR-gamma-like protein 1	1	0,007	PRDX2
A0A0A0MRM8	MYO6	Unconventional myosin-6	1	0,013	PRDX2
Q96H79	ZC3HAV1L	Zinc finger CCCH-type antiviral protein 1-like	1	0,013	PRDX2
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	1	0,017	PRDX2
Q15042	RAB3GAP1	Rab3 GTPase-activating protein catalytic subunit	1	0,023	PRDX2
095376	ARIH2	E3 ubiquitin-protein ligase ARIH2	1	0,027	PRDX2
O9P0M6	MACROH2A2	Core histone macro-H2A.2	1	0.046	PR DX2
015084	PDIA6	Protein disulfide isomerase A6	4.9	0	PR DX3
D13667	PDIA 4	Protein disulfide isomerase A/	4.9	0	DP DY2
00011/1/2	FDIA4		4,0	0	PRDA3
Q9INTU2	UGGII	ODP-glucose:glycoprotein glucosyltransferase 1	4,2	0	PRDAS
P1104/	LAMCI	Laminin subunit gamma-1	4	0	PRDX3
O00469	PLOD2	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	3,9	0	PRDX3
P07237	P4HB	Protein disulfide-isomerase	3,9	0	PRDX3
A0A087X054	HYOU1	Hypoxia up-regulated protein 1	3,9	0	PRDX3
Q12797	ASPH	Aspartyl/asparaginyl beta-hydroxylase	3,6	0	PRDX3
P11021	HSPA5	Endoplasmic reticulum chaperone BiP	3,5	0	PRDX3
P30101	PDIA3	Protein disulfide-isomerase A3	2,9	0	PRDX3
013217	DNAIC3	DnaI homolog subfamily C member 3	2.9	0	PR DX3
P12109	COLGAI	Collagen alpha-1(VI) chain	2.9	0.002	PR DX3
D50/5/	SEP DINILI	Coming U1	2,9	0,002	DP DY2
P 30434	CALD	Selpin III	2,0	0	PRDAJ
P2//9/	CALK		2,8	0	PRDAS
Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	2,8	0,04/	PRDX3
Q9Y680	FKBP7	Peptidyl-prolyl cis-trans isomerase FKBP7	2,7	0,002	PRDX3
P27824	CANX	Calnexin	2,6	0	PRDX3
P09972	ALDOC	Fructose-bisphosphate aldolase C	2,6	0,016	PRDX3
P14625	HSP90B1	Endoplasmin	2,4	0	PRDX3
D6RBV2	LMAN2	Vesicular integral-membrane protein VIP36	2,4	0,006	PRDX3
P55268	LAMB2	Laminin subunit beta-2	2,2	0,001	PRDX3
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	2,1	0,002	PRDX3
E9PFZ2	CP	Ceruloplasmin	2.1	0.012	PR DX3
012929	EPS8	Enidermal growth factor recentor kinase substrate 8	2	0.008	PR DX3
D07942	LAMB1	Laminin subunit bota 1	2	0,000	DP DY2
0121(2	DDDV4	Lammi subunit beta-1		0,015	DD DV2
Q15162	PRDA4	Peroxinedoxin-4	10	0	PRDAS
Q8IXBI	DNAJCIO	Dnaj homolog subramily C member 10	1,9	0	PRDX3
Q9BZQ6	EDEM3	ER degradation-enhancing alpha-mannosidase-like protein 3	1,9	0,012	PRDX3
Q9UKN8	GTF3C4	General transcription factor 3C polypeptide 4	1,9	0,015	PRDX3
P11717	IGF2R	Cation-independent mannose-6-phosphate receptor	1,9	0,018	PRDX3
P32119	PRDX2	Peroxiredoxin-2	1,8	0,002	PRDX3
Q8NBJ5	COLGALT1	Procollagen galactosyltransferase 1	1,7	0,031	PRDX3
Q16576	RBBP7	Histone-binding protein RBBP7	1,6	0,002	PRDX3
Q13151	HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	1,6	0,035	PRDX3
O8TEM1	NUP210	Nuclear pore membrane glycoprotein 210	1,5	0.001	PRDX3
P13674	P4H A 1	Prolyl 4-hydroxylase subunit alpha-1	15	0.002	PR DX3
A 0 A 2D 8V811	P DS14	40S ribosomal protoin \$14	1,9	0,002	DP DY2
OOLIDE (	DNAID11	Posthered and Costl Provident 11	1,4	0	PRDAJ
Q70034	DINAJDII	Of all complements of	1,4	0	PRDA3
P62/55	KP56	405 ribosomal protein 56	1,4	0,003	PKDX3
P06748	NPM1	Nucleophosmin	1,4	0,017	PRDX3
Q14696	MESD	LRP chaperone MESD	1,4	0,045	PRDX3
Q14697	GANAB	Neutral alpha-glucosidase AB	1,3	0,003	PRDX3
P62280	RPS11	40S ribosomal protein S11	1,3	0,004	PRDX3
O00116	AGPS	Alkyldihydroxyacetonephosphate synthase, peroxisomal	1,3	0,006	PRDX3
P18077	RPL35A	60S ribosomal protein L35a	1,2	0,003	PRDX3
P49257	LMAN1	Protein ERGIC-53	1,2	0,01	PRDX3
Q15424	SAFB	Scaffold attachment factor B1	1,2	0,014	PRDX3
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O43852	CALU	Calumenin	1,2	0,014	PRDX3
075821	EIF3G	Eukaryotic translation initiation factor 3 subunit G	1,1	0,003	PRDX3
Q9H0H5	RACGAP1	Rac GTPase-activating protein 1	1,1	0,008	PRDX3
Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	1,1	0,011	PRDX3
Q15020	SART3	Squamous cell carcinoma antigen recognized by T-cells 3	1,1	0,015	PRDX3
P18124	RPL7	60S ribosomal protein L7	1,1	0,032	PRDX3
P13667	PDIA4	Protein disulfide-isomerase A4	6	0	PRDX5
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	5,7	0	PRDX5
Q15084	PDIA6	Protein disulfide-isomerase A6	5	0	PRDX5
A0A087X054	HYOU1	Hypoxia up-regulated protein 1	4,2	0	PRDX5
Q12797	ASPH	Aspartyl/asparaginyl beta-hydroxylase	3,9	0	PRDX5
O9NYU2	UGGT1	UDP-glucose:glycoprotein glucosyltransferase 1	3,8	0	PRDX5
Q00469	PLOD2	Procollagen-lysine.2-oxoglutarate 5-dioxygenase 2	3.7	0	PR DX5
P07237	P4HB	Protein disulfide-isomerase	3.5	0	PR DX5
P11047	I AMC1	I aminin subunit gamma.	3,5	0	PR DX5
P50/5/	SER DINH1	Sernin H1	3.4	0	PR DY5
D11021	LISDAS	Endonlarmic raticulum chanarana BiD	2.2	0	DP DV5
012217	DNAIC2	Dral hamalag subfamily C mambar 2	3,2	0	DR DV5
Q1521/	DINAJC5	Nuclease subtaining Chemoter 3	2,9	0	PRDA3
Q8TEMI	NUP210	Nuclear pore membrane giycoprotein 210	2,9	0	PRDAS
P30101	PDIA3	Protein disulfide-isomerase A3	2,8	0	PRDX5
Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	2,8	0,036	PRDX5
Q9BZQ6	EDEM3	ER degradation-enhancing alpha-mannosidase-like protein 3	2,7	0,001	PRDX5
D6RBV2	LMAN2	Vesicular integral-membrane protein VIP36	2,7	0,002	PRDX5
P12109	COL6A1	Collagen alpha-1(VI) chain	2,6	0,001	PRDX5
P49257	LMAN1	Protein ERGIC-53	2,4	0,001	PRDX5
Q9Y680	FKBP7	Peptidyl-prolyl cis-trans isomerase FKBP7	2,4	0,002	PRDX5
P27824	CANX	Calnexin	2,2	0	PRDX5
P55268	LAMB2	Laminin subunit beta-2	2,2	0,002	PRDX5
P09110	ACAA1	3-ketoacyl-CoA thiolase, peroxisomal	2,1	0,001	PRDX5
Q96AC1	FERMT2	Fermitin family homolog 2	2,1	0,011	PRDX5
Q9BYN0	SRXN1	Sulfiredoxin-1	2,1	0,016	PRDX5
P22307	SCP2	Non-specific lipid-transfer protein	2	0	PRDX5
Q7Z406	MYH14	Myosin-14	2	0,001	PRDX5
Q13162	PRDX4	Peroxiredoxin-4	10,2	0	PRDX5
P27797	CALR	Calreticulin	1.9	0	PRDX5
O8IXB1	DNAIC10	Dnal homolog subfamily C member 10	1.9	0,001	PRDX5
013257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	1.9	0.002	PR DX5
P19105	MYI 12 A	Myosin regulatory light chain 12A	1.9	0.011	PR DX5
0151/9	DI FC	Dectin	1,9	0.025	PR DY5
D05782	VDT19	Karatin tuna Lautackalatal 18	1,9	0,025	DP DV5
E9DE72	CD	Carulanlasmin	1,0	0,003	DP DV5
09V224	DTD AF	P NA transprintion translation and transport factor protein	1,0	0,022	DP DV5
Q91224 D55084	LIADUR	Trifunctional and maintain and transport factor protein	1,8	0,02/	PRDA3
P55084	HADHD	Chaunian Cha	1,8	0,034	PRDAS
B8ZZC5	GLS	Glutaminase	1,/	0	PRDX5
P14625	HSP90B1	Endoplasmin	1,7	0	PRDX5
Q9BW92	TARS2	ThreoninetRNA ligase, mitochondrial	1,7	0,003	PRDX5
P31327	CPS1	Carbamoyl-phosphate synthase [ammonia], mitochondrial	1,7	0,012	PRDX5
G3V5X4	SYNE2	Nesprin-2	1,7	0,022	PRDX5
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	1,7	0,025	PRDX5
Q9H0H5	RACGAP1	Rac GTPase-activating protein 1	1,6	0	PRDX5
Q4VCS5	AMOT	Angiomotin	1,6	0,012	PRDX5
Q96KM6	ZNF512B	Zinc finger protein 512B	1,6	0,025	PRDX5
P07942	LAMB1	Laminin subunit beta-1	1,6	0,025	PRDX5
P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	1,6	0,025	PRDX5
P42345	MTOR	Serine/threonine-protein kinase mTOR	1,6	0,026	PRDX5
Q13813	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	1,6	0,034	PRDX5
P46013	MKI67	Proliferation marker protein Ki-67	1,6	0,035	PRDX5
P43897	TSFM	Elongation factor Ts, mitochondrial	1.5	0	PRDX5
A0A2R8YDO9	SUCLA2	SuccinateCoA ligase [ADP-forming] subunit beta, mitochondria]	1.5	0	PR DX5
09NY93	DDX56	Prohable ATP-dependent R NA helicase DDX56	1.5	0	PR DX5
0511928	USD17B10	2 hydrowyscyl CoA dobudrogopaso type 2	1,5	0	DP DV5
002241	VIE22	Vinsein like meetrin VIE22	1,5	0.002	DR DV5
Q02241	SUCL C1	Continue Co. Altico (ADD) CDD Continue la louise la loui	1,5	0,003	PRDA3
COD014	MACROHIDAG	Gene histore means U2A 2	1,5	0,004	PRDAS
Q7PUM6	MACKOH2A2	Core histone macro-H2A.2	1,5	0,005	PKDAS
QSJKX3	PIIKMI	Presequence protease, mitochondrial	1,5	0,007	PKDX5
Q6P2E9	EDC4	Enhancer of mKNA-decapping protein 4	1,5	0,008	PRDX5
Q5V W32	BROX	BKO1 domain-containing protein BROX	1,5	0,04	PKDX5
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	1,5	0,04	PRDX5
Q15477	SKIV2L	Helicase SKI2W	1,5	0,044	PRDX5

P27144	AK4	Adenvlate kinase 4, mitochondrial	1,4	0	PRDX5
P98175	RBM10	RNA-binding protein 10	1,4	0	PRDX5
A0A2R8YD50	HSD17B4	Peroxisomal multifunctional enzyme type 2	1,4	0	PRDX5
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	1,4	0,001	PRDX5
O9BSH4	TACO1	Translational activator of cytochrome c oxidase 1	1,4	0,002	PRDX5
O02252	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	1,4	0,002	PRDX5
O5ITZ9	AARS2	AlaninetRNA ligase, mitochondrial	1,4	0,002	PRDX5
08IYI6	EXOC8	Exocyst complex component 8	1.4	0.003	PR DX5
012849	GR SF1	G-rich sequence factor 1	1.4	0.003	PRDX5
P19338	NCL	Nucleolin	1.4	0.005	PRDX5
092616	GCN1	eIF-2-alpha kinase activator GCN1	1.4	0.013	PRDX5
015061	WDR43	WD repeat-containing protein 43	1.4	0.019	PRDX5
07L2E3	DHX30	ATP-dependent R NA helicase DHX 30	1,1	0.027	PR DX5
075367	MACROH2A1	Core histone macro-H2A 1	1,1	0.034	PR DX5
016762	TST	Thiosulfate sulfurtransferase	1,1	0.04	PR DX5
P11388	ТОР2А	DNA topoisomerase 2-alpha	1.4	0.042	PR DX5
098203	GSTK1	Glutathione S-transferase kanna 1	1,1	0.002	PR DX5
ADADAOMR M8	MYO6	Unconventional myosin-6	1,3	0.002	PR DY5
D1367/	D/H A 1	Prolyl 4 - hydroxylase subunit alpha.1	1,5	0.006	PR DY5
09NW13	R RM28	P NA binding protein 28	1,5	0.012	DR DY5
D82920	MP DS24	285 ribecomel protein 236 mitachondrial	1,5	0.025	DP DY5
012256	DDII 2	P INC ture F2 ubiquitin protein ligase DDU 2	1,3	0,025	DP DV5
Q15556	IICDD1	Last shash materia hata 1	1,5	0,03	DDDV5
P04/92	FCUSI	Fread Shock protein beta-1	1,2	0 002	PRDA5
P30084	ECH51	Enoyi-CoA nydratase, mitochondriai	1,2	0,002	PRDAS
P180//	RPL35A	Bost ribosomal protein L35a	1,2	0,003	PRDAS
GSEA31	SEC24C	Protein transport protein Sec24C	1,2	0,003	PRDAS
Q912R9	MRPS/	285 ribosomal protein 57, mitochondrial	1,2	0,004	PRDAS
P35580	MYH10	Myosin-10	1,2	0,004	PRDX5
094925	GLS	Glutaminase kidney isoform, mitochondrial	1,2	0,017	PRDX5
Q13509	TUBB3	Iubulin beta-3 chain	1,2	0,023	PRDX5
P33992	MCM5	DNA replication licensing factor MCM5	1,2	0,024	PRDX5
P0/196	NEFL	Neurofilament light polypeptide	1,2	0,035	PRDX5
Q9HCD5	NCOA5	Nuclear receptor coactivator 5	1,2	0,036	PRDX5
Q9H3U1	UNC45A	Protein unc-45 homolog A	1,2	0,044	PRDX5
Q9UBS4	DNAJB11	DnaJ homolog subtamily B member 11	1,1	0,001	PRDX5
Q9UBQ7	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	1,1	0,002	PRDX5
Q96KR1	ZFR	Zinc finger RNA-binding protein	1,1	0,003	PRDX5
O15381	NVL	Nuclear valosin-containing protein-like	1,1	0,004	PRDX5
P31942	HNRNPH3	Heterogeneous nuclear ribonucleoprotein H3	1,1	0,005	PRDX5
Q13085	ACACA	Acetyl-CoA carboxylase 1	1,1	0,005	PRDX5
Q9GZT3	SLIRP	SRA stem-loop-interacting RNA-binding protein, mitochondrial	1,1	0,011	PRDX5
P18583	SON	Protein SON	1,1	0,016	PRDX5
A0A0G2JNZ2	SCRIB	Protein scribble homolog	1,1	0,016	PRDX5
A0A0U1RRM6	ENAH	Protein enabled homolog	1,1	0,016	PRDX5
E9PEJ4	DLAT	Acetyltransferase component of pyruvate dehydrogenase complex	1,1	0,016	PRDX5
G5E9W7	MRPS22	28S ribosomal protein S22, mitochondrial	1,1	0,019	PRDX5
O43615	TIMM44	Mitochondrial import inner membrane translocase subunit TIM44	1,1	0,022	PRDX5
Q05655	PRKCD	Protein kinase C delta type	1,1	0,023	PRDX5
Q14258	TRIM25	E3 ubiquitin/ISG15 ligase TRIM25	1,1	0,023	PRDX5
Q9BQ69	MACROD1	ADP-ribose glycohydrolase MACROD1	1,1	0,024	PRDX5
P25685	DNAJB1	DnaJ homolog subfamily B member 1	1,1	0,025	PRDX5
P62879	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	1,1	0,026	PRDX5
O95861	BPNT1	3'(2'),5'-bisphosphate nucleotidase 1	1,1	0,031	PRDX5
Q13464	ROCK1	Rho-associated protein kinase 1	1,1	0,034	PRDX5
P50995	ANXA11	Annexin A11	1,1	0,034	PRDX5
Q5JTH9	RRP12	RRP12-like protein	1,1	0,035	PRDX5
P51570	GALK1	Galactokinase	1,1	0,042	PRDX5
Q00610	CLTC	Clathrin heavy chain 1	1,1	0,046	PRDX5
Q99798	ACO2	Aconitate hydratase, mitochondrial	1	0,001	PRDX5
Q15555	MAPRE2	Microtubule-associated protein RP/EB family member 2	1	0,002	PRDX5
P78406	RAE1	mRNA export factor	1	0,002	PRDX5
P40429	RPL13A	60S ribosomal protein L13a	1	0,005	PRDX5
O60701	UGDH	UDP-glucose 6-dehydrogenase	1	0,008	PRDX5
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	1	0,014	PRDX5
O75439	РМРСВ	Mitochondrial-processing peptidase subunit beta	1	0,016	PRDX5
P55795	HNRNPH2	Heterogeneous nuclear ribonucleoprotein H2	1	0,017	PRDX5
Q15042	RAB3GAP1	Rab3 GTPase-activating protein catalytic subunit	1	0,023	PRDX5
Q16352	INA	Alpha-internexin	1	0,032	PRDX5
Q8WYP5	AHCTF1	Protein ELYS	1	0,036	PRDX5

BADD         Disk         Disk <thdisk< th="">         Disk         Disk         <thd< th=""><th>Dc2701</th><th>Mette</th><th>DNA strend sector in Male</th><th>1</th><th>0.0/</th><th>DD DVC</th></thd<></thdisk<>	Dc2701	Mette	DNA strend sector in Male	1	0.0/	DD DVC
Partin         Principal and an end of the second start process of the proces of the process of the process o	P52/01 P48735	IDH2	JNA mismatch repair protein Msn6 Isocitrate debydrogenase [NADP] mitochondrial	1	0,04	PRDA5
PRUM<-open of the interaction         Processing interaction         Processinteracti	P60174	TPI1	Triosenhosnhate isomerase	1	0.043	PR DX5
0.847.0         MTA2         Metasabaseschind protein MTA2         7         0         PRI2           0.92760         HDAC         Histore description 2         5         0         PRR           0.92780         HDAC         Histore description 2         5         0         PRR           0.92780         PSR45         Protession excitents complex nutwint 3         4.6         0.0001         PRR           0.92928         PSR45         Protession excitents complex nutwint 3         4.6         0         PRR           0.92928         RBN4         Histone-Histon filt         4.1         0         PRR           PR355         RRN         Histone-Hostone filt in boom histone filt         5.8         0         PRR           PR354         RPR151         Protession signitis         PRR         5.8         0         PRR           PR354         Histone-Hostone filt in boom histone filt         1.5         0         PRR           PR154         Histone-Hostone filt in boom histone filt         1.5         0         PRR           PR354         Histone filt in boom histone filt in boom histone filt         1.5         0         PRR           PR154         Histone filt in boom histone filt in boom histone filt in boom histone filt in boom histone fil	PR DX5 -specific in	teractors	110septospiate isoliterase	1	0,045	T(DA)
Partial         Disory page in produce         6.4         0         PERA           Q2709         IIDAGC         Interest services         5         0         PERA           Q20201         PERA         Personin P         4.0         0.00         PERA           Q20202         RBH         Horesconte activator complex releants         4.0         0.00         PERA           Q20203         RBH         Horesconte activator complex releants         5.1         0         PERA           Q20203         RBH         Histone filtering protein P         5.1         0         PERA           Q20204         RBH         Histone filtering protein Protein RBH?         5.1         0         PERA           Q1554         RBH?         Histone filtering protein RBH?         5.2         0         PERA           Q1656         RBH?         Histone filtering protein Protein activator relation of protein RBH?         5.3         0         PERA           Q20204         IPENA         Periodin molecular sponter filtering protein Protein activator relation of protein RBH?         5.3         0         PERA           Q2050         IPENA         Periodin molecular sponter filtering protein protein protein protein protein protein protein protein activator relation activator relation activatore relation activator relati	094776	MTA2	Metastasis-associated protein MTA2	7	0	PR DX1
Q2709         H1Mc2         Histors descriptions <sup>2</sup> 6         0         PRA           PRA12         Protexin P         Protexin P         6.4         0.001         PRA           PR239         PSA15         Protexin present regions many frames and the second s	P49366	DHPS	Deaxyhynusine synthase	6.6	0	PR DX1
QQNNN         PEX19         Personser         4,0         0         PEX125           QQNNA         RNP-1         Histon-chaining protein RNP-1         4,1         0         PEX125           QUNNA         RNP-1         Histon-chaining protein RNP-1         4,1         0         PEX125           PAS356         H-C1         Histon-RNP interphysics         3,2         0         PEX125           QUNNA         RNP12         GS schlar differsomal growth P1         3,2         0         PEX125           QUNNA         RNP125         Desten anginine N methylinansfrars 5         3,8         0         PEX125           QUNNA         RNP127         Distances kinding protein RNP17         3,7         0         PEX125           QUNNA         HENDER Mages         3,6         0         PEX125         CAS25         0,001         PEX125           QUNNA         PENDA         Perfoldan shumh 4         3,5         0         PEX125         QUNNA         PENDA         Perfoldan shumh 4         3,5         0         PEX125           QUNNA         PENDA         Perfoldan shumh 4         3,5         0         PEX125         0         PEX125         0         PEX125         0         PEX125         0	092769	HDAC2	Histone deacetylase ?	5	0	PR DX1
PAC29         PSML1         Processors excitning complex advants J         4.6         0.001         PLT           PN366         RRPH         665 self-infosonal porein P1         4.1         0         PRT           PN365         RRPT         665 self-infosonal porein P1         4.1         0         PRT           PN365         PRTA         Section Advances P1         5.7         0         PRT           PN365         PRTA         Decoden agnines PA subpranders 2.5 NLD a guidency subunit B diplat bofem         5.8         0         PRT           P0364         PRTA         Discodent deported protein RBP7         5.7         0         PRT           P03054         PRTAS         Discodent deported protein RBP7         5.6         0.001         PRT           P03054         PRTAS         Discodent deported protein A L         5.6         0.001         PRT           P03054         PRTNA         Predidin subaria         1         5.5         0         PRT           P03054         PRTNA         Discodent deported protein A L         5.5         0         PRT           P03054         PRTNA         Discodent deported protein A L         5.5         0         PRT           P03054         PRTNA         Discoden	050NY5	PFX19	Perovin-19	49	0	PR DX1
DOUMS         RBPS         Histone-fooding predin PL         4.5         0         PL           D0256         RLP.2         656 solite filtoning predin PL         4.1         0         PR           D0256         HGL1         Histone Hall graphing predin PL         4.1         0         PR           D0257         Histone Isoling predin Prophysics 27 AS1D regulatory subanti Balpha Isofim         3.8         0         PR           D0474         PPS2A         ScienchProphysics 27 AS1D regulatory subanti Balpha Isofim         3.8         0         PR           D0475         RBP7         1.5         0         PR         2.6         0         PR           P1030         GARS1         Gigsine - RNAJBargo         5.6         0         PR         PR         2.6         0         PR           D0106         HAX1         HCS1 susscient protein protein serving phophysics exploratory subanti 3         5.5         0         PR	D(1289	DSME3	Protessame activator complex subunit 3	4.6	0.001	DR DX1
QC0500         AUT         Interior Harver         4.3         0         PTA           QC0500         HACL         Harver Harver         4.4         0         PTA           D04205         HACL         Harver Harver         4.4         PTA           D04314         PPRATS         Semical equitors in the merchine statements         3.8         0         PTA           D04574         PPRATS         Devints arginate in the merchine statements         3.8         0         PTA           Q04576         RABEP         Hinoso-banding protein RABP         3.8         0         PTA           Q04576         RABEP         Hinoso-banding protein RABP         3.6         0         PTA           Q0456         HAX         Homosech         3.6         0         PTA           Q04504         HAX         HCLSA suscituate protein NA         3.5         0         PTA           Q04504         HAX         HCLSA suscituate protein Samose in the state protein space in the state sta	000028	P PPD4	Listene highing metric D BBD4	4,6	0,001	PRDA1
Process         Process <t< td=""><td>Q09028</td><td>D DI D1</td><td>(OS acidia ciberand protein D1</td><td>4,5</td><td>0</td><td>PRDA1</td></t<>	Q09028	D DI D1	(OS acidia ciberand protein D1	4,5	0	PRDA1
Prod. Prod.         Finant Pro- transmission (PA2)         Finance hording account phosphatuse 2A 55 kD regulatory subunit B alpha tosform         57         0         PHL           Old*14         PRM33         Prosting againsing exponent phosphatuse 2A 55 kD regulatory subunit B alpha tosform         57         0         PHL           Q4576         RMB77         Hannos-boding ground RMB77         37         0         PHL           P8048         PRD33         Thiorostalis depondent persisk reductse, mitochondrial         36         0         PHL           P8049         PRD34         Hannos boding expondent persisk reductse, mitochondrial         36         0         PHL           P8049         PHD34         Herding in about expondent persisk reductse, mitochondrial         36         0         PHL           P80494         PHVB41         Isome framework in about expondent phosphatuse 6 regulatory subunit 3         35         0         PHL           P80496         STNCRUP         Hencorganosa nuclear framework phosphatuse 6 regulatory subunit 3         3         0         PHL           P80497         CALK         Christeria MTR 10         3         0         PHL           P80497         STNCRUP         Hencorganosa nuclear framework in an analysis in an anal	P03366	LI4C1	Uistana Ué	4,1	0	PRDA1
10101         1111100000         1011100000000000000000000000000000000	P62803	DDDDD 2 A	Ensione F14	4,1	0	PRDA1
Dir.Yi         PARAIS         From applied V methymmetrics         3.4         0         PAL           Q4556         RABP7         Hisnox-basing provide ResP         3.7         0         PRL           P0058         PRD23         Thiorebasine specific responses ResP         3.6         0         PRL           P00570         HPX         Henorebasing responses ResP         3.6         0         PRL           P00790         HPX         Henorebasing responses ResP         3.5         0         PRL           Q2NQP4         PTPN43         Semechanome proving hospharase 6 regularry subunit 3         3.5         0         PRL           Q2NQP4         PTPN44         Fromosphorebasing hospharase 6 regularry subunit 3         3.5         0         PRL           Q2157         HDACL         Histore base controls fromosphorebasing previous 2         3.4         0         PRL           Q3577         CALK         Caltercolule         3.3         0         PRL           Q3577         HDACL         Histore base controls fromosphore hybrid	P63151	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	3,9	0	PRDX1
QBD3.0         KBBP/         Histonic dunning protein holp/         3./         0         PEL           PAD048         PRLDX3         GARS1         Grychn-dRNA lipase         3.6         0         PRLT           PA1250         GARS1         Grychn-dRNA lipase         3.6         0.0001         PRLT           P02700         HYX         Hemopetin         3.5         0         PRLT           Q00163         HAX1         HCLS1-associated pretein X1         3.5         0         PRLT           Q00163         HAX1         HCLS1-associated pretein X1         3.5         0         PRLT           Q00164         HDX1         HCLS1-associated pretein X1         3.5         0         PRLT           Q0024         PPDN4         Holpschurdt dytoperate 2         3.5         0         PRLT           Q15547         HDXC1         Heterogeneous colder ribonind second pretein 2         3.3         0         PRLT           Q15547         HDXC1         Histoned date: ribonind pretein 58P72         3.2         0         PRLT           Q16540         SMR217         Signal recognition particle subuit 58P72         3.2         0         PRLT           Q15674         RPLP2         668 acidic ribbonind pretein 52P12	014/44	PKM15	Protein arginine N-methyltransferase 5	3,8	0	PRDXI
PM043         Intersolutin-dependent procents fourthal, minochoorinal         5.6         0         PRL           P01250         GARS1         Giysline-GRMA ligase         5.6         0         PRL           P01270         HIX         Hemoperatin         5.6         0         PRL           P01270         HIX         Hendshin subsmit 4         5.3         0         PRL           QPNQP4         PIDN4         Periodian subsmit 4         5.3         0         PRL           QPNQP4         PIDN4         Periodian subsmit 4         5.3         0         PRL           HOYAR         IMM04D         Inside departed departed expression subscient fibroanchoprotein Q         5.4         0         PRL           D6258         YWHAG         Histore decorprotein subscient fibroanchoprotein Q         5.4         0         PRL           D60596         SINCKIP         Histore decorprotein subscient fibroanchoprotein Q         3.4         0         PRL           D70597         CALR         Calarecopition particle subsnif 5R/P2         3.2         0         PRL           D70537         RPLP 2         O645 scient fibroanchoprotein P2         3.2         0         PRL           D93547         PREP         Podid achyperidase         <	Q165/6	R BBP/		3,/	0	PRDXI
PALESO         CARASI         Generation         3.6         0.001         PRCI           000165         HAXI         HECRSLassociated protein X1         3.5         0         PRCI           000165         HAXI         HECRSLassociated protein X1         3.5         0         PRCI           10017N2         PPR6AI         Scrinc/threenine-protein phorphartac (regulatory subunit 3         3.5         0         PRCI           10017N2         PPR043         Scrinc/threenine-protein phorphartac (regulatory subunit 3         3.5         0         PRCI           062566         SYNCKLP         Hetrogeneous noder: ribonal-coprotein Q         3.4         0         PRCI           025777         CALR         Calrecticulin         3.3         0         PRCI           076094         SRP72         3.2         0         PRCI	P30048	PKDX3	I hioredoxin-dependent peroxide reductase, mitochondrial	3,6	0	PRDXI
PMC290         HAX1         Hendpatz         J.b.         0.001         PGL           Q00165         HAX1         3.5         0         PRCI           QNQP4         PEDN4         Periodin subunit 4         3.5         0         PRCI           QNQP4         PEDN4         Periodin subunit 4         3.5         0         PRCI           HOYAL         IMUP12         Inside S-monphophate dehydrogenes 2         3.6         0         PRCI           HOYAL         IMUP12         Inside S-monphophate dehydrogenes 2         3.6         0         PRCI           D62596         SYNCRIP         Histore descerptise 1         3.3         0         PRCI           D25577         CALR         Calericular         3.3         0         PRCI           D76094         SRP72         Sigat recognition particle subunit SRP72         3.2         0         PRCI           D760587         RPLP2         GeN Scich Tobonal protein P2         3.2         0         PRCI           D78387         RPLP         Poli (colopeptidas         3.1         0         PRCI           D78387         RPLP         Poli (colopeptidas         3.1         0         PRCI           D78381         SYT1	P41250	GAKSI	GlycinetRINA ligase	3,6	0	PRDXI
000165         [HAX]         [HCD3]-associated protein X-1         3,5         0         [PKI]           HOTENI2         PPR083         Senter (threenine-protein phosphatze 6 regulatory subunit 3         3,5         0         [PKI]           HOYENI2         IMPOHA         Institute-form (threenine-protein phosphatze 6 regulatory subunit 3         3,5         0         [PKI]           PR2258         WHAE         IH-3.3 protein epsilon         3,5         0         [PKI]           R02596         SYNCRIP         Hetcreegroscons unclear ribonacleoprotein Q         3,4         0         [PKI]           R02597         HDAC1         Histome descrylase 1         3,3         0         [PKI]           P10599         TXN         Thioredoxin         3,2         0         [PKI]           P05847         RPLP2         605 acidic ribosomal protein P2         3,2         0         [PKI]           P05847         RPLP2         605 acidic ribosomal protein P2         3,2         0         [PKI]           P05847         RPLP2         605 acidic ribosomal protein P2         3,2         0         [PKI]           P08147         PRE         Proble ondoperdoxe         3,1         0         [PKI]           P08147         PRE <t< td=""><td>P02/90</td><td>HPX</td><td>Hemopexin</td><td>3,6</td><td>0,001</td><td>PRDXI</td></t<>	P02/90	HPX	Hemopexin	3,6	0,001	PRDXI
QPNQP4         PTDN4         Predidin submit 4         3.5         0         PRL           H0YEN2         PPPR45         Seriner/Freenophopsharae (regulatory subunit 3         3.5         0         PRL           H0YAR1         IMDP12         Inosiner-5-monophopsharae (regulatory subunit 3         3.5         0         PRL           D60596         SYNCRIP         Henrogeneous nuclear inhonachoprotein Q         3.4         0         PRL           Q15977         CALR         Calerical inhonachoprotein Q         3.3         0         PRL           P0599         TXN         Thioredoxin         3.2         0         PRL           Q26041         WDR77         Methylosome protein P2         3.2         0         PRL           Q962U8         PSME3P1         PSME3-interacting protein 12         3.2         0         PRL           Q962U8         PSME3P1         PSME3-interacting protein 12         3.1         0         PRL           Q972U8         PSME3 Methylosome protein 12         10         PRL         10         PRL           Q972U8         PSME3 Methylosome protein 12         10         10         PRL         10         10         10         10         10         10         10         10 <td>000165</td> <td>HAX1</td> <td>HCLS1-associated protein X-1</td> <td>3,5</td> <td>0</td> <td>PRDX1</td>	000165	HAX1	HCLS1-associated protein X-1	3,5	0	PRDX1
HOYEN.2         PPP6R3         Semicultare on phosphate desputance of equilatory subunit 3         3.5         0         PRIX           HOYAR.1         IMDD14         Insoines/Frances/Integration         3.5         0         PRIX           R0238         YW HAE         14-33 protein equilion         3.5         0         PRIX           R02387         HIDAC1         Histone descrytars 1         3.3         0         PRIX           R03597         TAN         Thioreductin         3.3         0         PRIX           P05999         TXN         Thioreductin         3.2         0         PRIX           P05837         RPLP2         668 addit rhosonal protein P2         3.2         0         PRIX           QPG2U8         PSME31         Toroprotein 90         3.2         0.002         PRIX           QPG2U4         PMR7         Methylosone protein 90         3.1         0         PRIX           QPG354         FSME17         PREP         Polylendopaptidase         3.1         0         PRIX           QPG354         ESTT1         Extended synaptotagnin-1         3         0.001         PRIX           QP4257         RCN2         Reticioallin-2         3         0.001         PRIX <td>Q9NQP4</td> <td>PFDN4</td> <td>Prefoldin subunit 4</td> <td>3,5</td> <td>0</td> <td>PRDX1</td>	Q9NQP4	PFDN4	Prefoldin subunit 4	3,5	0	PRDX1
H0Y4R1         IMOPD12         Incoine-5' monophosphate dehydrogenae 2         3.5         0         PRL           D60596         SYNCRIP         Heterogeneous nuclear ribonachoprotein Q         3.4         0         PRL           D60596         SYNCRIP         Heterogeneous nuclear ribonachoprotein Q         3.3         0         PRL           D27777         CALK         Calencialin         3.3         0         PRL           D76094         SRV72         Signal recognition particle subunit SRV72         3.2         0         PRL           D76094         SRV72         Signal recognition particle subunit SRV72         3.2         0         PRL           Q95387         RVL2         605 scific fichosomal protein P2         3.2         0         PRL           Q954218         PSMEJPI         PSMEJ-interacting protein         3.1         0         PRL           Q95218         PSMEJ         PSMEJ-interacting protein         3.1         0         PRL           Q95224         PAde/ Topognosin alpha + dain         3         0         PRL           Q12257         RCN2         Reciclocalbin-2         3         0,001         PRL           Q4257         RCN2         Reciclocalbin-2         3         0,001	H0YEN2	PPP6R3	Serine/threonine-protein phosphatase 6 regulatory subunit 3	3,5	0	PRDX1
Pic238         YWHAE         14-33 protein epalon         3.5         0         PRE           069056         SYNCRIP         Hetrogramosa nuckar thoundeoprotein Q         3.4         0         PRI           Q13547         HDAC1         Hitsone descrylar I         3.3         0         PRI           Q13547         HDAC1         Caltericulin         3.3         0         PRI           P10599         TXN         Thioredoxin         3.2         0         PRI           P05387         RPLP2         608 acidic ribosomal protein P2         3.2         0         PRI           Q76024         WDR77         Methylosome protein 50         3.1         0         PRI           Q78204         PME87         PREP         Prohylendopeptidas         3.1         0         PRI           Q78204         PMLCS         Multifunctional protein ADE2 [Include: Phosphoribosylaminoinidazole         3.1         0         PRI           P12234         PALCS         Multifunctional protein P2         3         0         PRI           Q4857         RCN2         Rericulocalin-2         3         0         PRI           Q42457         RCN2         Freatrosperije reprotein Paintochynintoperioding practino Paintochyniza practino Paintoc	H0Y4R1	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	3,5	0	PRDX1
060956         SYNCRIP         Histore descriptor         3.4         0         PRI           127777         CALR         Calericulin         3.3         0         PRI           127777         CALR         Calericulin         3.3         0         PRI           127777         CALR         Calericulin         3.2         0         PRI           076094         SRP72         Sigaal recognition particle subunit SRP72         3.2         0         PRI           195387         RPLP2         605 acidic ribosonal protein 50         3.2         0,002         PRI           2962QA1         WDR77         Methylosome protein 50         3.1         0         PRI           297224         PRIS         Proble despecipidas         3.1         0         PRI           297234         TPM4         Topoonyosin alpha-4 chain         3.1         0         PRI           297234         RCN2         Rcinal calibin-2         3         0,001         PRI           29818         EXYT1         Extended anyotogamin-1         3         0,001         PRI           204257         BCN2         Cricobronne coidae assembly factor?         3         0,001         PRI           20426442	P62258	YWHAE	14-3-3 protein epsilon	3,5	0	PRDX1
Q15347         HDAC1         Histone decerylase 1         3.3         0         PRL           P10959         TXN         Calericcilin         3.3         0         PRL           P10959         TXN         Thioredoxin         3.2         0         PRL           P05387         RPLP2         60S acidic ribosonal protein P2         3.2         0         PRL           Q05604         WDR77         Methylosome protein 50         3.1         0         PRL           Q057US         PSME31P         PSME31Protecting P301         3.1         0         PRL           P4147         PREP         Prohyl endopeptidaxe         3.1         0         PRL           P67356         TTPM4         Tropogrysion alpha + chain         3.1         0         PRL           Q4257         RCN2         Reinculocallin=2         accinco-acidinae assembly factor 7         3         0,001         PRL           Q4255         CAOT         Cycochrome coxidase assembly factor 7         3         0,001         PRL           Q42655         CAOT         Cycochrome coxidase assembly factor 7         3         0,001         PRL           Q42657         RCN2         Katiculocallin=2         Sternager 2,9         0	O60506	SYNCRIP	Heterogeneous nuclear ribonucleoprotein Q	3,4	0	PRDX1
P2777         CALR         Calericulin         3.3         0         PRI           076094         SRP12         Signal recognition particle subunit SRP2         3.2         0         PRI           076094         SRP12         G85 acide Hosonial porticle subunit SRP2         3.2         0         PRI           076094         WDR77         Mcdryboome protein 50         3.2         0.002         PRI           076094         PMEJ Interacting protein         3.1         0         PRI           076076         TPM4         Tropentyonia lpha-4 chain         3.1         0         PRI           PC3254         TPM4         Topentyonia lpha-4 chain         3.1         0         PRI           PC3254         TPM4         Topentyonia lpha-4 chain         3         0         PRI           Q4837         RCN2         Retriculo-calibin-2         3         0.001         PRI           Q4547         RCN2         Cycochrone coxidate assembly factor 7         3         0.001         PRI           Q4688         COA7         Cycochrone coxidate assembly factor 7         3         0.001         PRI           Q40024842         An0024842         An024842/An0248242/LIAUAR Mapartylaininopepridac, isoform CRA, b 2,9         0	Q13547	HDAC1	Histone deacetylase 1	3,3	0	PRDX1
Photogen         TXN         Thioredoxin         5,2         0         PRE           075604         SRP.12         Sign frequency limb particle submit SRP2         3,2         0         PRE           075604         WDR.77         Methylosome protein P2         3,2         0         PRE           07507         RPLP2         605 acids ribosomal protein P2         3,2         0         PRE           07507         Methylosome protein 50         3,2         0         PRE           07507         PKP         Prolylendoperidase         3,1         0         PRE           07536         TPM4         Troponyonia labia-4 chin         3,1         0         PRE           07236         TPX1         Extended synaptrotein ADE2 [Includes Phosphoribosylaminolimidzaole-         3,1         0         PRE           074237         RCN2         Retricule Calibia - 2         3         0,001         PRE           074247         RCN2         Retraincoperide repeat protein 19, mitochondrial         3         0,001         PRE           0746185         CAA7         Cyrochrome coxidae assembly factor 7         3         0,001         PRE           074619         PRE Acicula Calibia - 2         0         PRE         0	P27797	CALR	Calreticulin	3,3	0	PRDX1
076094         SRP72         Signal recognition particle subanti SRP72         S.2         0         PRE           095857         RPLI2         663 acidin ribosoma protein P2         S.2         0.002         PRE           096041         WDR7         Methylosome protein 50         S.2         0.002         PRE           0976078         PRK1P         PSME3-interacting protein and S.2         0         PRE           1         0         PRE         Protein decoperidase         S.1         0         PRE           1         Protein and Second Se	P10599	TXN	Thioredoxin	3,2	0	PRDX1
P05387         R.PLP2         60 Sacidic ribosome protein P2         3.2         0         PRT           Q96QA1         WDR.77         Metrylowne protein 50         3.2         0.002         PRT           Q96ZU8         PME1P1         PSME3 interacting protein and the stand stan	O76094	SRP72	Signal recognition particle subunit SRP72	3,2	0	PRDX1
QPBQA1         WDR77         Methylosome protein 50         3.2         0.002         PRI           QPSGZU8         PSME3PI         PSME3-interacting protein         3.1         0         PRI           P48147         PREP         Prolylendopeptidase         3.1         0         PRIC           P6736         TPM4         Tropomysin alpha-4 chain         3.1         0         PRIC           P4736         TPM4         Tropomysin alpha-4 chain         3.1         0         PRIC           P2234         PAICS         Multifunctional protein AD2 [Includes Phosphoribosytaminoimidazole- succinocarboxamide synthase         0         PRIC           Q48457         RCN2         Reticulocalbin-2         3         0.001         PRIC           Q6DKK2         TTC19         Tetratricopeptide repeat protein hanse subunit gamma-1         3         0.001         PRIC           Q64BK5         COA7         Cytochrome coidase assembly factor?         3         0.001         PRIC           Q46BK5         COA7         Cytochrome coidase assembly factor?         3         0.001         PRIC           Q46BK5         COA7         Cytochrome optiona Soperon CX9-Sofe CN=1>pyp(201LA0)DXPEP         4         HUMAN Aparyral aminopeptidase, isof         2         0	P05387	RPLP2	60S acidic ribosomal protein P2	3,2	0	PRDX1
QPCZU8         PSME3IP1         PSME3-interacting protein         3.1         0         PRE           PN847         PKEP         Prolylendopeptidase         3.1         0         PRE           PPC736         TPM4         Tropomyosin alphase 4 chain         3.1         0         PRE           PP2234         PALCS         Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidzole- saccinco-achacamide synthase         3.1         0         PRE           QB58         ESTT1         Extended synaprotegmini-1         3         0.001         PRE           Q465X         COA7         Cytochrome c caidase assembly factor 7         3         0.001         PRE           Q465K         COA7         Cytochrome c caidase assembly factor 7         3         0.001         PRE           P54619         PRKAGE         5-AM-Pactrixet protein kinase ubmin gamma-1         3         0.001         PRE           A0A024R442         A0A024R442         A0A024R442 [A0A024K442 [AUMAA Aspartyl aminopeptidae, isoform CRA, b         2,9         0         PRE           Q8N806         UBR7         Putative E3 abiguitin protein flage UBR7         2,9         0         PRE           Q96EW2         HISPBAH         HSPBA Esociectar protein flage UBR7         2,9         0	Q9BQA1	WDR77	Methylosome protein 50	3,2	0,002	PRDX1
PNR147         PREP         Prolylendopeptidase         3.1         0         PREP           P67936         TPM4         Tropomyosin alpha-4 chain         3.1         0         PRED           P22234         PAICS         Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase         3.1         0         PRED           QBS[8         ESTT1         Extendod synaptotagamin-1         3         0.0         PRED           Q4577         RCN2         Reticulocalibrio-2         3         0.001         PRED           Q60KK2         TTC19         Tetratricopeptide repeat protein 19, micochondrial         3         0,001         PRED           Q60RK5         COA7         Cytochrome coxidase assembly factor 7         3         0,001         PRED           A0A024R442         A0A024R442         br/A0A24R442         br/A0A24R442 </td <td>Q9GZU8</td> <td>PSME3IP1</td> <td>PSME3-interacting protein</td> <td>3,1</td> <td>0</td> <td>PRDX1</td>	Q9GZU8	PSME3IP1	PSME3-interacting protein	3,1	0	PRDX1
Pk7956         TPM4         Topomyosin alpha-4 chain         3.1         0         PR12           P22234         PAICS         Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboaumid synthase         3.1         0         PR1           QPBSJ8         ESYT1         Extended synaptotagmin-1         3         0         PR2           Q4527         RCN2         Reicolocalbin-2         3         0,001         PR2           Q6DKS2         COA7         Cytochome c oxidsae assembly factor 7         3         0,001         PR2           Q46BR5         COA7         Cytochome c oxidsae assembly factor 7         3         0,001         PR2           Q46DK24         PKAGI         S'AMP-activated protein kinase subuning amma-1         3         0,001         PR2           Q40A024R442         ValA024R442, HUMAN Aspartyl aminopeptidase, isoform CRA, b 2,9         0         PR2           Q40A024R442         ValA024R442, HUMAN Aspartyl aminopeptidase, iso         Q.9         Q         PR2           Q40A024R442         PUAAN Aspartyl aminopeptidase, Soform CRA, b 2,9         0         PR2           Q40EW2         HBPBAP1         HSPBAP1         SPB491         Q.9         Q.9           Q46EW2         HBPBAP1         HSPB41-sosocitated pro	P48147	PREP	Prolyl endopeptidase	3,1	0	PRDX1
P22234         PAICS         Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinoarboxamide symhase         9.1         PAICS           Q9BSJ8         ESYT1         Extended symaptocagmin-1         3         0         PRL           Q14237         RCN2         Reciculocalibn-2         3         0.01         PRL           Q46BS.         COA7         Cytochrome c oxidase assembly factor 7         3         0.001         PRL           Q46BS.         COA7         Cytochrome c oxidase assembly factor 7         3         0.001         PRL           Q46BAS.         COA7         Cytochrome c oxidase assembly factor 7         3         0.001         PRL           Q46BAS.         QA0024R442         MAD024R442 (AUANA) Asparyt aninoperptidace, looform CRA_b 2, 2, 0         PRL           Q45EMOS         DMO24R442         MAD024R442 (AUANA) Asparyt aninoperptidace Scienco NPREP DE-15V=15/x9L/2PR[ETETB3]EFETB3.HUMAN Asparyt aninoperptidace, DS-966 GN-DNPEP PE-1         2,9         0         PRL           Q985W2         IBSPBAP1         IBSPBAP1         IBSPBAP1         IBSPBAP1         PRE         PRL           P393S         SLC16A1         Monocarboxated protein 1         2,8         0         PRL           Q965W2         IBSPBAP1         HSPB1-associated protein ATA1         <	P67936	TPM4	Tropomyosin alpha-4 chain	3,1	0	PRDX1
QPBS/R         ESYT1         Extended synaptotagmin-1         3         0         PRL           Q14257         RCN2         Reticulocalbin-2         3         0,001         PRL           Q45K5         TC19         Tetratricopeptide repeat protein 19, mitochondrial         3         0,001         PRL           Q6BK5         COA7         Cytochrome coxidase assembly factor 7         3         0,001         PRL           Q46BK5         COA7         Cytochrome coxidase assembly factor 7         3         0,001         PRL           AA04024R442         AA0A024R442         AA0	P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase	3,1	0	PRDX1
Q14257         RCN2         Reticuloalbin-2         3         0         PRL           Q4DKX2         TTC19         Tetraricoperpide repertorein 19, micochondrial         3         0,001         PRL           Q60RK5         COA7         Cytochome coxidase assembly factor 7         3         0,001         PRL           P34619         PRKAGI         5'AMP-activated protein kinase subunit gamma.1         3         0,001         PRL           A0A024R442         >tri/A0A024R442_1MUANA Spartyl aminopeptidase, isoform CRA_b         2,9         0         PRL           A0A024R442         >tri/A0A024R442_1HUANA Aspartyl aminopeptidase, isoform CRA_b         2,9         0         PRL           Q45EW2         HSPBAP1         PtSTETTB3 <huana aminopeptidase,="" aspartyl="" cra_b<="" isoform="" td="">         2,9         0         PRL           Q46EW2         HSPBAP1         HSPB1-associated protein 1         2,9         0         PRL           Q46EW2         HSPBAP1         HSPB1-associated protein 1         2,9         0         PRL           Q45EW2         HSPBAP1         HSPB1-associated protein 2         2,8         0         PRL           Q45EW2         HSPBAP1         MSPB-associated protein 17         2,9         0         PRL           Q45EW2         HSPBAP1</huana>	Q9BSJ8	ESYT1	Extended synaptotagmin-1	3	0	PRDX1
Q6DKK2         TTC19         Tetratricopeptide repeat protein 19, mitochondrial         3         0,001         PRL           Q6BR5         COA7         Cytochrome c oxidase assembly factor 7         3         0,001         PRL           Q6BR5         COA7         Cytochrome c oxidase assembly factor 7         3         0,001         PRL           A0A024R442         PRKAG1         5-AMP-activated protein kinase subunit gamma-1         3         0,001         PRL           A0A024R442         xr[A0A024R442]         xr[A0A024R442]         Yr[A0A024R442]         VII/ANA Aspartyl aminopeptidase (Sof-Mono spiens OX=9606 CN=DNPEP PE-1 SV=1;>representation spiens OX=9606 CN=DNPEP PE-1 SV=1;>representation SV=1;         Q,9         Q         PRL	Q14257	RCN2	Reticulocalbin-2	3	0	PRDX1
Q96BR5COA7Cytochrome coxidase assembly factor 730,001PRLP54619PRKAG1S'AMP-activated protein kinase subunit gamma130,001PRLA0A024R442xe1QA0024R442LIQA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R442NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R4424NetTolA0024R44424NetTolA0024R4424NetTolA0024R442	Q6DKK2	TTC19	Tetratricopeptide repeat protein 19, mitochondrial	3	0,001	PRDX1
P54619PRKAG1S'-AMP-activated protein kinase subunit gamma-130,001PRLA0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A024R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442A0A0494R442<	Q96BR5	COA7	Cytochrome c oxidase assembly factor 7	3	0,001	PRDX1
A0A024R442       A0A024R442       >tr[A0A024R442]A0A024R442_HUMAN Aspartyl aminopeptidase, isoform CRA_b       2.9       0       PRE         DS=Homo sapiens OX=9606 GN=DNPEP PE = 1SV=1:syel[90LLA0]DNPEP_I       SV=1:str[E7ETB3]ETETB3_HUMAN Aspartyl aminopeptidase, iso       0       PRE         Q8N806       UBR7       Putative E3 ubiquitin-protein ligase UBR7       2.9       0       PRE         Q96EW2       HSPBAP1       HSPB1-associated protein 1       2.9       0       PRE         Q95EW2       HSPBAP1       HSPB1-associated protein 1       2.9       0       PRE         P49321       NASP       Nuclear autoantigenic sperm protein 2       2.9       0       PRE         P3985       SLC16A1       Monocarboxylate transporter 1       2.9       0       PRE         P53925       ALG4Y       Adenosylaborocysteinase       2.8       0       PRE         P23526       AHCY       Adenosylate transporterin MTA1       2.8       0       PRE         P23526       AHCY       Adenosylate transportenin MTA1       2.8       0       PRE         P23526       AHCY       Adenosylate consysteniase       2.8       0       PRE         P23526       AHCY       Adenosylate consysteniase       2.8       0       PRE	P54619	PRKAG1	5'-AMP-activated protein kinase subunit gamma-1	3	0,001	PRDX1
Q8N806UBR7Putative E3 ubiquitin-protein ligase UBR72,90PRLP20839IMPDH1Inosine-5'-monophosphate dehydrogenase 12,90PRLQ96EW2HSPBAP1HSPB1-associated protein 12,90PRLP49321NASPNuclear autoantigenic sperm protein2,90PRLP53985SLC16A1Monocarboxylate transporter 12,90PRLQ15008PSMD6265 protessome non-ATPase regulatory subunit 62,80PRLQ2526AHCYAdenosylhomocysteinase2,80PRLQ26EW2AHCYAdenosylhomocysteinase2,80PRLQ25008PSMD6266 protessome non-ATPase regulatory subunit 62,80PRLQ2526AHCYAdenosylhomocysteinase2,80PRLQ96D55RMDN1Regulator of microtubule dynamics protein 12,80,001PRLQ96EX6NUDCD1NudC domain-containing protein 12,70PRLQ90EY8ADD3Gamma-adducin2,70PRLQ90HV9PFDN2Prefoldin subunit22,60PRLQ91HV9PFDN2Prefoldin subunit22,60PRLQ914V9PFDN2Prefoldin subunit22,60PRLQ15276RABEP1Rab GTPase-binding effector protein 12,60PRLQ1513MAT2AS-adenosylmethionine synthase isoform type-22,60PRLQ15276RAB	A0A024R442	A0A024R442	>tr A0A024R442 A0A024R442_HUMAN Aspartyl aminopeptidase, isoform CRA_t OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>sp Q9ULA0 DNPEP_ HUMAN Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>tr E7ETB3]E7ETB3_HUMAN Aspartyl aminopeptidase, iso	2,9	0	PRDX1
P20839IMPDH1Inosine-5'-monophosphate dehydrogenase 12,90PRLQ96EW2HSPBAP1HSPB1-associated protein 12,90PRLP49321NASPNuclear autoantigenic sperm protein2,90PRLP53985SLC16A1Monocarboxylate transporter 12,90PRLA0A1C7CYX9DPYSL2Dihydropyrimidinase-related protein 22,80PRLQ15008PSMD6265 proteasome non-ATPase regulatory subunit 62,80PRLP23526AHCYAdenosylhomocysteinase2,80PRLQ96DB5RMDN1Regulator of microtubule dynamics protein 12,80,001PRLQ96R56NUDCD1NudC domain-containing protein 12,70PRLQ9UEY8ADD3Gamma-adducin2,70PRLQ9UHV9PFDN2Prefoldin subunit 22,60PRLQ9T4U8RABGGTBGeranylgeranyltransferase type-2 subunit beta2,60PRLQ91L976RABGGTBGeranylgeranyltransferase omega-12,60PRLQ91L976RABGGTBGeranylgeranyltransferase omega-12,60PRLQ91L976RABGGTBGeranylgeranyltransferase omega-12,60PRLQ91L976RABGGTBGeranylgeranyltransferase omega-12,60PRLQ91L97PFDN2Prefoldin subunit 22,60PRLQ91L97RABGGTBGeranylgeranyltransferase omega-12,60 <td>Q8N806</td> <td>UBR7</td> <td>Putative E3 ubiquitin-protein ligase UBR7</td> <td>2,9</td> <td>0</td> <td>PRDX1</td>	Q8N806	UBR7	Putative E3 ubiquitin-protein ligase UBR7	2,9	0	PRDX1
Q96EW2HSPBAP1HSPB1-associated protein 12,90PREP49321NASPNuclear autoantigenic sperm protein2,90PREP53985SLC16A1Monocarboxylate transporter 12,90PRED041C7CYX9DPYSL2Dihydropyrimidinase-related protein 22,80PREQ15008PSMD6265 proteasome non-ATPase regulatory subunit 62,80PREP25326AHCYAdenosylhomocysteinase2,80PREQ96DS5RMDN1Regulator of microtubule dynamics protein 12,70PREQ96RS6NUDCD1NudC domain-containing protein 12,70PREQ90EV8ADD3Gamma-adducin2,70PREQ91UFY8ADD3Gamma-adducin2,70PREQ91HV9PFDN2Prefoldin subunit 22,60PREQ91HV9PFDN2Prefoldin subunit 22,60PREQ912Y6RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PREQ914V9PFDN2Prefoldin subunit 22,60PREQ91526RABEP1Rab GTPase-binding effector protein 12,60PREQ915276RABEP1Rab GTPase-binding effector protein 12,60PREQ915276RABEP1Rab GTPase-binding effector 3 subunit G2,60PREQ91528CFL1Cofilin-12,60PREQ92528CFL1Cofilin-1<	P20839	IMPDH1	Inosine-5'-monophosphate dehydrogenase 1	2,9	0	PRDX1
P49321NASPNuclear autoantigenic sperm protein2,90PRDP53985SLC16A1Monocarboxylate transporter 12,90PRDA0A1C7CYX9DPYSL2Dihydropyrimidinase-related protein 22,80PRDQ15008PSMD6265 proteasome non-ATPase regulatory subunit 62,80PRDP25526AHCYAdenosylhomocysteinase2,80PRDQ96D85RMDN1Regulator of microtubule dynamics protein 12,80PRDQ90EY8ADD3Gamma-adducin2,70PRDQ90EY8ADD3Gamma-adducin2,70PRDQ2314UBA1Ubiquitin-like modifier-activating enzyme 12,70PRDQ91HV9PFDN2Prefoldin subunit 22,60PRDQ91HV9PFDN2Prefoldin subunit 22,60PRDQ914148RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRDQ91526RABEP1Rab GTPase-binding effector protein 12,60PRDQ915276RABEP1Rab GTPase-binding effector protein 12,60	Q96EW2	HSPBAP1	HSPB1-associated protein 1	2,9	0	PRDX1
P53985SLC16A1Monocarboxylate transporter 12,90PRIA0A1C7CYX9DPYSL2Dihydropyrimidinase-related protein 22,80PRIQ15008PSMD626S proteasome non-ATPase regulatory subunit 62,80PRIE7ESY4MTA1Metastasis-associated protein MTA12,80PRIQ95D5AHCYAdenosylhomocysteinase2,80PRIQ96B5RMDN1Regulator of microtubule dynamics protein 12,80,001PRIQ96RS6NUDCD1NudC domain-containing protein 12,70PRIQ91EY8ADD3Gamma-adducin2,70PRIQ2314UBA1Ubiquitin-like modifier-activating enzyme 12,70PRIQ91HV9PFDN2Prefoldin subunit 22,60PRIQ91HV9PFDN2Prefoldin subunit 22,60PRIQ1526RABEP1Rab GTPase-binding effector protein 12,60PRIQ1533MAT2AS-adenosylmethionine synthase isoform type-22,60PRIQ1526CFL1Cofilin-12,60PRIQ1528CFL1Cofilin-12,60PRIQ3528CFL1Cofilin-12,60PRIQ98PU6DPYSL5Dihydropyrimidinase-related protein 52,50PRIQ3528CFL1Cofilin-12,60PRIQ3528CFL1Cofilin-12,60PRI	P49321	NASP	Nuclear autoantigenic sperm protein	2,9	0	PRDX1
A0A1C7CYX9DPYSL2Dihydropyrimidinase-related protein 22,80PRDQ15008PSMD626S proteasome non-ATPase regulatory subunit 62,80PRDE7ESY4MTA1Metastasis-associated protein MTA12,80PRDP23526AHCYAdenosylhomocysteinase2,80PRDQ96DB5RMDN1Regulator of microtubule dynamics protein 12,80,001PRDQ96RS6NUDCD1NudC domain-containing protein 12,70PRDQ9UEY8ADD3Gamma-adducin2,70PRDQ9UEY8ADD3Gamma-adducin2,70PRDQ9UIV9PFDN2Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX152,60PRDQ9T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRDQ91S276RABEJP1Rab GTPase-binding effector protein 12,60PRDQ15276RABEJP1Rab GTPase-binding effector protein 12,60PRDQ15276RABEJP1<	P53985	SLC16A1	Monocarboxylate transporter 1	2,9	0	PRDX1
Q15008PSMD626S proteasome non-AT Pase regulatory subunit 62,80PRDE7ESY4MTA1Metastasis-associated protein MTA12,80PRDP23526AHCYAdenosylhomocysteinase2,80PRDQ96D85RMDN1Regulator of microtubule dynamics protein 12,80,001PRDQ96R86NUDCD1NudC domain-containing protein 12,70PRDQ91EY8ADD3Gamma-adducin2,70PRDP23314UBA1Ubiquitin-like modifier-activating enzyme 12,70PRDQ91HV9PFDN2Prefoldin subunit 22,60PRDQ914U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRDQ15276RABEP1Rab GTPase-binding effector protein 12,60PRDQ15276RABEP1Rab GTPase-binding effector as subunit G2,60PRDQ2528CFL1Cofilin-12,60PRDQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PRDQ9BPU6DPYSL5Dihydropyrimidinase-related protein 5 <td< td=""><td>A0A1C7CYX9</td><td>DPYSL2</td><td>Dihydropyrimidinase-related protein 2</td><td>2,8</td><td>0</td><td>PRDX1</td></td<>	A0A1C7CYX9	DPYSL2	Dihydropyrimidinase-related protein 2	2,8	0	PRDX1
E7ESY4MTA1Metastasis-associated protein MTA12,80PRDP23526AHCYAdenosylhomocysteinase2,80PRDQ96DB5RMDN1Regulator of microtubule dynamics protein 12,80,001PRDQ96RS6NUDCD1NudC domain-containing protein 12,70PRDQ90RV8ADD3Gamma-adducin2,70PRDQ91EY8ADD3Gamma-adducin2,70PRDP22314UBA1Ubiquitin-like modifier-activating enzyme 12,60PRDQ91HV9PFDN2Prefoldin subunit 22,60PRDQ91HV9PFDN2Prefoldin subunit 22,60PRDQ574U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRDQ15276RABEP1Rab GTPase-binding effector protein 12,60PRDQ75821EIF3GEukaryotic translation initiation factor 3 subunit G2,60PRDQ928V6PRKAA22S'-AMP-activated protein kinase catalytic subunit alpha-22,50PRDP3466PRKAA22S'-AMP-activated protein sinase catalytic subunit alpha-22,50PRDQ13200PSMD2268 proteasome non-ATPase regulatory subunit 22,50PRDQ94018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRD	Q15008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	2,8	0	PRDX1
P23526AHCYAdenosylhomocysteinase2,80PRDQ96DB5RMDN1Regulator of microtubule dynamics protein 12,80,001PRDQ96RS6NUDCD1NudC domain-containing protein 12,70PRDQ9UEY8ADD3Gamma-adducin2,70PRDP22314UBA1Ubiquitin-like modifier-activating enzyme 12,70PRD043143DHX15Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX152,60PRDQ9UHV9PFDN2Prefoldin subunit 22,60PRDQ5T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRDQ15276RABEP1Rab GTPase-binding effector protein 12,60PRDQ75821EIF3GEukaryotic translation initiation factor 3 subunit G2,60PRDQ3528CFL1Cofilin-12,60PRDQ35406PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PRDP3408USP39U4/U6.U5 tri-snRNP-associated protein 22,50PRD	E7ESY4	MTA1	Metastasis-associated protein MTA1	2,8	0	PRDX1
Q96DB5         RMDN1         Regulator of microtubule dynamics protein 1         2,8         0,001         PRD           Q96RS6         NUDCD1         NudC domain-containing protein 1         2,7         0         PRD           Q9UEY8         ADD3         Gamma-adducin         2,7         0         PRD           P22314         UBA1         Ubiquitin-like modifier-activating enzyme 1         2,7         0         PRD           Q43143         DHX15         Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15         2,6         0         PRD           Q9UHV9         PFDN2         Prefoldin subunit 2         2,6         0         PRD           Q5T4U8         RABGGTB         Geranylgeranyl transferase type-2 subunit beta         2,6         0         PRD           Q15276         RABEP1         Rab GPase-binding effector protein 1         2,6         0         PRD           Q15276         RABEP1         Rab GPase-binding effector protein 1         2,6         0         PRD           Q15276         RABEP1         Rab GrPase-binding effector protein 1         2,6         0         PRD           Q15276         RABEP1         Rab GrPase-binding effector protein 1         2,6         0         PRD           Q1528         <	P23526	AHCY	Adenosylhomocysteinase	2,8	0	PRDX1
Q96R\$6NUDCD1NudC domain-containing protein 12,70PRDQ9UEY8ADD3Gamma-adducin2,70PRDP22314UBA1Ubiquitin-like modifier-activating enzyme 12,70PRD043143DHX15Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX152,60PRDQ9UHV9PFDN2Prefoldin subunit 22,60PRDQ5T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRDQ1276RABEP1Glutathione S-transferase omega-12,60PRDQ15276RABEP1Rab GTPase-binding effector protein 12,60PRDQ15276RABEP1Rab GTPase-binding effector protein 12,60PRDP31153MAT2AS-adenosylmethionine synthase isoform type-22,60PRDQ2528CFL1Cofilin-12,60PRDP23528CFL1Cofilin-12,60PRDP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PRDQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PRDQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,40PRDB9A018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRD	Q96DB5	RMDN1	Regulator of microtubule dynamics protein 1	2,8	0,001	PRDX1
Q9UEY8ADD3Gamma-adducin2,70PRICP22314UBA1Ubiquitin-like modifier-activating enzyme 12,70PRICO43143DHX15Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX152,60PRICQ9UHV9PFDN2Prefoldin subunit 22,60PRICQ9UHV9PFDN2Prefoldin subunit 22,60PRICQ5T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRICQ15276RABEP1Rab GTPase-binding effector protein 12,60PRICQ15276RABEP1Rab GTPase-binding effector protein 12,60PRICQ2588CFL1Cofilin-12,60PRICP54646PRKAA25'-AMP-activated prote	Q96RS6	NUDCD1	NudC domain-containing protein 1	2,7	0	PRDX1
P22314UBA1Ubiquitin-like modifier-activating enzyme 12,70PRE043143DHX15Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX152,60PRE09UHV9PFDN2Prefoldin subunit 22,60PRE05T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PRE0758417GSTO1Glutathione S-transferase omega-12,60PRE075821RABEP1Rab GTPase-binding effector protein 12,60PRE075821EIF3GEukaryotic translation initiation factor 3 subunit G2,60PRE075828CFL1Cofilin-12,60PRE040A2U3TZY2CLPBCaseinolytic peptidase B protein homolog2,60PRE04546PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PRE04300PSMD226S proteasome non-ATPase regulatory subunit 22,50PRE043018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRE	Q9UEY8	ADD3	Gamma-adducin	2,7	0	PRDX1
Od3143DHX15Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX152,60PREQ9UHV9PFDN2Prefoldin subunit 22,60PREQ5T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PREQ5T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PREQ5T4U8RABGTBGeranylgeranyl transferase omega-12,60PREQ15276RABEP1Rab GTPase-binding effector protein 12,60PREQ15276RABEP1Rab GTPase-binding effector protein 12,60PREQ75821EIF3GEukaryotic translation initiation factor 3 subunit G2,60PREP23528CFL1Cofflin-1Caseinolytic peptidase B protein homolog2,60,001PREQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PREQ13200PSMD226S proteasome non-ATPase regulatory subuni	P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	2.7	0	PR DX1
Q9UHV9PFDN2Prefoldin subunit 22,60PREQ9UHV9PFDN2Prefoldin subunit 22,60PREQ5T4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PREQ78417GSTO1Glutathione S-transferase omega-12,60PREQ15276RABEP1Rab GTPase-binding effector protein 12,60PREQ15276RABEP1Rab GTPase-binding effector protein 12,60PREQ75821EIF3GEukaryotic translation initiation factor 3 subunit G2,60PREP23528CFL1Cofilin-12,60PREA0A2U3TZY2CLPBCaseinolytic peptidase B protein homolog2,60,001PREP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PREQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PREQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,40PREB9A018USP3	Q43143	DHX15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	2.6	0	PR DX1
QST4USRABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PREQST4U8RABGGTBGeranylgeranyl transferase type-2 subunit beta2,60PREQ15276RABEP1Rab GTPase-binding effector protein 12,60PREQ15276RABEP1Rab GTPase-binding effector protein 12,60PREP31153MAT2AS-adenosylmethionine synthase isoform type-22,60PREQ75821EIF3GEukaryotic translation initiation factor 3 subunit G2,60PREP23528CFL1Cofilin-12,60PREA0A2U3TZY2CLPBCaseinolytic peptidase B protein homolog2,60,001PREP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PREQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PREQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,40PREB9A018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRE	O9UHV9	PFDN2	Prefoldin subunit 2	2.6	0	PR DX1
Q1100Integration of the protein protein of the protein protein of the protein protein of the protein protein of the protein prote	05T4U8	RABGGTB	Geranylgeranyl transferase type-2 subunit beta	2.6	0	PR DX1
Q15276R ABEP1Rab GTPase-binding effector protein 12,60PREP31153MAT2AS-adenosylmethionine synthase isoform type-22,60PREP31153EIF3GEukaryotic translation initiation factor 3 subunit G2,60PREP23528CFL1Cofilin-12,60PREA0A2U3TZY2CLPBCaseinolytic peptidase B protein homolog2,60,001PREP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PREQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PREQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,50PREB9A018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRE	P78417	GSTO1	Glutathione S-transferase omega-1	2,6	0	PR DX1
Q2521Hubbr Hubbr	015276	R A BEP1	Rab GTPase-binding effector protein 1	2.6	0	PR DX1
ADALODescriptionStatus information syntaxe isoform (spr22)2,60PRLO75821EIF3GEukaryotic translation initiation factor 3 subunit G2,60PRLP23528CFL1Cofilin-12,60PRLDA0A2U3TZY2CLPBCaseinolytic peptidase B protein homolog2,60,001PRLP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PRLQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PRLQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,50PRLB9A018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRL	P31153	MAT2A	S-adenosylmethionine synthase isoform type-2	2.6	0	PR DY 1
D73524D135Enkalyout translation initiation factor 3 subunit of2,60PRLP23528CFL1Collin-12,60PREA0A2U3TZY2CLPBCaseinolytic peptidase B protein homolog2,60,001PREP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PREQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PREQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,50PREB9A018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRE	075821	FIF3C	Fukarvotic translation initiation factor 3 subunit C	2,0	0	DR DV1
P23220CFL1Contin-12,60PRLA0A2U3TZY2CLPBCaseinolytic peptidase B protein homolog2,60,001PRCP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PRCQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PRCQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,50PRCB9A018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRC	D22528	CEL 1		2,0	0	PRDA1
AURZUSTETZCLPDCaseInorytic peptidase B protein homotog2,60,001PRLP54646PRKAA25'-AMP-activated protein kinase catalytic subunit alpha-22,50PRLQ9BPU6DPYSL5Dihydropyrimidinase-related protein 52,50PRLQ13200PSMD226S proteasome non-ATPase regulatory subunit 22,50PRLB9A018USP39U4/U6.U5 tri-snRNP-associated protein 22,40PRL	123328	CLDD	Contraction of the Property Learning of the second	2,6	0.001	PRDAI
PY54646         PKKAA2         5-AMP-activated protein kinase catalytic subunit alpha-2         2,5         0         PRE           Q9BPU6         DPYSL5         Dihydropyrimidinase-related protein 5         2,5         0         PRE           Q13200         PSMD2         26S proteasome non-ATPase regulatory subunit 2         2,5         0         PRE           B9A018         USP39         U4/U6.U5 tri-snRNP-associated protein 2         2,4         0         PRE	AUAZU31ZYZ	ULPB DD V A A C	Casemorytic peptidase b protein homolog	2,6	0,001	PRDXI
QPBPUG         DPYSLS         Dihydropyrimidinase-related protein S         2,5         0         PRE           Q13200         PSMD2         26S proteasome non-ATPase regulatory subunit 2         2,5         0         PRE           B9A018         USP39         U4/U6.U5 tri-snRNP-associated protein 2         2,4         0         PRE	1')4646	PKKAA2	5 - AMP-activated protein kinase catalytic subunit alpha-2	2,5	0	PRDX1
Q15200         PSMD2         26S proteasome non-A1 Pase regulatory subunit 2         2,5         0         PRE           B9A018         USP39         U4/U6.U5 tri-snRNP-associated protein 2         2,4         0         PRE	Q9BPU6	DPYSL5	Dihydropyrimidinase-related protein 5	2,5	0	PRDX1
BYA018         USP39         U4/U6.U5 tri-snRNP-associated protein 2         2,4         0         PRE	Q13200	PSMD2	265 proteasome non-A I Pase regulatory subunit 2	2,5	0	PKDX1
	B9A018	USP39	U4/U6.U5 tri-snRNP-associated protein 2	2,4	0	PRDX1

D23588	FIF/B	Fukarvotic translation initiation factor /B	2 /	0	DR DY1
016531	DDB1	DNA damage-binding protein 1	2,1	0	DR DY1
D00/92	UDDT1	Hunovanthing guaning phoenhorihogyltransforaça	2,4	0.001	DP DV1
015/59	SE2 A 1	Splicing factor 2 A subunit 1	2,4	0,001	DR DV1
120079	DNDO	Splicing factor SA subulit 1	2,4	0,038	DR DV1
J3QQ29	PNPO	Tyridoxal 5 -phosphate synthase	2,3	0	PRDA1
P/83/1	UC12	1-complex protein 1 subunit beta	2,3	0	PRDXI
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	2,3	0	PRDX1
O00268	TAF4	Transcription initiation factor TFIID subunit 4	2,3	0	PRDX1
P35637	FUS	RNA-binding protein FUS	2,3	0,001	PRDX1
P38159	RBMX	RNA-binding motif protein, X chromosome	2,3	0,005	PRDX1
Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	2,2	0	PRDX1
P27348	YWHAQ	14-3-3 protein theta	2,2	0	PRDX1
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	2,2	0	PRDX1
Q13177	PAK2	Serine/threonine-protein kinase PAK 2	2,2	0	PRDX1
Q9Y3F4	STRAP	Serine-threonine kinase receptor-associated protein	2,2	0	PRDX1
Q9ULC3	RAB23	Ras-related protein Rab-23	2,2	0,001	PRDX1
P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	2,2	0,001	PRDX1
P12955	PEPD	Xaa-Pro dipeptidase	2,2	0,004	PRDX1
P43304	GPD2	Glycerol-3-phosphate debydrogenase, mitochondrial	2.2	0.004	PR DX1
000232	PSMD12	26S proteasome non-ATPase regulatory subunit 12	2.1	0	PR DX1
096BG2	DASK	PAS domain-containing sering/threening-protein kingse	2.1	0	DR DY1
D1527/	LICHI 2	Libiquitin carboyul terminal budralase icorume L2	2,1	0	DP DV1
	CORASPO	C lainear and the line and the	2,1	0	DD DV1
Q9H818	GORASP2		2,1	0	PRDAI
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	2,1	0	PRDXI
P40429	RPL13A	60S ribosomal protein L13a	2,1	0	PRDXI
P45973	CBX5	Chromobox protein homolog 5	2,1	0	PRDX1
A0A087WT45	GRIPAP1	GRIP1-associated protein 1	2,1	0,002	PRDX1
O00231	PSMD11	26S proteasome non-ATPase regulatory subunit 11	2	0	PRDX1
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	2	0	PRDX1
P36957	DLST	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate	2	0	PRDX1
		dehydrogenase complex, mitochondrial			
P31689	DNAJA1	DnaJ homolog subfamily A member 1	2	0	PRDX1
Q02750	MAP2K1	Dual specificity mitogen-activated protein kinase kinase 1	2	0	PRDX1
C9J4Z3	RPL37A	60S ribosomal protein L37a	2	0	PRDX1
Q93009	USP7	Ubiquitin carboxyl-terminal hydrolase 7	2	0	PRDX1
P61221	ABCE1	ATP-binding cassette sub-family E member 1	2	0	PRDX1
E5KLJ9	OPA1	Dynamin-like 120 kDa protein, form \$1	2	0,003	PRDX1
E9PGT1	TSN	Component 3 of promoter of RISC	2	0,003	PRDX1
H7C3C4	SLC4A7	Anion exchange protein	2	0.004	PRDX1
P52788	SMS	Spermine synthase	2.	0.007	PR DX1
HOYKUI	TMOD3	Tropomodulin-3	2	0.008	PR DX1
P30044	PR DX5	Peroviredovin-5 mitochondrial	10.1	0	PR DX1
0/2852	CALU	Calumonin	1.9	0	DP DV1
045652	CALU	Cardinerini 2	1,9	0	PRDA1
Q90BF2	COPG2	A still strengt (2011) De la service ATD se la service 1	1,9	0	PRDA1
D95455	AHSAI	Activator of 90 kDa neat snock protein A I Pase nomolog I	1,9	0	PRDAI
P34932	HSPA4	Heat shock /0 kDa protein 4	1,9	0	PRDXI
Q4J6C6	PREPL	Prolyl endopeptidase-like	1,9	0,001	PRDX1
Q13564	NAE1	NEDD8-activating enzyme E1 regulatory subunit	1,9	0,001	PRDX1
P62314	SNRPD1	Small nuclear ribonucleoprotein Sm D1	1,9	0,001	PRDX1
Q13185	CBX3	Chromobox protein homolog 3	1,9	0,001	PRDX1
Q9Y478	PRKAB1	5'-AMP-activated protein kinase subunit beta-1	1,9	0,004	PRDX1
P30041	PRDX6	Peroxiredoxin-6	1,9	0,005	PRDX1
Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	1,9	0,01	PRDX1
J3KPG2	TPT1	Translationally-controlled tumor protein	1,9	0,017	PRDX1
Q96A49	SYAP1	Synapse-associated protein 1	1,9	0,023	PRDX1
P61981	YWHAG	14-3-3 protein gamma	1,8	0	PRDX1
P06730	EIF4E	Eukaryotic translation initiation factor 4E	1,8	0	PRDX1
O99460	PSMD1	26S proteasome non-ATPase regulatory subunit 1	1.8	0	PRDX1
E9PLK3	NPEPPS	Aminopeptidase	1.8	0	PR DX1
O9BR P1	PDCD2I	Programmed cell death protein 2-like	1.8	0	PR DX1
015393	SE3B3	Splicing factor 3B subunit 3	1.8	0.001	DR DY1
	GEMIN/	Com-associated protein 6	1.8	0.001	DR DV1
ON IRSA	DNAIR11	Dra Lhomolog subfamily R momber 11	1.0	0,001	DD DV1
Q20034	ENIPD4	Enay homolog subtaining D member 11	1,0	0,005	PRDA1
Q0103A1	FINDP4	Conclusion in the second structure of the second struc	1,8	0,006	PRDAI
000483	NDUFA4	Cytochrome c oxidase subunit NDUFA4	1,8	0,009	PKDXI
Q15293	KCN1	Keticulocalbin-1	1,8	0,009	PRDX1
P12814	ACTN1	Alpha-actinin-1	1,8	0,012	PRDX1
Q9NVP1	DDX18	ATP-dependent RNA helicase DDX18	1,8	0,013	PRDX1
P62333	PSMC6	26S proteasome regulatory subunit 10B	1,7	0	PRDX1

P50502	ST13	Hsc70-interacting protein	1,7	0,001	PRDX1
P27824	CANX	Calnexin	1,7	0,004	PRDX1
P52888	THOP1	Thimet oligopeptidase	1,7	0,005	PRDX1
P46821	MAP1B	Microtubule-associated protein 1B	1,7	0,007	PRDX1
X6RM00	ERC1	ELKS/Rab6-interacting/CAST family member 1	1,7	0,009	PRDX1
Q9UHY1	NRBP1	Nuclear receptor-binding protein	1,7	0,009	PRDX1
O96019	ACTL6A	Actin-like protein 6A	1.7	0.01	PR DX1
D6R 400	ENOPH1	Finalese.phosphatase F1	17	0.012	DR DY1
DOKA00	D A DED2	P. I. CTD Line for a second secon	1,7	0,012	PRDA1
B4DHK0	KABEP2	Rab G I Pase-binding effector protein 2	1,/	0,013	PRDXI
Q53GQ0	HSD17B12	Very-long-chain 3-oxoacyl-CoA reductase	1,7	0,032	PRDX1
Q96CS3	FAF2	FAS-associated factor 2	1,6	0	PRDX1
Q9UJS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	1,6	0	PRDX1
O00487	PSMD14	26S proteasome non-ATPase regulatory subunit 14	1,6	0	PRDX1
E9PIF2	DDX10	RNA helicase	1,6	0	PRDX1
P52565	ARHGDIA	Rho GDP-dissociation inhibitor 1	1.6	0	PRDX1
P61923	COP71	Coatomer subunit zeta-1	1.6	0	PR DX1
D98175	R BM10	B NA binding protein 10	1.6	0	DR DY1
0011020	DA 2C 4	Dealiferation and interference 2C /	1,0	0	DR DV1
Q90Q80	PA2G4	ATTEN IN IN INCOME AND A STATEMENT	1,6	0	PRDAI
Q8NE/I	ABCFI	A I P-binding cassette sub-family F member 1	1,6	0	PRDXI
P34949	MPI	Mannose-6-phosphate isomerase	1,6	0	PRDX1
P26196	DDX6	Probable ATP-dependent RNA helicase DDX6	1,6	0	PRDX1
O43164	PJA2	E3 ubiquitin-protein ligase Praja-2	1,6	0,001	PRDX1
O15212	PFDN6	Prefoldin subunit 6	1,6	0,001	PRDX1
B1AK87	CAPZB	F-actin-capping protein subunit beta	1,6	0,002	PRDX1
075688	PPM1B	Protein phosphatase 1B	1.6	0.004	PR DX1
D29218	IMDA 1	Inocital manaphasahatasa 1	1.6	0.014	DP DV1
P27210	IMPA1		1,6	0,014	PRDAI
A0A08/WXS/	A0A08/WXS/	>tt/AUAUS / w XS / AUAUS / w XS / HUMAN A1 Pase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=1;>sp[O43681]ASNA_HUMAN ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2;>tr[K7ERW9]K7ERW9_ HUMAN Arsenical pump-driving ATPase (Fragment) OS=Homo sapiens OX=9606 G	1,6	0,03	PKDXI
O15372	EIF3H	Eukaryotic translation initiation factor 3 subunit H	1,5	0	PRDX1
O9UIG0	BAZ1B	Tyrosine-protein kinase BAZ1B	1.5	0	PRDX1
K7ER F1	EIF3K	Eukarvotic translation initiation factor 3 subunit K	1.5	0	PR DX1
096009	CDP ASD2	C protain coupled recenter associated serting protain 2	1,5	0	DP DV1
Q/0D0/	DVCI	Classical and the last free free free free free free free fre	1,5	0	DD DV1
P06/3/	PIGL	Giycogen phosphorylase, liver form	1,5	0	PRDAI
Q15029	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	1,5	0	PRDX1
P63104	YWHAZ	14-3-3 protein zeta/delta	1,5	0	PRDX1
E5RHG8	ELOC	Elongin-C	1,5	0	PRDX1
P30101	PDIA3	Protein disulfide-isomerase A3	1,5	0,001	PRDX1
O75832	PSMD10	26S proteasome non-ATPase regulatory subunit 10	1,5	0,001	PRDX1
O00273	DFFA	DNA fragmentation factor subunit alpha	1,5	0,002	PRDX1
043747	AP1G1	AP-1 complex subunit gamma-1	1.5	0.002	PR DX1
06IN85	DDD/R 3 A	Serine /three pine protein phosphatase / regulatory subunit 3 A	1.5	0.005	DR DY 1
Q011003	DCC1	Demol line on longing Correct	1,5	0,003	PRDX1
Q96125	KSF1		1,5	0,01	PKDAI
H/C128	BRD8	Bromodomain-containing protein 8	1,5	0,012	PRDXI
Q9HA64	FN3KRP	Ketosamine-3-kinase	1,5	0,017	PRDX1
Q9P287	BCCIP	BRCA2 and CDKN1A-interacting protein	1,5	0,018	PRDX1
Q13033	STRN3	Striatin-3	1,5	0,022	PRDX1
Q9NQ29	LUC7L	Putative RNA-binding protein Luc7-like 1	1,5	0,023	PRDX1
P19174	PLCG1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	1,5	0,024	PRDX1
086TI2	DPP9	Dipeptidyl peptidase 9	1.5	0.027	PR DX1
O9NTK5	OT A1	Oba-like ATPase 1	15	0.031	PR DX1
D20200	A PCD2	ATD his disc second for the Descent of 2	1,5	0,031	DR DV1
P20200	ABCDS	A I P-binding cassette sub-family D member 5	1,5	0,034	PRDAI
015144	ARPC2	Actin-related protein 2/3 complex subunit 2	1,5	0,035	PRDXI
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	1,5	0,044	PRDX1
Q9UL15	BAG5	BAG family molecular chaperone regulator 5	1,5	0,046	PRDX1
Q15691	MAPRE1	Microtubule-associated protein RP/EB family member 1	1,4	0	PRDX1
P15121	AKR1B1	Aldo-keto reductase family 1 member B1	1,4	0	PRDX1
E9PMI6	CLNS1A	Chloride channel, nucleotide sensitive 1A	1,4	0	PRDX1
O92598	HSPH1	Heat shock protein 105 kDa	1.4	0	PRDX1
P60900	PSM A6	Proteasome subunit alpha type-6	1.4	0	PR DX1
O8IWB7	WDFV1	WD repeat and FYVF domain-containing protein 1	1.4	0.001	PR DY1
U787147	7DD 1	7 Diegen protein 7DD 1	1,1	0,001	DD DV1
11/DLM/	LICD5		1,4	0,001	PRDAI
P45974	USP5	Ubiquitin carboxyl-terminal hydrolase 5	1,4	0,001	PRDX1
O43707	ACTN4	Alpha-actinin-4	1,4	0,002	PRDX1
E7EV99	ADD1	Alpha-adducin	1,4	0,002	PRDX1
Q9H0A0	NAT10	RNA cytidine acetyltransferase	1,4	0,006	PRDX1
F8W038	C17orf49	Chromosome 17 open reading frame 49	1,4	0,008	PRDX1
P42574	CASP3	Caspase-3	1,4	0.025	PRDX1
			-, -	0,027	
099598	TSNAV	Translin-associated protein X	1 /	0.029	DR DV1

O01085	TTAL1	Nucleolysin TI A R	1.4	0.033	PR DX1
O9NZL9	MAT2B	Methionine adenosyltransferase 2 subunit beta	1,1	0.037	PR DX1
Q9UKN8	GTF3C4	General transcription factor 3C polypeptide 4	1,1	0.045	PR DX1
Q8N999	C12orf29	Uncharacterized protein C12orf29	1,1	0.047	PR DX1
P32969	R PI 9	60S ribosomal protein [ 9	1.3	0,017	PR DX1
09NSD9	FARSB	PhenylalaninetR NA ligase beta subunit	13	0	PR DX1
09Y383	LUC7L2	Putative R NA-binding protein Luc7-like 2	13	0	PR DX1
P05023	ATPIA1	Sodium/notassium-transporting ATPase subunit alpha-1	1.3	0	PR DX1
AGNKB8	RNPFP	Aminopentidase B	1.3	0	PR DX1
P61247	R PS3A	40S ribosomal protein S3a	1.3	0	PR DX1
P62424	R PI 7A	60S ribosomal protein U7a	1.3	0	PR DX1
P60953	CDC42	Cell division control protein 42 homolog	1.3	0.001	PR DX1
O68E01	INTS3	Integrator complex subunit 3	1,3	0.001	PR DX1
F8VVI 1	DENR	Density-regulated protein	1,3	0.002	PR DX1
092688	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B	1,3	0.002	PR DX1
P18077	R PI 35A	60S ribosomal protein I 35a	1,3	0.003	PR DX1
000186	STXBP3	Syntaxin-binding protein 3	1,3	0.005	PR DX1
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1,3	0.005	PR DX1
P08133	ANXA6	Annevin A6	1,3	0.005	PR DX1
015291	R RRD5	Retipoblastoma binding protein S	1,3	0.005	DR DY1
Q19291 D/9750	VI DM1	VI P motif-containing protein 1	1,3	0.005	DR DY1
D55769	SNIL13	NHP2 like protein 1	1,3	0,005	DR DY1
075281	DEV14	Paravisanal membrana protain DEV14	1,5	0,008	DP DV1
D/1252	IAD \$1	Icologina tPNA ligan autoplasmia	1,5	0.018	DP DV1
D09759	ANVAS	Appavin AS	1,5	0,018	DP DV1
100/30	LIDE2A	Libraria matria liana E2A	1,5	0,022	PRDA1
FODINO	ACOTR	A sul as a subject to the sector of the sect	1,5	0,039	PRDA1
E3PJIN0	RCO18	Resistence of activitied protein Chinese 1	1,5	0,04	PRDA1
P65244	TED FOID	Receptor or activated protein C kinase 1	1,5	0,045	PRDA1
Q9N I D0	TERF2IP	College de la 1(W) de la	1,5	0,045	PRDA1
AUA 3D 31 3 V 3	COL4A1	Collagen alpha-1(1V) chain	1,5	0,049	PRDA1
Q13131	PKKAAI	5 -AMP-activated protein kinase catalytic subunit alpha-1	1,5	0,05	PRDA1
P40938	CLIC1	Chlorid investibility of the characteristic 1	1,2	0	PRDA1
D00299	CLICI	Chloride intracellular channel protein I	1,2	0	PRDXI
P0038/	CYB5R3	NADH-cytochrome b5 reductase 3	1,2	0	PRDXI
Q915V3	DADTA	Melanoma-associated antigen D1	1,2	0	PRDXI
P51149	KAB/A	Ras-related protein Rab-/a	1,2	0	PRDXI
060763	USOI	General vesicular transport factor p115	1,2	0	PRDXI
P23396	KPS3	405 ribosomal protein 53	1,2	0	PRDXI
01219	POLK2B	DNA-directed KNA polymerase subunit beta	1,2	0,001	PRDXI
Q32CQ8	11MM50	Mitochondrial import inner membrane translocase subunit 11M50	1,2	0,001	PRDXI
Q9H3P/	ACBD3		1,2	0,001	PRDXI
P51665	PSMD7	265 proteasome non-A1 Pase regulatory subunit /	1,2	0,001	PRDXI
<u>C9J019</u>	ZC3HCI	Nuclear-interacting partner of ALK	1,2	0,001	PRDXI
P43034	PAFAHIBI	Platelet-activating factor acetylhydrolase IB subunit beta	1,2	0,001	PRDXI
P14324	FDPS	Farnesyl pyrophosphate synthase	1,2	0,001	PRDXI
Q8ND82	ZNF280C	Zinc finger protein 280C	1,2	0,001	PRDXI
P09211	GSTP1	Glutathione S-transferase P	1,2	0,001	PRDX1
P628//	RBXI	E3 ubiquitin-protein ligase KBX1	1,2	0,002	PRDXI
Q0/020	RPL18	605 ribosomal protein L18	1,2	0,002	PRDXI
P25490	111 ZODUANU		1,2	0,003	PRDXI
Q96H/9	ZC3HAVIL	Zinc finger CCCH-type antiviral protein 1-like	1,2	0,004	PRDXI
Q9Y3Z3	SAMHDI	Deoxynucleoside triphosphate triphosphohydrolase SAMHDI	1,2	0,005	PRDXI
Q01831	XPC FIF2D	DNA repair protein complementing XP-C cells	1,2	0,005	PRDXI
P55884	EIF3B	Eukaryotic translation initiation factor 3 subunit B	1,2	0,005	PRDXI
Q90112	ATPOVIH	V-type proton AT Pase subunit H	1,2	0,006	PRDXI
Q915J1	UTP18	U3 small nucleolar KNA-associated protein 18 homolog	1,2	0,006	PRDXI
Q15843	NEDD8	NEDD8	1,2	0,008	PRDXI
P56192	MARSI	MethioninetRNA ligase, cytoplasmic	1,2	0,009	PRDXI
P19338	NCL	Nucleolin D. L. D. D. L. D.	1,2	0,015	PRDXI
Q9H0U4	RABIB	Ras-related protein Rab-IB	1,2	0,017	PRDXI
Q96RLI	UIMCI	BKCA1-A complex subunit KAP80	1,2	0,03	PRDX1
P30/40	SERPINB1	Leukocyte elastase inhibitor	1,2	0,033	PRDX1
Q93008	LINDAY	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	1,2	0,037	PKDX1
0752(0	UJF /A		1.2	0.0/1	DD DY's
075369	FLNB	Filamin-B	1,2	0,041	PRDX1
075369 E7EMC7	FLNB SQSTM1	Filamin-B Sequestosome-1	1,2 1,2	0,041 0,046	PRDX1 PRDX1
075369 E7EMC7 Q00325	FLNB SQSTM1 SLC25A3	Filamin-B Sequestosome-1 Phosphate carrier protein, mitochondrial	1,2 1,2 1,1	0,041 0,046 0	PRDX1 PRDX1 PRDX1
075369 E7EMC7 Q00325 P11310	FLNB SQSTM1 SLC25A3 ACADM	Filamin-B Sequestosome-1 Phosphate carrier protein, mitochondrial Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	1,2 1,2 1,1 1,1	0,041 0,046 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1
075369 E7EMC7 Q00325 P11310 Q96CX2	FLNB SQSTM1 SLC25A3 ACADM KCTD12	Filamin-B Sequestosome-1 Phosphate carrier protein, mitochondrial Medium-chain specific acyl-CoA dehydrogenase, mitochondrial BTB/POZ domain-containing protein KCTD12	1,2 1,2 1,1 1,1 1,1	0,041 0,046 0 0 0 0	PRDX1 PRDX1 PRDX1 PRDX1 PRDX1 PRDX1

O60934	NBN	Nibrin	1,1	0,002	PRDX1
O94826	TOMM70	Mitochondrial import receptor subunit TOM70	1,1	0,002	PRDX1
P45954	ACADSB	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	1,1	0,002	PRDX1
O94992	HEXIM1	Protein HEXIM1	1.1	0.003	PR DX1
P12236	SLC25A6	ADP/ATP translocase 3	11	0.003	PR DX1
P42166	TMPO	Lamina-associated polynentide 2 isoform alpha	11	0.004	PR DX1
P/32/6	MSH2	DNA mismatch repair protein Meh?	1 1	0.004	DR DY1
D52004	RI VD A	Biliverdin reductace A	1,1	0,004	DP DV1
1 3 3 0 0 4 D C X 4	CUI 1	Cullin 1	1,1	0,000	DR DV1
AUAUC4DGX4	CULI AD III2	Cullin-1	1,1	0,01	PRDAI
0953/6	AKIH2	E3 ubiquitin-protein ligase ARTH2	1,1	0,014	PRDXI
Q9UL25	RAB21	Ras-related protein Rab-21	1,1	0,015	PRDX1
O60784	TOM1	Target of Myb protein 1	1,1	0,02	PRDX1
Q15054	POLD3	DNA polymerase delta subunit 3	1,1	0,02	PRDX1
Q8IZ73	RPUSD2	RNA pseudouridylate synthase domain-containing protein 2	1,1	0,031	PRDX1
Q96SB4	SRPK1	SRSF protein kinase 1	1,1	0,033	PRDX1
P16435	POR	NADPHcytochrome P450 reductase	1,1	0,035	PRDX1
G3V529	DDX24	RNA helicase	1,1	0,044	PRDX1
P09960	LTA4H	Leukotriene A-4 hydrolase	1	0	PRDX1
Q99623	PHB2	Prohibitin-2	1	0,001	PRDX1
Q99613	EIF3C	Eukaryotic translation initiation factor 3 subunit C	1	0,002	PRDX1
O9NOW7	XPNPEP1	Xaa-Pro aminopeptidase 1	1	0,005	PRDX1
P07195	LDHB	L-lactate debydrogenase B chain	1	0.006	PR DX1
O9BY42	RTF2	Replication termination factor 2	1	0.007	PR DX1
O9LIPN7	DDD4R 1	Serine/threenine-protein phoenhatase 6 regulatory subunit 1	1	0,007	PR DY 1
Q/DFIN/	DARCO	A mentate a D NA lieses mite-shere deid	1	0,008	DR DV1
Q6P148	A D2D1	A D 2 second sec	1	0,012	PRDA1
000203	AP3B1	AP-3 complex subunit beta-1	1	0,013	PRDXI
0/6003	GLRX3	Glutaredoxin-3	1	0,035	PRDXI
F8W1A4	AK2	Adenylate kinase 2, mitochondrial	1	0,043	PRDXI
P20073	ANXA7	Annexin A7	1	0,047	PRDX1
P49366	DHPS	Deoxyhypusine synthase	6,9	0	PRDX2
O94776	MTA2	Metastasis-associated protein MTA2	6,7	0	PRDX2
H0YEN2	PPP6R3	Serine/threonine-protein phosphatase 6 regulatory subunit 3	4,1	0	PRDX2
Q16576	RBBP7	Histone-binding protein RBBP7	3,8	0	PRDX2
P63151	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	3,7	0	PRDX2
Q5QNY5	PEX19	Peroxin-19	3,7	0	PRDX2
H0Y4R1	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	3,7	0	PRDX2
P67936	TPM4	Tropomyosin alpha-4 chain	3,6	0	PRDX2
Q13547	HDAC1	Histone deacetylase 1	3,6	0	PRDX2
Q96BR5	COA7	Cytochrome c oxidase assembly factor 7	3,5	0	PRDX2
O00165	HAX1	HCLS1-associated protein X-1	3.4	0	PRDX2
O09028	R BBP4	Histone-binding protein R BBP4	3.4	0	PR DX2
P61289	PSME3	Proteasome activator complex subunit 3	3.4	0.023	PR DX2
096FW2	HSDRA D1	HSDBL-associated protein 1	3.1	0	DR DY2
0902118	DSME2ID1	DSME2 interacting protein	2	0	DP DY2
Q/G2.08	VDAC2	Our and the later	2	0	PRDA2
AUAUAUMKUZ	V DACZ	N IC I i i i i i i i i i i i i i i i i i	3	0	PRDX2
Q96R56	NUDCDI	NudC domain-containing protein 1	2,9	0	PRDX2
Q9NQP4	PFDN4	Prefoldin subunit 4	2,9	0	PRDX2
P62258	YWHAE	14-3-3 protein epsilon	2,9	0	PRDX2
A0A1C7CYX9	DPYSL2	Dihydropyrimidinase-related protein 2	2,8	0	PRDX2
O14744	PRMT5	Protein arginine N-methyltransferase 5	2,8	0,011	PRDX2
P23526	AHCY	Adenosylhomocysteinase	2,7	0	PRDX2
Q6DKK2	TTC19	Tetratricopeptide repeat protein 19, mitochondrial	2,7	0,003	PRDX2
P20839	IMPDH1	Inosine-5'-monophosphate dehydrogenase 1	2,6	0	PRDX2
Q96DB5	RMDN1	Regulator of microtubule dynamics protein 1	2,6	0,002	PRDX2
P78417	GSTO1	Glutathione S-transferase omega-1	2,5	0	PRDX2
Q15276	RABEP1	Rab GTPase-binding effector protein 1	2,5	0	PRDX2
P41250	GAR\$1	GlycinetRNA ligase	2,4	0	PRDX2
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosvlaminoimidazole-	2,4	0	PRDX2
		succinocarboxamide synthase			
			2 /		DP DV2
P78371	CCT2	1-complex protein 1 subunit beta	2,7	0	FRDAZ
P78371 075688	CCT2 PPM1B	I-complex protein I subunit beta Protein phosphatase 1B	2,4	0	PRDX2
P78371 075688 P27348	CCT2 PPM1B YWHAO	I-complex protein I subunit beta Protein phosphatase 1B 14-3-3 protein theta	2,4	0 0 0 0	PRDX2 PRDX2 PRDX2
P78371 O75688 P27348 O92769	CCT2 PPM1B YWHAQ HDAC2	I-complex protein I subunit beta Protein phosphatase 1B 14-3-3 protein theta Histone deacetylase 2	2,4 2,4 2,4 2,4	0 0 0	PRDX2 PRDX2 PRDX2 PRDX2
P78371 O75688 P27348 Q92769 O00268	CCT2 PPM1B YWHAQ HDAC2 TAF4	I-complex protein 1 subunit beta     Protein phosphatase 1B     14-3-3 protein theta     Histone deacetylase 2     Transcription initiation factor TEHD subunit 4	2,4 2,4 2,4 2,4 2,4 2,4	0 0 0 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
P78371 O75688 P27348 Q92769 O00268 P60900	CCT2 PPM1B YWHAQ HDAC2 TAF4 PSMAC	I-complex protein I subunit beta     Protein phosphatase 1B     14-3-3 protein theta     Histone deacetylase 2     Transcription initiation factor TFIID subunit 4     Protecome subunit alpha tune 6	2,4 2,4 2,4 2,4 2,3 2,2	0 0 0 0 0 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
P78371 O75688 P27348 Q92769 O00268 P60900 H7C3C4	CCT2 PPM1B YWHAQ HDAC2 TAF4 PSMA6 SLC447	I-complex protein I subunit beta     Protein phosphatase 1B     14-3-3 protein theta     Histone deacetylase 2     Transcription initiation factor TFIID subunit 4     Proteasome subunit alpha type-6     Anion exchange protein	2,4 2,4 2,4 2,4 2,3 2,2 2,2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
P78371 O75688 P27348 Q92769 O00268 P60900 H7C3C4	CCT2 PPM1B YWHAQ HDAC2 TAF4 PSMA6 SLC4A7 THCO2	I-complex protein I subunit beta Protein phosphatase 1B 14-3-3 protein theta Histone deacetylase 2 Transcription initiation factor TFIID subunit 4 Proteasome subunit alpha type-6 Anion exchange protein Transcript bit 2	2,4 2,4 2,4 2,4 2,3 2,2 2,2 2,2	0 0 0 0 0,002 0,003	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
P78371 O75688 P27348 Q92769 O00268 P60900 H7C3C4 H0YKU1 D00275	CCT2 PPM1B YWHAQ HDAC2 TAF4 PSMA6 SLC4A7 TMOD3 PBW66	I-complex protein I subunit beta     Protein phosphatase 1B     14-3-3 protein theta     Histone deacetylase 2     Transcription initiation factor TFIID subunit 4     Proteasome subunit alpha type-6     Anion exchange protein     Tropomodulin-3     DNM dulin-3	2,4 2,4 2,4 2,3 2,2 2,2 2,2 2,2	0 0 0 0 0,002 0,003 0,006	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
P78371 O75688 P27348 Q92769 O00268 P60900 H7C3C4 H0YKU1 P98175	CCT2 PPM1B YWHAQ HDAC2 TAF4 PSMA6 SLC4A7 TMOD3 RBM10	I-complex protein I subunit beta      Protein phosphatase 1B      14-3-3 protein theta      Histone deacetylase 2      Transcription initiation factor TFIID subunit 4      Proteasome subunit alpha type-6      Anion exchange protein      Tropomodulin-3      RNA-binding protein 10      Ithere is the set for the set for the set for the set of the s	2,4 2,4 2,4 2,3 2,2 2,2 2,2 2,2 2,1	0 0 0 0,002 0,003 0,006 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2

0/21/2	DUV16	D DNIA	2.1	0.00/	DDDV2
045145	DHAIS	Pre-mKNA-splicing factor ATP-dependent KNA helicase DHA15	2,1	0,004	PKDAZ
A0A2U3TZY2	CLPB	Caseinolytic peptidase B protein homolog	2,1	0,004	PRDX2
P52788	SMS	Spermine synthase	2,1	0,008	PRDX2
043852	CALU	Calumenin	2	0	PR DX2
U7D7)/7	ZDD 1	Zin Commenter ZDB 1	2	0	DDDV2
H/BZWI/	ZFKI		2	0	PRDA2
F8W1A4	AK2	Adenylate kinase 2, mitochondrial	2	0,005	PRDX2
P12814	ACTN1	Alpha-actinin-1	2	0,009	PRDX2
P30044	PR DX5	Peroxiredoxin-5 mitochondrial	12.4	0	PR DX2
000000	LIBERO	$(F_2 : 1 \dots 1 \dots )F_2$ limit in the second s	1.0	0	DDDV2
QUUCI	UBEZO	(E3-independent) E2 ubiquitin-conjugating enzyme	1,9	0	PKDA2
P31946	YWHAB	14-3-3 protein beta/alpha	1,9	0	PRDX2
Q9BPU6	DPYSL5	Dihydropyrimidinase-related protein 5	1,9	0	PRDX2
P/15973	CBY5	Chromobox protein homolog 5	19	0	DR DY2
<u>11))//5</u>	DD DV(		1,7	0 010	DD DV2
P30041	PRDX6	Peroxiredoxin-6	1,9	0,012	PRDX2
P61981	YWHAG	14-3-3 protein gamma	1,8	0	PRDX2
Q15008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	1,8	0	PRDX2
013200	DSMD2	26 protosomo pop ATDece regulatory subunit 2	1.9	0	DP DY2
Q15200	1 JMID2	200 proteasone non-7111 ase regulatory subunit 2	1,0	0	DD DWa
P11142	HSPA8	Heat shock cognate /1 kDa protein	1,8	0	PRDX2
O43164	PJA2	E3 ubiquitin-protein ligase Praja-2	1,8	0,001	PRDX2
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	1.8	0,001	PRDX2
130079	PNPO	Puridoval 5' phoenhate suppliese	1.8	0.001	DR DY2
<u></u>	PINFO	ryndoxal 5-phosphate synthase	1,0	0,001	PRDAZ
P629/9	KP\$2/A	Ubiquitin-408 ribosomal protein 82/a	1,8	0,001	PKDX2
Q14257	RCN2	Reticulocalbin-2	1,8	0,003	PRDX2
Q96RG2	PASK	PAS domain-containing serine/threonine-protein kinase	1,8	0,003	PRDX2
096B36	AKT1\$1	Proline-rich AKT1 substrate 1	1.8	0.015	PR DX2
2,00,00	DOTN		1,0	0,010	DDDV2
000399	DCIN6	Dynactin subunit 6	1,8	0,018	PKDX2
A0A087WXS7	A0A087WXS7	>tr A0A087WXS7 A0A087WXS7_HUMAN ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=1;>sp O43681 ASNA_HUMAN ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2;>tr K7ERW9 K7ERW9_	1,8	0,023	PRDX2
		HUMAN Arsenical pump-driving ATPase (Fragment) OS=Homo sapiens OX=9606 G			
O9UHV9	PFDN2	Prefoldin subunit 2	1.8	0,024	PRDX2
D6310/	VWH A 7	1/.3.3 protein zeta/delta	17	0	DR DY2
103104	1 W11112		1,7	0 005	DD DV2
A0A024K442	A0A024K442	>tr A0A024R442 A0A024R442_HUMAN Aspartyl aminopeptidase, isoform CRA_b	1,/	0,005	PRDX2
		OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>sp Q9ULA0 DNPEP_			
		HUMAN Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1			
		SV=1;>tr E7ETB3 E7ETB3_HUMAN Aspartyl aminopeptidase, iso			
O9NTK5	OLA1	Obg-like ATPase 1	1.7	0.022	PRDX2
Q9NTK5	OLA1	Obg-like ATPase 1	1,7	0,022	PRDX2
Q9NTK5 Q9NV56	OLA1 MRGBP	Obg-like ATPase 1 MRG/MORF4L-binding protein	1,7 1,7	0,022	PRDX2 PRDX2
Q9NTK5 Q9NV56 B4DHR0	OLA1 MRGBP RABEP2	Obg-like ATPase 1 MRG/MORF4L-binding protein Rab GTPase-binding effector protein 2	1,7 1,7 1,7	0,022 0,025 0,025	PRDX2 PRDX2 PRDX2
Q9NTK5 Q9NV56 B4DHR0 Q13131	OLA1 MRGBP RABEP2 PRKAA1	Obg-like ATPase 1 MRG/MORF4L-binding protein Rab GTPase-binding effector protein 2 5'AMP-activated protein kinase catalytic subunit alpha-1	1,7 1,7 1,7 1,7	0,022 0,025 0,025 0,03	PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS	Obg-like ATPase 1 MRG/MORF4L-binding protein Rab GTPase-binding effector protein 2 5'AMP-activated protein kinase catalytic subunit alpha-1 Aminopentidase	1,7 1,7 1,7 1,7 1,7	0,022 0,025 0,025 0,03 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           O22009	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS	Obg-like ATPase 1 MRG/MORF4L-binding protein Rab GTPase-binding effector protein 2 5'-AMP-activated protein kinase catalytic subunit alpha-1 Aminopeptidase	1,7 1,7 1,7 1,7 1,6 1,6	0,022 0,025 0,025 0,03 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q23009	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7	Obg-like ATPase 1 MRG/MORF4L-binding protein Rab GTPase-binding effector protein 2 5'-AMP-activated protein kinase catalytic subunit alpha-1 Aminopeptidase Ubiquitin carboxyl-terminal hydrolase 7	1,7 1,7 1,7 1,7 1,6 1,6	0,022 0,025 0,025 0,03 0 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5	Obg-like ATPase 1 MRG/MORF4L-binding protein Rab GTPase-binding effector protein 2 5'-AMP-activated protein kinase catalytic subunit alpha-1 Aminopeptidase Ubiquitin carboxyl-terminal hydrolase 7 Proteasome subunit alpha type-5	1,7 1,7 1,7 1,7 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0 0 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           O32MZ4	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           O2HX18	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 CTF3C4	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         Consert transcription forces 3C polynomials 4	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,012 0,023	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q92KN8	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,012 0,032	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,012 0,033 0,038	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,5	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,012 0,033 0,038 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,001 0,012 0,033 0,038 0 0 0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           O15424	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15424	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,012 0,033 0,038 0 0 0 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15424           Q15424           Q15424           Q15424           Q15843	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8	Obg-like ATPase 1         MRG/MOR F4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,012 0,033 0,038 0 0 0 0,001 0,001 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UBE0	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,033 0,038 0 0 0,001 0,001 0,001 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UBE0           Q9UEY8	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,001 0,001 0,001 0,001 0,001 0,001 0,001 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UBE0           Q9UEY8           A0A087X0K9	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TID1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tirbt injection protein ZOc1	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,012 0,033 0,038 0 0 0,001 0,001 0,001 0,001 0,001 0,001 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UBE0           Q9UEY8           A0A087X0K9	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSCC	Obg-like ATPase 1         MRG/MOR F4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,022 0,025 0,025 0,03 0 0 0 0,001 0,001 0,003 0,003 0,003 0,038 0 0 0,001 0,001 0,001 0,001 0,001 0,001 0,001 0,001 0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,033           0,033           0,033           0,033           0,034           0,001           0,0304           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1	Obg-like ATPase 1         MRG/MOR F4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q92KN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           O98S18	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 FSYT1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1	1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,017           0,035	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15843           Q9UEV8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BJ8           Q90KP	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 EST14EDWT	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,033           0,038           0           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,027	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q8NK00	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Y-box-binding protein 1	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q8N6R0           Q9BY42	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2	Obg-like ATPase 1         MRG/MOR F4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,012           0,012           0,017           0,035           0,037           0,04           0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q92KN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UEY8           A0A087X0K9           Q3PKV6           A0A087WT45           P67809           Q9BSI8           Q8N6R0           Q9BY42           P35998	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 ESYT1 ESYT1 ESYT1 ESYT1 ESF1AKNMT RTF2 PSMC2	Obg-like ATPase 1         MRG/MOR F4L-binding protein         Rab GTPase-binding effector protein 2         S'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,017           0,035           0,037           0,004           0,004	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UEV8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q8M6R0           Q9BY42           P35998           O9Y3F4	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,025           0,03           0           0,001           0,012           0,033           0,033           0,033           0,033           0,038           0           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087XWT45           P67809           Q9BSJ8           Q8N6R0           Q9BY42           P35998           Q9YF4           Q013185	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBY3	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDB8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Charactive protein boxedor 3	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q8N6R0           Q9Y3F4           Q1305	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3	Obg-like ATPase 1         MRG/MOR F4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,012           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002           0,021	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q92KN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UEY8           A0A087X0K9           Q9BEJ8           Q9BSJ8           Q9BY42           P35998           Q9Y3F4           Q13185           H7C128	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         S'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0,001           0,012           0,033           0,033           0,001           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,017           0,035           0,037           0,044           0           0,001           0,002           0,021           0,031	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087X0T45           P67809           Q9BSJ8           Q8N6R0           Q9Y3F4           Q13185           H7C128           Q8N806	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Sylaw and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein ligase UBR7	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,017           0,035           0,037           0,04           0           0,001           0,002           0,021           0,031           0,032	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q9RKV6           A0A087XWT45           P67809           Q9BSJ8           Q8N6R0           Q9Y3F4           Q13185           H7C128           Q8N806           P15104	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NED08 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7 GLUL	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein ligase UBR7         Glutamine synthetase <td><math display="block">\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6</math></td> <td>0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002           0,001           0,002           0,031           0,032           0</td> <td>PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2</td>	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002           0,001           0,002           0,031           0,032           0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q9Y3F4           Q13185           H7C128           Q8N806           P15104           P23528	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7 GLUL CFL1	Obg-like ATPase 1         MRG/MOR F4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein 8         Putative E3 ubiquitin-protein 1 </td <td><math display="block">\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6</math></td> <td>0,022           0,025           0,025           0,03           0           0           0,001           0,033           0,033           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002           0,021           0,032           0</td> <td>PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 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Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15843           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q8N6R0           Q93598           Q973F4           Q13185           H7C128           Q8N806           P15104           P23528	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7 GLUL CFL1 TTPN	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein ligase UBR7         Glutamine synthetase <td><math display="block">\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6</math></td> <td>0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,033           0,038           0           0,001           0,001           0,001           0,001           0,001           0,001           0,017           0,035           0,037           0,04           0           0,001           0,002           0,001           0,002           0,021           0,033           0           0,031           0,032           0           0</td> <td>PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 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Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087X0K9           Q9BSJ8           Q8NoR0           Q9BY42           P35998           Q9Y3F4           Q13185           H7C128           Q8N806           P15104           P23528           P12270	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7 GLUL CFL1 TPR	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         S'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Synae and N-terminal methyltransferase         Replication termination factor 2         265 proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein ligase UBR7         Glutamine synthetase     <	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002           0,021           0,032           0           0           0           0	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q15424           Q9UBE0           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q8N6R0           Q9Y3F4           Q13185           H7C128           Q8N806           P15104           P23528           P12270           Q96D09	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NED08 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 EXYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7 GLUL CFL1 TPR GPRASP2	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein ligase UBR7         Glutamine synthetase <td><math display="block">\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6</math></td> <td>0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002           0,021           0,031           0,032           0           0           0,001</td> <td>PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2</td>	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,012           0,033           0,033           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,011           0,012           0,017           0,035           0,037           0,04           0           0,001           0,002           0,021           0,031           0,032           0           0           0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2
Q9NTK5           Q9NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UE80           Q9UEY8           A0A087X0K9           Q5RKV6           A0A087WT45           P67809           Q9BSJ8           Q9Y3F4           Q13185           H7C128           Q8N806           P15104           P23528           P12270           Q9CD09           P62191	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7 GLUL CFL1 TPR GPRASP2 PSMC1	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'-AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Y-box-binding protein 1         X-box-binding protein 1         Extended synaptotagmin-1         eEF1A lysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein ligase UBR7	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,022           0,025           0,025           0,03           0           0           0,001           0,033           0,033           0,001           0,033           0,001           0,033           0,001           0,001           0,001           0,001           0,001           0,001           0,001           0,017           0,017           0,035           0,037           0,001           0,002           0,021           0,032           0           0,031           0,032           0           0,001           0,001           0,001           0,001	PRDX2
Q9NTK5           Q2NV56           B4DHR0           Q13131           E9PLK3           Q93009           P28066           O15212           Q32MZ4           Q9UKN8           P57076           C9J019           E7ESY4           Q15424           Q9UEV8           A0A087X0K9           Q9BEJ8           Q9BSJ8           Q9BSJ8           Q9BY42           P35998           Q9Y3F4           Q13185           H7C128           Q8N806           P15104           P23528           P12270           Q96D09           P62191           O9UPN7	OLA1 MRGBP RABEP2 PRKAA1 NPEPPS USP7 PSMA5 PFDN6 LRRFIP1 GTF3C4 CFAP298 ZC3HC1 MTA1 SAFB NEDD8 SAE1 ADD3 TJP1 EXOSC6 GRIPAP1 YBX1 ESYT1 EEF1AKNMT RTF2 PSMC2 STRAP CBX3 BRD8 UBR7 GLUL CFL1 TPR GPRASP2 PSMC1 PPPC81	Obg-like ATPase 1         MRG/MORF4L-binding protein         Rab GTPase-binding effector protein 2         5'AMP-activated protein kinase catalytic subunit alpha-1         Aminopeptidase         Ubiquitin carboxyl-terminal hydrolase 7         Proteasome subunit alpha type-5         Prefoldin subunit 6         Leucine-rich repeat flightless-interacting protein 1         General transcription factor 3C polypeptide 4         Cilia- and flagella-associated protein 298         Nuclear-interacting partner of ALK         Metastasis-associated protein MTA1         Scaffold attachment factor B1         NEDD8         SUMO-activating enzyme subunit 1         Gamma-adducin         Tight junction protein ZO-1         Exosome complex component MTR3         GRIP1-associated protein 1         Y-box-binding protein 1         Subo-binding protein 1         Extended synaptotagmin-1         eEF1 Alysine and N-terminal methyltransferase         Replication termination factor 2         26S proteasome regulatory subunit 7         Serine-threonine kinase receptor-associated protein         Chromobox protein homolog 3         Bromodomain-containing protein 8         Putative E3 ubiquitin-protein ligase UBR7         Glutamine synthetase	1,7         1,7         1,7         1,7         1,6         1,6         1,6         1,6         1,6         1,6         1,6         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,4         1,4         1,4         1,4         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2         1,2          1,2          1,2          1,2	0,022           0,025           0,025           0,025           0,03           0           0,001           0,012           0,033           0,033           0,033           0,033           0,033           0,038           0           0,001           0,001           0,001           0,001           0,001           0,001           0,017           0,035           0,037           0,04           0           0,001           0,002           0,021           0,032           0           0           0,001           0,002           0,031           0,032           0           0,001           0,001           0,001	PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 PRDX2 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F5KT 19	OPA 1	Dynamin-like 120 kDa protein form \$1	12	0.011	PR DX2
01356/	NAF1	NEDDS activating enzyme E1 regulatory subunit	1.2	0.025	PR DY 2
D22588	EIE/B	Fulcevotic translation initiation factor /B	1,2	0,029	DP DY2
014545	TD A FD1	TD A Example from domain containing methics 1	1,2	0,037	PRDA2
014545	TRAFDI	I KAP-type zinc ninger domain-containing protein 1	1,1	0	PRDAZ
Q32CQ8	11MM50	Mitochondrial import inner membrane translocase subunit 11M50	1,1	0,001	PRDX2
Q9NX63	CHCHD3	MICOS complex subunit MIC19	1,1	0,001	PRDX2
C9J2Y9	POLR2B	DNA-directed RNA polymerase subunit beta	1,1	0,003	PRDX2
P25786	PSMA1	Proteasome subunit alpha type-1	1,1	0,003	PRDX2
015355	PPM1G	Protein phosphatase 1G	1,1	0,008	PRDX2
Q9BTE6	AARSD1	Alanyl-tRNA editing protein Aarsd1	1,1	0,011	PRDX2
Q9NXF7	DCAF16	DDB1- and CUL4-associated factor 16	1,1	0,013	PRDX2
099504	EYA3	Eves absent homolog 3	11	0.015	PR DX2
D/81/7	DRED	Prolylendonentidase	1 1	0.031	DR DY2
D20210	IMDA 1	In a site large period as the set of the set	1,1	0,031	DR DX2
P29218	IMPAI		1,1	0,031	PRDA2
Q8N999	C12orf29	Uncharacterized protein C12orf29	1,1	0,035	PRDX2
Q13177	PAK2	Serine/threonine-protein kinase PAK 2	1,1	0,039	PRDX2
O00429	DNM1L	Dynamin-1-like protein	1,1	0,047	PRDX2
P20020	ATP2B1	Plasma membrane calcium-transporting ATPase 1	1	0,003	PRDX2
Q68E01	INTS3	Integrator complex subunit 3	1	0,012	PRDX2
Q96K76	USP47	Ubiquitin carboxyl-terminal hydrolase 47	1	0,016	PRDX2
P53985	SLC16A1	Monocarboxylate transporter 1	1	0,02	PRDX2
060784	TOM1	Target of Myb protein 1	1	0.022	PR DX2
D/9588	A A D S1	Alapina +P NA ligage gutaplesmic	1	0.022	DP DY2
P47588	AARSI	AlaninetKINA ligase, cytoplasmic	1	0,035	PRDA2
X6RM00	ERCI	ELKS/Rab6-interacting/CAS1 family member 1	1	0,035	PRDX2
094776	MTA2	Metastasis-associated protein MTA2	7	0	PRDX3
P49366	DHPS	Deoxyhypusine synthase	7	0	PRDX3
P61289	PSME3	Proteasome activator complex subunit 3	5	0	PRDX3
Q16576	RBBP7	Histone-binding protein RBBP7	5	0	PRDX3
P67936	TPM4	Tropomyosin alpha-4 chain	4,9	0	PRDX3
H0Y4R1	IMPDH2	Inosine-5'-monophosphate dehvdrogenase 2	4.6	0	PRDX3
P41250	GAR S1	GlycinetRNA ligase	43	0	PR DX3
D22224	DATCS	Multifunctional protein ADE2 [Includes: Dheepheriheestlemineimidezele	4.2	0	DP DY 2
122234	TAICS	suscinosarboramida surbasa	4,5	0	FRDAJ
01/7/ /	DD MCTC	Describeration Newsle lange Court	2.0	0	DD DV2
014/44	PRM15	Protein arginine N-metnyitransrerase 5	3,9	0	PRDA3
Q9NQP4	PFDN4	Prefoldin subunit 4	3,7	0	PRDX3
Q96BR5	COA7	Cytochrome c oxidase assembly factor 7	3,6	0	PRDX3
Q09028	RBBP4	Histone-binding protein RBBP4	3,6	0	PRDX3
O00165	HAX1	HCLS1-associated protein X-1	3,4	0	PRDX3
E7EVA0	MAP4	Microtubule-associated protein	3,4	0,001	PRDX3
P20839	IMPDH1	Inosine-5'-monophosphate dehvdrogenase 1	3.3	0	PRDX3
P30041	PR DX6	Peroxiredoxin-6	3.3	0	PR DX3
0967118	PSMF3IP1	PSMF3.interacting protein	3.2	0	PR DX3
Q/0208	LICDD A D1	USDP1 second anticia 1	2.2	0	DR DX2
Q76EW2	NUDODI	HSPBI-associated protein 1	3,2	0	PRDAS
Q96RS6	NUDCDI	NudC domain-containing protein 1	3,1	0	PRDX3
Q9UEY8	ADD3	Gamma-adducin	3,1	0	PRDX3
Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	3,1	0	PRDX3
Q9UHV9	PFDN2	Prefoldin subunit 2	3	0	PRDX3
Q13547	HDAC1	Histone deacetylase 1	3	0	PRDX3
Q6DKK2	TTC19	Tetratricopeptide repeat protein 19, mitochondrial	3	0,001	PRDX3
P63151	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	3	0,001	PRDX3
043143	DHX15	Pre-mR NA-splicing factor ATP-dependent R NA belicase DHX15	2.9	0	PR DX3
0221/74	L D D EID1	I aurine aich annat flichdass internation materin 1	2,9	0	DR DX2
Q32MZ4	LKKFIFI	Leuchie-rich repeat inghtiess-interacting protein 1	2,9	0	PRDAS
J3QQZ9	PNPO	Pyridoxal 5'-phosphate synthase	2,9	0	PRDX3
A0A024R442	A0A024R442	>tr A0A024R442 A0A024R442_HUMAN Aspartyl aminopeptidase, isoform CRA_b	2,7	0	PRDX3
		OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>sp Q9ULA0 DNPEP_			
		HUMAN Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1			
		SV=1;>tr E7ETB3 E7ETB3_HUMAN Aspartyl aminopeptidase, iso			
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	2,7	0	PRDX3
H0YEN2	PPP6R3	Serine/threonine-protein phosphatase 6 regulatory subunit 3	2,7	0	PRDX3
P10599	TXN	Thioredoxin	2,7	0,002	PRDX3
O99598	TSNAX	Translin-associated protein X	2.6	0	PRDX3
O5ONY5	PEX19	Peroxin-19	2.6	0	PR DX3
090000	LIBE2O	(F3 independent) F2 ubiquitin-conjugating enzyme	2,6	0	DR DY3
Q/C0C/	MAT2A	Colored have been been and an information of the second se	2,5	0	DD DV2
P31155	MAIZA	5-adenosylmethionine synthase isoform type-2	2,5	0	PRDA3
Q92/69	HDAC2	Histone deacetylase 2	2,5	0	PKDX3
A0A2U3TZY2	CLPB	Caseinolytic peptidase B protein homolog	2,5	0,001	PRDX3
A0A087WT45	GRIPAP1	GRIP1-associated protein 1	2,5	0,001	PRDX3
P12955	PEPD	Xaa-Pro dipeptidase	2,5	0,002	PRDX3
Q9C0C2	TNKS1BP1	182 kDa tankyrase-1-binding protein	2,5	0,005	PRDX3
O9BOA1	WDR77	Methylosome protein 50	2,5	0.008	PRDX3
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O8N3X1	FNBP4	Formin-binding protein 4	2,4	0	PRDX3
P62258	YWHAE	14-3-3 protein epsilon	2,4	0	PRDX3
P48147	PREP	Prolyl endopeptidase	2,4	0	PRDX3
H7C3C4	SLC4A7	Anion exchange protein	2.4	0.001	PRDX3
O96DB5	RMDN1	Regulator of microtubule dynamics protein 1	2,4	0.003	PRDX3
Q9BPU6	DPYSL5	Dihydropyrimidinase-related protein 5	2,3	0	PRDX3
Q9Y478	PRKAB1	5'-AMP-activated protein kinase subunit beta-1	2,3	0,001	PRDX3
O8NC51	SER BP1	Plasminogen activator inhibitor 1 RNA-binding protein	2,3	0.001	PRDX3
H0YKU1	TMOD3	Tropomodulin-3	2,3	0,002	PRDX3
P36551	CPOX	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	2,3	0,034	PRDX3
O95831	AIFM1	Apoptosis-inducing factor 1, mitochondrial	2,2	0	PRDX3
Q15276	RABEP1	Rab GTPase-binding effector protein 1	2,2	0	PRDX3
P23526	AHCY	Adenosylhomocysteinase	2,2	0	PRDX3
E7EV99	ADD1	Alpha-adducin	2,1	0	PRDX3
Q9BRP1	PDCD2L	Programmed cell death protein 2-like	2,1	0	PRDX3
Q9NT62	ATG3	Ubiquitin-like-conjugating enzyme ATG3	2,1	0,001	PRDX3
Q9HA64	FN3KRP	Ketosamine-3-kinase	2,1	0,002	PRDX3
013131	PRKAA1	5'-AMP-activated protein kinase catalytic subunit alpha-1	2,1	0.004	PRDX3
P52788	SMS	Spermine synthase	2,1	0,004	PRDX3
A0A0C4DGB5	CAST	Calpain inhibitor	2,1	0,006	PRDX3
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	2	0	PRDX3
015212	PFDN6	Prefoldin subunit 6	2	0	PRDX3
Q9Y3F4	STRAP	Serine-threonine kinase receptor-associated protein	2	0	PRDX3
O96D09	GPRASP2	G-protein coupled receptor-associated sorting protein 2	2	0	PRDX3
P29218	IMPA1	Inositol monophosphatase 1	2	0.004	PRDX3
09Y266	NUDC	Nuclear migration protein nudC	2	0.006	PRDX3
P30044	PRDX5	Peroxiredoxin-5. mitochondrial	13.2	0	PRDX3
A0A1C7CYX9	DPYSL2	Dihydropyrimidinase-related protein 2	1.9	0	PRDX3
015181	PPA1	Inorganic pyrophosphatase	1.9	0	PRDX3
013200	PSMD2	26S proteasome non-ATPase regulatory subunit 2	1.9	0	PRDX3
F5GZS6	SLC3A2	4F2 cell-surface antigen heavy chain	1.9	0.006	PRDX3
O96B36	AKT1S1	Proline-rich AKT1 substrate 1	1.9	0.006	PRDX3
A0A087WXS7	A0A087WXS7	>trlA0A087WXS7lA0A087WXS7_HUMAN ATPase ASNA1 OS=Homo sapiens	1.9	0.008	PRDX3
		OX=9606 GN=ASNA1 PE=1 SV=1;>sp O43681 ASNA_HUMAN ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2;>tr K7ERW9 K7ERW9_ HUMAN Arsenical pumo-driving ATPase (Fragment) OS=Homo sapiens OX=9606 G			
O9NTK5	OLA1	Obg-like ATPase 1	1.9	0.008	PRDX3
013177	PAK2	Serine/threonine-protein kinase PAK 2	1.8	0	PR DX3
013564	NAE1	NEDD8-activating enzyme E1 regulatory subunit	1.8	0	PR DX3
B7Z7F3	R ANBP3	Ran-binding protein 3	1.8	0.004	PR DX3
F8W1A4	AK2	Adenvlate kinase 2. mitochondrial	1.8	0.004	PRDX3
P54619	PRKAG1	5'-AMP-activated protein kinase subunit gamma-1	1.8	0.005	PRDX3
P61758	VBP1	Prefoldin subunit 3	1.8	0.005	PRDX3
H7C128	BR D8	Bromodomain-containing protein 8	1.8	0.006	PRDX3
O9H773	DCTPP1	dCTP pyrophosphatase 1	1.8	0.007	PRDX3
O8IVM0	CCDC50	Coiled-coil domain-containing protein 50	1,8	0.011	PRDX3
Q9UKN8	GTF3C4	General transcription factor 3C polypeptide 4	1,8	0,012	PRDX3
Q9BRS2	RIOK1	Serine/threonine-protein kinase RIO1	1,8	0,012	PRDX3
Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	1,8	0,016	PRDX3
O43164	PJA2	E3 ubiquitin-protein ligase Praja-2	1,7	0	PRDX3
Q5T4U8	RABGGTB	Geranylgeranyl transferase type-2 subunit beta	1,7	0,003	PRDX3
E9PGT1	TON	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		0,005	PRDX3
	15N	Component 3 of promoter of RISC	1,7		
P52888	THOP1	Component 3 of promoter of RISC Thimet oligopeptidase	1,7 1,7	0,005	PRDX3
P52888 P85037	THOP1 FOXK1	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1	1,7 1,7 1,7	0,005	PRDX3 PRDX3
P52888 P85037 Q8N999	THOP1 FOXK1 C12orf29	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29	1,7 1,7 1,7 1,7	0,005 0,006 0,012	PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7	THOP1 FOXK1 C12orf29 FAF1	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1	1,7 1,7 1,7 1,7 1,7 1,7	0,005 0,006 0,012 0,019	PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5	THOP1 FOXK1 C12orf29 FAF1 TACC3	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3	1,7 1,7 1,7 1,7 1,7 1,7 1,7	0,005 0,006 0,012 0,019 0,022	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5 Q96HC4	THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,6	0,005 0,006 0,012 0,019 0,022 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5 Q96HC4 P07195	TSN THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,6 1,6	0,005 0,006 0,012 0,019 0,022 0 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5 Q96HC4 P07195 O75821	TSN THOP1 FOXK1 C12orf29 FAF1 TACC3 PDL1M5 LDHB EIF3G	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,6 1,6 1,6	0,005 0,006 0,012 0,019 0,022 0 0 0 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5 Q96HC4 P07195 O75821 H7BZM7	TSN THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888       P85037       Q8N999       B1ANM7       Q9Y6A5       Q96HC4       P07195       O75821       H7BZM7       P23528	TSN THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5 Q96HC4 P07195 O75821 H7BZM7 P23528 P32119	TSN THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1 PRDX2	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1 Peroxiredoxin-2	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\$	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0,002	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888       P85037       Q8N999       B1ANM7       Q9Y6A5       Q96HC4       P07195       O75821       H7BZM7       P23528       P32119       Q9HB71	TSN THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1 PRDX2 CACYBP	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1 Peroxiredoxin-2 Calcyclin-binding protein	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0,002 0,002	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888         P85037         Q8N999         B1ANM7         Q9Y6A5         Q96HC4         P07195         O75821         H7BZM7         P23528         P32119         Q9HB71         B4DHR0	TSN THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1 PRDX2 CACYBP RABEP2	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1 Peroxiredoxin-2 Calcyclin-binding protein Rab GTPase-binding effector protein 2	1,7 1,7 1,7 1,7 1,7 1,7 1,7 1,6 1,6 1,6 1,6 1,6 1,6 1,6 1,6	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0 0,002 0,002 0,002 0,002 0,013	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888         P85037         Q8N999         B1ANM7         Q9Y6A5         Q96HC4         P07195         O75821         H7BZM7         P23528         P32119         Q9HB71         B4DHR0         P11802	THOP1 FOXK1 Cl2orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1 PRDX2 CACYBP RABEP2 CDK4	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1 Peroxiredoxin-2 Calcyclin-binding protein Rab GTPase-binding effector protein 2 Cyclin-dependent kinase 4	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0 0,002 0,002 0,002 0,002 0,013 0,021	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888         P85037         Q8N999         B1ANM7         Q9Y6A5         Q96HC4         P07195         O75821         H7BZM7         P23528         P32119         Q9HB71         B4DHR0         P11802         P53985	THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1 PRDX2 CACYBP RABEP2 CDK4 SLC16A1	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1 Peroxiredoxin-2 Calcyclin-binding protein Rab GTPase-binding effector protein 2 Cyclin-dependent kinase 4 Monocarboxylate transporter 1	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5 Q96HC4 P07195 O75821 H7BZM7 P23528 P32119 Q9HB71 B4DHR0 P11802 P53985 P45973	THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1 PRDX2 CACYBP RABEP2 CDK4 SLC16A1 CBX5	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1 Peroxiredoxin-2 Calcyclin-binding protein 2 Calcyclin-binding effector protein 2 Cyclin-dependent kinase 4 Monocarboxylate transporter 1 Chromobox protein homolog 5	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3
P52888 P85037 Q8N999 B1ANM7 Q9Y6A5 Q96HC4 P07195 O75821 H7BZM7 P23528 P32119 Q9HB71 B4DHR0 P11802 P53985 P53985 P45973 E5KLJ9	THOP1 FOXK1 C12orf29 FAF1 TACC3 PDLIM5 LDHB EIF3G ZPR1 CFL1 PRDX2 CACYBP RABEP2 CDK4 SLC16A1 CBX5 OPA1	Component 3 of promoter of RISC Thimet oligopeptidase Forkhead box protein K1 Uncharacterized protein C12orf29 FAS-associated factor 1 Transforming acidic coiled-coil-containing protein 3 PDZ and LIM domain protein 5 L-lactate dehydrogenase B chain Eukaryotic translation initiation factor 3 subunit G Zinc finger protein ZPR1 Cofilin-1 Peroxiredoxin-2 Calcyclin-binding effector protein 2 Cyclin-dependent kinase 4 Monocarboxylate transporter 1 Chromobox protein homolog 5 Dynamin-like 120 kDa protein, form S1	$\begin{array}{c} 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,7\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6$	0,005 0,006 0,012 0,019 0,022 0 0 0 0 0 0 0 0 0 0 0 0 0	PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3 PRDX3

P23381	WARS1	TryptophantRNA ligase, cytoplasmic	1,5	0	PRDX3
O43852	CALU	Calumenin	1,5	0,001	PRDX3
P60900	PSMA6	Proteasome subunit alpha type-6	1,5	0,001	PRDX3
O94992	HEXIM1	Protein HEXIM1	1,5	0,002	PRDX3
P27348	YWHAQ	14-3-3 protein theta	1,5	0,005	PRDX3
Q12929	EPS8	Epidermal growth factor receptor kinase substrate 8	1,5	0,03	PRDX3
Q13541	EIF4EBP1	Eukaryotic translation initiation factor 4E-binding protein 1	1,5	0,03	PRDX3
O95825	CRYZL1	Quinone oxidoreductase-like protein 1	1,5	0,034	PRDX3
E9PLK3	NPEPPS	Aminopeptidase	1.4	0	PRDX3
O9NXF7	DCAF16	DDB1- and CUL4-associated factor 16	1.4	0.001	PR DX3
P61981	YWHAG	14-3-3 protein gamma	1.4	0.001	PR DX3
015008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	1.4	0.001	PR DX3
P40222	TYI NA	Alpha-tavilin	1,1	0.004	PR DY 3
D/7985	LIOCE ES1	Cutochtome b.cl. complex subunit Rieske, mitochondrial	1,1	0.008	PR DY 3
D78371	CCT2	T-complex protein 1 subunit beta	1,4	0.011	PR DY 3
00D259	RCC2	Destrice DCC2	1,4	0,011	DR DV2
Q7F256	SCAE11	Protein RCC2	1,4	0,016	PRDA3
F8V AG/	DEDNI		1,4	0,035	PRDX3
ESKGS4	PFDNI	Prefoldin subunit 1	1,4	0,045	PRDX3
C9J019	ZC3HC1	Nuclear-interacting partner of ALK	1,3	0	PRDX3
F8VVL1	DENR	Density-regulated protein	1,3	0	PRDX3
A0A2R8Y811	RPS14	40S ribosomal protein \$14	1,3	0	PRDX3
Q3ZCQ8	TIMM50	Mitochondrial import inner membrane translocase subunit TIM50	1,3	0	PRDX3
P61221	ABCE1	ATP-binding cassette sub-family E member 1	1,3	0	PRDX3
Q06203	PPAT	Amidophosphoribosyltransferase	1,3	0,001	PRDX3
Q9NUQ3	TXLNG	Gamma-taxilin	1,3	0,004	PRDX3
P06748	NPM1	Nucleophosmin	1,3	0,014	PRDX3
Q9NPH2	ISYNA1	Inositol-3-phosphate synthase 1	1,3	0,017	PRDX3
P78356	PIP4K2B	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta	1,3	0,035	PRDX3
P62191	PSMC1	26S proteasome regulatory subunit 4	1,2	0	PRDX3
P63104	YWHAZ	14-3-3 protein zeta/delta	1,2	0	PRDX3
Q9Y230	RUVBL2	RuvB-like 2	1,2	0	PRDX3
O93009	USP7	Ubiquitin carboxyl-terminal hydrolase 7	1.2	0	PRDX3
O9UHY1	NR BP1	Nuclear receptor-binding protein	1.2	0	PRDX3
P62826	RAN	GTP-binding nuclear protein Ran	1.2	0	PR DX3
09Y265	RUVBL1	RuvB-like 1	1.2	0.001	PR DX3
Q94811	LUMC1	BRCA1.A complex subunit R A D80	1,2	0.011	PR DY 3
ONLIBED	SA E1	SUMO activating approve subunit 1	1,2	0.015	DP DV2
D/220/	CDD2	Clusteral 2 phoenhate debudregenese mitochondrial	1,2	0,022	DP DV2
P45504	GPD2 MRCPD	MRC/MORE/L his discusses	1,2	0,022	PRDA3
Q910 V 36	MKGDP	MRG/MORP4L-binding protein	1,2	0,031	PRDA3
P11142	HSPAð		1,1	0	PRDA3
P545/8	USP14	Ubiquitin carboxyl-terminal hydrolase 14	1,1	0,002	PRDX3
Q92598	HSPHI	Heat shock protein 105 kDa	1,1	0,002	PRDX3
P550/2	VCP	I ransitional endoplasmic reticulum A I Pase	1,1	0,006	PRDX3
P34932	HSPA4	Heat shock 70 kDa protein 4	1,1	0,012	PRDX3
A0A087X0K9	TJP1	Tight junction protein ZO-1	1,1	0,016	PRDX3
P05386	RPLP1	60S acidic ribosomal protein P1	1,1	0,016	PRDX3
O00487	PSMD14	26S proteasome non-ATPase regulatory subunit 14	1	0,004	PRDX3
P49321	NASP	Nuclear autoantigenic sperm protein	1	0,018	PRDX3
P31946	YWHAB	14-3-3 protein beta/alpha	1	0,025	PRDX3
Q9UKK9	NUDT5	ADP-sugar pyrophosphatase	1	0,028	PRDX3
Q96RG2	PASK	PAS domain-containing serine/threonine-protein kinase	1	0,035	PRDX3
Q9BRX5	GINS3	DNA replication complex GINS protein PSF3	1	0,037	PRDX3
Q13185	CBX3	Chromobox protein homolog 3	1	0,046	PRDX3
O94776	MTA2	Metastasis-associated protein MTA2	7	0	PRDX4
P49366	DHPS	Deoxyhypusine synthase	6,8	0	PRDX4
P41250	GARS1	GlycinetRNA ligase	5,7	0	PRDX4
P61289	PSME3	Proteasome activator complex subunit 3	5,5	0	PRDX4
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-	5	0	PRDX4
D/2151	DDDDD 2 A	Soring/throoping protein phoephatace 2A 55 kDa regulatory subunit B alpha isoform	4.9	0	DP DV/
D67936	TDM4	Tropomyosin alpha, 4 chain	4.8	0	DR DV4
10//J0 10V/D1	I LUDDI I 2	Tropolityoshi alpha-+ chain	4.2	0	PR DV
	IMPDH2	Description 10	4,2	0	PKDX4
QSQNIS	PEA19	reroxin-19	4	0	PKDX4
Q96KB5	PBK	Lymphokine-activated killer 1-cell-originated protein kinase	3,9	0	PRDX4
Q92769	HDAC2	Histone deacetylase 2	3,7	0	PRDX4
000165	HAX1	HCLS1-associated protein X-1	3,6	0	PRDX4
O14744	PRMT5	Protein arginine N-methyltransferase 5	3,6	0,001	PRDX4
Q96BR5	COA7	Cytochrome c oxidase assembly factor 7	3,5	0	PRDX4
P30041	PRDX6	Peroxiredoxin-6	3,5	0	PRDX4

D5/6/6	DR Κ Δ Δ 2	5' A MP activated protein kinase catalytic subunit alpha 2	3.5	0	DR DY/
OPNOD4	DEDN/4	Desfeldie suburit 4	25	0	DR DV4
01527(	D A DED1	Pierorani subunit 4	25	0	DR DV4
Q132/6	RADEP1	Rab G 1 Pase-bilding effector protein 1	3,3	0	PRDA4
Q9GZU8	PSME5IPI	PSME5-Interacting protein	3,4	0	PRDX4
Q9BSJ8	ESYII	Extended synaptotagmin-1	3,4	0	PRDX4
Q13547	HDAC1	Histone deacetylase 1	3,4	0	PRDX4
Q16576	RBBP7	Histone-binding protein RBBP7	3,4	0	PRDX4
P10599	TXN	Thioredoxin	3,3	0	PRDX4
Q9UHV9	PFDN2	Prefoldin subunit 2	3,3	0	PRDX4
P23526	AHCY	Adenosylhomocysteinase	3,3	0	PRDX4
O43143	DHX15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	3,2	0	PRDX4
Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	3,2	0	PRDX4
130079	PNPO	Pyridoxal 5'-phosphate synthase	3.2	0	PR DX4
06DKK2	TTC19	Tetratricopentide repeat protein 19 mitochondrial	3.2	0.001	PR DX4
A0A024P442	1101/ A0A024P442	Stel A0A024P442IA0A024P442 HUMAN Aspertul aminopentidase isoform CPA h	2.1	0,001	DP DV4
101102410442	10/102+10++2	OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>sp[Q9ULA0 DNPEP_ HUMAN Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1	5,1	Ū	TRDA
		SV=1;>tr E/E1B3 E/E1B3_HUMAN Aspartyl aminopeptidase, iso			
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	3	0	PRDX4
Q96EW2	HSPBAP1	HSPB1-associated protein 1	3	0	PRDX4
P20839	IMPDH1	Inosine-5'-monophosphate dehydrogenase 1	3	0	PRDX4
Q96DB5	RMDN1	Regulator of microtubule dynamics protein 1	3	0,001	PRDX4
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	2,9	0	PRDX4
O9BOA1	WDR77	Methylosome protein 50	2.9	0.003	PR DX4
P42574	CASP3	Caspase-3	2,9	0	PR DX4
000028	D DDD4	Ulistense hin Jine meterin D DDD4	2,0	0	DR DV4
Q09028	RDDP4	Histone-binding protein KDDP4	2,8	0	PRDX4
P4814/	PREP	Prolylendopeptidase	2,8	0	PRDX4
Q96A49	SYAP1	Synapse-associated protein 1	2,8	0,001	PRDX4
A0A2U3TZY2	CLPB	Caseinolytic peptidase B protein homolog	2,8	0,001	PRDX4
P61758	VBP1	Prefoldin subunit 3	2,6	0	PRDX4
O15212	PFDN6	Prefoldin subunit 6	2,6	0	PRDX4
H0YEN2	PPP6R3	Serine/threonine-protein phosphatase 6 regulatory subunit 3	2,6	0	PRDX4
P11802	CDK4	Cyclin-dependent kinase 4	2,6	0,001	PRDX4
P54619	PRKAG1	5'-AMP-activated protein kinase subunit gamma-1	2,6	0,001	PRDX4
094992	HFXIM1	Protein HFXIM1	2.5	0	PR DX4
D(2258	VWLLAE	1/ 2.2 protoin angilon	2,5	0	DP DV4
00114(4	T WITAL	Karana 21 ince	2,5	0 001	PRDA4
Q9HA64	FINSKRP	Ketosamine-3-kinase	2,5	0,001	PRDX4
Q6F181	CIAPINI	Anamorsin	2,5	0,001	PRDX4
P12955	PEPD	Xaa-Pro dipeptidase	2,5	0,002	PRDX4
Q96RS6	NUDCD1	NudC domain-containing protein 1	2,4	0	PRDX4
H7BXI1	ESYT2	Extended synaptotagmin-2	2,4	0	PRDX4
Q99598	TSNAX	Translin-associated protein X	2,4	0	PRDX4
A0A1C7CYX9	DPYSL2	Dihydropyrimidinase-related protein 2	2,4	0	PRDX4
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	2,4	0	PRDX4
E9PGT1	TSN	Component 3 of promoter of RISC	2,4	0,001	PRDX4
O9UEY8	ADD3	Gamma-adducin	2,3	0	PRDX4
08N3X1	FNBP4	Formin-binding protein 4	2.3	0	PR DX4
013564	NAF1	NEDD8-activating enzyme F1 regulatory subunit	2,3	0	PR DY/
012177	DAV2	Serie (herening motin hinter DAK 2	2,5	0	DR DV4
Q131/7	PAK2	Serme/threomne-protein kinase PAK 2	2,5	0	PRDA4
Q913F4	SIKAP	Serine-threeonine kinase receptor-associated protein	2,5	0	PRDX4
Q9BRPI	PDCD2L	Programmed cell death protein 2-like	2,3	0	PRDX4
Q9NPH2	ISYNA1	Inositol-3-phosphate synthase 1	2,3	0,001	PRDX4
P85037	FOXK1	Forkhead box protein K1	2,3	0,001	PRDX4
A0A087WT45	GRIPAP1	GRIP1-associated protein 1	2,3	0,001	PRDX4
Q9Y266	NUDC	Nuclear migration protein nudC	2,3	0,004	PRDX4
P78371	CCT2	T-complex protein 1 subunit beta	2,2	0	PRDX4
F8W1A4	AK2	Adenylate kinase 2, mitochondrial	2,2	0,001	PRDX4
Q5T4U8	RABGGTB	Geranylgeranyl transferase type-2 subunit beta	2,2	0,002	PRDX4
013131	PRKAA1	5'-AMP-activated protein kinase catalytic subunit alpha-1	2.2	0.005	PR DX4
Q10101	SPDI 1	Protein Spindly	2,2	0.008	PR DY/
F7FV99	ADD1	Alpha-adducin	2.1	0	PR DY4
D21152	MAT2A	S adapasel mathianing synthese inform two 2	2,1	0	DD DV4
012200	MAIZA	5-adenosymethionine synthase isoform type-2	2,1	0	PKDA4
Q13200	PSMD2	265 proteasome non-A 1 Pase regulatory subunit 2	2,1	0	PKDX4
H7C3C4	SLC4A7	Anion exchange protein	2,1	0,001	PRDX4
Q9NT62	ATG3	Ubiquitin-like-conjugating enzyme ATG3	2,1	0,001	PRDX4
P52888	THOP1	Thimet oligopeptidase	2,1	0,001	PRDX4
P60900	PSMA6	Proteasome subunit alpha type-6	2,1	0,001	PRDX4
Q9Y478	PRKAB1	5'-AMP-activated protein kinase subunit beta-1	2,1	0,002	PRDX4
H0YKU1	TMOD3	Tropomodulin-3	2,1	0,004	PRDX4
A0A0C4DGB5	CAST	Calpain inhibitor	2.1	0,005	PRDX4
			/		

H7BZM7	ZPR1	Zinc finger protein ZPR1	2	0	PRDX4
P11142	HSPA8	Heat shock cognate 71 kDa protein	2	0	PRDX4
Q9H974	QTRT2	Queuine tRNA-ribosyltransferase accessory subunit 2	2	0,002	PRDX4
Q96RG2	PASK	PAS domain-containing serine/threonine-protein kinase	2	0,003	PRDX4
B7Z7F3	RANBP3	Ran-binding protein 3	2	0,003	PRDX4
P49903	SEPHSI	Selenide, water dikinase 1	2	0,006	PRDX4
P32/88	5M5	Spermine synthase	12.5	0,009	PRDA4
P 50044 D49592	DDM1E	Provincio phorphatase 1E	19,5	0	PRDA4
09RDU6	DPVSI 5	Dibudropyrimidinase-related protein 5	1,9	0	PRDX4
F9DI K3	NPFPPS	Aminopentidase	1,9	0	PR DX4
P23528	CFL1	Cofilin-1	1.9	0	PR DX4
P31689	DNAIA1	Dnal homolog subfamily A member 1	1,9	0.001	PR DX4
P27348	YWHAO	14-3-3 protein theta	1.9	0.001	PR DX4
O8N806	UBR7	Putative E3 ubiquitin-protein ligase UBR7	1,9	0,001	PRDX4
E5KLI9	OPA1	Dynamin-like 120 kDa protein, form S1	1,9	0,001	PRDX4
Q9NV56	MRGBP	MRG/MORF4L-binding protein	1,9	0,002	PRDX4
O43164	PJA2	E3 ubiquitin-protein ligase Praja-2	1,9	0,004	PRDX4
Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	1,9	0,032	PRDX4
Q9C0C2	TNKS1BP1	182 kDa tankyrase-1-binding protein	1,9	0,046	PRDX4
B1AK87	CAPZB	F-actin-capping protein subunit beta	1,8	0	PRDX4
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	1,8	0,003	PRDX4
H7C128	BRD8	Bromodomain-containing protein 8	1,8	0,007	PRDX4
Q9H773	DCTPP1	dCTP pyrophosphatase 1	1,8	0,012	PRDX4
Q9BV44	THUMPD3	THUMP domain-containing protein 3	1,7	0	PRDX4
E7ESY4	MTA1	Metastasis-associated protein MTA1	1,7	0	PRDX4
Q96D09	GPRASP2	G-protein coupled receptor-associated sorting protein 2	1,7	0	PRDX4
P31946	YWHAB	14-3-3 protein beta/alpha	1,7	0,001	PRDX4
P43304	GPD2	Glycerol-3-phosphate dehydrogenase, mitochondrial	1,7	0,008	PRDX4
A0A087WXS7	A0A087WXS7	>tr[A0A087WXS7]A0A087WXS7_HUMAN ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=1;>sp[O43681]ASNA_HUMAN ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2;>tr[K7ERW9 K7ERW9_ HUMAN Arsenical pump-driving ATPase (Fragment) OS=Homo sapiens OX=9606 G	1,7	0,017	PRDX4
Q9UL15	BAG5	BAG family molecular chaperone regulator 5	1,7	0,027	PRDX4
A0A087X0K9	TJP1	Tight junction protein ZO-1	1,6	0	PRDX4
Q15738	NSDHL	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	1,6	0	PRDX4
Q15008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	1,6	0	PRDX4
Q9NXF7	DCAF16	DDB1- and CUL4-associated factor 16	1,6	0,001	PRDX4
P30740	SERPINB1	Leukocyte elastase inhibitor	1,6	0,019	PRDX4
Q9BRS2	RIOK1	Serine/threonine-protein kinase RIO1	1,6	0,024	PRDX4
B4DHR0	RABEP2	Rab GTPase-binding effector protein 2	1,6	0,032	PRDX4
Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	1,6	0,033	PRDX4
A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6	1,6	0,04	PRDX4
Q96K76	USP47	Ubiquitin carboxyl-terminal hydrolase 47	1,5	0	PRDX4
E9PM16	CLNSIA	Chloride channel, nucleotide sensitive 1A	1,5	0	PRDX4
Q06203	PPAI	Amidophosphoribosyltransferase	1,5	0	PRDX4
Q92598	HSPHI	Heat shock protein 105 kDa	1,5	0	PRDX4
D(2101	PSMD14 DSMC1	265 proteasome non-A I Pase regulatory subunit 14	1,5	0	PRDA4
012022	PSMC1 STD N2	265 proteasome regulatory subunit 4	1,5	0	PRDA4
Q15055 D(2104	VWUA7	Striatili-5	1,5	0	PRDA4
D3/932	HSDA/	Heat chock 70 kDa protein /	1,5	0.001	PRDX4
0911669	NUDT5	A DP-sugar pyrophosphatase	1,5	0.001	PR DX4
P35998	PSMC2	26S proteasome regulatory subunit 7	1,5	0.001	PR DX4
A0A0C4DGO6	R PR D1 A	Regulation of nuclear pre-mRNA domain-containing protein 1A	1.5	0.002	PR DX4
095831	AIFM1	Apoptosis-inducing factor 1, mitochondrial	1,5	0.003	PRDX4
0/)0)1		Chromohov protein homolog 2	1.6	-,	PR DX4
Q13185	CBX3		1,5	0,006	1 1(1)/11
Q13185 O95295	CBX3 SNAPIN	SNARE-associated protein Snapin	1,5	0,006	PRDX4
Q13185 O95295 U3KQC1	CBX3 SNAPIN WDR18	SNARE-associated protein Snapin WD repeat-containing protein 18	1,5 1,5 1,5	0,006 0,011 0,017	PRDX4 PRDX4
Q13185 O95295 U3KQC1 Q8N6T3	CBX3 SNAPIN WDR18 ARFGAP1	SNARE-associated protein formous 5 SWD repeat-containing protein 18 ADP-ribosylation factor GTPase-activating protein 1	1,5 1,5 1,5 1,5	0,006 0,011 0,017 0,018	PRDX4 PRDX4 PRDX4 PRDX4
Q13185 O95295 U3KQC1 Q8N6T3 P00492	CBX3 SNAPIN WDR18 ARFGAP1 HPRT1	SNARE-associated protein formous 5 WD repeat-containing protein 18 ADP-ribosylation factor GTPase-activating protein 1 Hypoxanthine-guanine phosphoribosyltransferase	1,5 1,5 1,5 1,5 1,5	0,006 0,011 0,017 0,018 0,019	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
Q13185 O95295 U3KQC1 Q8N6T3 P00492 Q8N999	CBX3 SNAPIN WDR18 ARFGAP1 HPRT1 C12orf29	SNARE-associated protein formoig 5 SNARE-associated protein 18 ADP-ribosylation factor GTPase-activating protein 1 Hypoxanthine-guanine phosphoribosyltransferase Uncharacterized protein C12orf29	1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,006 0,011 0,017 0,018 0,019 0,025	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
Q13185 O95295 U3KQC1 Q8N6T3 P00492 Q8N999 J3KN87	CBX3 SNAPIN WDR18 ARFGAP1 HPRT1 C12orf29 J3KN87	Chronibodx protein holinolog 5 SNARE-associated protein Snapin WD repeat-containing protein 18 ADP-ribosylation factor GTPase-activating protein 1 Hypoxanthine-guanine phosphoribosyltransferase Uncharacterized protein C12orf29 >tr[J3KN87]J3KN87_HUMAN Serine/threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=1;>sp[O14757]CHK1_HUMAN Serine/ threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=2;>tr[E7EPP6]E7EPP6 HUMAN Serine/threonine-protein k	1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,006 0,011 0,017 0,018 0,019 0,025 0,032	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
Q13185 O95295 U3KQC1 Q8N6T3 P00492 Q8N999 J3KN87 P22966	CBX3 SNAPIN WDR18 ARFGAP1 HPRT1 C12orf29 J3KN87 MARCKS	Chroniolox protein homolog 5 SNARE-associated protein Snapin WD repeat-containing protein 18 ADP-ribosylation factor GTPase-activating protein 1 Hypoxanthine-guanine phosphoribosyltransferase Uncharacterized protein C12orf29 >tr[J3KN87[J3KN87_HUMAN Serine/threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=1;>sp[O14757]CHK1_HUMAN Serine/ threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=2;>tr[E7EPP6[E7EPP6_HUMAN Serine/threonine-protein k Myristoylated alanine-rich C-kinase substrate	1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,006 0,011 0,017 0,018 0,019 0,025 0,032	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
Q13185           Q95295           U3KQC1           Q8N6T3           P00492           Q8N999           J3KN87           P29966           Q3ZCQ8	CBX3 SNAPIN WDR18 ARFGAP1 HPRT1 C12orf29 J3KN87 MARCKS TIMM50	Chroniolox protein homolog 5 SNARE-associated protein Snapin WD repeat-containing protein 18 ADP-ribosylation factor GTPase-activating protein 1 Hypoxanthine-guanine phosphoribosyltransferase Uncharacterized protein C12orf29 >tr[J3KN87]J3KN87_HUMAN Serine/threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=1;>sp[O14757]CHK1_HUMAN Serine/ threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=2;>tr[E7EPP6[E7EPP6_HUMAN Serine/threonine-protein k Myristoylated alanine-rich C-kinase substrate Mitochondrial import inner membrane translocase subunit TIM50	1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,006 0,011 0,017 0,018 0,019 0,025 0,032 0,032	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4
Q13185           Q95295           U3KQC1           Q8N6T3           P00492           Q8N999           J3KN87           P29966           Q3ZCQ8           Q9NSD9	CBX3 SNAPIN WDR18 ARFGAP1 HPRT1 C12orf29 J3KN87 MARCKS TIMM50 FARSB	SNARE-associated protein nonholg 5 SNARE-associated protein Snapin WD repeat-containing protein 18 ADP-ribosylation factor GTPase-activating protein 1 Hypoxanthine-guanine phosphoribosyltransferase Uncharacterized protein C12orf29 >tr[J3KN87]J3KN87_HUMAN Serine/threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=1;>sp[O14757]CHK1_HUMAN Serine/ threonine-protein kinase Chk1 OS=Homo sapiens OX=9606 GN=CHEK1 PE=1 SV=2;>tr[E7EPP6[E7EPP6_HUMAN Serine/threonine-protein k Myristoylated alanine-rich C-kinase substrate Mitochoondrial import inner membrane translocase subunit TIM50 PhenylalaninetRNA ligase beta subunit	1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5 1,5	0,006 0,011 0,017 0,018 0,019 0,025 0,032 0,032	PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4 PRDX4

P61981	YWHAG	14-3-3 protein gamma	1,4	0,001	PRDX4
P31930	UQCRC1	Cytochrome b-c1 complex subunit 1, mitochondrial	1,4	0,001	PRDX4
P29218	IMPA1	Inositol monophosphatase 1	1,4	0,004	PRDX4
Q14C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	1,4	0,008	PRDX4
B1ANM7	FAF1	FAS-associated factor 1	1,4	0,039	PRDX4
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	1,4	0,043	PRDX4
P31939	ATIC	Bifunctional purine biosynthesis protein ATIC	1,3	0	PRDX4
Q9Y230	RUVBL2	RuvB-like 2	1,3	0	PRDX4
P23381	WARS1	TryptophantRNA ligase, cytoplasmic	1,3	0	PRDX4
P15104	GLUL	Glutamine synthetase	1,3	0	PRDX4
Q9Y265	RUVBL1	RuvB-like 1	1,3	0,001	PRDX4
C9J0I9	ZC3HC1	Nuclear-interacting partner of ALK	1,3	0,001	PRDX4
P22695	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	1,3	0,003	PRDX4
Q9UJS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	1,3	0,004	PRDX4
P0DMV9	HSPA1B	Heat shock 70 kDa protein 1B	1,3	0,006	PRDX4
Q9UHD1	CHORDC1	Cysteine and histidine-rich domain-containing protein 1	1,3	0,009	PRDX4
O96B36	AKT1S1	Proline-rich AKT1 substrate 1	1,3	0,012	PRDX4
O9H0U4	RAB1B	Ras-related protein Rab-1B	1,3	0,016	PRDX4
I3KN29	PSMD9	26S proteasome non-ATPase regulatory subunit 9	1.3	0,02	PRDX4
P12814	ACTN1	Alpha-actinin-1	1.3	0.035	PRDX4
016204	CCDC6	Coiled-coil domain-containing protein 6	1.3	0.043	PRDX4
P78356	PIP4K2B	Phosphatidylinositol 5-phosphate 4-kinase type-2 heta	13	0.045	PR DX4
P25705	ATP5F1A	ATP synthase subunit alpha mitochondrial	1,3	0	PR DX4
P05023	ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	1.2	0	PR DX4
08WXD5	GEMIN6	Gem-associated protein 6	1.2	0	PR DX4
P20020	ATP2B1	Plasma membrane calcium-transporting ATPase 1	1.2	0.001	PR DX4
P3/897	SHMT2	Serine bydrovymethyltraneferase mitochondrial	1.2	0.005	DR DY/
K7EIO8	HDHD2	Haloacid debalogenase like bydrolase domain containing protein 2	1.2	0,009	DR DY/
P/2771	CDKN24	Cyclin.dependent kingse inhibitor 2 A	1,2	0.01	DR DY4
050PM7	DSME1	Protessome inhibitor PI31 subunit	1,2	0.013	DR DY4
D(2222	PSMC(	26S protossome regulatory subunit 10B	1,2	0.014	DP DV4
D15274	LICHI 2	Libiquitin carboryl terminal hydrolass isograms L2	1,2	0.014	DP DV4
OSIVMO	CCDC50	Coiled coil domain containing protoin 50	1,2	0.022	DP DV4
000231	DSMD11	26S protossome pop ATDese regulatory subunit 11	1,2	0,032	DP DV4
012045	FUI	Distain diskelses 1 homolog	1,2	0,032	DR DV4
Q13043	FADSA	Dhamdalaning AD NA lines alpha subunit	1,1	0	DR DV4
Q/1285	ACADM	Madium ahain masifa and CaA dahudaaanaa mitaahan daid	1,1	0	DR DV4
P11510	DCM1	Dheanhachachachachachachachachachachachachach	1,1	0 001	PRDA4
P 566/1	APCEI	ATD his Jing constants sub family E-member 1	1,1	0,001	PRDA4
P61221	ADCE1		1,1	0,001	PRDA4
P06/33	DSMC5	Alpha-enolase	1,1	0,002	PRDA4
P62173	LDUA	265 proteasonie regulatory subunit 8	1,1	0,002	PRDA4
PU0358		Alamit & DNA adising masterin A and 1	1,1	0,002	PRDA4
Q9B1E6	CPV5	Charmachan materia hamalaa 5	1,1	0,004	PRDA4
P459/3	CDAS		1,1	0,005	PRDX4
043242	PSMD3	265 proteasome non-A I Pase regulatory subunit 3	1,1	0,006	PRDX4
P0/195	LDHB	L-lactate dehydrogenase B chain	1,1	0,007	PRDX4
Q15181	PPAI	Inorganic pyrophosphatase	1,1	0,008	PRDX4
P55072	VCP	Transitional endoplasmic reticulum AT Pase	1,1	0,009	PRDX4
P53985	SLC16A1	Monocarboxylate transporter 1	1,1	0,009	PRDX4
095453	PARN	Poly(A)-specific ribonuclease PARN	1,1	0,01	PRDX4
P05386	RPLP1	60S acidic ribosomal protein P1	1,1	0,015	PRDX4
P52907	CAPZA1	F-actin-capping protein subunit alpha-1	1,1	0,017	PRDX4
Q9HB71	CACYBP	Calcyclin-binding protein	1,1	0,022	PRDX4
P49321	NASP	Nuclear autoantigenic sperm protein	1,1	0,023	PRDX4
Q99536	VAT1	Synaptic vesicle membrane protein VAT-1 homolog	1	0,001	PRDX4
O60884	DNAJA2	DnaJ homolog subfamily A member 2	1	0,001	PRDX4
Q99460	PSMD1	26S proteasome non-ATPase regulatory subunit 1	1	0,003	PRDX4
Q8NBU5	ATAD1	ATPase family AAA domain-containing protein 1	1	0,029	PRDX4

## Table S3: peroxidatic cysteine-dependent interactors ( $C_{R}S$ )

uniprot ID PRDX1 cysteine-de	gene pendent interactors	protein	log ratio	p-value
Q53H12	AGK	Acylglycerol kinase, mitochondrial	4,1	< 0.001
075531	BANF1	Barrier-to-autointegration factor	3,9	< 0.001
P27824	CANX	Calnexin	3,7	< 0.001
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	3,4	0,001
P68133	ACTA1	Actin, alpha skeletal muscle	3,4	0,006
A0A024R4E5	HDLBP	High density lipoprotein binding protein	3,3	< 0.001
P55084	HADHB	Trifunctional enzyme subunit beta, mitochondrial	3,3	< 0.001
O9NY93	DDX56	Probable ATP-dependent RNA helicase DDX56	3.3	0.001
O9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	3.2	< 0.001
O9UHV9	PFDN2	Prefoldin subunit 2	3.2	< 0.001
P55735	SEC13	Protein SEC13 homolog	3.2	0.001
P43897	TSFM	Flongation factor Ts mitochondrial	3.2	0.001
P21964	COMT	Catechol O-methyltransferase	3.2	0.001
P62316	SNR PD2	Small nuclear ribonucleon ratein Sm D2	3.1	<0.001
P53621	COPA	Contomer subunit alpha	3.1	<0.001
06P587	FAHD1	Acylpyruwse FAHD1 mitochondrial	3.1	0.001
001081	LI2 A F1	Splicing factor I/2 A F 35 kDa subunit	3.1	0.006
Q01001	LADS1	Lausing a PNA lises autoplasmic	2	<0.001
Q7P2J5	LAKSI	LeucinetRINA ligase, cytoplasmic		<0.001
P06132	D ANDD2	D li li contra c	3	0,009
B/Z/F3	KANBP3	Kan-binding protein 3	2,9	<0.001
Q16513	PKN2	Serine/threonine-protein kinase N2	2,9	0,003
Q15654	TRIP6	I hyroid receptor-interacting protein 6	2,9	0,003
O00148	DDX39A	A I P-dependent RNA helicase DDX 39A	2,9	0,008
P35268	RPL22	60S ribosomal protein L22	2,8	< 0.001
C9JZR2	CTNND1	Catenin delta-1	2,8	< 0.001
P62829	RPL23	60S ribosomal protein L23	2,8	< 0.001
Q86V48	LUZP1	Leucine zipper protein 1	2,8	< 0.001
P24666	ACP1	Low molecular weight phosphotyrosine protein phosphatase	2,8	0,001
Q9C0C2	TNKS1BP1	182 kDa tankyrase-1-binding protein	2,8	0,001
O14744	PRMT5	Protein arginine N-methyltransferase 5	2,8	0,002
Q96DH6	MSI2	RNA-binding protein Musashi homolog 2	2,8	0,003
Q15149	PLEC	Plectin	2,8	0,004
E7ETK0	RPS24	40S ribosomal protein S24	2,8	0,004
P39023	RPL3	60S ribosomal protein L3	2,7	< 0.001
Q7Z406	MYH14	Myosin-14	2,7	< 0.001
Q06124	PTPN11	Tyrosine-protein phosphatase non-receptor type 11	2,7	< 0.001
Q9UHB6	LIMA1	LIM domain and actin-binding protein 1	2,7	< 0.001
P52788	SMS	Spermine synthase	2,7	0,001
P27694	RPA1	Replication protein A 70 kDa DNA-binding subunit	2,7	0,002
Q9Y262	EIF3L	Eukaryotic translation initiation factor 3 subunit L	2,7	0,013
A0A087WTZ5	UBXN1	UBX domain-containing protein 1	2,6	< 0.001
O94979	SEC31A	Protein transport protein Sec31A	2,6	< 0.001
P48634	PR RC2A	Protein PR R C 2 A	2.6	<0.001
P31689	DNAIA1	DnaI homolog subfamily A member 1	2.6	< 0.001
F7FX90	DCTN1	Dynactin subunit 1	2.6	0.002
D51/52	DUSP3	Dynactin subdinit 1	2,0	0.004
0967T3	SI IR P	SR A stem-loop-interacting R NA-binding protein mitochondrial	2,0	0.005
0994(0	DSMD1	2/S protocomo non ATDeco regulatory orbunit 1	2,0	0,005
Q))460	P A P11FID1	265 proteasonie non-A i Pase regulatory subunit i	2,6	0,003
Q6WKZ4	RADIIFIPI FODAC	Rabii ramiiy-interacting protein 1	2,6	0,006
Q5V1K3	ECPAS	Proteasome adapter and scatfold protein ECM29	2,6	0,007
Q96ACI	FERM12	Permitin ramity homolog 2	2,6	0,009
043143	DHX15	Pre-mKNA-splicing factor ATP-dependent KNA helicase DHX15	2,6	0,009
095373	IPO7	Importin-7	2,6	0,01
Q8IWZ3	ANKHD1	Ankyrin repeat and KH domain-containing protein 1	2,5	< 0.001
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	2,5	< 0.001
P48444	ARCN1	Coatomer subunit delta	2,5	< 0.001
P62258	YWHAE	14-3-3 protein epsilon	2,5	< 0.001
Q13185	CBX3	Chromobox protein homolog 3	2,5	< 0.001
Q15075	EEA1	Early endosome antigen 1	2,5	0,01
P11387	TOP1	DNA topoisomerase 1	2,5	0,011
Q5SW79	CEP170	Centrosomal protein of 170 kDa	2,4	< 0.001
Q9BSH4	TACO1	Translational activator of cytochrome c oxidase 1	2,4	< 0.001
P15170	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	2,4	< 0.001
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	2,4	< 0.001
Q14204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	2,4	0,001
P15924	DSP	Desmoplakin	2,4	0,002
O95747	OXSR1	Serine/threonine-protein kinase OSR1	2.4	0,005
O6IAA8	LAMTOR 1	Ragulator complex protein LAMTOR1	2 4	0.006
Xuiiiio	LITTLE CIVI		2,T	0,000

P08559	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	2,4	0,006
Q9Y5Y2	NUBP2	Cytosolic Fe-S cluster assembly factor NUBP2	2,4	0,009
Q12948	FOXC1	Forkhead box protein C1	2,4	0,011
Q8TAT6	NPLOC4	Nuclear protein localization protein 4 homolog	2,4	0,014
Q51701	GTF3C5	General transcription factor 3C polypeptide 5	2,3	<0.001
Q/262/ 01/2/7	CTTN	ES ubiquitin-protein ligase FLO W E1	2,3	<0.001
Q1424/ Q9UHB9	SR P68	Signal recognition particle subunit SR P68	2,3	0.001
Q9BO67	GRWD1	Glutamate-rich WD repeat-containing protein 1	2,3	0.002
A0A087WZ13	RAVER1	Ribonucleoprotein PTB-binding 1	2,3	0,003
P19525	EIF2AK2	Interferon-induced, double-stranded RNA-activated protein kinase	2,3	0,009
A0A087X1A5	STAU1	Double-stranded RNA-binding protein Staufen homolog 1	2,3	0,011
Q9NP97	DYNLRB1	Dynein light chain roadblock-type 1	2,3	0,014
P27708	CAD	CAD protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase	2,3	0,017
Q9BYG3	NIFK	MKI67 FHA domain-interacting nucleolar phosphoprotein	2,3	0,02
Q15061	WDR43	WD repeat-containing protein 43	2,3	0,025
E5RGR0	LYPLA1	Acyl-protein thioesterase 1	2,3	0,049
P41252	IARS1	IsoleucinetRNA ligase, cytoplasmic	2,2	< 0.001
P35658	NUP214	Nuclear pore complex protein Nup214	2,2	< 0.001
Q90G54	MAP3K/	Mitogen-activated protein kinase kinase	2,2	<0.001
P55809	DACII D D D1 D	Succinyl-CoA:5-ketoacid coenzyme A transferase 1, mitochondrial	2,2	0,001
D39748	FEN1	Flap endopyclesse 1	2,2	0.002
P37108	SR P14	Signal recognition particle 14 kDa protein	2,2	0.008
F5H6F2	MYO1C	Unconventional myosin-Ic	2,2	0.01
P13807	GYSI	Glycopen [starch] synthase, muscle	2.2	0.013
O8WUH6	TMEM263	Transmembrane protein 263	2,2	0,015
Q43795	MYO1B	Unconventional myosin-Ib	2,2	0,016
075663	TIPRL	TIP41-like protein	2,2	0,018
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	2,2	0,03
E9PF10	NUP155	Nuclear pore complex protein Nup155	2,2	0,032
E9PDU5	WDR6	WD repeat-containing protein 6	2,1	< 0.001
Q5T6F2	UBAP2	Ubiquitin-associated protein 2	2,1	< 0.001
P22307	SCP2	Non-specific lipid-transfer protein	2,1	0,001
Q9Y6Y8	SEC23IP	SEC23-interacting protein	2,1	0,001
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	2,1	0,001
Q9BSJ8	ESYT1	Extended synaptotagmin-1	2,1	0,002
O75436	VPS26A	Vacuolar protein sorting-associated protein 26A	2,1	0,003
Q9UQE7	SMC3	Structural maintenance of chromosomes protein 3	2,1	0,007
P35579	MYH9	Myosin-9	2,1	0,012
Q92797	SYMPK	Symplekin	2,1	0,015
0/58/4	TRCIDIOR	TRC1 denvis fumile much as 10P	2,1	0,018
Q4KMP/ Q7L0V3	TRMT10C	T DC1 domain ramily memoer 10D	2,1	0.02
016822	PCK2	Phosphoenolpyruwate carboxykinase [GTP]_mitochondria]	2,1	0.021
007021	CIOBP	Complement component 1 O subcomponent-binding protein mitochondrial	2,1	0.021
P29144	TPP2	Tripeptidyl-peptidase 2	2,1	0,023
015645	TRIP13	Pachytene checkpoint protein 2 homolog	2,1	0,025
Q8NCA5	FAM98A	Protein FAM98A	2,1	0,026
P50542	PEX5	Peroxisomal targeting signal 1 receptor	2,1	0,028
Q9HD26	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein	2,1	0,048
Q9Y2R4	DDX52	Probable ATP-dependent RNA helicase DDX52	2,1	0,049
Q9UNE7	STUB1	E3 ubiquitin-protein ligase CHIP	2	< 0.001
Q14166	TTLL12	Tubulintyrosine ligase-like protein 12	2	< 0.001
Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	2	< 0.001
Q14157	UBAP2L	Ubiquitin-associated protein 2-like	2	< 0.001
P63272	SUPT4H1	Transcription elongation factor SPT4	2	0,001
P08708	RPS17	40S ribosomal protein S17	2	0,001
P30520	ADSS2	Adenylosuccinate synthetase isozyme 2	2	0,001
AUAU8/WVM4	COPOIC	Consistent of the constant of	2	0,001
Q90LV4	COROIC CD DE 4	Coronin-IC Sing development ide 54 hDe mentric	2	0,002
O9UKD2	MRTO/	mR NA turnover protein / homolog	2	0,005
014683	SMC1A	Structural maintenance of chromosomes protein 1 A	2	0.005
P42704	LR PPR C	Leucine-rich PPR motif.containing protein mitochondrial	2	0.007
Q9H0C8	ILKAP	Integrin-linked kinase-associated serine/threonine phosphatase 2C.	2	0.007
O14929	HAT1	Histone acetyltransferase type B catalytic subunit	2	0,008
Q86VP6	CAND1	Cullin-associated NEDD8-dissociated protein 1	2	0,014
P11388	TOP2A	DNA topoisomerase 2-alpha	2	0,015
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	2	0,016
Q13144	EIF2B5	Translation initiation factor eIF-2B subunit epsilon	2	0,017
P34949	MPI	Mannose-6-phosphate isomerase	2	0,018
O43660	PLRG1	Pleiotropic regulator 1	2	0,024

Q15750	TAB1	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	2	0,026
P23258	TUBG1	Tubulin gamma-1 chain	2	0,029
G3V1C3	API5	Apoptosis inhibitor 5	2	0,035
Q9H840	GEMIN7	Gem-associated protein 7	2	0,048
Q16204	CCDC6	Coiled-coil domain-containing protein 6	2	0,048
P19105	MYL12A DCARL	Myosin regulatory light chain 12A	2	0,049
Q9NXF/	DCAFI6	DDBI- and CUL4-associated factor 16	1,9	<0.001
E/EVA0	MAP4	Microtubule-associated protein	1,9	<0.001
Q90HDI D40221	NASP	Cysteine and histidine-rich domain-containing protein 1	1,9	<0.001
P47521	NASP SLC(ALAD	Nuclear autoantigenic sperm protein	1,7	<0.001
AUAU8/AUM4	SLC4AIAP VDM2R	Kanadaptin	1,7	<0.001
Q/LDC6	ENAL	Directoin enchlod homolog	1,7	<0.001
D48643	CCT5	T complex protein 1 subunit encilon	1,9	<0.001
OSND83	SLAIN1	SLAIN motif containing protein 1	1,9	<0.001
060784	TOM1	Target of Myb protein 1	1,9	0.001
P00568	AK1	Adenvlate kinase isoenzyme 1	1,9	0.001
0%GD0	PDXP	Pyridoxal phosphate phosphatase	1,9	0.001
075832	PSMD10	26S proteasome non-ATPase regulatory subunit 10	1.9	0.001
P57740	NUP107	Nuclear pore complex protein Nup107	1.9	0.002
P46459	NSF	Vesicle-fusing ATPase	1.9	0.002
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	1.9	0,003
O43837	IDH3B	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	1,9	0,004
P33991	MCM4	DNA replication licensing factor MCM4	1,9	0,007
E7ESP9	NEFM	160 kDa neurofilament protein	1,9	0,008
Q9Y3I0	RTCB	RNA-splicing ligase RtcB homolog	1,9	0,008
O43719	HTATSF1	HIV Tat-specific factor 1	1,9	0,009
O00399	DCTN6	Dynactin subunit 6	1,9	0,01
Q9Y2L1	DIS3	Exosome complex exonuclease RRP44	1,9	0,015
Q9Y2V2	CARHSP1	Calcium-regulated heat-stable protein 1	1,9	0,015
H3BPE1	MACF1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	1,9	0,016
Q9NQ88	TIGAR	Fructose-2,6-bisphosphatase TIGAR	1,9	0,027
P09110	ACAA1	3-ketoacyl-CoA thiolase, peroxisomal	1,9	0,028
P23919	DTYMK	Thymidylate kinase	1,9	0,029
E9PLK3	NPEPPS	Aminopeptidase	1,9	0,031
P46940	IQGAP1	Ras GTPase-activating-like protein IQGAP1	1,9	0,034
P40939	HADHA	Trifunctional enzyme subunit alpha, mitochondrial	1,9	0,038
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	1,9	0,039
P40222	TXLNA	Alpha-taxilin	1,9	0,041
E9PKP7	UBTF	Nucleolar transcription factor 1	1,9	0,043
O00487	PSMD14	26S proteasome non-ATPase regulatory subunit 14	1,9	0,045
P62333	PSMC6	26S proteasome regulatory subunit 10B	1,8	< 0.001
E7EPN9	PRRC2C	Protein PRRC2C	1,8	< 0.001
B1AK87	CAPZB	F-actin-capping protein subunit beta	1,8	< 0.001
Q9BQ69	MACROD1	ADP-ribose glycohydrolase MACROD1	1,8	< 0.001
Q14126	DSG2	Desmoglein-2	1,8	< 0.001
P46776	RPL27A	60S ribosomal protein L27a	1,8	< 0.001
P13861	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory subunit	1,8	< 0.001
Q13428	TCOF1	Treacle protein	1,8	0,001
A0A3B3IRI2	CTPS1	CTP synthase	1,8	0,001
P62753	RPS6	40S ribosomal protein S6	1,8	0,001
A0A3B3IRP5	CDC73	Parafibromin	1,8	0,002
P11802	CDK4	Cyclin-dependent kinase 4	1,8	0,003
B4DDF4	CNN2	Calponin	1,8	0,003
Q9UPN7	PPP6R1	Serine/threonine-protein phosphatase 6 regulatory subunit 1	1,8	0,003
P43490	NAMPT	Nicotinamide phosphoribosyltransferase	1,8	0,003
P49790	NUP153	Nuclear pore complex protein Nup153	1,8	0,004
Q13561	DCTN2	Dynactin subunit 2	1,8	0,005
Q9BZE4	GTPBP4	Nucleolar GTP-binding protein 1	1,8	0,005
O00154	ACOT7	Cytosolic acyl coenzyme A thioester hydrolase	1,8	0,006
M0QXL5	FBL	rRNA 2'-O-methyltransferase fibrillarin	1,8	0,008
Q6P2E9	EDC4	Enhancer of mRNA-decapping protein 4	1,8	0,008
Q14152	EIF3A	Eukaryotic translation initiation factor 3 subunit A	1,8	0,009
Q9BV P2	GNL3	Guanine nucleotide-binding protein-like 3	1,8	0,013
Q99959	PKP2	Plakophilin-2	1,8	0,017
Q14008	CKAP5	Cytoskeleton-associated protein 5	1,8	0,017
P25205	MCM3	DNA replication licensing factor MCM3	1,8	0,022
Q9NQX3	GPHN	Gephyrin [Includes: Molybdopterin adenylyltransferase	1,8	0,026
P82673	MRPS35	285 ribosomal protein 535, mitochondrial	1,8	0,03
P52594	AGFG1	Art-GAP domain and FG repeat-containing protein 1	1,8	0,034
Q15084	PDIA6	Protein disulfide-isomerase A6	1,8	0,036
Q6P9B6	MEAK7	M I OR-associated protein MEAK7	1,8	0,036
Q9BR76	CORO1B	Coronin-1B	1,8	0,037

O60832	DKC1	H/ACA ribonucleoprotein complex subunit DKC1	1,8	0,037
Q92973	TNPO1	Transportin-1	1,8	0,04
P30154	PPP2R1B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	1,8	0,041
O76021	RSL1D1	Ribosomal L1 domain-containing protein 1	1.8	0,05
O6PKG0	LAR P1	La-related protein 1	17	<0.001
QOPW20	MD I1	Mathulthiasibase 1 phoenhate isomorese	1.7	<0.001
Q75V20	CR622	LIDE0.688 martine Country	1,7	<0.001
Q9H/E9	C80ff 33	UPP0488 protein C8orr35	1,/	<0.001
Q00796	SORD	Sorbitol dehydrogenase	1,7	< 0.001
Q9H0B6	KLC2	Kinesin light chain 2	1,7	0,001
X1WI28	RPL10	60S ribosomal protein L10	1,7	0,001
P30566	ADSL	Adenylosuccinate lyase	1,7	0,001
O99497	PARK7	Parkinson disease protein 7	1.7	0,002
P51553	IDH3G	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	1.7	0.002
P12004	DCNA	Droliferating cell puclear antigen	1.7	0.002
P12004	FCNA 6T12	Fiomerating cen indices and gen	1,7	0,002
P50502	5113	Hsc/0-interacting protein	1,7	0,002
Q99615	DNAJC7	DnaJ homolog subfamily C member 7	1,7	0,003
O60684	KPNA6	Importin subunit alpha-7	1,7	0,004
Q14694	USP10	Ubiquitin carboxyl-terminal hydrolase 10	1,7	0,004
Q15417	CNN3	Calponin-3	1,7	0,005
Q9UG63	ABCF2	ATP-binding cassette sub-family F member 2	1,7	0,006
O9UHI6	DDX20	Probable ATP-dependent RNA helicase DDX20	1.7	0,006
000178	GTPBP1	GTP-binding protein 1	17	0.006
015160	POL R 1C	DNA directed R NA polymerases I and III subunit R DAC1	1.7	0.006
D/(0(0	D ANCADI		1,7	0,000
P46060	KANGAPI	Kan G I Pase-activating protein 1	1,7	0,012
Q92667	AKAP1	A-kinase anchor protein 1, mitochondrial	1,7	0,014
Q8IY81	FTSJ3	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3	1,7	0,016
Q12849	GRSF1	G-rich sequence factor 1	1,7	0,018
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	1,7	0,022
O75533	SF3B1	Splicing factor 3B subunit 1	1,7	0,029
A0A0A0MRT6	ABI1	Abl interactor 1	1.7	0.03
098283	NOP58	Nucleolar protein 58	1.7	0.032
Q/12AJ	MIE	Marconal protein 38	1,7	0,032
P141/4	MIF	Macrophage migration inhibitory ractor	1,/	0,035
P62906	RPL10A	60S ribosomal protein L10a	1,7	0,043
Q9UGV2	NDRG3	Protein NDRG3	1,7	0,045
Q96P70	IPO9	Importin-9	1,7	0,048
Q3ZCQ8	TIMM50	Mitochondrial import inner membrane translocase subunit TIM50	1,7	0,048
A0A0C4DGQ6	RPRD1A	Regulation of nuclear pre-mRNA domain-containing protein 1A	1,6	< 0.001
O95816	BAG2	BAG family molecular chaperone regulator 2	1.6	< 0.001
012955	ANK3	Ankvrin-3	16	<0.001
0755(0	DRVRJ	The second state of the se	1,0	(0.001
0/5569	PKKKA	D L ( Q) L L L	1,6	<0.001
Q15365	PCBP1	Poly(rC)-binding protein 1	1,6	<0.001
09U080		Proliferation-associated protein 2G4		< 0.001
0.0	PA2G4		1,6	
P13797	PA2G4 PLS3	Plastin-3	1,6 1,6	< 0.001
P13797 Q9BTE6	PA2G4 PLS3 AARSD1	Plastin-3 Alanyl-tRNA editing protein Aarsd1	1,6 1,6 1,6	<0.001 <0.001
P13797 Q9BTE6 Q9UNY4	PA2G4 PLS3 AARSD1 TTF2	Plastin-3 Alanyl-tRNA editing protein Aarsd1 Transcription termination factor 2	1,6 1,6 1,6 1,6	<0.001 <0.001 0,001
P13797 Q9BTE6 Q9UNY4 P33993	PA2G4 PLS3 AARSD1 TTF2 MCM7	Plastin-3 Alanyl-tRNA editing protein AarsdI Transcription termination factor 2 DNA replication licensing factor MCM7	1,6 1,6 1,6 1,6 1,6	<0.001 <0.001 0,001 0,001
P13797 Q9BTE6 Q9UNY4 P33993 Q00170	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP	Plastin-3 Alanyl-tRNA editing protein Aarsd1 Transcription termination factor 2 DNA replication licensing factor MCM7 AH receptor-interacting protein	1,6 1,6 1,6 1,6 1,6 1,6	<0.001 <0.001 0,001 0,001 0.002
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R 1A	Plastin-3 Alanyl-tRNA editing protein Aarsd1 Transcription termination factor 2 DNA replication licensing factor MCM7 AH receptor-interacting protein Series (hreceptor-interacting protein	1,6 1,6 1,6 1,6 1,6 1,6 1,6	<0.001 <0.001 0,001 0,001 0,002
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A EAPD5	Plastin-3 Alanyl-tRNA editing protein Aarsd1 Transcription termination factor 2 DNA replication licensing factor MCM7 AH receptor-interacting protein Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	1,6 1,6 1,6 1,6 1,6 1,6 1,6	<0.001 <0.001 0,001 0,002 0,002
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           O021002	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5	Plastin-3 Alanyl-tRNA editing protein Aarsd1 Transcription termination factor 2 DNA replication licensing factor MCM7 AH receptor-interacting protein Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform Fatty acid-binding protein 5	1,6 1,6	<0.001 <0.001 0,001 0,002 0,002 0,002
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,002 0,003
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,002 0,003 0,003
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68	PA2G4           PLS3           AARSD1           TTF2           MCM7           AIP           PPP2R1A           FABP5           SLK           RPS8           SERBP1           DIAPH1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q0H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1 DIAPH1 PSPC1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,004
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A040G2JH68           Q8WXF1           Q8IWX8	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1 DIAPH1 PSPC1 CHERP	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein	$ \begin{array}{c c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P49588	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RP58 SERBP1 DIAPH1 PSPC1 CHERP AARS1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P49588           P53618	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1 DIAPH1 PSPC1 CHERP AARS1 COPB1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P49588           P53618           OSCOCO	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1 DIAPH1 PSPC1 CHERP AARS1 COPB1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         Alanine-tRNA ligase, cytoplasmic         Coatomer subunit beta	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           D9C26	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1 DIAPH1 PSPC1 CHERP AARS1 COPB1 UBE2O	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,005
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2]H68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           P26368	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1 DIAPH1 PSPC1 CHERP AARS1 COPB1 UBE2O U2AF2	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threconine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threconine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,005 0,006
Q13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8WXS8           P49588           P53618           Q9C0C9           P26368           Q15185	PA2G4 PLS3 AARSD1 TTF2 MCM7 AIP PPP2R1A FABP5 SLK RPS8 SERBP1 DIAPH1 PSPC1 CHERP AARS1 COPB1 UBE2O U2AF2 PTGES3 CONTER	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,005 0,006 0,006
Q13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2]H68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2	$\begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P45588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q9BUF5	PA2G4           PLS3           AARSD1           TTF2           MCM7           AIP           PPP2R1A           FABP5           SLK           RPS8           SERBP1           DIAPH1           PSPC1           CHERP           AARS1           COPB1           UBE2O           U2AF2           PTGES3           DPYSL2           TUBB6	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2]H68           Q8WXF1           Q8WXF1           Q8WXS           P45588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q9BUF5           Q9Y450	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropryrimidinase-related protein 2         Tubulin beta-echain         HBS1-like protein	1,6     1,6	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,008
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8WXF1           Q8WX8           P49588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q9BUF5           Q9Y450           P40937	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5	1,6     1,6	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,008 0,009
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P45888           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q98UF5           Q97450           P47897	PA2G4           PLS3           AARSD1           TTF2           MCM7           AIP           PPP2R1A           FABP5           SLK           RPS8           SERBP1           DIAPH1           PSPC1           CHERP           AARS1           COPB1           UBE2O           U2AF2           PTGES3           DPYSL2           TUBB6           HBS1L           RFC5           OARS1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,008 0,009 0,009
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q9BUF5           Q9Y450           P40937           P47897           P09543	PA2G4           PLS3           AARSD1           TTF2           MCM7           AIP           PPP2R1A           FABP5           SLK           RPS8           SERBP1           DIAPH1           PSPC1           CHERP           AARS1           COPB1           UBE2O           U2AF2           PTGES3           DPYSL2           TUBB6           HBS1L           RFC5           QARS1           CNP	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2'. 3'-cryclic-nucleotide 3'-phosphodiesterase	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,008 0,009 0,009 0,001
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2]H68           Q8WXF1           Q8WXF1           Q8WXF3           P45588           P53618           Q9C0C9           P26368           Q155           Q9Y450           P40937           P47897           P09543           Oewuvy3	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         DP DE 11	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropryrimidinase-related protein 2         Tubulin beta-e chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2',3'-cyclic-nucleotide 3'-phosphodiesterase         L'A' Ll' Comul In udaes ribourcleaoprotein Pro*2'	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,008 0,009 0,009 0,01
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2]H68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           P26368           Q15185           A0A1c7CYX9           Q9BUF5           Q9Y450           P40937           P47897           P09543           Q8WWY3	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         PRPF31	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2',3'-cyclic-nucleotid 3'-phosphodiesterase         U4/U6 small nuclear ribonucleoprotein Prp31	$ \begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,006 0,008 0,009 0,009 0,01 0,01 0,01 0,01 0,01 0,01 0,01 0,01 0,01 0,01 0,002 0,002 0,002 0,002 0,002 0,002 0,002 0,002 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,006 0,007 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,007 0,007 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,007 0,007 0,007 0,007 0,006 0,006 0,007 0,0
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8WXF1           Q8UX58           P45588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q98UF5           Q97450           P40937           P47897           P09543           Q8WWY3           Q43395           Q43395	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         PRPF31         PRPF31	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta - 6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2',3'-cyclic-nucleotid 3'-phosphodiesterase         U4/U6 small nuclear ribonucleoprotein Prp3         TUR tier	1,6     1,6	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,006 0,006 0,006 0,006 0,008 0,009 0,009 0,001 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,011 0,002 0,002 0,002 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,006 0,007 0,006 0,006 0,006 0,007 0,006 0,006 0,007 0,007 0,007 0,006 0,006 0,007 0,007 0,007 0,007 0,006 0,006 0,007 0,007 0,007 0,007 0,007 0,007 0,006 0,007
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2]H68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q9BUF5           Q9Y450           P40937           P47897           P09543           Q8WWY3           O43395           Q2TAY7	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         PRPF31         PRPF3         SMU1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2',3'-cyclic-nucleotide 3'-phosphodiesterase         U4/U6 small nuclear ribonucleoprotein Prp31         U4/U6 small nuclear ribonucleoprotein Prp3         WD40 repeat-containing protein SMU1	1,6     1,6	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,006 0,008 0,009 0,009 0,01 0,011 0,012
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2]H68           Q8WXF1           Q8WXF1           Q8WXF3           P45588           P53618           Q9C0C9           P26368           Q1555           Q9Y450           P40937           P47897           P09543           Q8WWY3           Q43395           Q2TAY7           Q95861	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         PRPF31         PRPF3         SMU1         BPNT1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein S8         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropryrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2',3'-cyclic-nucleotide 3'-phosphodiesterase         2',3'-cyclic-nucleotide 3'-phosphodiesterase         2',3'-cyclic-nucleotide 3'-phosphodiesterase         2',3'-cyclic-nucleotide 3'-phosphodiesterase         2',3'-cyclic-nucleotide 3'-phosphodiesterase         2',3'-cyclic-nucleotide 3'-phosphodiesterase	$\begin{array}{c} 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\ 1,6\\$	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,006 0,008 0,009 0,009 0,011 0,011 0,012 0,014
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           P263668           Q15185           A0A1C7CYX9           Q9BUF5           Q9Y450           P40937           P47897           P05543           Q8TMY3           O43395           Q2TAY7           O95861           Q5JRX3	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         PRPF31         PRPF3         SMU1         BPNT1         PITRM1	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2; 3'-cyclic-nucleotide 3'-phosphodiesterase         U4/U6 small nuclear ribonucleoprotein Prp31         U4/U6 small nuclear ribonucleoprotein Prp3         WD40 repeat-containing protein SMU1         3'(2'),5'-bisphosphate nucleotidase 1         Presequence protease, mitochondrial	1,6     1,6	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,006 0,006 0,009 0,009 0,001 0,011 0,012 0,014 0,014
P13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8WXF1           Q8UX58           P49588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q98UF5           Q97450           P40937           P40937           P47897           P09543           Q8WWY3           Q43395           Q2TAY7           Q95861           Q5JRX3           Q75152	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         PRPF31         PRPF3         SMU1         BPNT1         PITRM1         ZC3H11A	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2', 3'-cyclic-nucleotid 3'-phosphodiesterase         U4/U6 small nuclear ribonucleoprotein Prp31         U4/U6 small nuclear ribonucleoprotein Prp3         WD40 repeat-containing protein SMU1         3'(2'),5'-bisphosphate nucleotidase 1         Presequence protease, mitochondrial         Zi	1,6     1,6	<0.001 <0.001 0,001 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,006 0,006 0,006 0,006 0,006 0,008 0,009 0,009 0,009 0,001 0,011 0,014 0,014 0,015
Q13797           Q9BTE6           Q9UNY4           P33993           O00170           P30153           Q01469           Q9H2G2           P62241           Q8NC51           A0A0G2JH68           Q8WXF1           Q8IWX8           P49588           P53618           Q9C0C9           P26368           Q15185           A0A1C7CYX9           Q9BUF5           Q9Y450           P40937           P47897           P05543           Q8WWY3           O43395           Q2TAY7           O55861           Q5JRX3           O75152           O75131	PA2G4         PLS3         AARSD1         TTF2         MCM7         AIP         PPP2R1A         FABP5         SLK         RPS8         SERBP1         DIAPH1         PSPC1         CHERP         AARS1         COPB1         UBE2O         U2AF2         PTGES3         DPYSL2         TUBB6         HBS1L         RFC5         QARS1         CNP         PRPF31         PRPF3         SMU1         BPNT1         PITRM1         ZC3H11A         CPNE3	Plastin-3         Alanyl-tRNA editing protein Aarsd1         Transcription termination factor 2         DNA replication licensing factor MCM7         AH receptor-interacting protein         Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform         Fatty acid-binding protein 5         STE20-like serine/threonine-protein kinase         40S ribosomal protein 58         Plasminogen activator inhibitor 1 RNA-binding protein         Protein diaphanous homolog 1         Paraspeckle component 1         Calcium homeostasis endoplasmic reticulum protein         AlaninetRNA ligase, cytoplasmic         Coatomer subunit beta         (E3-independent) E2 ubiquitin-conjugating enzyme         Splicing factor U2AF 65 kDa subunit         Prostaglandin E synthase 3         Dihydropyrimidinase-related protein 2         Tubulin beta-6 chain         HBS1-like protein         Replication factor C subunit 5         GlutaminetRNA ligase         2',3' cyclic-nucleotide 3'-phosphodiesterase         U4/U6 small nuclear ribonucleoprotein Prp31         U4/U6 small nuclear ribonucleoprotein Prp3         WD40 repeat-containing protein SMU1         3'(2'),5'-bisphosphate nucleotidase 1         Presequence protease, mitochondrial         Zi	1,6     1,6	<0.001 <0.001 0,001 0,002 0,002 0,002 0,003 0,003 0,003 0,003 0,003 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,004 0,005 0,006 0,006 0,006 0,006 0,006 0,008 0,009 0,009 0,001 0,011 0,011 0,012 0,014 0,015 0,016

Q96RP9	GFM1	Elongation factor G, mitochondrial	1,6	0,016
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	1,6	0,017
P08754	GNAI3	Guanine nucleotide-binding protein G(i) subunit alpha	1,6	0,017
Q92879	CELF1	CUGBP Elav-like family member 1	1,6	0,03
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	1,6	0,037
P42566	EPS15	Epidermal growth factor receptor substrate 15	1,6	0,046
Q6YN16	HSDL2	Hydroxysteroid dehydrogenase-like protein 2	1,5	< 0.001
Q5JSZ5	PRRC2B	Protein PRRC2B	1,5	< 0.001
Q8N0X7	SPART	Spartin	1,5	< 0.001
Q6Y7W6	GIGYF2	GRB10-interacting GYF protein 2	1,5	< 0.001
P26640	VARS1	ValinetRNA ligase	1,5	0,001
015371	EIF3D	Eukaryotic translation initiation factor 3 subunit D	1,5	0,001
O14802	POLR3A	DNA-directed RNA polymerase III subunit RPC1	1,5	0,001
P22102	GART	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase	1,5	0,001
P62873	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	1,5	0,001
Q96S44	TP53RK	EKC/KEOPS complex subunit TP53RK	1,5	0,002
O43159	RRP8	Ribosomal RNA-processing protein 8	1,5	0,002
M0R0F0	RPS5	40S ribosomal protein S5	1,5	0,003
F8WB06	ATXN2	Ataxin-2	1,5	0,003
Q15003	NCAPH	Condensin complex subunit 2	1,5	0,003
P05198	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	1,5	0,003
Q15042	RAB3GAP1	Rab3 GTPase-activating protein catalytic subunit	1,5	0,003
P78344	EIF4G2	Eukaryotic translation initiation factor 4 gamma 2	1,5	0,004
O95336	PGLS	6-phosphogluconolactonase	1,5	0,004
P62244	RPS15A	40S ribosomal protein S15a	1.5	0,005
095573	ACSL3	Long-chain-fatty-acidCoA ligase 3	1.5	0.005
P55795	HNR NPH2	Heterogeneous nuclear ribonucleoprotein H2	15	0.005
D55081	MEA D1	Microfibrillar associated protein 1	1,5	0.007
09UBT2	UBA2	SUMO-activating enzyme subunit 2	1,5	0.007
013136	DDFLA 1	Liprin alpha 1	1,5	0,007
A0A0C2IN72	SCDID	Destain caribble homolog	1,5	0,008
ONIOTS	EVOSC2	Execome complex component P. P. D/0	1,5	0,007
0011162	LIOOK1	Exosonie complex component RKF40	1,5	0,01
418202	CUADVIDAD	Protein Flook nomolog 1	1,5	0,014
AIA283	SH3PAD2B	SH3 and PA domain-containing protein 2B	1,5	0,014
Q8NIG4	LKKC4/	Leucine-rich repeat-containing protein 4/	1,5	0,014
Q86156	DNAAFS	Dynein assembly factor 5, axonemal	1,5	0,015
B4E1N1	ARMC6	Armadillo repeat-containing protein 6	1,5	0,016
Q00610	CLIC	Clathrin heavy chain 1	1,5	0,017
P20042	E1F2S2	Eukaryotic translation initiation factor 2 subunit 2	1,5	0,017
P04637	TP53	Cellular tumor antigen p53	1,5	0,018
P63165	SUM01	Small ubiquitin-related modifier 1	1,5	0,018
Q9HB71	CACYBP	Calcyclin-binding protein	1,5	0,02
Q8WVM8	SCFD1	Sec1 family domain-containing protein 1	1,5	0,026
Q08J23	NSUN2	RNA cytosine C(5)-methyltransferase NSUN2	1,5	0,026
Q9Y696	CLIC4	Chloride intracellular channel protein 4	1,5	0,029
075934	BCAS2	Pre-mRNA-splicing factor SPF27	1,5	0,031
Q8N9T8	KRI1	Protein KRI1 homolog	1,5	0,036
Q9BY32	ITPA	Inosine triphosphate pyrophosphatase	1,5	0,041
E9PGZ1	CALD1	Caldesmon	1,5	0,047
Q9BQG0	MYBBP1A	Myb-binding protein 1A	1,5	0,049
Q9NSD9	FARSB	PhenylalaninetRNA ligase beta subunit	1,4	< 0.001
Q8WUM4	PDCD6IP	Programmed cell death 6-interacting protein	1,4	< 0.001
Q86TB9	PATL1	Protein PAT1 homolog 1	1,4	< 0.001
O94826	TOMM70	Mitochondrial import receptor subunit TOM70	1,4	0,001
Q14151	SAFB2	Scaffold attachment factor B2	1,4	0,001
Q16658	FSCN1	Fascin	1,4	0,001
P17987	TCP1	T-complex protein 1 subunit alpha	1,4	0,001
Q96FW1	OTUB1	Ubiquitin thioesterase OTUB1	1,4	0,002
P25325	MPST	3-mercaptopyruvate sulfurtransferase	1.4	0,005
P52701	MSH6	DNA mismatch repair protein Msh6	1.4	0,011
07L2H7	EIE3M	Fukarvotic translation initiation factor 3 subunit M	1.4	0.015
095782	A P2 A 1	A P.2 complex subunit alpha-1	1.4	0.02
096F45	ZNF503	Zinc finger protein 503	1,1	0.023
0%N67	DOCK7	Dedicator of cytokinesis protein 7	1.4	0.023
P55265	ADAP	Double.stranded R NA-specific adenosine deaminase	1.4	0,020
O9NR 12	PDI IM7	DDD and LIM domain protein 7	1.4	0.025
Q9INR12	PDLIM/	r DZ and LIM domain protein /	1,4	0,027
000425	IGF2BP3	Insulin-like growth factor 2 mK NA-binding protein 3	1,4	0,031
Q81151	PM20D2	reptidase M20 domain-containing protein 2	1,4	0,031
Q916G9	DINCILII	Cytoplasmic dynein 1 light intermediate chain 1	1,4	0,034
Q9P258	RCC2	Protein KCC2	1,4	0,037
Q96I25	RBM17	Splicing factor 45	1,4	0,041
O75439	PMPCB	Mitochondrial-processing peptidase subunit beta	1,4	0,041
P62851	RPS25	40S ribosomal protein \$25	1,4	0,041

P61163	ACTR1A	Alpha-centractin	1,4	0,042
Q99569	PKP4	Plakophilin-4	1,4	0,042
E9PD53	SMC4	Structural maintenance of chromosomes protein	1,4	0.044
P46821	MAP1B	Microtubule-associated protein 1B	1.4	0.049
D(2172	D DI 29	(OS sibacamal protein 12	1.2	<0.001
<u>F631/3</u>	KFL38		1,5	<0.001
Q96A33	CCDC4/	Coiled-coil domain-containing protein 4/	1,3	0,001
P11908	PRPS2	Ribose-phosphate pyrophosphokinase 2	1,3	0,001
Q16643	DBN1	Drebrin	1,3	0,001
P62195	PSMC5	26S proteasome regulatory subunit 8	1,3	0,001
P61158	ACTR3	Actin-related protein 3	1,3	0.001
0133/7	FIF3I	Fukarvatic translation initiation factor 3 subunit I	1.3	0.003
Q1334/	LITDN		1,5	0,003
P46939	UIRN	Utrophin	1,3	0,003
P31948	STIP1	Stress-induced-phosphoprotein 1	1,3	0,003
O60343	TBC1D4	TBC1 domain family member 4	1,3	0,003
O75792	RNASEH2A	Ribonuclease H2 subunit A	1,3	0,004
P51114	FXR1	Fragile X mental retardation syndrome-related protein 1	1,3	0.004
O8WVD5	AHCTE1	Protein FLVS	1.3	0.007
Q8W115			1,5	0,007
P13804	EIFA	Electron transfer flavoprotein subunit alpha, mitochondrial	1,3	0,007
Q9Y5A9	YTHDF2	YTH domain-containing family protein 2	1,3	0,007
Q14C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	1,3	0,007
P42696	RBM34	RNA-binding protein 34	1,3	0,007
P55060	CSE1L	Exportin-2	13	0.007
002252		Mathulmalanata comialdohudo dohudrogonaco [agulating] mitochondrial	1.2	0.007
Q02232	ALDHOAT	Methymatonate-semialdenyde denydrogenase [acytating], mitochondriai	1,5	0,007
P63241	EIF5A	Eukaryotic translation initiation factor 5A-1	1,3	0,009
Q9Y2U8	LEMD3	Inner nuclear membrane protein Man1	1,3	0,011
P54136	RARS1	ArgininetRNA ligase, cytoplasmic	1,3	0,011
Q96AG4	LRRC59	Leucine-rich repeat-containing protein 59	1,3	0,011
P46779	R PI 28	60S ribosomal protein L 28	13	0.012
00N/719	ICE20D1	Lewlin like second forter 2 m P.NA kin dia second in 1	1,5	0.012
QINZIS	IGF2BP1	Insulin-like growth factor 2 mk/NA-binding protein 1	1,5	0,015
P45974	USP5	Ubiquitin carboxyl-terminal hydrolase 5	1,3	0,013
P35580	MYH10	Myosin-10	1,3	0,013
Q9BRX2	PELO	Protein pelota homolog	1,3	0,014
P49736	MCM2	DNA replication licensing factor MCM2	1,3	0,014
C9IR15	LIMD1	I IM domain-containing protein 1	13	0.014
D(2285	MTDEX		1,5	0.01(
P42285	MIKEA	Exosome KINA nelicase M I K4	1,5	0,016
H0Y5D5	CIZI	Cip1-interacting zinc finger protein	1,3	0,017
Q9BPU6	DPYSL5	Dihydropyrimidinase-related protein 5	1,3	0,017
P18615	NELFE	Negative elongation factor E	1,3	0,018
Q14318	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8	1,3	0,018
0521.10	FA M 98B	Protein FA M98B	13	0.02
D102/7	HV1	Hereliness 1	1.2	0.025
F1/36/	TIKI	rickokinase-i	1,5	0,023
Q13509	TUBB3	Tubulin beta-3 chain	1,3	0,026
Q1KMD3	HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	1,3	0,026
P52272	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	1,3	0,027
F8W0J6	NAP1L1	Nucleosome assembly protein 1-like 1	1,3	0,029
13OR09	RPL19	Ribosomal protein L19	1.3	0.031
013526	PIN1	Pantidul prolulicie transisomerasa NIM & interacting 1	1.3	0.031
Q13320			1,5	0,001
Q90BE0	SAEI	SUMO-activating enzyme subunit 1	1,3	0,034
Q9P0K7	RAI14	Ankycorbin	1,3	0,035
Q16543	CDC37	Hsp90 co-chaperone Cdc37	1,3	0,036
P62854	RPS26	40S ribosomal protein S26	1,3	0,041
Q9NR45	NANS	Sialic acid synthase	1,3	0,043
P25685	DNAIB1	Dual homolog subfamily B member 1	13	0.0/18
0120/5	ELU ELU		1,5	0,040
Q13045	FLII	Protein flightless-1 homolog	1,2	<0.001
Q9P2I0	CPSF2	Cleavage and polyadenylation specificity factor subunit 2	1,2	0,001
P42771	CDKN2A	Cyclin-dependent kinase inhibitor 2A	1,2	0,002
Q9HC35	EML4	Echinoderm microtubule-associated protein-like 4	1,2	0,003
A0A0A0MR M8	MYO6	Unconventional myosin-6	1.2	0.003
096036	DVCR 2	Pueroline 5 carboxylate reductore 2	1.2	0.003
Q70C30	VDC/A		1,2	0,005
Q90N3/	VP84A	Vacuolar protein sorting-associated protein 4A	1,2	0,004
Q9UMS4	PRPF19	Pre-mRNA-processing factor 19	1,2	0,006
Q9Y2Z0	SUGT1	Protein SGT1 homolog	1,2	0,008
P31939	ATIC	Bifunctional purine biosynthesis protein ATIC	1,2	0,008
K7EIL1	AP1M1	AP-1 complex subunit mu-1	1.2	0,008
FSVVFS	PPP1CC	Serine/threanine_protein_phoenhatase	1.2	0.009
001/00	TT NI	or me, encounte-protein phosphatase	1,2	0,008
Q91490	I LNI	1alin-1	1,2	0,009
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	1,2	0,009
P98175	RBM10	RNA-binding protein 10	1,2	0,014
P49368	CCT3	T-complex protein 1 subunit gamma	1,2	0,015
P13489	RNH1	Ribonuclease inhibitor	1.2	0.017
	7NE220	Zing funger protein 220	1.2	0.017
Q71332	LINF 330		1,2	0,01/
Q9H0D6	AKN2	5-5 exoribonuclease 2	1,2	0,018
Q12904	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	1,2	0,019

P36542	ATP5F1C	ATP synthase subunit gamma, mitochondrial	1,2	0,019
P36915	GNLI		1,2	0,02
Q13907	TAGEND	Isopentenyl-diphosphate Delta-isomerase I	1,2	0,02
P3/802	TAGLINZ	fransgein-2	1,2	0,021
AUA2K81DQ5	SUCLAZ	DucinateCoA ngase [ADP-forming] subunit beta, mitochondriai	1,2	0,023
GSEA31	SEC24C	Protein transport protein Sec24C	1,2	0,027
0/2290	LIND NDD	Heterogeneous pueleer silverueleen retein P	1,2	0,029
D41240	CSV	Turoring protoin kinese CSK	1,2	0,022
09NW82	WDP 70	WD spect containing protein 70	1,2	0,033
Q/INW62	WDR/0	SAEP like transmining protein 70	1,2	0,033
094904	DD DEC	Dra mP NA processing factor (	1,2	0,035
094908	PHIP	PH-interacting protein	1,2	0,035
D33176	KIESB	Kingsin 1 heavy chain	1,2	0.036
D28838	I A D3	Cutocol aminopentidose	1,2	0.037
P27540	ARNT	Arvl hydrocarbon receptor nuclear translocator	1,2	0.045
P39687	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A	1,2	0.046
O9BY44	FIF2A	Fukarvotic translation initiation factor 2A	1,2	0.047
P53384	NUBP1	Cytosolic Fe-S cluster assembly factor NUBP1	1,2	0.049
P29692	EEF1D	Elongation factor 1-delta	1.1	0.001
05IXI8	FHL1	Four and a half LIM domains protein 1	1.1	0.001
Q43684	BUB3	Mitotic checkpoint protein BUB3	1,1	0.004
C91019	ZC3HC1	Nuclear-interacting partner of ALK	1,1	0.004
013451	FKBP5	Peptidyl-prolyl cis-trans isomerase FKBP5	1,1	0.004
O2TAM5	RELA	RELA protein	1,1	0,006
P43487	RANBP1	Ran-specific GTPase-activating protein	1,1	0,007
O9H3K6	BOLA2	BolA-like protein 2	1,1	0.009
P30084	ECHS1	Enovl-CoA hydratase, mitochondrial	1,1	0.009
P62701	RPS4X	40S ribosomal protein S4, X isoform	1,1	0,01
A0A1B0GWF2	STXBP1	Syntaxin-binding protein 1	1,1	0,01
P46778	RPL21	60S ribosomal protein L21	1,1	0,01
Q6ZN17	LIN28B	Protein lin-28 homolog B	1,1	0,01
P43246	MSH2	DNA mismatch repair protein Msh2	1,1	0,011
Q16527	CSRP2	Cysteine and glycine-rich protein 2	1,1	0,011
Q8IWS0	PHF6	PHD finger protein 6	1,1	0,012
Q5TDH0	DDI2	Protein DDI1 homolog 2	1,1	0,012
G3XAH6	PAPOLA	Poly(A) polymerase	1,1	0,012
P45973	CBX5	Chromobox protein homolog 5	1,1	0,012
Q15126	PMVK	Phosphomevalonate kinase	1,1	0,014
P84095	RHOG	Rho-related GTP-binding protein RhoG	1,1	0,014
Q02790	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	1,1	0,015
A0A087WXM6	RPL17	60S ribosomal protein L17	1,1	0,016
Q9UPQ9	TNRC6B	Trinucleotide repeat-containing gene 6B protein	1,1	0,017
M0R3C3	TECR	Very-long-chain enoyl-CoA reductase	1,1	0,017
Q99829	CPNE1	Copine-1	1,1	0,019
Q71RC2	LARP4	La-related protein 4	1,1	0,019
P60660	MYL6	Myosin light polypeptide 6	1,1	0,021
P49207	RPL34	60S ribosomal protein L34	1,1	0,021
Q10567	AP1B1	AP-1 complex subunit beta-1	1,1	0,023
P63092	GNAS	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	1,1	0,025
Q9UN86	G3BP2	Ras GTPase-activating protein-binding protein 2	1,1	0,027
P51116	FXR2	Fragile X mental retardation syndrome-related protein 2	1,1	0,027
H0YNW5	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase	1,1	0,028
H7C5E4	XRN1	5'-3' exoribonuclease 1	1,1	0,031
P52294	KPNA1	Importin subunit alpha-5	1,1	0,031
P15880	RPS2	40S ribosomal protein S2	1,1	0,031
P31946	YWHAB	14-3-3 protein beta/alpha	1,1	0,036
O14893	GEMIN2	Gem-associated protein 2	1,1	0,037
K4DI93	CUL4B	Cullin 4B, isoform CRA_e	1,1	0,042
Q9UKM9	RALY	RNA-binding protein Raly	1,1	0,043
P54578	USP14	Ubiquitin carboxyl-terminal hydrolase 14	1,1	0,046
C9J0J7	PFN2	Profilin	1,1	0,046
Q8IYI6	EXOC8	Exocyst complex component 8	1,1	0,048
P50991	CCT4	T-complex protein 1 subunit delta	1	0,007
P32322	PYCR1	Pyrroline-5-carboxylate reductase 1, mitochondrial	1	0,008
P07814	EPRS1	Bifunctional glutamate/prolinetRNA ligase	1	0,011
Q9NUQ9	CYRIB	CYFIP-related Rac1 interactor B	1	0,013
Q16576	RBBP7	Histone-binding protein RBBP7	1	0,017
A0A087WY55	VTA1	Chromosome 6 open reading frame 55, isoform CRA_b	1	0,022
Q7RTV0	PHF5A	PHD finger-like domain-containing protein 5A	1	0,022
P38117	ETFB	Electron transfer flavoprotein subunit beta	1	0,024
B5MCF9	PES1	Pescadillo homolog	1	0,024
A0A2R8Y855	SMARCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	1	0,027
Q9UJ83	HACL1	2-hydroxyacyl-CoA lyase 1	1	0,029
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Q9BZE9	ASPSCR1	Tether containing UBX domain for GLUT4	1	0,034
P55884	EIF3B	Eukaryotic translation initiation factor 3 subunit B	1	0,036
Q15370	ELOB	Elongin-B	1	0,04
Q9ULC4	MCTS1	Malignant T-cell-amplified sequence 1	1	0,043
P26358	DNMT1	DNA	1	0,045
A0A024RAC6	ELOA	Elongin-A	1	0,047
PRDX2 cysteine-depend	ent interactors			
Q9C0C2	TNKS1BP1	182 kDa tankyrase-1-binding protein	6,4	< 0.001
Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	5,2	< 0.001
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	5,2	< 0.001
P07355	ANXA2	Annexin A2	5,1	< 0.001
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	4,9	< 0.001
Q9NQX3	GPHN	Gephyrin [Includes: Molybdopterin adenylyltransferase	4,9	< 0.001
E7EVA0	MAP4	Microtubule-associated protein	4,9	< 0.001
Q9UHV9	PFDN2	Prefoldin subunit 2	4,5	< 0.001
Q9BQA1	WDR77	Methylosome protein 50	4,2	< 0.001
O60547	GMDS	GDP-mannose 4,6 dehydratase	4,2	< 0.001
Q9Y266	NUDC	Nuclear migration protein nudC	4,1	< 0.001
A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6	4,1	< 0.001
P11802	CDK4	Cyclin-dependent kinase 4	4,1	< 0.001
Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	4,1	< 0.001
Q9NPH2	ISYNA1	Inositol-3-phosphate synthase 1	4	< 0.001
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	4	< 0.001
Q9HBH5	RDH14	Retinol dehydrogenase 14	4	0,004
P12955	PEPD	Xaa-Pro dipeptidase	3,9	0,001
P61289	PSME3	Proteasome activator complex subunit 3	3,9	0,005
B/Z/F3	RANBP3	Ran-binding protein 3	3,8	<0.001
014/44	PKM15	Protein arginine N-methyltransferase 5	3,/	<0.001
AGNGPS	JP12 TDV2	Jupiter microtubule-associated homolog 2	3,/	<0.001
Q90LW0	IPA2 MADIR	Targeting protein for Akip2	3,/	0,001
01/2/7	CTTN	Microtubule-associated protein 1B	3,6	<0.001
Q1424/	NDUEA	Sre substrate cortactin	3,6	<0.001
000485	SDDI 1	Cytochrome c oxidase subunit NDOFA4	3,5	<0.001
05T6F2		Ubiquitin associated protein 2	3,5	<0.001
Q9H773	DCTPP1	dCTP pyrophosphatase 1	3.3	<0.001
Q911775	SFR BP1	Plasminogen activator inhibitor 1 R NA-binding protein	33	<0.001
05SW79	CFP170	Centrosomal protein of 170 kDa	3.2	<0.001
Q96KB5	PBK	I ymphokine-activated killer T-cell-originated protein kinase	3.2	0.002
O9BR P1	PDCD2L	Programmed cell death protein 2-like	3.1	0.001
P06132	UROD	Uroporphyrinogen decarboxylase	3.1	0.004
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	3,1	0,042
O9NUO3	TXLNG	Gamma-taxilin	3	0,002
Q86V48	LUZP1	Leucine zipper protein 1	2,9	< 0.001
O43809	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	2,9	0,001
Q9H2U2	PPA2	Inorganic pyrophosphatase 2, mitochondrial	2,9	0,001
Q9NUP9	LIN7C	Protein lin-7 homolog C	2,9	0,002
P40222	TXLNA	Alpha-taxilin	2,9	0,002
P61758	VBP1	Prefoldin subunit 3	2,9	0,004
O60664	PLIN3	Perilipin-3	2,9	0,008
H0YNW5	DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase	2,8	< 0.001
E7EPN9	PRRC2C	Protein PRRC2C	2,8	< 0.001
Q8N3X1	FNBP4	Formin-binding protein 4	2,8	0,001
Q13541	EIF4EBP1	Eukaryotic translation initiation factor 4E-binding protein 1	2,8	0,006
O75223	GGCT	Gamma-glutamylcyclotransferase	2,8	0,011
P19174	PLCG1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	2,7	0,002
O75381	PEX14	Peroxisomal membrane protein PEX14	2,7	0,004
E9PGZ1	CALD1	Caldesmon	2,7	0,004
Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	2,7	0,004
Q8IWB7	WDFY1	WD repeat and FYVE domain-containing protein 1	2,7	0,004
P10599	TXN	Thioredoxin	2,6	< 0.001
Q9P258	RCC2	Protein RCC2	2,6	< 0.001
P26599	PTBP1	Polypyrimidine tract-binding protein 1	2,6	< 0.001
P30041	PRDX6	Peroxiredoxin-6	2,6	0,002
O43143	DHX15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	2,6	0,002
K7EJQ8	HDHD2	Haloacid dehalogenase-like hydrolase domain-containing protein 2	2,6	0,004
P30740	SERPINB1	Leukocyte elastase inhibitor	2,6	0,005
Q8WVC2	RPS21	40S ribosomal protein S21	2,6	0,006
Q16204	CCDC6	Coiled-coil domain-containing protein 6	2,6	0,011
H3BRL3	UBFD1	Ubiquitin domain-containing protein UBFD1	2,6	0,014
152888	THOPI	I nimet oligopeptidase	2,5	<0.001
J3N.IN29	P3MD9	265 proteasome non-A 1 Pase regulatory subunit 9	2,5	<0.001

Q9Y570	PPME1	Protein phosphatase methylesterase 1	2,5	< 0.001
O14929	HAT1	Histone acetyltransferase type B catalytic subunit	2,5	< 0.001
P48634	PRRC2A	Protein PRRC2A	2,5	< 0.001
Q9HA64	FN3KRP	Ketosamine-3-kinase	2,5	0,002
Q8TAQ2	SMARCC2	SWI/SNF complex subunit SMARCC2	2,5	0,003
A0A087WTM1	ROBO1	Roundabout homolog 1	2,5	0,004
Q6IQ49	SDE2	Replication stress response regulator SDE2	2,5	0,004
Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	2,5	0,005
Q9P2B4	CTTNBP2NL	CTTNBP2 N-terminal-like protein	2,5	0,006
O99598	TSNAX	Translin-associated protein X	2.5	0,008
P49903	SEPHS1	Selenide water dikinase 1	25	0.009
K7FLV2	SEH1U SEH1U	Nucleoporin SFH1	2,5	0.01
0135/2	FIE/FRD2	Fukervotic translation initiation factor /F hinding protein 2	2,5	0.045
Q13342	EIF4EDF2	Effect your translation initiation factor 4E-binding protein 2	2,5	0,043
CODVIO	SLC3A2	4r2 cell-surrace antigen neavy chain	2,4	<0.001
Q9BXJ9	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	2,4	0,003
P35520	CBS	Cystathionine beta-synthase	2,3	<0.001
Q13428	ICOFI	I reacle protein	2,3	<0.001
P42771	CDKN2A	Cyclin-dependent kinase inhibitor 2A	2,3	< 0.001
Q15019	SEPTIN2	Septin-2	2,3	0,009
Q9Y3B7	MRPL11	39S ribosomal protein L11, mitochondrial	2,3	0,017
Q8N6M0	OTUD6B	Deubiquitinase OTUD6B	2,3	0,017
Q49A26	GLYR1	Putative oxidoreductase GLYR1	2,3	0,037
P52907	CAPZA1	F-actin-capping protein subunit alpha-1	2,2	< 0.001
Q13547	HDAC1	Histone deacetylase 1	2,2	0,002
Q14257	RCN2	Reticulocalbin-2	2,2	0,004
Q9UQE7	SMC3	Structural maintenance of chromosomes protein 3	2,2	0,006
O5IRA6	MIA3	Transport and Golgi organization protein 1 homolog	2.2	0,007
E9PS17	SCYL1	N-terminal kinase-like protein	2.2	0.008
000629	KPNA4	Importin subunit alpha-3	2,2	0,009
094992	HFXIM1	Protein HFXIM1	2,2	0.01
09(E45	7NES02	Zing frager protein 502	2,2	0.012
Q76F45	ADD1	Alaba addacia	2,2	0,015
E/EV99	ADDI	Alpha-adducin	2,2	0,014
P38159	RBMX	RNA-binding motif protein, X chromosome	2,2	0,014
Q96GD0	PDXP	Pyridoxal phosphate phosphatase	2,2	0,015
E9PM92	C11orf58	Small acidic protein	2,2	0,017
A4D1S0	KLRG2	Killer cell lectin-like receptor subfamily G member 2	2,2	0,027
C9J0I9	ZC3HC1	Nuclear-interacting partner of ALK	2,1	< 0.001
P35237	SERPINB6	Serpin B6	2,1	< 0.001
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	2,1	0,004
Q9UBS4	DNAJB11	DnaJ homolog subfamily B member 11	2,1	0,014
Q9Y2R9	MRPS7	28S ribosomal protein S7, mitochondrial	2,1	0,015
O95104	SCAF4	SR-related and CTD-associated factor 4	2,1	0,016
F5H8D7	XRCC1	DNA repair protein XRCC1	2,1	0,016
Q9NVP1	DDX18	ATP-dependent RNA helicase DDX18	2,1	0,018
O86WA6	BPHL.	Valacyclovir hydrolase	2.1	0.026
O6PKG0	LARP1	I a-related protein 1	2,1	<0.001
006126	DTDN11	Twocine protein phosphatase non recentor type 11	2	<0.001
D1 A V 97	CADZD		2	<0.001
DIANO/	DRKAAD	r-actin-capping protein subunit beta	2	<0.001
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	2	0,007
P41250	GARSI	GlycinetRNA ligase	2	0,013
Q9H3S7	PTPN23	Tyrosine-protein phosphatase non-receptor type 23	2	0,014
Q9NXF7	DCAF16	DDB1- and CUL4-associated factor 16	2	0,016
O94903	PLPBP	Pyridoxal phosphate homeostasis protein	2	0,017
P29373	CRABP2	Cellular retinoic acid-binding protein 2	2	0,018
Q8IVM0	CCDC50	Coiled-coil domain-containing protein 50	2	0,021
O15143	ARPC1B	Actin-related protein 2/3 complex subunit 1B	2	0,025
P23588	EIF4B	Eukaryotic translation initiation factor 4B	2	0,049
Q16576	RBBP7	Histone-binding protein RBBP7	1,9	< 0.001
O93034	CUL5	Cullin-5	1.9	0,001
09C0C9	UBE2O	(E3-independent) E2.ubiquitin-conjugating enzyme	1.9	0.001
P52732	KIF11	Kinesin-like protein KIF11	19	0.002
O8N6T3	ARECAD1	A DP ribosylation factor GTPase activating protein 1	19	0.016
09/17/	LICD47	Libiquitie asthory terminal hydrolass 47	1,7	0,010
Q16240	EIE(A)	Eulermentic initiation foren (A. H	1,7	0,02
014240	EIF4A2	Eukaryotic initiation ractor 4A-11	1,7	0,02
A1X283	SH3PXD2B	SH3 and PX domain-containing protein 2B	1,9	0,026
Q9Y3D0	CIAO2B	Cytosolic iron-sulfur assembly component 2B	1,9	0,031
P42574	CASP3	Caspase-3	1,9	0,042
Q16531	DDB1	DNA damage-binding protein 1	1,8	< 0.001
P51452	DUSP3	Dual specificity protein phosphatase 3	1,8	< 0.001
Q9Y3F4	STRAP	Serine-threonine kinase receptor-associated protein	1,8	< 0.001
P31153	MAT2A	S-adenosylmethionine synthase isoform type-2	1,8	0,001
A0A1B0GW38	CBL	E3 ubiquitin-protein ligase CBL	1,8	0,003
Q9Y6Y8	SEC23IP	SEC23-interacting protein	1,8	0,005
		V1		

Q12948	FOXC1	Forkhead box protein C1	1,8	0,014
Q12800	TFCP2	Alpha-globin transcription factor CP2	1,8	0,024
Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	1,8	0,026
Q2M1P5	KIF7	Kinesin-like protein KIF7	1,8	0,026
E9POV9	DCUN1D5	DCN1-like protein	1,8	0,032
O9BT25	HAUS8	HAUS augmin-like complex subunit 8	1.8	0.038
Q60826	CCDC22	Coiled-coil domain-containing protein 22	1.8	0.047
006203	PPAT	A midonhoshorihosyltransferase	1.7	<0.001
Q00205	EDC2	Enhances of m DNA decomping protein 2	1,7	0.004
Q76F86	EDC5 6AE1	SUMO activities any machine 1	1,7	0,004
Q90BE0	SAEI		1,/	0,006
A0A08/X054	HYOUI	Hypoxia up-regulated protein 1	1,/	0,008
A0A3B3ISG5	IDE	Insulin-degrading enzyme	1,7	0,014
Q6P2Q9	PRPF8	Pre-mRNA-processing-splicing factor 8	1,7	0,014
P52788	SMS	Spermine synthase	1,7	0,023
E9PGT1	TSN	Component 3 of promoter of RISC	1,7	0,031
O43815	STRN	Striatin	1,7	0,039
Q6UN15	FIP1L1	Pre-mRNA 3'-end-processing factor FIP1	1,7	0,042
Q9BXP5	SRRT	Serrate RNA effector molecule homolog	1,7	0,045
Q92783	STAM	Signal transducing adapter molecule 1	1,7	0,048
O5OPM7	PSMF1	Proteasome inhibitor PI31 subunit	1.6	< 0.001
O9UKG1	APPL1	DCC-interacting protein 13-alpha	16	< 0.001
014C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	1,6	0.001
015202	CE2P2	Solicion factor 2D subunit 2	1,0	0,001
Q13373	313D3		1,6	0,001
Q90N3/	VPS4A	vacuolar protein sorting associated protein 4A	1,6	0,004
075663	TIPRL	11P41-like protein	1,6	0,007
A0A087WTZ5	UBXN1	UBX domain-containing protein 1	1,6	0,01
P63000	RAC1	Ras-related C3 botulinum toxin substrate 1	1,6	0,018
O00165	HAX1	HCLS1-associated protein X-1	1,6	0,025
P49750	YLPM1	YLP motif-containing protein 1	1,6	0,038
O75533	SF3B1	Splicing factor 3B subunit 1	1,6	0,039
Q9Y265	RUVBL1	RuvB-like 1	1,5	0,001
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	1,5	0,002
E9PLA9	CAPRIN1	Caprin-1	1,5	0,002
A0A087X2B5	BSG	Basigin	1.5	0.005
007666	KHDR BS1	KH domain-containing RNA-binding signal transduction-associated protein 1	15	0.01
Q07000	GTSF1	G2 and S phase expressed protein 1	1,5	0.01
Q IN I Z J	CT3D2	Selician Grand 2 million 2	1,5	0.01/
Q96WJ5	35303	Splicing factor 3D subunit 5	1,5	0,014
Q9266/	AKAPI	A-kinase anchor protein 1, mitochondrial	1,5	0,022
P61106	RAB14	Kas-related protein Kab-14	1,5	0,035
095347	SMC2	Structural maintenance of chromosomes protein 2	1,5	0,041
O60493	SNX3	Sorting nexin-3	1,5	0,047
Q96A33	CCDC47	Coiled-coil domain-containing protein 47	1,4	< 0.001
Q8N5F7	NKAP	NF-kappa-B-activating protein	1,4	< 0.001
Q13045	FLII	Protein flightless-1 homolog	1,4	< 0.001
A0A0A0MRM8	MYO6	Unconventional myosin-6	1,4	0,001
Q92598	HSPH1	Heat shock protein 105 kDa	1,4	0,001
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	1,4	0,002
Q60343	TBC1D4	TBC1 domain family member 4	1.4	0.002
P20020	ATP2B1	Plasma membrane calcium-transporting ATPase 1	1.4	0.002
A0A024RCR6	BAC6	BCL2 associated athanogene 6	1,4	0.002
Of BK71	ZNE22/	DRID D complex suburity (NIE22)	1,4	0,003
QSBKZI	ZINF326	2 CO AND COMPLEX SUDURIT ZINF 326	1,4	0,005
Q7UNM6	PSMD13	265 proteasome non-A 1 Pase regulatory subunit 13	1,4	0,003
P61981	YWHAG	14-5-5 protein gamma	1,4	0,005
P62333	PSMC6	26S proteasome regulatory subunit 10B	1,4	0,006
P15374	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	1,4	0,006
O00170	AIP	AH receptor-interacting protein	1,4	0,007
P35998	PSMC2	26S proteasome regulatory subunit 7	1,4	0,008
P50213	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	1,4	0,012
P31946	YWHAB	14-3-3 protein beta/alpha	1,4	0,013
Q7Z6Z7	HUWE1	E3 ubiquitin-protein ligase HUWE1	1,4	0,018
Q9UPN7	PPP6R1	Serine/threonine-protein phosphatase 6 regulatory subunit 1	1,4	0,024
094905	ERLIN2	Erlin-2	1.4	0.028
O95801	TTC4	Tetratricopeptide repeat protein 4	1.4	0,03
096T23	R SF1	Remodeling and spacing factor 1	1.4	0.033
01/97/	DDD1D 12 A	Destein phoepheteos 1 roculators subunit 12 A	1,4	0,033
0147/4 D12707	PPPIKIZA DI 62	Protein phosphatase 1 regulatory subunit 12A	1,4	0,038
r13/7/	PL33	riastin-5	1,3	< 0.001
P62191	PSMC1	26S proteasome regulatory subunit 4	1,3	0,001
Q9Y230	RUVBL2	RuvB-like 2	1,3	0,001
P25786	PSMA1	Proteasome subunit alpha type-1	1,3	0,001
O00151	PDLIM1	PDZ and LIM domain protein 1	1,3	0,002
Q7LBC6	KDM3B	Lysine-specific demethylase 3B	1,3	0,004
Q96D09	GPRASP2	G-protein coupled receptor-associated sorting protein 2	1,3	0,006
P08240	SRPRA	Signal recognition particle receptor subunit alpha	1,3	0,011

P55072	VCP	Transitional endoplasmic reticulum ATPase	1,3	0,012
Q9UJV9	DDX41	Probable ATP-dependent RNA helicase DDX41	1,3	0,021
Q92769	HDAC2	Histone deacetylase 2	1,3	0,023
P41214	EIF2D	Eukaryotic translation initiation factor 2D	1,3	0,024
A0MZ66	SHTN1	Shootin-1	1,3	0,024
A0A1C7CYX9	DPYSL2	Dihydropyrimidinase-related protein 2	1,3	0,025
Q15417	CNN3	Calponin-3	1,3	0,027
000267	SUPT5H	Transcription elongation factor SPT5	1.3	0.027
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	13	0.029
015276	R A REP1	R ab GTPase-binding effector protein 1	13	0.039
094(50	VTUDC2	2' 5' P NA holioso VTHDC2	1,5	0.044
0011014	D A D1D	3-3 KNA hencase 1111DC2	1,5	0,044
Q9H0U4	CEVNI	Cil d : 1	1,5	0,046
Q9H9B4	SFANI	Sideroffexin-1	1,2	0,001
Q6NUK1	SLC25A24	Calcium-binding mitochondrial carrier protein SCaMC-1	1,2	0,001
Q9UKX7	NUP50	Nuclear pore complex protein Nup50	1,2	0,002
Q15046	KARS1	LysinetRNA ligase	1,2	0,003
O00487	PSMD14	26S proteasome non-ATPase regulatory subunit 14	1,2	0,005
P06737	PYGL	Glycogen phosphorylase, liver form	1,2	0,005
Q9UJZ1	STOML2	Stomatin-like protein 2, mitochondrial	1,2	0,005
Q9UNF1	MAGED2	Melanoma-associated antigen D2	1,2	0,006
Q7Z4H7	HAUS6	HAUS augmin-like complex subunit 6	1,2	0,006
Q9UHD1	CHORDC1	Cysteine and histidine-rich domain-containing protein 1	1,2	0,01
P22695	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	1,2	0,011
O9GZT9	EGLN1	Egl nine homolog 1	1.2	0.012
097549	YTHDF2	VTH domain-containing family protein 2	1.2	0.013
000273	DEFA	DNA fragmentation factor subunit alpha	1.2	0.014
D5 95 4/	MTDN	Mustenhin	1,2	0.02
P (2)(77	D DC27		1,2	0,02
P426//	KPS2/	405 ribosomai protein 52/	1,2	0,026
54K3H4	ACINI	Apoptotic chromatin condensation inducer in the nucleus	1,2	0,027
Q9BTE3	мсмвр	Mini-chromosome maintenance complex-binding protein	1,2	0,027
M0QY97	ZC3H4	Zinc finger CCCH domain-containing protein 4	1,2	0,028
Q14739	LBR	Delta(14)-sterol reductase LBR	1,2	0,03
P52701	MSH6	DNA mismatch repair protein Msh6	1,2	0,031
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	1,2	0,035
P55265	ADAR	Double-stranded RNA-specific adenosine deaminase	1,2	0,04
Q8NI27	THOC2	THO complex subunit 2	1,2	0,046
P49790	NUP153	Nuclear pore complex protein Nup153	1,2	0,048
Q14137	BOP1	Ribosome biogenesis protein BOP1	1,2	0,049
P00387	CYB5R3	NADH-cytochrome b5 reductase 3	1,1	0,001
O6P4A7	SFXN4	Sideroflexin-4	1.1	0.002
O9Y295	DRG1	Developmentally-regulated GTP-binding protein 1	1.1	0.003
014566	MCM6	DNA replication licensing factor MCM6	11	0.003
D00228	I DUA	L lastata dabudeananaa A ahain	1,1	0,005
D40502	DDM1E	Destrin phoephateos 1E	1,1	0,005
P47575	PPMIF		1,1	0,005
AUAUC4DGX4	CULI	Cullin-1	1,1	0,006
Q13200	PSMD2	26S proteasome non-ATPase regulatory subunit 2	1,1	0,006
P22570	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial	1,1	0,007
P13861	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory subunit	1,1	0,007
E9PLK3	NPEPPS	Aminopeptidase	1,1	0,009
P05023	ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	1,1	0,009
095573	ACSL3	Long-chain-fatty-acidCoA ligase 3	1,1	0,009
Q9NZB2	FAM120A	Constitutive coactivator of PPAR-gamma-like protein 1	1,1	0,012
Q96P70	IPO9	Importin-9	1,1	0,013
H0YDU8	PPP5C	Serine/threonine-protein phosphatase	1,1	0,014
Q04917	YWHAH	14-3-3 protein eta	1,1	0,016
096KR1	ZFR	Zinc finger R NA-binding protein	11	0.016
OGUWP7	LCLAT1	Lysocardiolinin acyltransferase 1	11	0.018
OWWWV9	CVAD2		1,1	0.021
Q8WWK9	DA71D		1,1	0,021
Q901G0	BAZIB	Tyrosine-protein kinase BAZIB	1,1	0,024
AUAU8/WWP4	KBM15	KNA-binding protein 15	1,1	0,024
Q99504	EYA3	Eyes absent homolog 3	1,1	0,025
Q9H936	SLC25A22	Mitochondrial glutamate carrier 1	1,1	0,028
Q14694	USP10	Ubiquitin carboxyl-terminal hydrolase 10	1,1	0,028
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	1,1	0,038
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	1,1	0,038
Q9NZL9	MAT2B	Methionine adenosyltransferase 2 subunit beta	1,1	0,04
O60832	DKC1	H/ACA ribonucleoprotein complex subunit DKC1	1,1	0,04
Q8WXF1	PSPC1	Paraspeckle component 1	1,1	0,041
P49588	AARS1	AlaninetRNA ligase, cytoplasmic	1,1	0,043
P98175	R BM10	RNA-binding protein 10	11	0.049
D7924/	P DD20	Dihanudassa Darotain subunit n20	1	0,047
Cell Llo	STAT2	Signal transducer and estimator of transcription	1	0,000
GojLH9	51A13	Signal transducer and activator or transcription	1	0,009
A0A087WUX8	APOOL	MICOS complex subunit	1	0,01

Q92597	NDRG1	Protein NDRG1	1	0,011
P46939	UTRN	Utrophin	1	0,014
Q2NKX8	ERCC6L	DNA excision repair protein ERCC-6-like	1	0,016
P09936	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	1	0,017
Q86YP4	GATAD2A	Transcriptional repressor p66-alpha	1	0,024
Q16512	PKN1	Serine/threonine-protein kinase N1	1	0,025
P60228	EIF3E	Eukaryotic translation initiation factor 3 subunit E	1	0,026
Q8ND82	ZNF280C	Zinc finger protein 280C	1	0,035
O95684	CEP43	Centrosomal protein 43	1	0,038
O43765	SGTA	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	1	0,044
O43242	PSMD3	26S proteasome non-ATPase regulatory subunit 3	1	0,048
PRDX3 cysteine-depend	ent interactors			
P40616	ARL1	ADP-ribosylation factor-like protein 1	4,8	< 0.001
Q5SZR4	TDRKH	Tudor and KH domain containing, isoform CRA_a	4,6	< 0.001
P11766	ADH5	Alcohol dehydrogenase class-3	4,6	< 0.001
F8VYE8	PPP1CC	Serine/threonine-protein phosphatase	4,4	< 0.001
B3KUS5	USP30	Ubiquitin carboxyl-terminal hydrolase	4,1	< 0.001
Q9NWV4	CZIB	CXXC motif containing zinc binding protein	4,1	< 0.001
Q7L2H7	EIF3M	Eukaryotic translation initiation factor 3 subunit M	4	< 0.001
Q07820	MCL1	Induced myeloid leukemia cell differentiation protein Mcl-1	3,9	< 0.001
A0A0B4J1Z1	SRSF7	Serine/arginine-rich-splicing factor 7	3,9	< 0.001
P05386	RPLP1	60S acidic ribosomal protein P1	3,9	< 0.001
Q07021	C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial	3,9	< 0.001
H3BTA2	PPP4C	Serine/threonine-protein phosphatase	3,9	< 0.001
P07355	ANXA2	Annexin A2	3,9	< 0.001
Q14964	RAB39A	Ras-related protein Rab-39A	3,9	0,036
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	3,8	< 0.001
Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	3,7	0,001
Q8N5K1	CISD2	CDGSH iron-sulfur domain-containing protein 2	3,6	0,001
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	3,6	0,001
C9JAW5	C9JAW5	HIG1 domain-containing protein	3,6	0,001
Q9BYN0	SRXN1	Sulfiredoxin-1	3,5	0,002
G5EA06	MRPS27	28S ribosomal protein S27, mitochondrial	3,5	0,009
Q6IBS0	TWF2	Twinfilin-2	3,4	< 0.001
Q9HD26	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein	3,4	0,001
P06132	UROD	Uroporphyrinogen decarboxylase	3,4	0,001
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	3,4	0,001
O43809	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	3,3	< 0.001
P61106	RAB14	Ras-related protein Rab-14	3,3	< 0.001
Q6DKI1	RPL7L1	60S ribosomal protein L7-like 1	3,3	0,001
P14174	MIF	Macrophage migration inhibitory factor	3,3	0,001
P19022	CDH2	Cadherin-2	3,3	0,001
Q9BQA1	WDR77	Methylosome protein 50	3,2	< 0.001
Q92667	AKAP1	A-kinase anchor protein 1, mitochondrial	3,2	< 0.001
P51809	VAMP7	Vesicle-associated membrane protein 7	3,2	0,006
Q9NQG6	MIEF1	Mitochondrial dynamics protein MID51	3,2	0,046
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	3,1	< 0.001
D6RA00	ENOPH1	Enolase-phosphatase E1	3,1	< 0.001
P51148	RAB5C	Ras-related protein Rab-5C	3,1	0,008
Q16698	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	3	0,001
P30041	PRDX6	Peroxiredoxin-6	3	0,002
O75600	GCAT	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	3	0,002
Q9NS69	TOMM22	Mitochondrial import receptor subunit TOM22 homolog	3	0,002
Q96EA4	SPDL1	Protein Spindly	3	0,005
Q92990	GLMN	Glomulin	2,9	< 0.001
Q9Y3D0	CIAO2B	Cytosolic iron-sulfur assembly component 2B	2,9	0,001
Q9BTE1	DCTN5	Dynactin subunit 5	2,9	0,002
Q8WVC2	RPS21	40S ribosomal protein S21	2,9	0,002
P02790	HPX	Hemopexin	2,9	0,007
Q15814	TBCC	Tubulin-specific chaperone C	2,9	0,03
Q9BSJ8	ESYT1	Extended synaptotagmin-1	2,8	< 0.001
Q9Y5Y2	NUBP2	Cytosolic Fe-S cluster assembly factor NUBP2	2,8	0,001
Q5SY16	NOL9	Polynucleotide 5'-hydroxyl-kinase NOL9	2,8	0,001
Q15084	PDIA6	Protein disulfide-isomerase A6	2,8	0,001
Q9H9P8	L2HGDH	L-2-hydroxyglutarate dehydrogenase, mitochondrial	2,8	0,002
K7EJQ8	HDHD2	Haloacid dehalogenase-like hydrolase domain-containing protein 2	2,8	0,002
Q5T749	KPRP	Keratinocyte proline-rich protein	2,8	0,006
Q8N6T3	ARFGAP1	ADP-ribosylation factor GTPase-activating protein 1	2,7	0,001
M0R026	ILVBL	2-hydroxyacyl-CoA lyase 2	2,7	0,001
Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	2,7	0,002
Q9NP61	ARFGAP3	ADP-ribosylation factor GTPase-activating protein 3	2,7	0,003
B4DJ81	NDUF\$1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	2,6	0,001
Q96S44	TP53RK	EKC/KEOPS complex subunit TP53RK	2,6	0,002

Q96IU4	ABHD14B	Protein ABHD14B	2,6	0,005
A0A087WU06	TUBGCP3	Gamma-tubulin complex component	2,6	0,007
Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	2,6	0,008
Q5VW32	BROX	BRO1 domain-containing protein BROX	2,6	0,011
P18669	PGAM1	Phosphoglycerate mutase 1	2,6	0,015
Q15388	TOMM20	Mitochondrial import receptor subunit TOM20 homolog	2,6	0,02
Q9NZ45	CISD1	CDGSH iron-sulfur domain-containing protein 1	2,6	0,025
O60566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	2,6	0,035
Q9P287	BCCIP	BRCA2 and CDKN1A-interacting protein	2,5	0,001
Q96A49	SYAP1	Synapse-associated protein 1	2,5	0,002
P78346	RPP30	Ribonuclease P protein subunit p30	2,5	0,002
E9PJN0	ACOT8	Acyl-coenzyme A thioesterase 8	2,5	0,003
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	2,5	0,005
P30740	SERPINB1	Leukocyte elastase inhibitor	2,5	0,006
Q8N6M0	OTUD6B	Deubiquitinase OTUD6B	2,5	0,007
095295	SNAPIN	SNARE-associated protein Snapin	2,5	0,007
Q8N6R0	EEF1AKNMT	eEF1A lysine and N-terminal methyltransferase	2,5	0,008
F5H008	VPS33B	Vacuolar protein sorting-associated protein 33B	2,5	0,009
Q9H840	GEMIN7	Gem-associated protein 7	2,5	0,009
Q16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	2,5	0,021
Q5VUJ6	LRCH2	Leucine-rich repeat and calponin homology domain-containing protein 2	2,5	0,028
A6NDU8	C5ort51	UPF0600 protein C5orf51	2,5	0,034
Q7L5D6	GET4	Golgi to ER traffic protein 4 homolog	2,5	0,036
X6RM00	ERC1	ELKS/Rab6-interacting/CAST family member 1	2,4	0,003
Q9UKK9	NUDT5	ADP-sugar pyrophosphatase	2,4	0,004
Q9NYK5	MRPL39	39S ribosomal protein L39, mitochondrial	2,4	0,006
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	2,4	0,008
Q86WA6	BPHL	Valacyclovir hydrolase	2,4	0,011
Q66PJ3	ARL61P4	ADP-ribosylation factor-like protein 6-interacting protein 4	2,4	0,011
P63151	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	2,4	0,016
P21/96	VDACI	Voltage-dependent anion-selective channel protein 1	2,4	0,026
Q9H6K0	DHA33	A I P-dependent KNA helicase DHX33	2,4	0,032
P11802	CDK4	Cyclin-dependent kinase 4	2,3	<0.001
Q9BQC3	DPH2 DNDC1	2-(3-amino-5-carboxypropyl)histidine synthase subunit 2	2,3	0,003
H3BV80	KNP51	KNA-binding protein with serine-rich domain 1	2,3	0,005
Q81V32	DIOV2	Bikessen lemman 2	2,3	0,006
Q81018	NOP1	Ribosomai oxygenase 2	2,3	0,007
D5707(	CEAD200	Cilia and feaglla appointed protein 208	2,3	0,011
004/01/0	SDE2L1	Stromal coll derived factor 2 like protein 1	2,3	0,011
01/7//	DP MT5	Destain argining N methyltranoferase 5	2,2	0,003
0405/7	CMDS	CDP manpace / 6 debudratace	2,2	0,008
O9ND97	DVNI R B1	Dynain light chain readblock type 1	2,2	0,003
09BP72	SPIN2R	Spindlin-2B	2,2	0.026
Q/UI 22	UOCC3	Ubiquinal-cutochrome-c reductase complex assembly factor 3	2,2	0.045
P62879	GNB2	Guanine nucleoride-hinding protein G(I)/G(S)/G(T) subunit heta-2	2,2	0.001
043237	DYNC1LI2	Cytoplasmic dynein 1 light intermediate chain 2	2,1	0,001
A0A0A0MTB8	WDR 36	WD repeat.containing protein 36	2,1	0.009
013509	TUBB3	Tubulin beta 3 chain	2,1	0.012
092785	DPF2	Zinc finger protein ubi-d4	2,1	0.012
016204	CCDC6	Coiled-coil domain-containing protein 6	2,1	0.037
09868	SEC23IP	SEC23-interacting protein	2,1	0.001
014318	FKBP8	Pentidyl-prolyl cis-trans isomerase FKBP8	2	0.001
Q11510 Q95801	TTC4	Tetratricopentide repeat protein 4	2.	0.008
013257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	2	0.009
08NDI1	FHBP1	FH domain-binding protein 1	2	0.01
Q96BW9	TAMM41	Phosphatidate cytidylyltransferase, mitochondrial	2.	0.01
O9BZX2	UCK2	Uridine-cytidine kinase 2.	2.	0.011
O9UOR0	SCML2	Sex comb on midleg-like protein 2.	2.	0.011
043815	STRN	Striatin	2.	0.015
O9H974	OTRT2	Queuine tRNA-ribosyltransferase accessory subunit 2	2	0.016
015019	SEPTIN2	Sentin-2	2	0.024
P49903	SEPHS1	Selenide, water dikinase 1	2.	0.045
P35520	CBS	Cystathionine beta-synthase	19	0.003
O9UI30	TRMT112	Multifunctional methyltransferase subunit TR M112-like protein	1 9	0.004
P52788	SMS	Spermine synthase	1.9	0.012
016718	NDUFA5	NADH dehydrogenase [ubiquinone] 1 alpha subcompley subunit 5	1.9	0.012
×10/10	111/01/11	The second secon	1,7	0,015
015291	R BBD5	Retinoblastoma-binding protein 5	1 0	11112
Q15291	RBBP5	Ketinoblastoma-binding protein 5 Lipid droplet-regulating VLDL assembly factor AUD1	1,9	0.014
Q15291 Q9Y679 OSNIBLIS	RBBP5 AUP1 ATADI	Retinoblastoma-binding protein 5 Lipid droplet-regulating VLDL assembly factor AUP1 ATDree femily A A domain containing protein 1	1,9	0,014
Q15291 Q9Y679 Q8NBU5	RBBP5 AUP1 ATAD1 ACADSP	Retinoblastoma-binding protein 5 Lipid droplet-regulating VLDL assembly factor AUP1 ATPase family AAA domain-containing protein 1 Shore themeshed abaia amorfic and CaA dobridge accuration big doi:1	1,9 1,9 1,9	0,014 0,014 0,016 0,016
Q15291 Q9Y679 Q8NBU5 P45954 Q96 4 T 9	RBBP5 AUP1 ATAD1 ACADSB PDF	Retinoblastoma-binding protein 5 Lipid droplet-regulating VLDL assembly factor AUP1 ATPase family AAA domain-containing protein 1 Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial B lipulose phocebara 3 emigrates	1,9 1,9 1,9 1,9 1,9	0,014 0,014 0,016 0,016
Q15291 Q9Y679 Q8NBU5 P45954 Q96AT9 OolUB71	RBBP5 AUP1 ATAD1 ACADSB RPE CACVED	Retinoblastoma-binding protein 5 Lipid droplet-regulating VLDL assembly factor AUP1 ATPase family AAA domain-containing protein 1 Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial Ribulose-phosphate 3-epimerase	1,9 1,9 1,9 1,9 1,9 1,9	0,014 0,014 0,016 0,016 0,018

Q9UHD2	TBK1	Serine/threonine-protein kinase TBK1	1,9	0,022
095551	TDP2	Tyrosyl-DNA phosphodiesterase 2	1,9	0,025
075146	HIP1R	Huntingtin-interacting protein 1-related protein	1.9	0.036
096859	R ANBP9	Ran-binding protein 9	1.9	0.037
P62979	R PS27A	Ubiquitin-40S ribosomal protein \$27a	1.8	0.002
P10599	TXN	Thioredovin	1.8	0.011
09NOX3	GPHN	Genhvrin [Includes: Molyhdonterin adenylyltransferase	1,8	0.025
D2489(	SHMT1	Soring hydrowymethylaransforage awteoplie	1,0	0.029
P17252	DR KCA	Denorie kie oo Coleko eme	1,0	0,050
P1/252	PERCA	Protein kinase C alpha type	1,8	0,042
P18031	PIPNI	Tyrosine-protein prospiratase non-receptor type 1	1,7	0,007
Q914B6	DCAFI	DDBI- and CUL4-associated factor I	1,/	0,045
Q5QPM7	PSMF1	Proteasome inhibitor P131 subunit	1,6	<0.001
Q8TDH9	BLOCISS	Biogenesis of lysosome-related organelles complex 1 subunit 5	1,6	0,002
P21964	COMT	Catechol O-methyltransferase	1,6	0,003
Q9UH62	ARMCX3	Armadillo repeat-containing X-linked protein 3	1,6	0,006
Q2M2I8	AAK1	AP2-associated protein kinase 1	1,6	0,036
H7C155	RAF1	Non-specific serine/threonine protein kinase	1,6	0,047
O95831	AIFM1	Apoptosis-inducing factor 1, mitochondrial	1,5	0,002
Q96TC7	RMDN3	Regulator of microtubule dynamics protein 3	1,5	0,002
B4E1N1	ARMC6	Armadillo repeat-containing protein 6	1,5	0,007
Q9UL25	RAB21	Ras-related protein Rab-21	1,5	0,012
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	1,5	0,014
Q16543	CDC37	Hsp90 co-chaperone Cdc37	1,5	0,016
O15269	SPTLC1	Serine palmitoyltransferase 1	1,5	0,018
P35268	RPL22	60S ribosomal protein L22	1,5	0,035
O75688	PPM1B	Protein phosphatase 1B	1,5	0,038
O9Y266	NUDC	Nuclear migration protein nudC	1.5	0.047
Q60825	PFKFB2	6-phosphofructo-2-kinase/fructose-2 6-bisphosphatase 2	15	0.049
016576	R BBP7	Histone-binding protein R BBP7	1,5	0.002
D(0953	CDC/2	Cell division control protein (2 homolog	1,4	0.002
OTC07	TRC1D15	TPC1 domain family momber 15	1,4	0.005
Qarcu/	NDPC2	Destein NDP C2	1,4	0.01
Q70012	P DC25	400 sile score di accessi a 625	1,4	0.01
P62851	RP325	405 ribosomai protein 525	1,4	0,01
Q\$1760	SKSFII	Serine/arginine-rich-splicing factor 11	1,4	0,01
0/5663	TIPKL	11P41-like protein	1,4	0,034
Q90L15	BAG5	BAG family molecular chaperone regulator 5	1,4	0,038
Q147X3	NAA30	N-alpha-acetyltransferase 30	1,4	0,047
Q8IXI1	RHOT2	Mitochondrial Rho GTPase 2	1,3	0,001
Q9GZS3	WDR61	WD repeat-containing protein 61	1,3	0,003
P51553	IDH3G	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	1,3	0,014
Q8TEX9	IPO4	Importin-4	1,3	0,024
Q5VT66	MTARC1	Mitochondrial amidoxime-reducing component 1	1,3	0,028
P19367	HK1	Hexokinase-1	1,3	0,035
P62820	RAB1A	Ras-related protein Rab-1A	1,3	0,04
Q9Y570	PPME1	Protein phosphatase methylesterase 1	1,3	0,047
P35237	SERPINB6	Serpin B6	1,2	0,002
O60784	TOM1	Target of Myb protein 1	1,2	0,006
P55072	VCP	Transitional endoplasmic reticulum ATPase	1,2	0,018
P20042	EIF2S2	Eukaryotic translation initiation factor 2 subunit 2	1,2	0,023
Q9NQT5	EXOSC3	Exosome complex component RRP40	1,2	0,026
P29558	RBMS1	RNA-binding motif, single-stranded-interacting protein 1	1,2	0,027
P26368	U2AF2	Splicing factor U2AF 65 kDa subunit	1,2	0,038
O9H0U4	RAB1B	Ras-related protein Rab-1B	1,2	0,045
P62873	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	1,1	0.009
015738	NSDHI	Sterol-4-alpha-carboxylate 3-dehydrogenase decarboxylating	11	0.024
P31040				0.027
P09211	SDHA	Succinate dehydrogenase [ubiquinone] flavonrotein subunit, mitochondria]	11	
053EL 6	SDHA GSTP1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	1,1	0.027
	SDHA GSTP1 PDCD4	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4	1,1 1,1	0,027
01/126	SDHA GSTP1 PDCD4 DSG2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Dermodein 2	1,1 1,1 1,1	0,027 0,047 0.012
Q14126	SDHA GSTP1 PDCD4 DSG2 OTUB1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitie a bioexterces OTUB1	1,1 1,1 1,1 1	0,027 0,047 0,012
Q14126 Q96FW1	SDHA GSTP1 PDCD4 DSG2 OTUB1 P P P1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Pitocompile DNA menoresing protein 1 hemelog A	1,1 1,1 1,1 1 1	0,027 0,047 0,012 0,019
Q14126 Q96FW1 P56182	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 CEP PINUL	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A	1,1 1,1 1,1 1 1 1	0,027 0,047 0,012 0,019 0,026
Q14126 Q96FW1 P56182 P50454 Q14498	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 PDV20	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 DNA his disc serucia 20	1,1 1,1 1,1 1 1 1 1 1	0,027 0,047 0,012 0,019 0,026 0,029
Q14126 Q96FW1 P56182 P50454 Q14498	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 D N27	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 (of the particular of 20	1,1 1,1 1,1 1 1 1 1 1 1 1	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,027
Q14126 Q96FW1 P56182 P50454 Q14498 P62081	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 DC2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein S7	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,037
Q14126 Q26FW1 P56182 P50454 Q14498 P62081 P16435 PD P1V	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein S7 NADPHcytochrome P450 reductase	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1 1 1	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,037 0,041
Q14126 Q26FW1 P56182 P50454 Q14498 P62081 P16435 <b>PRDX4 cysteine-depend</b>	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR POR	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein S7 NADPHcytochrome P450 reductase	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,037 0,041
Q14126 Q26FW1 P56182 P50454 Q14498 P62081 P16435 <b>PRDX4 cysteine-depend</b> Q12797	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR leat interactors ASPH	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein 57 NADPHcytochrome P450 reductase Aspartyl/asparaginyl beta-hydroxylase	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1 1 3,9	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,037 0,041 <0.001
Q14126 Q96FW1 P56182 P50454 Q14498 P62081 P16435 PRDX4 cysteine-depend Q12797 I3L1P8	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR RPS7 POR Lent interactors ASPH SLC25A11	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein 37 NADPHcytochrome P450 reductase NADPHcytochrome P450 reductase Aspartyl/asparaginyl beta-hydroxylase Mitochondrial 2-oxoglutarate/malate carrier protein	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1 3,9 3,5	0.027 0.047 0.012 0.019 0.026 0.029 0.037 0.037 0.041 <0.001 <0.001
Q14126 Q26FW1 P56182 P50454 Q14498 P62081 P16435 <b>PRDX4 cysteine-depend</b> Q12797 I3L1P8 A0A0B4J1Z1	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR elet interactors ASPH SLC25A11 SRSF7	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein 57 NADPHcytochrome P450 reductase Aspartyl/asparaginyl beta-hydroxylase Mitochondrial 2-oxoglutarate/malate carrier protein Serine/arginine-rich-splicing factor 7	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1 3,9 3,5 3,1	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,037 0,041 <0.001 <0.001 0,002
Q14126 Q96FW1 P56182 P50454 Q14498 P62081 P16435 <b>PRDX4 cysteine-depend</b> Q12797 I3L1P8 A0A0B4J1Z1 F5H6E2	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR lent interactors ASPH SLC25A11 SRSF7 MYO1C	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein 57 NADPHcytochrome P450 reductase Aspartyl/asparaginyl beta-hydroxylase Mitochondrial 2-oxoglutarate/malate carrier protein Serine/arginine-rich-splicing factor 7 Unconventional myosin-Ic	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1 3,9 3,5 3,1 2,9	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,037 0,041 <0.001 <0.001 0,002 0,001
Q14126 Q26FW1 P56182 P50454 Q14498 P62081 P16435 PRDX4 cysteine-depend Q12797 I3L1P8 A0A0B4J1Z1 F5H6E2 O00469	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR POR RPS7 POR SEC25A11 SRSF7 MYO1C PLOD2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein S7 NADPHcytochrome P450 reductase Aspartyl/asparaginyl beta-hydroxylase Mitochondrial 2-oxoglutarate/malate carrier protein Serine/arginine-rich-splicing factor 7 Unconventional myosin-Ic Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 3,9 3,5 3,1 2,9 2,8	0,027 0,047 0,012 0,019 0,026 0,029 0,035 0,037 0,041 <0.001 <0.001 0,002 0,001 0,03
Q14126 Q26FW1 P56182 P50454 Q14498 P62081 P16435 <b>PRDX4 cysteine-depend</b> Q12797 I3L1P8 A0A0B4J1Z1 F5H6E2 O00469 Q9NVP1	SDHA GSTP1 PDCD4 DSG2 OTUB1 RRP1 SERPINH1 RBM39 RPS7 POR POR ent interactors ASPH SLC25A11 SRSF7 MYO1C PLOD2 DDX18	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial Glutathione S-transferase P Programmed cell death protein 4 Desmoglein-2 Ubiquitin thioesterase OTUB1 Ribosomal RNA processing protein 1 homolog A Serpin H1 RNA-binding protein 39 40S ribosomal protein 37 NADPHcytochrome P450 reductase Aspartyl/asparaginyl beta-hydroxylase Mitochondrial 2-oxoglutarate/malate carrier protein Serine/arginine-rich-splicing factor 7 Unconventional myosin-Ic Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 ATP-dependent RNA helicase DDX18	1,1 1,1 1,1 1 1 1 1 1 1 1 1 1 1 1 1 3,9 3,5 3,1 2,9 2,8 2,6	0,027 0,047 0,012 0,019 0,026 0,035 0,037 0,041 <0.001 <0.001 0,002 0,001 0,03 0,007

Q9Y2R4	DDX52	Probable ATP-dependent RNA helicase DDX52	2,3	0,024
Q13618	CUL3	Cullin-3	2,2	0,013
Q9Y2R5	MRPS17	28S ribosomal protein S17, mitochondrial	2,2	0,03
D6RA00	ENOPH1	Enolase-phosphatase E1	2,1	0,017
P30154	PPP2R1B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	2,1	0,021
075592	MYCBP2	E3 ubiquitin-protein ligase MYCBP2	2,1	0,027
Q8NBS9	TXNDC5	Thioredoxin domain-containing protein 5	1,9	0,007
P84103	SRSF3	Serine/arginine-rich splicing factor 3	1,9	0,028
Q12905	ILF2	Interleukin enhancer-binding factor 2	1,9	0,032
P29372	MPG	DNA-3-methyladenine glycosylase	1,9	0,039
Q7KZ85	SUPT6H	Transcription elongation factor SPT6	1,9	0,043
Q92783	STAM	Signal transducing adapter molecule 1	1,8	0,041
Q66K74	MAP1S	Microtubule-associated protein 1S	1,8	0,049
A0A2R8Y7S2	SMARCA4	Transcription activator BRG1	1,7	0,008
B4DJ81	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	1,7	0,039
Q81U18	CRLF3	Cytokine receptor-like factor 3	1,7	0,049
Q8W X93	PALLD	Palladin Number of the test of tes	1,/	0,049
Q1469/	GANAB	Neutral alpha-glucosidase AB	1,6	0,001
P11802	UVOU1		1,6	0,011
A0A08/X054	HYOUI	Hypoxia up-regulated protein 1	1,6	0,019
P49593	PPMIF	Protein phosphatase IF	1,5	0,015
0/560/	NPM5	Tutcieopiasmin-3	1,5	0,022
Q14152	EIF3A DDD1D124	Eukaryotic translation initiation factor 3 subunit A	1,5	0,025
0147/4 09RVD2	CNU 2	Frotein prospiratase 1 regulatory subunit 12A	1,5	0.024
090002	UNL3 TNK\$1RD1	Suanne nucleotide-ofinding protein-like 3	1,5	0.0/2
Q/C0C2	SDE2L1	Stromal call derived factor 2 like protein 1	1,5	0,043
016513	DKN2	Serine/threening protein kingse N2	1,4	0,002
043809	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	1.4	0.028
092974	AR HGFF2	R ho guanine nucleotide exchange factor 2	1.3	0.002
Q55W79	CFP170	Centrosomal protein of 170 kDa	13	0.013
O9UOR0	SCML2	Sex comb on midleg-like protein 2	13	0.016
014318	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8	1.3	0.02
P27824	CANX	Calnexin	1.3	0.022
P49411	TUFM	Elongation factor Tu, mitochondrial	1,3	0,022
O9BWF3	RBM4	RNA-binding protein 4	1,3	0.038
Q16543	CDC37	Hsp90 co-chaperone Cdc37	1,3	0,039
A0A087WY71	AP2M1	AP-2 complex subunit mu	1,2	0,014
P18858	LIG1	DNA ligase 1	1,2	0,014
Q12904	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	1,2	0,019
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	1,2	0,033
Q8TCG1	CIP2A	Protein CIP2A	1,2	0,04
P62249	RPS16	40S ribosomal protein S16	1,2	0,043
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	1,1	0,006
E7EPN9	PRRC2C	Protein PRRC2C	1,1	0,018
Q99567	NUP88	Nuclear pore complex protein Nup88	1,1	0,032
P30520	ADSS2	Adenylosuccinate synthetase isozyme 2	1,1	0,035
Q07020	RPL18	60S ribosomal protein L18	1,1	0,036
P13489	RNH1	Ribonuclease inhibitor	1	0,03
PRDX5 cysteine-dej	pendent interactors			
P36551	CPOX	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	6,4	< 0.001
Q6DKK2	TTC19	Tetratricopeptide repeat protein 19, mitochondrial	3,9	< 0.001
Q96A49	SYAP1	Synapse-associated protein 1	3,9	< 0.001
O00165	HAX1	HCLS1-associated protein X-1	3,7	< 0.001
A0A0C4DGQ6	RPRD1A	Regulation of nuclear pre-mRNA domain-containing protein 1A	2,9	0,002
P78371	CCT2	T-complex protein 1 subunit beta	2,7	< 0.001
P85037	FOXK1	Forkhead box protein K1	2,6	0,012
A0A024R442	A0A024R442	>tr A0A024R442 A0A024R442_HUMAN Aspartyl aminopeptidase, isoform CRA_b OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>sp Q9ULA0 DNPEP_HUMAN Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>tr E7ETB3 E7ETB3_HUMAN Aspartyl aminopeptidase, iso	2,6	0,012
P30740	SERPINB1	Leukocyte elastase inhibitor	2,3	0,016
Q2TAM5	RELA	RELA protein	2,2	0,013
Q10713	PMPCA	Mitochondrial-processing peptidase subunit alpha	2,2	0,018
A0A075B6R9	IGKV2D-24	Probable non-functional immunoglobulin kappa variable 2D-24	2,2	0,041
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	2,1	< 0.001
O95801	TTC4	Tetratricopeptide repeat protein 4	2,1	0,025
Q6PID6	TTC33	Tetratricopeptide repeat protein 33	2,1	0,043
Q96HS1	PGAM5	Serine/threonine-protein phosphatase PGAM5, mitochondrial	2	0,005
P13667	PDIA4	Protein disulfide-isomerase A4	2	0,018
O00483	NDUFA4	Cytochrome c oxidase subunit NDUFA4	2	0,025
Q96DH6	MSI2	RNA-binding protein Musashi homolog 2	2	0,044
P62979	RPS27A	Ubiquitin-40S ribosomal protein \$27a	1,9	0,001
P07355	ANXA2	Annexin A2	1,9	0,007

E9PGZ1	CALD1	Caldesmon	1,8	0,023
O95831	AIFM1	Apoptosis-inducing factor 1, mitochondrial	1,6	0,001
Q9NZL9	MAT2B	Methionine adenosyltransferase 2 subunit beta	1,6	0,006
H7C128	BRD8	Bromodomain-containing protein 8	1,6	0,011
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	1,6	0,013
P43304	GPD2	Glycerol-3-phosphate dehydrogenase, mitochondrial	1,6	0,015
P43686	PSMC4	26S proteasome regulatory subunit 6B	1,6	0,016
E5KLJ9	OPA1	Dynamin-like 120 kDa protein, form S1	1,5	0,004
P26599	PTBP1	Polypyrimidine tract-binding protein 1	1,5	0,006
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	1,5	0,02
Q96IZ0	PAWR	PRKC apoptosis WT1 regulator protein	1,4	0,013
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	1,4	0,016
Q8N3X1	FNBP4	Formin-binding protein 4	1,3	0,009
C9J4Z3	RPL37A	60S ribosomal protein L37a	1,3	0,022
P31689	DNAJA1	DnaJ homolog subfamily A member 1	1,2	0,003
Q9HB71	CACYBP	Calcyclin-binding protein	1,2	0,018
Q8NC51	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	1,2	0,028
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	1,2	0,035
Q9NX63	CHCHD3	MICOS complex subunit MIC19	1,1	0,004
Q5QPM7	PSMF1	Proteasome inhibitor PI31 subunit	1,1	0,007
Q14C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	1,1	0,02
P40222	TXLNA	Alpha-taxilin	1,1	0,048

Table S4: all cysteine-dependent interactors (wild-type and  $C_R S$ )

uniprot ID	gene	protein	inte_action
PRDX1 cysteine-dep	endent interactors	•	r
P62273	RPS29	40S ribosomal protein S29	WT
P13667	PDIA4	Protein disulfide-isomerase A4	WT
O60762	DPM1	Dolichol-phosphate mannosyltransferase subunit 1	WT
Q15185	PTGES3	Prostaglandin E synthase 3	WT, C <sub>.</sub> S
P31323	PRKAR2B	cAMP-dependent protein kinase type II-beta regulatory subunit	WT
P50570	DNM2	Dynamin-2	WT
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	WT
A0A3B3IUD2	MSTO1	Protein misato homolog 1	WT
Q96FV9	THOC1	THO complex subunit 1	WT
P15924	DSP	Desmoplakin	WT, C.S
Q9Y2V2	CARHSP1	Calcium-regulated heat-stable protein 1	WT, C.S
Q9H845	ACAD9	Complex I assembly factor ACAD9, mitochondrial	WT
P83731	RPL24	60S ribosomal protein L24	WT
Q9BY32	ITPA	Inosine triphosphate pyrophosphatase	WT, C.S
O94760	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	WT
P62266	RPS23	40S ribosomal protein S23	WT
Q8WWH5	TRUB1	Probable tRNA pseudouridine synthase 1	WT
Q6P1L8	MRPL14	39S ribosomal protein L14, mitochondrial	WT
Q99961	SH3GL1	Endophilin-A2	WT
P08559	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	WT, C.S
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	WT
I3L2Z5	MAZ	Myc-associated zinc finger protein	WT
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	WT, C.S
Q14008	CKAP5	Cytoskeleton-associated protein 5	WT, C S
Q7L2E3	DHX30	ATP-dependent RNA helicase DHX30	WT
O14964	HGS	Hepatocyte growth factor-regulated tyrosine kinase substrate	WT
Q5JTH9	RRP12	RRP12-like protein	WT
P49841	GSK3B	Glycogen synthase kinase-3 beta	WT
P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	WT
Q15149	PLEC	Plectin	WT, C.S
E3W994	CLASP2	CLIP-associating protein 2	WT
Q16698	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	WT
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	WT, C.S
E7EVH7	E7EVH7	Kinesin light chain	WT
Q15717	ELAVL1	ELAV-like protein 1	WT
P22626	HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	WT
Q99615	DNAJC7	DnaJ homolog subfamily C member 7	WT, C <sub>.</sub> S
Q7L1Q6	BZW1	Basic leucine zipper and W2 domain-containing protein 1	WT
Q01813	PFKP	ATP-dependent 6-phosphofructokinase, platelet type	WT
Q8N1F7	NUP93	Nuclear pore complex protein Nup93	WT
O95801	TTC4	Tetratricopeptide repeat protein 4	WT
P63165	SUMO1	Small ubiquitin-related modifier 1	WT, C <sub>s</sub> S
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	WT, CS
D6RBD7	EEF1E1	Eukaryotic translation elongation factor 1 epsilon-1	WT
Q99543	DNAJC2	DnaJ homolog subfamily C member 2	WT

Q9NW13	RBM28	RNA-binding protein 28	WT
Q08211	DHX9	ATP-dependent RNA helicase A	WT
A0A1W2PRV5	SMN2	Survival motor neuron protein	WT
O60493	SNX3	Sorting nexin-3	WT
P62318	SNRPD3	Small nuclear ribonucleoprotein Sm D3	WT
Q9Y5K6	CD2AP	CD2-associated protein	WT
Q02241	KIF23	Kinesin-like protein KIF23	WT
P19623	SRM	Spermidine synthase	WT
P24534	EEF1B2	Elongation factor 1-beta	WT
Q9BV44	THUMPD3	THUMP domain-containing protein 3	WT
Q9BQG0	MYBBP1A	Myb-binding protein 1A	WT, C,S
A0A0C4DGX4	CUL1	Cullin-1	WT
P51153	RAB13	Ras-related protein Rab-13	WT
Q8TCG1	CIP2A	Protein CIP2A	WT
P62851	RPS25	40S ribosomal protein S25	WT, C <sub>r</sub> S
Q92879	CELF1	CUGBP Elav-like family member 1	WT, C <sub>r</sub> S
014617	AP3D1	AP-3 complex subunit delta-1	WT
P53582	METAP1	Methionine aminopeptidase 1	WT
Q71UI9	H2AZ2	Histone H2A.V	WT
Q96I25	RBM17	Splicing factor 45	WT, C <sub>r</sub> S
075369	FLNB	Filamin-B	WT
P43686	PSMC4	26S proteasome regulatory subunit 6B	WT
O43447	PPIH	Peptidyl-prolyl cis-trans isomerase H	WT
Q13595	TRA2A	Transformer-2 protein homolog alpha	WT
P36915	GNL1	Guanine nucleotide-binding protein-like 1	WT, C <sub>s</sub> S
P24666	ACP1	Low molecular weight phosphotyrosine protein phosphatase	WT, C <sub>s</sub>
P61081	UBE2M	NEDD8-conjugating enzyme Ubc12	WT
P46940	IQGAP1	Ras GTPase-activating-like protein IQGAP1	WT, C <sub>r</sub> S
P61011	SRP54	Signal recognition particle 54 kDa protein	WT, C S
Q13247	SRSF6	Serine/arginine-rich splicing factor 6	WT
Q9HAV4	XPO5	Exportin-5	WT
E9PD53	SMC4	Structural maintenance of chromosomes protein	WT, C_S
O15446	POLR1G	DNA-directed RNA polymerase I subunit RPA34	WT
Q96N67	DOCK7	Dedicator of cytokinesis protein 7	WT, C.S
A0A2R8YDQ9	SUCLA2	SuccinateCoA ligase [ADP-forming] subunit beta, mitochondrial	WT, CS
P49207	RPL34	60S ribosomal protein L34	WT, C.S
Q9GZT3	SLIRP	SRA stem-loop-interacting RNA-binding protein, mitochondrial	WT, CS
Q8WTT2	NOC3L	Nucleolar complex protein 3 homolog	WT
P62280	RPS11	40S ribosomal protein S11	WT
P61160	ACTR2	Actin-related protein 2	WT
Q92615	LARP4B	La-related protein 4B	WT
A0A0A0MRM9	NOLC1	Nucleolar and coiled-body phosphoprotein 1	WT
O14974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	WT
P49790	NUP153	Nuclear pore complex protein Nup153	WT, CS
Q9H6T3	RPAP3	RNA polymerase II-associated protein 3	WT
P07196	NEFL	Neurofilament light polypeptide	WT
P61313	RPL15	60S ribosomal protein L15	WT
A0A087WZ13	RAVER1	Ribonucleoprotein PTB-binding 1	WT, C S
O15305	PMM2	Phosphomannomutase 2	WT
E7EX90	DCTN1	Dynactin subunit 1	WT, C S
Q9H0C8	ILKAP	Integrin-linked kinase-associated serine/threonine phosphatase 2C	WT, C_S
Q9BUQ8	DDX23	Probable ATP-dependent RNA helicase DDX23	WT
Q9BQ39	DDX50	ATP-dependent RNA helicase DDX50	WT
Q9UQE7	SMC3	Structural maintenance of chromosomes protein 3	WT, C_S
Q9H2G2	SLK	STE20-like serine/threonine-protein kinase	WT, C_S
Q13363	CTBP1	C-terminal-binding protein 1	WT
Q13813	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	WT
A0A1B0GV47	KIF21A	Kinesin-like protein KIF21A	WT
O43707	ACTN4	Alpha-actinin-4	WT
Q8N9T8	KRI1	Protein KRI1 homolog	WT, CS
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	WT
P61163	ACTR1A	Alpha-centractin	WT, C S
A0A1W2PPZ5	TCEA1	Transcription elongation factor A protein 1	WT
F8W8I6	TIA1	Nucleolysin TIA-1 isoform p40	WT
P23258	TUBG1	Tubulin gamma-1 chain	WT.C.S
	RPL6	60S ribosomal protein L6	WT
002878	VV1	Transcriptional repressor protein VV1	W I W/T
Q02878 P25490		mansemptional repressor protein 1.11	W 1
Q02878 P25490	CTNNP1	Catenin hera 1	WT
Q02878 P25490 A0A2R8Y804 B5MCE9	CTNNB1 DES1	Catenin beta-1	WT
Q02878 P25490 A0A2R8Y804 B5MCF9 Q9NSK0	CTNNB1 PES1	Catenin beta-1 Pescadillo homolog Vincein light chain (	WT WT, CS
Q02878 P25490 A0A2R8Y804 B5MCF9 Q9NSK0 Q9CBK(	CTNNB1 PES1 KLC4 P PM16	Catenin beta-1 Pescadillo homolog Kinesin light chain 4 PNIA biodica generatio 14	WT WT, C, S WT
Q02878 P25490 A0A2R8Y804 B5MCF9 Q9NSK0 Q96PK6 ONULUC	CTNNB1 PES1 KLC4 RBM14 DDX20	Catenin beta-1 Pescadillo homolog Kinesin light chain 4 RNA-binding protein 14 Prohebite ATD dependent PNA beliense DDV20	WT WT, C, S WT WT
Q02878 P25490 A0A2R8Y804 B5MCF9 Q9NSK0 Q96PK6 Q9UHI6 U28P81	CTNNB1 PES1 KLC4 RBM14 DDX20	Catenin beta-1 Pescadillo homolog Kinesin light chain 4 RNA-binding protein 14 Probable ATP-dependent RNA helicase DDX20 Miserbale arguments lichtic from 1/2/2/2	WT WT, C, S WT WT WT, C, S

	MID OF		
Q15813	TBCE	Iubulin-specific chaperone E	W1
Q8WVM8	SCFD1	Sec1 family domain-containing protein 1	WT, C.S
016352	INIA	Alpha internevin	WT
Q16332	11NA	Alpha-Internexin	
P19338	NCL	Nucleolin	WT
A0A087X2D5	MRPL45	39S ribosomal protein L45, mitochondrial	WT
ADADAD) (DTC	A BI1	Ablinger 1	WT C S
AUAUAUMIK16	ADII	ADI Interactor 1	w1,C <sub>5</sub>
P48507	GCLM	Glutamatecysteine ligase regulatory subunit	WT
O9H9A6	LRRC40	Leucine-rich repeat-containing protein 40	WT
2,11,110	D ( NO ( D)		
P46060	RANGAPI	Ran G I Pase-activating protein 1	WT, C, S
Q9ULV4	CORO1C	Coronin-1C	WT, C S
ESCW/T/	WNK1	Non specific corino/throoping protein kinese	WT
13G w 14	WINKI	Non-specific serme/ threenine protein kinase	w 1
A0A3B3ISG5	IDE	Insulin-degrading enzyme	WT
P14174	MIF	Macrophage migration inhibitory factor	WT.CS
00005/	ADVICEE		
Q929/4	ARHGEF2	Kho guanine nucleotide exchange factor 2	W I
Q13561	DCTN2	Dynactin subunit 2	WT, C.S
OPHOR	KI C2	Vincein light shein 2	WTCS
QUIIODO	KL02	Kincsin ngiteenan 2	w1,C3
Q9NR12	PDLIM7	PDZ and LIM domain protein 7	WT, C <sub>s</sub>
014684	R R P1B	R ibosomal R NA processing protein 1 homolog B	WT C S
	CNOT I		
A5YKK6	CNOTI	CCR4-NO1 transcription complex subunit 1	W I
P31942	HNRNPH3	Heterogeneous nuclear ribonucleoprotein H3	WT
D08243	ASNIS	A charge in a synthetase [alutamine hydrolyzing]	WТ
100245	10100		
Q96MU7	YTHDC1	YTH domain-containing protein 1	WT
P78316	NOP14	Nucleolar protein 14	WT
0.001/2702	F43(4004		107741
Q9NZB2	FAM120A	Constitutive coactivator of PPAR-gamma-like protein 1	W 1
Q5JRX3	PITRM1	Presequence protease, mitochondrial	WT, C.S
096D71	R FPS1	R aIRPLassociated Ensidemain-containing protein 1	WT
Q)0D/1	ICLI 51	Kandi Fassociated Eps domani-containing protein 1	WI
Q14683	SMC1A	Structural maintenance of chromosomes protein 1A	WT, C <sub>s</sub>
O9UG63	ABCF2	ATP-binding cassette sub-family F member 2	WT.CS
OTTUN	DDD		WT CC
QSIDHO	DDI2	Protein DD11 nomolog 2	w1,C5
P82921	MRPS21	28S ribosomal protein S21, mitochondrial	WT
075717	WDHD1	WD repeat and HMG has DNA hinding protein 1	WТ
0/)/1/	w D11D1	w Diepert and Timo-box Divisioning protein T	w 1
Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	WT
P27144	AK4	Adenvlate kinase 4. mitochondrial	WT
FZECDO	NICENC		WT CC
E/ESP9	NEFM	160 kDa neuroniament protein	w1,C <sub>5</sub>
Q9Y237	PIN4	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	WT
F8WB06	ATXN2	Atayin-2	WT C S
1000000	III AIV2	Indanie 2	W1,00
P54578	USP14	Ubiquitin carboxyl-terminal hydrolase 14	WT, C <sub>s</sub>
P20042	EIF2S2	Eukaryotic translation initiation factor 2 subunit 2	WT, C S
OSWWKS	CKAD2	Cutophalatan associated protein 2	WT
Qowwk)	CKAF2	Cytoskeleton-associated protein 2	w 1
P52948	NUP98	Nuclear pore complex protein Nup98-Nup96	WT
007666	KHDR BS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	WT.CS
207000			
P46013	MK16/	Proliferation marker protein K1-6/	W I
P55084	HADHB	Trifunctional enzyme subunit beta, mitochondrial	WT, C.S
D18031	DTDN1	Tyracine protein phosphatase non recentor type 1	WT
110031	111111	Tyrosine-protein phosphatase non-receptor type 1	WI
Q15654	TRIP6	Thyroid receptor-interacting protein 6	WT, C <sub>s</sub>
O9Y2Z4	YARS2	TyrosinetRNA ligase, mitochondrial	WT
01/259	TD D (25		XV7'T*
Q14258	1 KIM25	E3 ubiquitin/15G15 ligase 1 K1M25	W 1
O00425	IGF2BP3	Insulin-like growth factor 2 mRNA-binding protein 3	WT, C.S
P35659	DFK	Protein DFK	WT
075500	N/VODDa		NV741
0/5592	M YCBP2	E3 ubiquitin-protein ligase MYCBP2	W I
O00273	DFFA	DNA fragmentation factor subunit alpha	WT
09H2U1	DHY36	ATD dependent DNA / P NA belicase DHY36	WТ
×/11201	DDIAJO		
P29558	KBMS1	KNA-binding motif, single-stranded-interacting protein 1	WT
Q9BXP5	SRRT	Serrate RNA effector molecule homolog	WT
014974	KPNR1	Importin subunit beta-1	WT
X14)/4	ATIND1	Importin subunit Deta-1	wi
Q96RP9	GFM1	Elongation factor G, mitochondrial	WT, C <sub>s</sub>
O02252	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	WT.CS
A DADA (D. (D.	LIDI DD	······································	
AUAU24R4E5	HDLBP	High density lipoprotein binding protein	W1,C5
Q9GZS1	POLR1E	DNA-directed RNA polymerase I subunit RPA49	WT
D38/32	COU	Coilin	WТ
00102	UEOTEN		
Q90L18	HECTDI	E3 ubiquitin-protein ligase HEC1D1	W I
Q13838	DDX39B	Spliceosome RNA helicase DDX39B	WT
071862	LARD4	La related protein A	WT CS
X/1KC2	LART <sup>4</sup>	Lanciacu protein 4	w 1,00
Q9UGI8	TES	Testin	WT
002543	R PI 18A	60S ribosomal protein L 18a	WT
	TELEON		
1′/8344	E1F4G2	Eukaryotic translation initiation factor 4 gamma 2	w1,C5
P60174	TPI1	Triosephosphate isomerase	WT
076003	CLR Y3	Chutaradavin 3	WT
070003	ULKAJ		1 1
O43252	PAPSS1	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	WT
P55010	EIF5	Eukarvotic translation initiation factor 5	WT
001101/2	CUDADOD		
Q9UQN3	CHMP2B	Charged multivesicular body protein 2b	W 1
Q14677	CLINT1	Clathrin interactor 1	WT
013283	C3BD1	Place CTPase activating protain hinding protein 1	WT
U1.320.3	CODLI	ixas o 11 asc-activating protein-binding protein 1	YV 1

P35249	RFC4	Replication factor C subunit 4	WT
Q9Y5X1	SNX9	Sorting nexin-9	WT
O9NYI8	TAB2	TGF-beta-activated kinase 1 and MAP3K7-binding protein 2	WT
P19367	HK1	Hexokinase-1	WT.C.S
O9UNE7	STUB1	F3 ubiquitin-protein ligase CHIP	WT CS
FADBAD	нка	Hevolvinase	WT
077(77	LILIWE1	F2 ubiquitia protoin ligase HI JWF1	WT CS
Q/262/	HU WEI		w 1, C 3
F611Q0	PDE12	2,5-phosphodiesterase 12	W I
Q5JTZ9	AARS2	AlaninetRNA ligase, mitochondrial	WT
014497	ARID1A	AT-rich interactive domain-containing protein 1A	WT
Q86U42	PABPN1	Polyadenylate-binding protein 2	WT
P37802	TAGLN2	Transgelin-2	WT, C <sub>r</sub> S
Q9BVJ6	UTP14A	U3 small nucleolar RNA-associated protein 14 homolog A	WT
Q8N163	CCAR2	Cell cycle and apoptosis regulator protein 2	WT
Q86VS8	HOOK3	Protein Hook homolog 3	WT
P39023	RPL3	60S ribosomal protein L3	WT, C <sub>S</sub>
Q14161	GIT2	ARF GTPase-activating protein GIT2	WT
Q86UK7	ZNF598	E3 ubiquitin-protein ligase ZNF598	WT
P04637	TP53	Cellular tumor antigen p53	WT, C S
095453	PARN	Poly(A)-specific ribonuclease PARN	WT
086VP4	GATAD2A	Transcriptional repressor p.66 alpha	WT
D22207	SCD2	Non anaifa linid transfor protain	WTCS
015042	D A D2C A D1	D.12 CTD	wi, CS
Q15042	KAB3GAPI	Rabs G I Pase-activating protein catalytic subunit	w 1, C, S
P23246	SFPQ	Splicing factor, proline- and glutamine-rich	W1
P00519	ABL1	1yrosine-protein kinase ABL1	WT
Q9U130	TRMT112	Multifunctional methyltransferase subunit TR M112-like protein	WT
P26373	RPL13	60S ribosomal protein L13	WT
A0A087WVZ9	POLR2E	DNA-directed RNA polymerase II subunit E	WT
M0R0F0	RPS5	40S ribosomal protein S5	WT, C <sub>r</sub> S
Q86WJ1	CHD1L	Chromodomain-helicase-DNA-binding protein 1-like	WT
Q14151	SAFB2	Scaffold attachment factor B2	WT, C <sub>.</sub> S
P28838	LAP3	Cytosol aminopeptidase	WT, C.S
P46777	RPL5	60S ribosomal protein L5	WT
O95782	AP2A1	AP-2 complex subunit alpha-1	WT. C S
O9H3U1	UNC45A	Protein unc-45 homolog A	WT
09H0H5	R ACGAP1	Rac GTPase-activating protein 1	WT
001081	LI2 A F1	Splicing factor U2 A F 35 kDa subunit	WTCS
095229	VIE4A	Chromosome accessisted kinesin KIE/A	WT
D12237	CKD	Construction Const	W I
P122//	CKB	Creatine kinase B-type	w I
A0A087WY71	AP2M1	AP-2 complex subunit mu	W1
P55809	OXCII	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	W1, C <sub>p</sub> S
C9JP00	MBNL1	Muscleblind-like protein 1	WT
P52732	KIF11	Kinesin-like protein KIF11	WT
Q14204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	WT, C <sub>r</sub> S
Q13509	TUBB3	Tubulin beta-3 chain	WT, C <sub>r</sub> S
P46063	RECQL	ATP-dependent DNA helicase Q1	WT
P51114	FXR1	Fragile X mental retardation syndrome-related protein 1	WT, C <sub>2</sub> S
Q5HYI8	RABL3	Rab-like protein 3	WT
P42166	TMPO	Lamina-associated polypeptide 2, isoform alpha	WT
O8TD19	NEK9	Serine/threonine-protein kinase Nek9	WT
07Z4H3	HDDC2	5'-deoxynucleotidase HDDC2	WT
09HD26	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein	WTCS
052110/	DVCP 2	Durralian 5 comb ovulato reductore 2	WT
Q3311/6	DCD1A	Pyrionne-3-carboxylate reductase 5	W I
Q9INP16	DCPIA	and the set of the set	W I
Q9B1N8	MKP526	285 ribosomai protein 526, mitochondriai	w I
Q9NYZ3	GTSE1	G2 and S phase-expressed protein 1	WT
O94927	HAUS5	HAUS augmin-like complex subunit 5	WT
P57740	NUP107	Nuclear pore complex protein Nup107	WT, C, S
P54920	NAPA	Alpha-soluble NSF attachment protein	WT
P17252	PRKCA	Protein kinase C alpha type	WT
F8W8R3	POLD2	DNA polymerase delta subunit 2	WT
Q9H814	PHAX	Phosphorylated adapter RNA export protein	WT
P15170	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	WT, C S
O43837	IDH3B	Isocitrate dehydrogenase [NAD] subunit beta. mitochondrial	WT. C S
014966	ZNF638	Zinc finger protein 638	WT
07R TV0	DHE5A	PHD finger-like domain-containing protein 54	WT CS
D53597	SUCI C1	Succinate CoA ligase [ADD/CDD forming] suburity links with the diff.	W1, C5 W/T
1 33377 OONID 20	DDV21	Nuclealer DNA holicers 2	w 1
Q9NK30	DDX21	Nucleolar KNA helicase 2	W 1
E9PQV9	DCUN1D5	DCN1-like protein	WT
O00231	PSMD11	26S proteasome non-ATPase regulatory subunit 11	WT
P25786	PSMA1	Proteasome subunit alpha type-1	WT
P51570	GALK1	Galactokinase	WT
Q8NB90	SPATA5	ATPase family protein 2 homolog	WT
		· · · · · · · · · · · · · · · · · · ·	

A0A3B3IRP5	CDC73	Parafibromin	WT, C S
Q9H2P0	ADNP	Activity-dependent neuroprotector homeobox protein	WT
Q13464	ROCK1	Rho-associated protein kinase 1	WT
Q52LJ0	FAM98B	Protein FAM98B	WT, C_S
Q15233	NONO	Non-POU domain-containing octamer-binding protein	WT
Q9P2J5	LARS1	LeucinetRNA ligase, cytoplasmic	WT, C.S
P60228	EIF3E	Eukarvotic translation initiation factor 3 subunit E	WT
C9IZR2	CTNND1	Catenin delta-1	WT.C.S
P49959	MR F11	Double-strand break renair protein MR F11	WT
D33240	CSTE2	Cleavage stimulation factor subunit 2	WT
01/512	DVN2	Social Appropriate protocol suburiti 2	WTCS
Q10313	P DC2	400 rik com al motoria \$2	wi,C,S
P15880	RP32	405 Hoosomai protein 52	wi,C,S
043264	Z W 10	Centromere/kinetochore protein zw10 homolog	W I
Q08/52	PPID	Peptidyl-prolyl cis-trans isomerase D	W I
P35221	CTNNA1	Catenin alpha-1	WT
Q14669	TRIP12	E3 ubiquitin-protein ligase TRIP12	WT
P46778	RPL21	60S ribosomal protein L21	WT, C <sub>2</sub> S
P50213	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	WT
Q8N1G4	LRRC47	Leucine-rich repeat-containing protein 47	WT, C S
O43237	DYNC1LI2	Cytoplasmic dynein 1 light intermediate chain 2	WT
Q14152	EIF3A	Eukaryotic translation initiation factor 3 subunit A	WT, C <sub>2</sub> S
Q6P2E9	EDC4	Enhancer of mRNA-decapping protein 4	WT, C <sub>S</sub>
P23919	DTYMK	Thymidylate kinase	WT, C.S
P63272	SUPT4H1	Transcription elongation factor SPT4	WT, C.S
P52597	HNRNPF	Heterogeneous nuclear ribonucleoprotein F	WT
O15785	TOMM34	Mitochondrial import receptor subunit TOM34	WT
P13804	FTFA	Flectron transfer flavonrotein subunit alpha, mitochondrial	WT C S
010567	A D1 B1	A D 1 complex subunit hera 1	WT CS
D/7897	OAP S1	Clutaming +P NA ligan	WT CS
P4/8//	D DC1	GiulannietRivA ngase	w 1, C 5
P62249	RPS16	405 ribosomai protein 516	W I
Q92616	GCNI	elF-2-alpha kinase activator GCNI	W1
P19525	EIF2AK2	Interferon-induced, double-stranded KNA-activated protein kinase	w1,CS
Q8NCW5	NAXE	NAD(P)H-hydrate epimerase	WI
Q16527	CSRP2	Cysteine and glycine-rich protein 2	WT, C <sub>2</sub> S
Q15637	SF1	Splicing factor 1	WT
P31689	DNAJA1	DnaJ homolog subfamily A member 1	WT, C <sub>z</sub> S
A0A087WXM6	RPL17	60S ribosomal protein L17	WT, C, S
Q9UG54	MAP3K7	Mitogen-activated protein kinase kinase kinase	WT, C, S
Q6Y7W6	GIGYF2	GRB10-interacting GYF protein 2	WT, C, S
P08708	RPS17	40S ribosomal protein S17	WT, C <sub>2</sub> S
K4DI93	CUL4B	Cullin 4B, isoform CRA_e	WT, C <sub>2</sub> S
P63010	AP2B1	AP-2 complex subunit beta	WT
Q9NZI8	IGF2BP1	Insulin-like growth factor 2 mRNA-binding protein 1	WT, C.S
P57772	EEFSEC	Selenocysteine-specific elongation factor	WT
O96AG4	LRRC59	Leucine-rich repeat-containing protein 59	WT.CS
P43246	MSH2	DNA mismatch repair protein Msh2	WT.C.S
013136	PPFIA1	Liprin-alpha-1	WT.C.S
076021	R SI 1D1	Ribosomal I 1 domain-containing protein 1	WT C S
09UNM6	DSMD13	26S protessome non ATDase regulatory subunit 13	WT
ADA 1BOGWE2	STYBD1	Syntaxin binding protein 1	WT C S
008122	NEUND	P NA outocine C(5) mothylaraneforace NSUN2	WT CS
<u>200125</u>	FDC2	Takanoor of mD NA doonning protein 2	WT
0755(0	DDVDA	Enhancer of http://www.uccapping.protein.p	WT CC
0/5569	PKKKA	The line of the stranded KNA-dependent protein kinase activator A	w1,C,S
AUAU8/AUK9	IJF1	Pile Levis To	W I
J3QR09	RPL19	Ribosomal protein L19	w1,C,S
Q15154	PCM1	Pericentriolar material 1 protein	WI
O60701	UGDH	UDP-glucose 6-dehydrogenase	WT
D6R938	CAMK2D	Calcium/calmodulin-dependent protein kinase	WT
Q13451	FKBP5	Peptidyl-prolyl cis-trans isomerase FKBP5	WT, C <sub>2</sub> S
P62829	RPL23	60S ribosomal protein L23	WT, C <sub>s</sub> S
O75874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	WT, C, S
P56545	CTBP2	C-terminal-binding protein 2	WT
P30084	ECHS1	Enoyl-CoA hydratase, mitochondrial	WT, C <sub>S</sub>
O75150	RNF40	E3 ubiquitin-protein ligase BRE1B	WT
Q9Y613	FHOD1	FH1/FH2 domain-containing protein 1	WT
H7C5E4	XRN1	5'-3' exoribonuclease 1	WT, C S
Q15021	NCAPD2	Condensin complex subunit 1	WT
P50995	ANXA11	Annexin A11	WT
O43290	SART1	U4/U6.U5 tri-snRNP-associated protein 1	WT
P30153	PPP2R1A	Serine/threenine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	WTCS
015555	MAPR F2	Microtubule-associated protein R P/FR family member 2	WT
O8WYP5	AHCTE1	Protein FLVS	WT CS
043390	HNRNPP	Heteroreneous nuclear ribonucleonrotein R	WT CS
073370	TITATVICINEIC	received inclusion inclusion inclusion in the inclusion of the inclusion in the inclusion of the inclusion o	w 1, C, S

Q9Y2Z0	SUGT1	Protein SGT1 homolog	WT, C <sub>.</sub> S
Q96G46	DUS3L	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	WT
Q9ULX3	NOB1	RNA-binding protein NOB1	WT
Q14847	LASP1	LIM and SH3 domain protein 1	WT
O60783	MRPS14	28S ribosomal protein S14, mitochondrial	WT
P61586	RHOA	Transforming protein RhoA	WT
P08754	GNAI3	Guanine nucleotide-binding protein G(i) subunit alpha	WT, C <sub>r</sub> S
P49591	SARS1	SerinetRNA ligase, cytoplasmic	WT
A0A087WY55	VTA1	Chromosome 6 open reading frame 55, isoform CRA_b	WT, C <sub>r</sub> S
P56192	MARS1	MethioninetRNA ligase, cytoplasmic	WT
Q5SW79	CEP170	Centrosomal protein of 170 kDa	WT, C <sub>r</sub> S
Q9Y490	TLN1	Talin-1	WT, C <sub>z</sub> S
P42765	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	WT, C <sub>z</sub> S
Q9BY77	POLDIP3	Polymerase delta-interacting protein 3	WT
P55265	ADAR	Double-stranded RNA-specific adenosine deaminase	WT, C <sub>z</sub> S
B4DY08	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	WT
Q92878	RAD50	DNA repair protein RAD50	WT
Q99569	PKP4	Plakophilin-4	WT, C <sub>z</sub> S
P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	WT, C <sub>s</sub>
Q9UPQ9	TNRC6B	Trinucleotide repeat-containing gene 6B protein	WT, C <sub>z</sub> S
O14654	IRS4	Insulin receptor substrate 4	WT
P33991	MCM4	DNA replication licensing factor MCM4	WT, C <sub>z</sub> S
Q9UHD8	SEPTIN9	Septin-9	WT
P00568	AK1	Adenylate kinase isoenzyme 1	WT, C <sub>2</sub> S
Q9BW92	TARS2	ThreoninetRNA ligase, mitochondrial	WT
Q96J01	THOC3	THO complex subunit 3	WT
Q9BXJ9	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	WT
P46939	UTRN	Utrophin	WT, C,S
P11387	TOP1	DNA topoisomerase 1	WT, C,S
H0YDU8	PPP5C	Serine/threonine-protein phosphatase	WT
P49368	CCT3	T-complex protein 1 subunit gamma	WT, C,S
P18615	NELFE	Negative elongation factor E	w1,CS
P27708	CAD	CAD protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase	W1, C, S
J3K1A4	DDX5	DEAD box protein 5	W1
P60660	MYL6	Myosin light polypeptide 6	w1,C5
095/85	WIZ	Protein Wiz	W I
A6NDG6	PGP	Glycerol-3-phosphate phosphatase	W I
P62269	RP518	40S ribosomai protein 518	WI OS
AUAUUIKKM6	ENAH	Protein enabled homolog	w1,C5
075(42	EIF4A5	Eukaryotic initiation factor 4A-111	W I
0/3643	SINKINP200	Com avanimularitation 7	WT CS
Q7F1840	GEMIN/	Gent-associated protein /	wit, C.5
Q15424 Q15160	DOL R 1C	DNA directed P NA polymeraces Land III subunit P DAC1	WT CS
D55795	HNR NDH2	Heterogeneous nuclear ribonucleoprotein H2	WT CS
B14K87	CAP7B	E actin camping protein subunit beta	WT CS
OSOJE6	DNTTIP?	Deoxypucleoridyltransferase terminal-interacting protein 2	WT
Q9Q126	PSPC1	Parasneckle component 1	WT CS
O9NTI5	PDS5B	Sister chromatid cohesion protein PDS5 homolog B	WT
000571	DDX3X	ATP-dependent R NA helicase DDX 3X	WT
08WX93	PALLD	Palladin	WT
099497	PARK7	Parkinson disease protein 7	WT CS
P62913	R PL11	60S ribosomal protein L11	WT
A0A1C7CYX9	DPYSL2	Dihydropyrimidinase-related protein 2.	WT.C.S
P40939	HADHA	Trifunctional enzyme subunit alpha, mitochondrial	WT.C.S
A0A0A0MR M8	MYO6	Unconventional myosin-6	WT.C.S
P29144	TPP2	Tripeptidyl-peptidase 2	WT, C S
O9BWF3	RBM4	RNA-binding protein 4	WT
P35658	NUP214	Nuclear pore complex protein Nup214	WT, C S
F8W0]6	NAP1L1	Nucleosome assembly protein 1-like 1	WT, CS
095347	SMC2	Structural maintenance of chromosomes protein 2	WT
O99613	EIF3C	Eukarvotic translation initiation factor 3 subunit C	WT
P38117	ETFB	Electron transfer flavoprotein subunit beta	WT, C S
A0A0A6YYL4	CORO7-PAM16	Coronin	WT
075534	CSDE1	Cold shock domain-containing protein E1	WT
015226	NKRF	NF-kappa-B-repressing factor	WT
P46776	RPL27A	60S ribosomal protein L27a	WT.C.S
P41252	IARS1	IsoleucinetRNA ligase, cytoplasmic	WT. C.S
Q9NVH2	INTS7	Integrator complex subunit 7	WT
O9GZL7	WDR12	Ribosome biogenesis protein WDR12	WT
P55060	CSE1L	Exportin-2	WT CS
P25325	MPST	3-mercaptopyruvate sulfurtransferase	WT.CS
P61758	VBP1	Prefoldin subunit 3	WT
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P51572	BCAP31	B-cell receptor-associated protein 31	WT
086¥56	DNA AF5	Dynein assembly factor 5 axonemal	WTCS
013573	SNW1	SNW domain containing protein 1	WT
Q15375	CCT2	Six w domani-containing protein 1	WT
P/85/1	CC12	1-complex protein 1 subunit beta	W1
Q9P0K7	KA114	Ankycorbin	W1,C5
Q9BTY7	HGH1	Protein HGH1 homolog	WT
Q13625	TP53BP2	Apoptosis-stimulating of p53 protein 2	WT
P09525	ANXA4	Annexin A4	WT
P52701	MSH6	DNA mismatch repair protein Msh6	WT, C <sub>p</sub> S
Q14690	PDCD11	Protein RRP5 homolog	WT
P62633	CNBP	Cellular nucleic acid-binding protein	WT
P13861	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory subunit	WT.C.S
O9BR X2	PELO	Protein pelota homolog	WT C S
0/0884	DNAIA2	Deal homolog undergring A member 2	WT
D10105	DINAJA2		WT CC
P19105	MILIZA	Myosin regulatory light chain 12A	w1,C,S
A0A087WVM4	MTHFD1L	Formyltetrahydrofolate synthetase	W1, C S
P10606	COX5B	Cytochrome c oxidase subunit 5B, mitochondrial	WT
Q99460	PSMD1	26S proteasome non-ATPase regulatory subunit 1	WT, C <sub>2</sub> S
B4DLN1	B4DLN1	cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier	WT
Q9NXH9	TRMT1	tRNA	WT
P33176	KIF5B	Kinesin-1 heavy chain	WT, CS
P26640	VARS1	ValinetRNA lipase	WT.C.S
099959	PK P2	Plakonbilin,2	WTCS
D/0227	CCT(A		w/T
P4022/	CCIGA	1-complex protein 1 subunit zeta	W 1
Q90J06	DRUT		W 1
P46783	RPS10	40S ribosomal protein S10	WT
P29692	EEF1D	Elongation factor 1-delta	WT, C,S
A0A2R8Y5F1	TSC2	Tuberin	WT
Q9NR45	NANS	Sialic acid synthase	WT, C <sub>.</sub> S
A0A0G2JNZ2	SCRIB	Protein scribble homolog	WT, C.S
P52272	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	WT.C.S
09P2R 3	ANKFY1	Rahankyrin-5	WT
075152	7021114	Zing finger CCCH domain containing protein 11 Å	WTCS
0/5152	ZCOHIIA		w1,C5
0/5/92	KNASEHZA	Kibonuclease H2 subunit A	W1,C5
P62906	RPL10A	60S ribosomal protein L10a	WT, C S
A0A2R8Y880	RBBP6	E3 ubiquitin-protein ligase RBBP6	WT
P36578	RPL4	60S ribosomal protein L4	WT
Q9BZE9	ASPSCR1	Tether containing UBX domain for GLUT4	WT, C <sub>.</sub> S
P52294	KPNA1	Importin subunit alpha-5	WT, C.S
G5EA36	CDC27	Cell division cycle 27. isoform CRA c	WT
09Y6G9	DYNC1L11	Cytoplasmic dynein 1 light intermediate chain 1	WT.C.S
013155	AIMP2	A minoacyl tR NA synthese complex interacting multifunctional protein 2	WT
Q13135	AGA 41		WT CC
P09110	ACAAI	3-ketoacyi-CoA thiolase, peroxisomal	w1,C,5
P111/2	UMPS	Uridine 5 - monophosphate synthase	W 1
M0R3C3	TECR	Very-long-chain enoyl-CoA reductase	WT, C,S
Q5TFE4	NT5DC1		
P34897		5'-nucleotidase domain-containing protein 1	WT
Q8IWB7	SHMT2	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial	WT WT
	SHMT2 WDFY1	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1	WT WT WT
Q9UBT2	SHMT2 WDFY1 UBA2	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2	WT WT WT,CS
Q9UBT2 O8WVI2	SHMT2 WDFY1 UBA2 NUDCD2	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2	WT WT WT, C,S WT
Q9UBT2 Q8WVJ2 Q7Z417	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2 Nuclear frasile X mental retrardation-interacting protein 2	WT WT WT, C, S WT WT
Q9UBT2 Q8WVJ2 Q7Z417 Q02790	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2 Nuclear fragile X mental retardation-interacting protein 2 Pentidel-production-trans isomerase FKBP4	WT WT WT, C, S WT WT C, S
Q9UBT2 Q8WVJ2 Q7Z417 Q02790 Q02NSV4	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein dimbanauk homelog 3	WT WT WT, C, S WT WT WT, C, S WT
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           D07214	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EXPR64	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Differential talana and the subscription of	WT WT WT, C,S WT WT WT, C,S WT WT C
Q9UBT2 Q8WVJ2 Q7Z417 Q02790 Q9NSV4 P07814 Q1665	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 EVCN	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase	WT WT WT, C,S WT WT, C,S WT WT, C,S WT WT, C,S WT WT, C,S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin	WT WT WT, C, S WT WT, C, S WT, C, S WT, C, S WT, C, S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43	WT WT WT, C, S WT WT, C, S WT, C, S WT, C, S WT, C, S WT
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/proline-tRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha	WT WT WT, C, S WT WT, C, S WT, C, S WT, C, S WT WT, C, S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q13658           Q13148           P53621           Q9Y30	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog	WT WT WT, C, S WT WT, C, S WT WT, C, S WT, C, S WT WT, C, S WT, C, S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q13148           P53621           Q9Y310           Q9BT25	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 NudC domain-containing protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8	WT WT WT,CS WT WT,CS WT WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9YI0           Q9BT25           Q00399	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6	WT WT WT, C, S WT WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S WT WT, C, S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Rihosomal B NA-processing protein 8	WT WT WT, C, S WT WT, C, S WT, C, S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159           Q8KV16	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 FXOC8	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/proline-tRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Fvoryst complex component 8	WT WT WT,C,S WT WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y3I0           Q9BT25           O00399           O43159           Q8IY16           A0A140T2P1	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 EXOC8	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Exocyst complex component 8	WT WT WT CS WT WT CS WT WT, CS WT WT, CS WT WT, CS WT WT, CS WT WT, CS WT WT, CS WT WT, CS WT, CS WT, CS WT, CS WT, CS WT, CS WT, CS WT, CS WT, CS WT WT
Q9UBT2         Q8WVJ2         Q7Z417         Q02790         Q9NSV4         P07814         Q16658         Q13148         P53621         Q9Y310         Q9BT25         O00399         O43159         Q8IY16         A0A140T9R1	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin	WT WT WT,C,S WT WT,C,S WT WT,C,S WT WT,C,S WT
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Dates	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 APIM1 PR 2005	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Florillin AP-1 complex subunit mu-1	WT WT WT, C, S WT WT, C, S WT,
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q92973	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 AP1M1 TNPO1	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit mu-1 Transportin-1	WT WT WT, C, S WT WT, C, S WT, C, S
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q92973           Q5BKZ1	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 APIM1 TNPO1 ZNF326	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit ZNF326	WT WT WT, C,S WT WT, C,S WT, C,S WT WT WT, C,S WT, C,S WT WT, C,S WT
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y3I0           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q92B73           Q5BKZ1           Q15084	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 APIM1 TNP01 ZNF326 PDIA6	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit mu-1 Transportin-1 DBIRD complex subunit ZNF326 Protein disulfide-isomerase A6	WT WT WT CS WT WT WT, CS WT WT, CS WT, CS WT
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q92973           Q8KZ1           Q15084           C9JRJ5	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RAP8 EXOC8 FLOT1 APIM1 TNP01 ZNF326 PDIA6 LIMD1	5'-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit mu-1 Transportin-1 DBIRD complex subunit ZNF326 Protein disulfide-isomerase A6 LIM domain-containing protein 1	WT WT WT CS WT WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT,CS WT WT,CS WT WT,CS WT,CS WT WT,CS WT,CS WT,CS WT WT,CS
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9Y310           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q22973           Q3BKZ1           Q15084           C29IRJ5           Q9Y2L1	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 APIM1 TNP01 ZNF326 PDIA6 LIMD1 DIS3	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit mu-1 Transportin-1 DBIRD complex subunit ZNF326 Protein disulfide-isomerase A6 LIM domain-containing protein 1 Exosome complex conclease RRP44	WT WT WT WT, C, S WT WT, C, S WT, C, S WT
Q9UBT2         Q8WVJ2         Q7Z417         Q02790         Q9NSV4         P07814         Q16658         Q13148         P53621         Q9Y310         Q9BT25         O00399         O43159         Q8IY16         A0A140T9R1         K7EJL1         Q92973         Q5BKZ1         Q15084         C9JRJ5         Q9Y2L1         A0A040C4DGA6	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 AP1M1 TNPO1 ZNF326 PDIA6 LIMD1 DIS3 HLTF	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/proline-tRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit TNF326 Protein disulfide-isomerase AG LIM domain-containing protein 1 Exosome complex exonuclease RRP44 Helicase-like transcription factor	WT WT WT WT, C, S WT WT, C, S WT, C, S WT
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q92973           Q5BKZ1           Q15084           C9JRJ5           Q9Y2L1           A0A04C4DGA6           Q14157	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 APIM1 TNPO1 ZNF326 PDIA6 LIMD1 DIS3 HLTF UBAP2L	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA, processing protein 8 Exocyst complex component 8 Florillin AP-1 complex subunit ZNF326 Protein disulfide-isomerase A6 LIM domain-containing protein 1 Exosome complex exonuclease RRP44 Helicase-like transcription factor	WT WT WT CS WT WT WT, CS WT WT, CS WT WT, CS WT, CS WT WT, CS WT, CS WT WT, CS WT, CS WT, CS WT WT, CS WT, CS WT
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y3I0           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q92973           Q5BKZ1           Q15084           C9JRJ5           Q9Y2L1           A0A0C4DGA6           Q14157           O9Y5A9	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 APIM1 TNP01 ZNF326 PDIA6 LIMD1 DIS3 HLTF UBAP2L YTHDF2	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit mu-1 Transportin-1 DBIRD complex subunit ZNF326 Protein disulfide-isomerase A6 LIM domain-containing protein 1 Exosome complex exonuclease RRP44 Helicase-like transcription factor Ubiquitin-associated protein 2.	WT WT WT WT WT,C,S WT WT,C,S W
Q9UBT2           Q8WVJ2           Q7Z417           Q02790           Q9NSV4           P07814           Q16658           Q13148           P53621           Q9Y310           Q9BT25           O00399           O43159           Q8IY16           A0A140T9R1           K7EJL1           Q15084           C3IRJ5           Q9Y2L1           A0A0C4DGA6           Q14157           Q9Y5A9           D3565	SHMT2 WDFY1 UBA2 NUDCD2 NUFIP2 FKBP4 DIAPH3 EPRS1 FSCN1 TARDBP COPA RTCB HAUS8 DCTN6 RRP8 EXOC8 FLOT1 AP1M1 TNP01 ZNF326 PDIA6 LIMD1 DIS3 HLTF UBAP2L YTHDF2 DNA1B1	5-nucleotidase domain-containing protein 1 Serine hydroxymethyltransferase, mitochondrial WD repeat and FYVE domain-containing protein 1 SUMO-activating enzyme subunit 2 Nuclear fragile X mental retardation-interacting protein 2 Peptidyl-prolyl cis-trans isomerase FKBP4 Protein diaphanous homolog 3 Bifunctional glutamate/prolinetRNA ligase Fascin TAR DNA-binding protein 43 Coatomer subunit alpha RNA-splicing ligase RtcB homolog HAUS augmin-like complex subunit 8 Dynactin subunit 6 Ribosomal RNA-processing protein 8 Exocyst complex component 8 Flotillin AP-1 complex subunit ru-1 Transportin-1 DBIRD complex subunit ZNF326 Protein disulfide-isomerase A6 LIM domain-containing protein 1 Exosome complex conclease RRP44 Helicase-like transcription factor Ubiquitin-associated protein 2-1 Evaluation 12 Nuter 12 Series 12 Seri	WT WT WT WT, C, S WT WT, C, S WT, C, S

P50502	ST13	Hsc70-interacting protein	WT, C <sub>r</sub> S
M0QXL5	FBL	rRNA 2'-O-methyltransferase fibrillarin	WT, C <sub>r</sub> S
Q8WUM4	PDCD6IP	Programmed cell death 6-interacting protein	WT, C <sub>s</sub> S
Q9UKF6	CPSF3	Cleavage and polyadenylation specificity factor subunit 3	WT
P62316	SNRPD2	Small nuclear ribonucleoprotein Sm D2	WT, C <sub>r</sub> S
Q13435	SF3B2	Splicing factor 3B subunit 2	WT
P11177	PDHB	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	WT
Q9UQ35	SRRM2	Serine/arginine repetitive matrix protein 2	WT
O94979	SEC31A	Protein transport protein Sec31A	WT, C <sub>r</sub> S
P37108	SRP14	Signal recognition particle 14 kDa protein	WT, C <sub>s</sub> S
Q7Z406	MYH14	Myosin-14	WT, C,S
G3V1C3	API5	Apoptosis inhibitor 5	WT, C,S
P13807	GYS1	Glycogen [starch] synthase, muscle	WT, C <sub>z</sub> S
E9PF10	NUP155	Nuclear pore complex protein Nup155	WT, C <sub>z</sub> S
Q1KMD3	HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	WT, C <sub>z</sub> S
P41240	CSK	Tyrosine-protein kinase CSK	WT, C <sub>z</sub> S
O15020	SPTBN2	Spectrin beta chain, non-erythrocytic 2	WT
P35250	RFC2	Replication factor C subunit 2	WT
Q8WUH6	TMEM263	Transmembrane protein 263	WT, C <sub>z</sub> S
P46779	RPL28	60S ribosomal protein L28	WT, C <sub>2</sub> S
Q9BSD7	NTPCR	Cancer-related nucleoside-triphosphatase	WT
Q06210	GFPT1	Glutaminefructose-6-phosphate aminotransferase [isomerizing] 1	WT
Q2TAL8	QRICH1	Glutamine-rich protein 1	WT
Q9BQ69	MACROD1	ADP-ribose glycohydrolase MACROD1	WT, C,S
P48444	ARCN1	Coatomer subunit delta	WT, C,S
Q16204	CCDC6	Coiled-coil domain-containing protein 6	WT, C,S
Q15031	LARS2	Probable leucinetRNA ligase, mitochondrial	WT
Q06124	PTPN11	Tyrosine-protein phosphatase non-receptor type 11	WT, C,S
P14866	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	W1
X1W128	RPL10	60S ribosomal protein L10	w1,CS
Q9UGV2	NDRG3	Protein NDRG3	WI,CS
095336	PGLS	6-phosphogluconolactonase	wi, c.s
Q9C0C2	I NKSIBPI	182 kDa tankyrase-1-binding protein	wi, c,s
Q0/021	CIQBP	Complement component I Q subcomponent-binding protein, mitochondrial	
P18585	JUEDI 2	Protein SON	WT CS
Q611N16	HSDL2	286 rik compalance in 221 minute and rid	wT
Q92665	MKP531	285 ribosomai protein 531, mitochondriai	W I
Q81285	D DL 0	Aldenyde denydrogenase ramily 16 member A1	W I
012(18	CUL 2	Cullin 2	WT
P31948	STIP1	Stress-induced-phosphoprotein 1	WTCS
09HC35	FMI 4	Febinoderm microtubule-associated protein-like 4	WT CS
P19022	CDH2	Cadherin-2	WT
B4DDF4	CNN2	Caloonin	WTCS
099426	TBCB	Tubulin-folding cofactor B	WT
O5IXI8	FHL1	Four and a half LIM domains protein 1	WT.C.S
O9UKM9	RALY	RNA-binding protein Raly	WT, C S
P78347	GTF2I	General transcription factor II-I	WT
095861	BPNT1	3'(2').5'-bisphosphate nucleotidase 1	WT.C.S
P50991	CCT4	T-complex protein 1 subunit delta	WT, C S
Q92597	NDRG1	Protein NDRG1	WT
A0A087X1A5	STAU1	Double-stranded RNA-binding protein Staufen homolog 1	WT, CS
P09622	DLD	Dihydrolipoyl dehydrogenase, mitochondrial	WT
O75131	CPNE3	Copine-3	WT, CS
P61158	ACTR3	Actin-related protein 3	WT, C S
O00267	SUPT5H	Transcription elongation factor SPT5	WT
P18858	LIG1	DNA ligase 1	WT
Q53EL6	PDCD4	Programmed cell death protein 4	WT
Q9H0E2	TOLLIP	Toll-interacting protein	WT
P39748	FEN1	Flap endonuclease 1	WT, C <sub>S</sub>
Q15750	TAB1	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	WT, C.S
C9J4Z3	RPL37A	60S ribosomal protein L37a	WT
Q05048	CSTF1	Cleavage stimulation factor subunit 1	WT
Q00610	CLTC	Clathrin heavy chain 1	WT, C,S
Q12904	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	WT, C,S
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	WT, C S
O43660	PLRG1	Pleiotropic regulator 1	WT, C.S
O14980	XPO1	Exportin-1	WT
P53396	ACLY	ATP-citrate synthase	WT
Q9BV20	MRI1	Methylthioribose-1-phosphate isomerase	WT, C.S
Q8IWS0	PHF6	PHD finger protein 6	WT, C.S
P30520	ADSS2	Adenylosuccinate synthetase isozyme 2	WT, C.S
Q14126	DSG2	Desmoglein-2	WT, C.S
-			

Q9BUF5	TUBB6	Tubulin beta-6 chain	WT, C S
P26368	U2AF2	Splicing factor U2AF 65 kDa subunit	WT, C.S
O95232	LUC7L3	Luc7-like protein 3	WT
P27540	ARNT	A ryl bydrocarbon receptor nuclear translocator	WTCS
02TAM5	DELA	P EL A protein	WT C S
QZIAMJ	KELA	RELA piotein	w1,C5
F2Z212	XPA	DNA repair protein-complementing XP-A cells	W I
O94906	PRPF6	Pre-mRNA-processing factor 6	WT, C <sub>s</sub>
E7EPN9	PRRC2C	Protein PRRC2C	WT, C <sub>s</sub> S
Q15003	NCAPH	Condensin complex subunit 2	WT, C.S
O9UPT5	EXOC7	Exocyst component 7	WT
D26639	TAP S1	Threaning tP NA ligase 1 cytoplasmic	WT
0011000	DAGC	Delt for the stand of 200	WT CC
Q90Q80	PA2G4	Proliferation-associated protein 2G4	w 1, C, S
043615	TIMM44	Mitochondrial import inner membrane translocase subunit TIM44	WT
Q12849	GRSF1	G-rich sequence factor 1	WT, C, S
P63241	EIF5A	Eukaryotic translation initiation factor 5A-1	WT, C <sub>s</sub>
B4E1N1	ARMC6	Armadillo repeat-containing protein 6	WT, C S
P46459	NSF	Vesicle-fusing ATPase	WT.C.S
D1((15	ATD2 A 2	Saraan laamia (on dan laamia natiau lum aalaium ATDasa 2	WT C S
P1001)	TOPAA	Sarcopiasini /endopiasini /endo	w1,C3
P11388	TOP2A	DNA topoisomerase 2-alpha	W1, C.S
Q5UIP0	RIF1	Telomere-associated protein RIF1	WT
Q15008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	WT
Q9BR76	CORO1B	Coronin-1B	WT, C.S
015075	EEA1	Early endosome antigen 1	WT.CS
01529/	OCT	UDD N according monorming, populde N according program invitation of proses 110 kDa suburgit	WT
013274	001	ODF-N-acetyightCosamine-peptide N-acetyightCosaminyitransierase 110 kDa subunit	W I
P55884	EIF3B	Eukaryotic translation initiation factor 3 subunit B	W1,CS
O60684	KPNA6	Importin subunit alpha-7	WT, C <sub>s</sub> S
F5H6E2	MYO1C	Unconventional myosin-Ic	WT, C <sub>s</sub> S
Q5VYK3	ECPAS	Proteasome adapter and scaffold protein ECM29	WT, C.S
013045	FLII	Protein flightless-1 homolog	WT.C.S
ONWH9	SLTM	SAFB like transcription modulator	WT C S
Q)INWII)	NDLOG		w1,0,5
Q81A16	NPLOC4	Nuclear protein localization protein 4 homolog	W 1, C, S
Q9NSD9	FARSB	PhenylalaninetRNA ligase beta subunit	WT, C <sub>s</sub>
Q8ND24	RNF214	RING finger protein 214	WT
E7EVA0	MAP4	Microtubule-associated protein	WT, C.S
O9UHB6	LIMA1	LIM domain and actin-binding protein 1	WT.C.S
O8WWO0	DHID	DH interacting protein	WTCS
Q0W WQ0	I ANTOD 1		wr.c.c
Q6IAA8	LAMIORI	Ragulator complex protein LAM I OR I	W1, C.S
A0A2R8Y855	SMARCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	WT, C <sub>s</sub>
Q7Z478	DHX29	ATP-dependent RNA helicase DHX29	WT
P49327	FASN	Fatty acid synthase	WT
015371	EIF3D	Eukarvotic translation initiation factor 3 subunit D	WT, C S
O9HCD5	NCOAS	Nuclear recentor coactivator 5	WT
0100/7	(FTD14		W I
01504/	SEIDIA	Histone-lysine N-methyltransferase SE I DIA	W 1
P12004	PCNA	Proliferating cell nuclear antigen	WT, CS
Q9Y3S2	ZNF330	Zinc finger protein 330	· · ·
P42696		Enterniger protein 550	WT, C,S
	RBM34	RNA-binding protein 34	WT, C S WT, C S
A0A0G2IH68	RBM34 DIAPH1	RNA-binding protein 34 Protein diaphanous homolog 1	WT, C,S WT, C,S WT, C S
A0A0G2JH68	RBM34 DIAPH1 PRRC2B	RNA-binding protein 34 Protein diaphanous homolog 1 Protein DB P C2B	WT, C,S WT, C,S WT, C,S WT, C,S
A0A0G2JH68 Q5JSZ5	RBM34 DIAPH1 PRRC2B	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B	WT, C,S WT, C,S WT, C,S WT, C,S WT, C,S
A0A0G2JH68 Q5JSZ5 O00487	RBM34 DIAPH1 PRRC2B PSMD14	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14	WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S
A0A0G2JH68           Q5JSZ5           O00487           Q09666	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK	WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S WT, C, S
A0A0G2JH68           Q5JSZ5           O00487           Q09666           Q14C86	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1	WT, C, S WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VP89 domain-containing protein 1 SLAIN motif-containing protein 1	WT, C, S WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1	WT, C,S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8KD83 Q867B9 P30154	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q09Y81	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B ETC12	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform res or BVA 23 O attors PMA angebrare FTR12	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q81Y81 Q81Y81	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 One of the state of t	WT, C,S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3	WT, C, S
A0A0G2JH68 Q5J5Z5 O00487 Q09666 Q14C86 Q8KD83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPT2R1B FTSJ3 GNL3 RPS4X	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein S4, X isoform	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8KD83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9Y5Y2	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PP2R1B FTSJ3 GNL3 RP54X NUBP2	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9Y5Y2 P48634	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein S4, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A	WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9FY22 P48634 O9H7E9	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RP54X NUBP2 PRRC2A C8orG33	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33	WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 O09KV8	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C8orf33 SEC23ID	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein S4, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein CSorf33 SEC73 Interacting protein	WT, C, S
A0A0G2JH68 Q5J5Z5 O00487 Q09666 Q14C86 Q8KD83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9H7E9 Q9Y6Y8 Q9H7E9 Q9Y6Y8	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PP2R1B FTSJ3 GNL3 RP54X NUBP2 PRRC2A C8orf33 SEC23IP	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2 <sup>2</sup> -0-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BYP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9Y6Y8 Q9C0C9	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C&orf33 SEC23IP UBE2O	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein S4, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme	WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9C0C9 P33993	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C&orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7	WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q920C9 P33993 P22102	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RP54X NUBP2 PRRC2A C&orf33 SEC23IP UBE2O MCM7 GART	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein S4, X isoform Cytosolic Fe-S-cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9Y6Y8 Q9C0C9 P33993 P32993 P22102 Q00170	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C&orf33 SEC23IP UBE2O MCM7 GART AIP	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein protein 1 Stanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q8IY81 Q9BYP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9Y6Y8 Q9C0C9 P33993 P22102 O00170 Q8IWZ3	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C&orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein	WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9BVP2 P48634 Q9H7E9 Q9Y6Y8 Q9H7E9 Q9Y6Y8 Q9C0C9 P33993 P22102 O00170 Q8IWZ3 P51452	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1 DUISP3	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein Ankyrin repeat and KH domain-containing protein 1 Drula processing factor MCM7	WT, C, S         WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q92C0C9 P33993 P22102 O00170 Q8IWZ3 P51452 O20172	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RP54X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1 DUSP3 EXOCC2	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein S4, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein Ankyrin repeat and KH domain-containing protein 1 Dual specificity protein phosphatase 3 Ference and the Dual	WT, C, S         WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q8IY81 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9C0C9 P33993 P22102 O00170 Q8IWZ3 P51452 Q9NQT5	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C&orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1 DUSP3 EXXSC3	RNA-binding protein 34 RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein Ankyrin repeat and KH domain-containing protein 1 Dual specificity protein phosphatase 3 Exosome complex component R.RP40	WT, C, S         WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q8BYP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9Y6Y8 Q9C0C9 P33993 P22102 O00170 Q8IWZ3 P51452 Q9NQT5 O94826	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RP54X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1 DUSP3 EXOSC3 TOMM70	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein 1 Dual specificity protein phosphatase 3 Exosome complex component RRP40 Mitochondrial import receptor subunit TOM70	WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BVP2 P62701 Q9FY22 P48634 Q9H7E9 Q9Y6Y8 Q9C0C9 P33993 P22102 O00170 Q8IWZ3 P51452 Q9NQT5 O94826 Q16543	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1 DUSP3 EXOSC3 TOMM70 CDC37	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C&orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein Ankyrin repeat and KH domain-containing protein 1 Dual specificity protein phosphatase 3 Exosome complex component RRP40 Mitochondrial import receptor subunit TOM70 Hsp90 co-chaperone Cdc37	WT, C, S
A0A0G2JH68 Q5JSZ5 Q00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q81Y81 Q9BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9Y6Y8 Q9C0C9 P33993 P22102 Q00170 Q8IWZ3 P51452 Q9NQT5 Q9NQT5 Q9S43 Q9UMS4	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PP2R1B FTSJ3 GNL3 RP54X NUBP2 PRRC2A C8orf33 SEC23IP UBE20 MCM7 GART AIP ANKHD1 DUSP3 EXOSC3 TOMM70 CDC37 PRPF19	RNA-binding protein 34 RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-rihose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein S4, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein 1 Dual specificity protein phosphatase 3 Exosome complex component R.RP40 Mitochondrial import receptor subunit TOM70 Hsp90 co-chaperone Cdc37 Pre-mRNA-processing factor 19	WT, C, S         WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q9BYP2 P62701 Q9SY2 P48634 Q9H7E9 Q9Y6Y8 Q9C0C9 P33993 P22102 O00170 Q8IWZ3 P51452 Q9NQT5 O94826 Q14C543 Q9UMS4 Q9UN54 Q9UN54	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PP2R1B FTSJ3 GNL3 RPS4X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1 DUSP3 EXOSC3 TOMM70 CDC37 PRPF19 PPP6R1	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein 1 Dual specificity protein phosphatase 3 Exosome complex component RRP40 Mitochondrial import receptor subunit TOM70 Hsp90 co-chaperone Cdc37 Pre-mRNA-processing factor 19 Serine/threonine-protein phosphatase 6 regulatory subunit 1	WT, C, S         WT, C, S
A0A0G2JH68 Q5JSZ5 O00487 Q09666 Q14C86 Q8ND83 Q86TB9 P30154 Q8IY81 Q8BVP2 P62701 Q9Y5Y2 P48634 Q9H7E9 Q9Y6Y8 Q9C0C9 P33993 P22102 O00170 Q8IWZ3 P51452 Q9NQT5 O94826 Q16543 Q9UMS4 Q9UNS4 Q9UN7 O99450	RBM34 DIAPH1 PRRC2B PSMD14 AHNAK GAPVD1 SLAIN1 PATL1 PPP2R1B FTSJ3 GNL3 RP54X NUBP2 PRRC2A C8orf33 SEC23IP UBE2O MCM7 GART AIP ANKHD1 DUSP3 EXOSC3 TOMM70 CDC37 PRPF19 PPP6R1 HBSU	RNA-binding protein 34 Protein diaphanous homolog 1 Protein PRRC2B 26S proteasome non-ATPase regulatory subunit 14 Neuroblast differentiation-associated protein AHNAK GTPase-activating protein and VPS9 domain-containing protein 1 SLAIN motif-containing protein 1 Protein PAT1 homolog 1 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 Guanine nucleotide-binding protein-like 3 40S ribosomal protein 54, X isoform Cytosolic Fe-S cluster assembly factor NUBP2 Protein PRRC2A UPF0488 protein C8orf33 SEC23-interacting protein (E3-independent) E2 ubiquitin-conjugating enzyme DNA replication licensing factor MCM7 Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamineglycine ligase AH receptor-interacting protein 1 Dual specificity protein phosphatase 3 Exosome complex component RRP40 Mitochondrial import receptor subunit TOM70 Hsp90 co-chaperone Cdc37 Pre-mRNA-processing factor 19 Serine/threonine-protein phosphatase 6 regulatory subunit 1 HBSI-like protein	WT, C, S         WT, C, S

H0Y5D5	CIZ1	Cip1-interacting zinc finger protein	WT, C,S
E9PKP7	UBTF	Nucleolar transcription factor 1	WT, C.S
Q9BSH4	TACO1	Translational activator of cytochrome c oxidase 1	WT, C.S
O60832	DKC1	H/ACA ribonucleoprotein complex subunit DKC1	WT, CS
Q9NY93	DDX56	Probable ATP-dependent RNA helicase DDX56	WT, C.S
Q13347	EIF3I	Eukaryotic translation initiation factor 3 subunit I	WT, C.S
095573	ACSL3	Long-chain-fatty-acidCoA ligase 3	WT, CS
Q15370	ELOB	Elongin-B	C,S
P62244	RPS15A	40S ribosomal protein S15a	WT, C.S
Q00796	SORD	Sorbitol dehydrogenase	WT, CS
E9PGZ1	CALD1	Caldesmon	C,S
P30566	ADSL	Adenylosuccinate lyase	WT, C.S
P49736	MCM2	DNA replication licensing factor MCM2	WT, C S
Q15126	PMVK	Phosphomevalonate kinase	WT, C S
O9BY44	EIF2A	Eukarvotic translation initiation factor 2A	C S
P25205	MCM3	DNA replication licensing factor MCM3	WT.C.S
P55735	SEC13	Protein SEC13 homolog	WT.C.S
09BWD1	ACAT2	Acetyl-CoA acetyltransferase cytosolic	WT CS
09UN86	G3BP2	R as GTPase-activating protein-binding protein 2	WT CS
Q9H0D6	XRN2	5'-3' evoribonuclease 2	WT CS
095816	BAG2	BAC family molecular changeone regulator 2	WT CS
O8N0Y7	SDART	Sportin	WT CS
D(2222	DSMC(	2(S protosomo rozulatory subunit 10P	WT CS
096036	DVCD 2	Durroline S carboxylate reductere 2	wit cs
Q26C36	CHER D	r y 10mie-5-cardoxylate reductase 2	wit, CS
Q81WX8	CHERP	Calcium homeostasis endoplasmic reticulum protein	w1,CS
	PFN2	Profilin	C3
Q16822	PCK2	Phosphoenolpyruvate carboxykinase [G I P], mitochondrial	W1,C5
Q13144	EIF2B5	Iranslation initiation factor eIF-2B subunit epsilon	W1, CS
P45974	USP5	Ubiquitin carboxyl-terminal hydrolase 5	WI, CS
Q15417	CNN3	Calponin-3	WT, C, S
A0A087WTZ5	UBXN1	UBX domain-containing protein 1	WT, C,S
O43395	PRPF3	U4/U6 small nuclear ribonucleoprotein Prp3	WT, C,S
Q8NCA5	FAM98A	Protein FAM98A	WT, C, S
P27694	RPA1	Replication protein A 70 kDa DNA-binding subunit	WT, C, S
Q13526	PIN1	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	C.S.
P63092	GNAS	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	C <sub>r</sub> S
O95747	OXSR1	Serine/threonine-protein kinase OSR1	WT, C <sub>r</sub> S
P21964	COMT	Catechol O-methyltransferase	WT, C,S
Q3ZCQ8	TIMM50	Mitochondrial import inner membrane translocase subunit TIM50	C <sub>r</sub> S
Q5T7U1	GTF3C5	General transcription factor 3C polypeptide 5	WT, C <sub>z</sub> S
Q86V48	LUZP1	Leucine zipper protein 1	WT, C <sub>r</sub> S
P35579	MYH9	Myosin-9	WT, C,S
P49321	NASP	Nuclear autoantigenic sperm protein	WT, C <sub>s</sub> S
E5RGR0	LYPLA1	Acyl-protein thioesterase 1	C <sub>r</sub> S
P54136	RARS1	ArgininetRNA ligase, cytoplasmic	WT, C,S
P50542	PEX5	Peroxisomal targeting signal 1 receptor	WT, C <sub>s</sub> S
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	C.S
Q9BZE4	GTPBP4	Nucleolar GTP-binding protein 1	WT, C.S
Q13907	IDI1	Isopentenyl-diphosphate Delta-isomerase 1	WT, C.S
E7ETK0	RPS24	40S ribosomal protein S24	WT, C.S
P35580	MYH10	Myosin-10	WT, C.S
P49588	AARS1	AlaninetRNA ligase, cytoplasmic	WT, C.S
Q9ULC4	MCTS1	Malignant T-cell-amplified sequence 1	C.S
P52594	AGFG1	Arf-GAP domain and FG repeat-containing protein 1	C.S.
Q14247	CTTN	Src substrate cortactin	WT, C.S
P45973	CBX5	Chromobox protein homolog 5	CS
P52788	SMS	Spermine synthase	WT, C S
P62195	PSMC5	26S proteasome regulatory subunit 8	WT, CS
O9UN37	VPS4A	Vacuolar protein sorting-associated protein 4A	WT.C.S
075436	VPS26A	Vacuolar protein sorting-associated protein 26A	WT.C.S
P17987	TCP1	T-complex protein 1 subunit alpha	WT CS
09BTF6	A A R SD1	Alapyl-tR NA editing protein Aarsd1	WT CS
Q96GD0	PDXP	Puridoval phosphate phosphatase	WT CS
015365	PCBP1	Poly(rC)-binding protein 1	WT CS
07L0Y3	TR MT10C	tRNA methyltransferase 10 homolog C	WTCS
OPUNV/	TTE2	Transcription termination factor 2	WTCS
095272	1112 IDO7	Importin 7	WI, CS
0733/3 D2/5/2	ATDODA	ATD	w 1, C <sub>1</sub> S
r 36342	ATPSFIC LINCOR	A 1 i' synthase subunit gamma, mitochondrial	<u> </u>
Q62N1/	LIN28B	Protein III-28 nomolog B	
0/5934	BCA52	Pre-mKNA-splicing factor SPF2/	<u> </u>
Q99829	CPNE1	Copine-1	<u>C</u> S
P06132	UROD	Uroporphyrinogen decarboxylase	WT, C S
Q14166	TTLL12	Tubulintyrosine ligase-like protein 12	WT, C <sub>.</sub> S

P43490	NAMPT	Nicotinamide phosphoribosyltransferase	WT, C S
Q9BSJ8	ESYT1	Extended synaptotagmin-1	WT, C.S
O43143	DHX15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	WT, C.S
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	WT, CS
P62241	RPS8	40S ribosomal protein S8	WT, CS
043719	HTATSF1	HIV Tat-specific factor 1	WTCS
014893	GEMIN2	Gem-associated protein 2	C.S.
P09543	CNP	2' 3'-cyclic-nucleotide 3'-nhosnhodiesterase	WTCS
D12/80	DNUI	P ib an along in biblion	w1,0,5
001469	EADDE	Ribonuclease inhibitor	US WT CS
Q01469	FABPS	Fatty acid-binding protein 5	wi,cs
E9PDU5	WDR6	WD repeat-containing protein 6	WT, C,S
Q92797	SYMPK	Symplekin	WT, C <sub>r</sub> S
Q13428	TCOF1	Treacle protein	WT, C S
Q4KMP7	TBC1D10B	TBC1 domain family member 10B	WT, C,S
P26358	DNMT1	DNA	C_S
Q5T6F2	UBAP2	Ubiquitin-associated protein 2	WT, C <sub>s</sub>
P43487	RANBP1	Ran-specific GTPase-activating protein	C_S
Q92667	AKAP1	A-kinase anchor protein 1, mitochondrial	WT, C.S
P98175	RBM10	RNA-binding protein 10	CS
P31946	YWHAB	14-3-3 protein beta/alpha	C.S.
P13797	PI \$3	Plastin-3	WT C S
091103	HOOK1	Protein Heak homolog 1	WT CS
0001000	WDB 70	WD ment contribution and in 70	w1,0,5
Q9IN W82	WDK/0		C <sub>5</sub>
P4389/	1 SFM	Elongation factor 1s, mitochondrial	W1,C5
Q9Y696	CLIC4	Chloride intracellular channel protein 4	C <sub>s</sub>
P40937	RFC5	Replication factor C subunit 5	WT, C S
P39687	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A	C <sub>z</sub> S
Q9BYG3	NIFK	MKI67 FHA domain-interacting nucleolar phosphoprotein	WT, C <sub>r</sub> S
Q9Y2R4	DDX52	Probable ATP-dependent RNA helicase DDX52	C_S
Q86VP6	CAND1	Cullin-associated NEDD8-dissociated protein 1	WT, C,S
P48643	CCT5	T-complex protein 1 subunit epsilon	WT, C.S
A0A3B3IRI2	CTPS1	CTP synthase	WT, CS
O00154	ACOT7	Cytosolic acyl coenzyme A thioester hydrolase	WT, CS
P31939	ATIC	Bifunctional purine biosynthesis protein ATIC	CS
09N088	TIGAR	Fructose-2 6-bisnbosnbatase TIGAR	C S
01/218	EV DDo	Dentidul neglul ais trans icometeos EKPDS	C S
Q14518	CDDCO	Cite and a strength of the str	UJS WT CC
Q90HB9	5KP68	Signal recognition particle subunit SRP68	w1,C,S
P51116	FXR2	Fragile X mental retardation syndrome-related protein 2	<u>C</u> S
Q9UJ83	HACL1	2-hydroxyacyl-CoA lyase 1	C <sub>s</sub>
P53618	COPB1	Coatomer subunit beta	WT, C,S
P42566	EPS15	Epidermal growth factor receptor substrate 15	CS
O75439	PMPCB	Mitochondrial-processing peptidase subunit beta	C <sub>z</sub> S
G5EA31	SEC24C	Protein transport protein Sec24C	C_S
F8VYE8	PPP1CC	Serine/threonine-protein phosphatase	C_S
Q9NUQ9	CYRIB	CYEIP-related Racl interactor B	
Q9BQ67			C_S
G3XAH6	GRWD1	Glutamate-rich WD repeat-containing protein 1	C_S WT, C S
0.7444440	GRWD1 PAPOLA	Glutanate-rich WD repeat-containing protein 1 Polv(A) polymerase	C_S WT, C_S C S
P84095	GRWD1 PAPOLA RHOG	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Boc-related GTP-binding protein B hoG	C,S WT,C,S C,S
P84095	GRWD1 PAPOLA RHOG DVNLR B1	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Durasien lights chain readblock turns 1	C,S WT,C,S C,S C,S WT,C,S
P84095 Q9NP97 QCPKC0	GRWD1 PAPOLA RHOG DYNLRB1	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Dynein light chain roadblock-type 1	C,S WT,C,S C,S WT,C,S WT,C,S
P84095           Q9NP97           Q6PKG0           O8HP71	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYRP	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Dynein light chain roadblock-type 1 La-related protein 1	C,S WT,C,S C,S C,S WT,C,S WT,C,S C,S
P84095           Q9NP97           Q6PKG0           Q9HB71           Q1202/2	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Dynein light chain roadblock-type 1 La-related protein 1 Calcyclin-binding protein	C,S WT,C,S C,S C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S
D84095           Q9NP97           Q6PKG0           Q9HB71           Q12948	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Dynein light chain roadblock-type 1 La-related protein 1 Calcyclin-binding protein Forkhead box protein C1	C,S WT,C,S C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S
D31000000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Dynein light chain roadblock-type 1 La-related protein 1 Calcyclin-binding protein Forkhead box protein C1 40S ribosomal protein S6	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S
D311113           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 3	C,S WT,C,S C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S
D311113           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Dynein light chain roadblock-type 1 La-related protein 1 Calcyclin-binding protein Forkhead box protein C1 40S ribosomal protein S6 Ran-binding protein 3 Unconventional myosin-Ib	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S
D3111113           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MY01B YWHAE	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 56         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S
0537773           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 36         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S C,S
053           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MY01B YWHAE NUBP1 TIPRL	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein S6         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S
D31000000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35	Glutamate-rich WD repeat-containing protein 1 Poly(A) polymerase Rho-related GTP-binding protein RhoG Dynein light chain roadblock-type 1 La-related protein 1 Calcyclin-binding protein Forkhead box protein C1 40S ribosomal protein S6 Ran-binding protein 3 Unconventional myosin-Ib 14-3-3 protein epsilon Cytosolic Fe-S cluster assembly factor NUBP1 TIP41-like protein 28S ribosomal protein S35, mitochondrial	C,S WT,C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S
D311113           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663           P82673           P68133	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein S6         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein S35, mitochondrial         Actin, alpha skeletal muscle	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
053mins           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663           P86273           P68133           Q9NQX3	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein S35, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
0537478           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663           P82673           P68133           Q9NQX3           P32322	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein 1         Calcyclin-binding protein 1         Forkhead box protein C1         40S ribosomal protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein 535, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pvrroline-5-carboxylate reductase 1. mitochondrial	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
0511113           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663           P82673           P68133           Q9NQX3           P32322           O2TAV7	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 36         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein S35, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdoprerin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WDa0 repeat-containing protein SMU1	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
03571113           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663           P82673           P68133           Q9NQX3           P32322           Q2TAY7           O94544	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TDP3P K	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 56         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein S35, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein S35MU1         EVC/K FORS complex eutomic TS38 K	C,S WT,C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
DSMARD           P84095           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663           P82673           P68133           Q9NQX3           P32322           Q2TAY7           Q96844           O21101	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TPS3RK CUOR DCC	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 36         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein 33, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Convisor of binitions on the protein subunit TP53RK	C,S WT,C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
05.000000           Q9NP97           Q6PKG0           Q9HB71           Q12948           P62753           B7Z7F3           O43795           P62258           P53384           O75663           P82673           P68133           Q9NQX3           P32322           Q2TAY7           Q96S44           Q9UHD1           Q56412	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TP53RK CHORDC1	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein 61         40S ribosomal protein 56         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein 3, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Cysteine and histidine-rich domain-containing protein 1	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
05.00000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TP53RK CHORDC1 AGK	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein 1         Value         A0S ribosomal protein 56         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fc-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein 355, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Cysteine and histidine-rich domain-containing protein 1         Acylglycerol kinase, mitochondrial	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
05.00000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TP53RK CHORDC1 AGK KDM3B	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein 335, mitochondrial         Actrin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5- carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Cysteine and histidine-rich domain-containing protein 1         Acylglycerol kinase, mitochondrial         Lysine-specific demethylase 3B	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
05.00000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TP53RK CHORDC1 AGK KDM3B DUT	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 56         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein S35, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Cysteine and histidine-rich domain-containing protein 1         Acylglycerol kinase, mitochondrial         Lysine-specific demethylase 3B         Deoxyuridine 5'-triphosphate nucleotidohydrolase	C,S WT,C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
05.00000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRP355 ACTA1 GPHN PYCR1 SMU1 TP53RK CHORDC1 AGK KDM3B DUT MPI	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 36         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein 35, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Cysteine and histidine-rich domain-containing protein 1         Acylg/ycerol kinase, mitochondrial         Lysine-specific demethylase 3B         Deoxyuridine 5'-triphosphate nucleotidohydrolase         Mannose-6-phosphate isomerase	C,S WT,C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
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05.00000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TP53RK CHORDC1 AGK KDM3B DUT MPI DBN1 FAHD1	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein 1         Calcyclin-binding protein         Forkhead box protein 56         Ran-binding protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fe-S cluster assembly factor NUBP1         TIP41-like protein         288 ribosomal protein 355, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Cysteine and histidine-rich domain-containing protein 1         Acylglycerol kinase, mitochondrial         Upeoxyuridine 5 <sup>1</sup> -triphosphate nucleotidohydrolase         Mannose-6-phosphate isomerase         Drebrin         Acylpyruvase FAHD1, mitochondrial	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
05.00000000000000000000000000000000000	GRWD1 PAPOLA RHOG DYNLRB1 LARP1 CACYBP FOXC1 RPS6 RANBP3 MYO1B YWHAE NUBP1 TIPRL MRPS35 ACTA1 GPHN PYCR1 SMU1 TP53RK CHORDC1 AGK KDM3B DUT MPI DBN1 FAHD1 BOD1L1	Glutamate-rich WD repeat-containing protein 1         Poly(A) polymerase         Rho-related GTP-binding protein RhoG         Dynein light chain roadblock-type 1         La-related protein 1         Calcyclin-binding protein         Forkhead box protein C1         40S ribosomal protein 3         Unconventional myosin-Ib         14-3-3 protein epsilon         Cytosolic Fc-S cluster assembly factor NUBP1         TIP41-like protein         28S ribosomal protein s35, mitochondrial         Actin, alpha skeletal muscle         Gephyrin [Includes: Molybdopterin adenylyltransferase         Pyrroline-5-carboxylate reductase 1, mitochondrial         WD40 repeat-containing protein SMU1         EKC/KEOPS complex subunit TP53RK         Cysteine and histidine-rich domain-containing protein 1         Acylglycerol kinase, mitochondrial         Lysine-specific demethylas 3B         Deoxyuridine 5 <sup>*</sup> triphosphate nucleotidohydrolase         Mannose-6-phosphate isomerase         Drebrin         Acylpyruvase FAHD1, mitochondrial	C,S WT,C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S

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LPRAS     NPLPS     Anilographics     C3       LPRAS     NPLPS     Missenting points 28     C5       PNOB     MISPIT     Microfiellite sociard cross 1     C5       PNOB     MISPIT     Microfiellite sociard cross 1     C5       PNOB     MISPIT     Encode and implementer 4     C5       PALSM     MTRIX     Encode NM MisPIT     C5       PALSM     MTRIX     Encode NM MisPIT     C5       PALSM     POLIA     DNA discosed RNA polymers 21     C5       PALSM     POLIA     DNA discosed RNA polymers 21     C5       PALSM     POLIA     DNA discosed RNA polymers 21     C5       PALSM     POLIA     Adiacesed RNA polymers 21     C5       PALSM     POLIA     DNA discosed RNA polymers 21     C5       PALSM     POLIA     POLIA     C5       PALSM     PoliA     POLIA </td <td>Q9BPU6</td> <td>DPYSL5</td> <td>Dihydropyrimidinase-related protein 5</td> <td><u> </u></td>	Q9BPU6	DPYSL5	Dihydropyrimidinase-related protein 5	<u> </u>
0.1029         0.10900         0.00000         0.5           0.10100         0.000000         0.5         0.5           0.0011         MARP         Maccinetize scattering protein 1         0.5           0.0013         TRCID+         TSCI.domain family members 4         0.5           0.0013         CCDC47         CeleIcol domain-contraining protein 87         0.5           0.01402         POLEJA         DDA directed RA hoppmane Dillowink IPC1         0.5           0.01402         POLEJA         DDA directed RA hoppmane Dillowink IPC1         0.5           0.01402         TRLMA         Alphareatilin         0.5           0.0173         RTJSA         Off Stationand protein 158         0.5           0.0173         RTJSA         Alphareatilin         0.5           0.0174         OTF Ibanding protein 148         0.5         0.5           0.0173         RTJSA         Alpharin         0.5         0.5           0.0174         OTF Ibanding protein 148         0.5         0.5         0.5           0.0174         OTF Ibanding protein 148         0.5         0.5         0.5           0.0174         DIPAN         DiPAN control ibandina 149         0.7         0.5           0.0154	E9PLK3	NPEPPS CUADVDAR	Aminopeptidase	<u> </u>
School         MARI         Machine and constraint         5           School         TRC1Data         TRC1 down in only member 4         5           School         TRC1Data         TRC1 down in only member 4         5           School         CCDC c <sup>2</sup> Celebest down in only member 4         5           School         DRLAM         DRLAM in only member 4         5           School         DRLAM         DRLAM in only member 4         5           School         DRLAM         DRLAM in only member 4         5           School         DRLAM         Add in only member 4         5           School         DRLAM         DRLAM         School           School         DRLAM         DRLAM         School           School         DRLAM         DRLAM         DRLAM         School           School <td< td=""><td>A1A285</td><td>NODS8</td><td>SH3 and PA domain-containing protein 2D</td><td>C \$</td></td<>	A1A285	NODS8	SH3 and PA domain-containing protein 2D	C \$
2003         TPC 104         TPC 14 should for fully should at 1         0.6           2023         MTB X         Lassenge RNA blarks MTB 4         0.5           004302         DOLK 3A         DNA discost RNA physics at 11 should PC1         0.5           004302         DOLK 3A         DNA discost RNA physics at 11 should PC1         0.5           004302         DOLK 3A         Alpha cath         0.5           004302         TXLMA         Alpha cath         0.5           004302         TXLMA         Alpha cath         0.5           004078         GTRBafing porein 1         C.5         0.5           004078         GTRBafing porein 1         C.5         0.5           017352         RAKS         Alpha cath         0.5         0.5           017353         RANFI         Burnice-sancting pretrin 32         C.5         0.5           017351         SIRBH         Protein appliate for the sand 30         WT, C.5         0.5           017351         SIRBH         Protein appliate for the sand 30         WT, C.5         0.5           01744         PRAT5         Protein appliate for the sand 30         WT, C.5         0.5           01745         PRAT5         Protein appliate for the sand 30         WT,	Q712A3	MEAD1	Nucleolar protein 58	<u> </u>
Pa23*MTRXLessen PAA Melicar MTH4C5QP6433CCDC 47Callef-301 disan accorating protes 47C5D14802POLEAADNA dirccel RNA polymerse III advant PC1C5PN272TK1AMAlpheratinC5PN272TK1AMAlpheratin Bart from Composers P13C5QWWYYPRPF11U/U/a mall andcar thomach operator P131C5QUITYNGTP8P1GTP8holing protein 1C5QUITYNPRPF11U/U/a mall andcar thomach operator P131C5QUITYNPRPF11U/U/a mall andcar thomach operator P131C5QUITYNPRPF11U/U/a mall protein 52C5QUITYNPRPF11Drafadin subasit 2C5QUITYNPRD3Protein protein 52C5QUITYNPRD3Protein protein 52C5QUISISLADPProtein protein 52C5QUISISLADPProtein protein 53C5QUISIBAND1Bor protein strain adult at 1NA binding proteinC5QUISIWRADW Depare containing protein 1NA binding proteinC5QUISIBAND2Bor protein strain adult at 1NA binding proteinC5QUISIBAND3Bor protein strain adult at 1NA binding proteinC5QUISIWRADBor protein strain adult at 1NA binding proteinC5QUISIBAND2Bor protein strain adult at 1NA binding protein 1C5QUISIBAND3Bor protein strain adult at 1NA binding protein 1C5QUISIBAND3Bor protei	060343	TBC1D4	TBC1 domain family member 4	<u> </u>
OptA33         CCC497         Cold-cold-senie optimizing protein 47         Cs           NAM2         DNA Adjaces (RA Applements III) Hounk IPC1         Cs           NAU2         RLIAS         Gest Indone (RA Applements III) Hounk IPC1         Cs           QUIVY         PRP13         U/U/C multi-mackar rhomachopoten Prp1         Cs           QUIVYS         PRP13         D/Tobicamo context Transmitter Protein Prp1         Cs           QUIVS         RNS         BANFIN         Barticiter autointer protein Prot	P42285	MTREX	Fxosome R NA helicase MTR4	C.S.
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PA222TKIAAAlpha satinC.S.QRWYDPRP31U/L/Sami luncar brokenogroen Pp1C.S.Q0075GTPP1GTP banding protein 1C.S.QU119VPTDN2Profolds advanit 2WT.C.S.Q01119VPTDN2Profolds advanit 3WT.C.S.Q01119VPTDN2Profolds advanit 6C.S.Q01119VPTDN2Star protein 470 are regulatory value 10WT.C.S.Q1581BANFIBarrier canoningering factor actionWT.C.S.Q1581BANFIBarrier canoningering factor actionWT.C.S.Q1581BANFIBarrier canoningering factor actionWT.C.S.Q1581GK3Chromobog protein 43WT.C.S.Q1581GK3Chromobog protein 41WT.C.S.Q1581GK3Chromobog protein factor fac	P63173	RPL38	60S ribosomal protein L38	C \$
QWWY0PKP31UAUkanal mader homouchopoten Pg31C 5QU295ATNAArkytin 5C 5QU295MNS1Ankytin 5WT.C 5PK284RP5086 thonomal proten 50WT.C 5PK284RP5026 protens one AT bere arguincy valuania 10WT.C 5PK284RP5026 protens one AT bere arguincy valuania 10WT.C 5QU591BANTIExperimenta ATT bere arguincy valuania 10WT.C 5QU591WTR45WT.C science arguincy valuania 10WT.C 5QU591WTR45Concolor potent homolog 3WT.C 5QU404PKNT3Concolor potent homolog 3WT.C 5QU604MS12ENAbore potent homolog 2WT.C 5QU604MS12ENAbore hotophate propeholokinse 2QCQu604MS12ENAbore hotophate propeholokinse 2WT.C 5QU504TR1H3Potence checkpoint potent Actional potent MLS7C 5QU504TR1H3Fubrue checkpoint potent MLS7C 5QU504LR BR14Lawaresic transfulfich interinseting protein 11C 5QU504LR BR14Lawaresic transfulfich interinseting protein 12C 5QU505MLS4MOLAMCC2C 5QU504RLS4MLS4MLS4MLS4 <td>P40222</td> <td>TXLNA</td> <td>Alpha-taxilin</td> <td>C S</td>	P40222	TXLNA	Alpha-taxilin	C S
OWDCTRPHCSQ2295ANK3AlxKrib.3CSQ21947PTDN2Perfoldin submit 2.WT.CSQ21947PTDN2Perfoldin submit 2.WT.CSQ2584KB254463 theomal protein 324WT.CSQ75812PADD025 protessome non ATDne regulatory submit 10WT.CSQ75814MANF1Barber to antiongration factorWT.CSQ1586MANF1Barber to antiongration factorWT.CSQ1586GK3CSCSQ1874PBAT5Protein agrinion N analybranefactorWT.CSQ1874PBAT5Protein agrinion N analybranefactorWT.CSQ1874PBAT5Protein agrinion N analybranefactor 5WT.CSQ46704OTUBHoppitter protein factor factorCSQ46704OTUBHoppitter protein factor factorCSQ46704ITUBDUB add CUL4 social factor factorCSQ46704ITUBITUBCSQ4734ITUBDUB add CUL4 social factor factorCSQ4744ITUBDUB add CUL4 social factor factorCSQ4757ITUBDUB add CUL4 social factor factorCSQ47670ITUBITUBCSQ4774ITUBITUB	Q8WWY3	PRPF31	U4/U6 small nuclear ribonucleoprotein Prp31	CS
Q2195         ANS1         Akstrin         C.S.           QVUIVY         PFDN2         Nordia Submit 2         W.C.G.S.           PX254         PSD2         465 fiboomal protein S26         C.S.           O7551         BANF1         Barrisers-autiointegration facor         WTL C.S.           QVISV3         SERBPI         Paramission cond/The regulatory adouts 10         C.S.           QVISV1         SERBPI         Paramission cond/The regulatory adouts 10         C.S.           QVISV1         SERBPI         Paramission cond/the regulatory adouts 10         WTL C.S.           QVISV1         SERBPI         Paramission cond/the regulatory adouts 20         WTL C.S.           QVISV1         RERS2         Reloce/pather protein/Patheranticose 2         WTL C.S.           QVISV1         OTUBI         Usignatin indicererator 01081         C.S.           QVISV1         OTUBI         Usignatin indicererator 01081         C.S.           QVISV2         DRAFIE         DRAFIE         C.S.           QVISV2         DRAFIE         DRAFIE         DRAFIE         C.S.           QVISV2         IFPS1         Early ortubin MLAF7         C.S.           QVISV2         IFPS1         Early ortubin MLAF7         C.S.	O00178	GTPBP1	GTP-binding protein 1	C S
QPUIPYPINAPerfodian submit 2WT. C. S.PGEMAPISS2487 document precess 2014SCOTS31BAND263 processome and PDe regulatory pubnit 10WT. C. S.OTS31BANFRarcisc-cumoting ratio factor factorWT. C. S.Q1504WD. VD. S.WD. repear-containing protein 43SCQ1505SERBPPassing activator tabibitory 11NA-Mading protein 12NA-Mading protein 12NA-Madi	Q12955	ANK3	Ankyrin-3	C.S.
PacebasePRS2640% relevances non Pregulary submit 0CSOTS931PSM10026 proteomating ary trequisary submit 0WT c, SOTS91NDR4WT c, Second submit ary submit 0CSQMNG1ST&BP1Busingen scriwer inhibiter 1 NDA banding proteinCSQMNG1GR31Charbone protein bone of pacebaseWT c, SQMNG4PRM75Porein arginin Protein Manah bonelog 2WT c, SQM9H6MS12Rabone phosphar proteopholy RaiseCSQM9H7OTUBDepartman argin of phosphar proteopholy RaiseCSQM970ITUBUbagetin discentrace OTUBCSQM970ITUBDepartman argin of phosphar proteopholy RaiseCSQM970ITUBDepartman argin oppharingCSQM171DCAFAGDBIs and CUL* ansociated factor 16CSQM172LCAFAGDBIs and CUL* ansociated factor 16CSQM173DCAFAGDBIs and CUL* ansociated factor 16CSQM174LRAFIPILardine-drin protein BUISCSQM175DCAFAGDBIs and CUL* ansociated factor 16CSQM174LRAFMTCA scociated diprogenase (NAD) submit gamma, mitochondrialCSQM175DI-GARole ancolated scholar protein GU/GG/GU/GU/GU/GU/GU/GU/GU/GU/GU/GU/GU/G	Q9UHV9	PFDN2	Prefoldin subunit 2	WT, C.S
07581PSND9265 protecome on ATP are regulatory subant 10VT. C.S07581NAN1Referee subant regutation factorVT. C.S08591NDRA3WD repersionaling protein A3 factory and the regutation of the regutation and the regutatio	P62854	RPS26	40S ribosomal protein \$26	C.S.
O7551MNIBarriesto autoingration factorVT, CSQ5961WDRA 30WDrepertontining protein A30CSQ4NC51STRBPPlanningen activate inhibitor 1 NAA hading proteinWT, CSQ3135CRA3Choose protein housely 30WT, CSQ4D144PRMT5Protein arginine N-methyltranoferas 5WT, CSQ4D145MS12RAMS-beinghurgen probenghurgen p	O75832	PSMD10	26S proteasome non-ATPase regulatory subunit 10	WT, C.S
QiSolaWDr speac-outsning protein 43CSQNSC51SER.BP1Panapose at store infoliator 1 NAA-binding proteinCSQ1348CRX1Chromobex protein homolog 3.WT.CSQ1346MS21RAA-binding protein Ansahi homolog 2.WT.CSQ400H6MS22RAA-binding protein Masshi homolog 2.CSQ407H7OTUB1Ubiquitin discentrace OTUB1CSQ407H7OTUB1Ubiquitin discentrace OTUB1CSQ407H7DOP.1Importin 9CSQ407H7DOP.1DDB1 and CUL4-associated factor 16CSQ407H7DCA17BDDB1 and CUL4-associated factor 16CSQ5454TRUP3Rad-stored factor 16CSQ5454RDS1Max-sociated factor 10CSQ5454RDS1Max-sociated factor 10CSQ5454RDS3Moteic chcyclang tradition inticiato factor 2 ubunit1CSQ5454RDS1Statter chcyclang tradition inticiato factor 2 ubunit1CSQ5455RDS2Rose chcyclang tradition inticiato factor 2 ubunit1CSQ5456RDS1Statter chcyclang tradition inticiato factor 2 ubunit1CSQ5456RDS1Statter chcyclang tradition inticiato factor 2 ubunit3CSQ4756RDS1Rose chcyc	O75531	BANF1	Barrier-to-autointegration factor	WT, C,S
QNNC31SRAP1Plasminogen activator inhibitor I RNA-binding protein monoles 3CRQ1335CRX3Chronobes protein homoles 3WT, CSQ01744PKMT5Protein arginine N-methyltranofrans 5WT, CSQ01740MS12RNA-binding protein Massubh homolog 2WT, CSQ04770OTUBIUbayinin hisesense OTUBICSQ04771IPO5ImportineCSQ16454TRU3Pachetee declopion protein 2 homologCSQ18454TRU3Pachetee declopion protein 2 homologCSQ18454TRU13Pachetee declopion protein 1 homologCSQ18454TRU13Pachetee declopion protein 1 homologCSQ18454TRU3Pachetee declopion protein 1 homologCSQ18454TRU3Pachetee declopion protein 1 homologCSQ18454RLRSILOTA-associated factor 16CSQ18454BUB3Mitote declopion protein BUB3CSQ18454BUB3Mitote declopion protein BUB3CSQ19456BOLA2Protein BCC2CSQ19456ZNF930Zantein declopioni protein G(I)CG(S)(CT) submit bers 1CSQ28456ZNF930GRGauine molecule-binding protein G(I)CG(S)(CT) submit bers 1CSQ19457RAB11FIPRab11 family-interacting protein 1CSQ28456ZNF930Gauine molecule-binding protein G(I)CG(S)(CT) submit bers 1CSQ28456ZNF930Gauine molecule-binding protein G(I)CG(S)(CT) submit bers 1CSQ28456ZNF	Q15061	WDR43	WD repeat-containing protein 43	C,S
Q1318CBX3Chromobor protein homolog 3WT, C, S.Q45741PRATYSProtein arquine X-methylkramforase 5WT, C, S.Q460F116MS12R.NA-honding protein Musahi homolog 2WT, C, S.Q13080PRAS2R.Boscephophate protein Musahi homolog 2C, S.Q467V1OTUB1Ubiquitin fluiscenze OTUB1C, S.Q467V7IPO3Importin-9C, S.Q457V7DCAF16DDB1-ad CUL4-suociated factor 16C, S.Q3NZ4LRRFIP1Lackine-icht protein fluiscenze protein 1WT, C, S.Q3NZ4LRRFIP1Lackine-icht protein fluiscenze protein 1WT, C, S.Q5384BUB3Horicic checkpoint protein BUB3C, S.Q4986MEAX7MTOR suscical protein MEAX7C, S.Q4986BOLA2BolA file protein 2C, S.Q4987RCC2Protein BCC2C, S.Q4988RCC2Protein BCC2C, S.Q4984BOLA2BolA file protein 30C, S.Q4985RCC2Protein BCC2C, S.Q4984MTONE checkpoint protein G1/PG(S)/G(T) subanit jamma, mitochondrialC, S.Q4985RCD2Protein BCC2C, S.Q4986BOLA2BolA file protein 30C, S.Q4987RCD1Ratin randordic Hondring protein 2C, S.Q4987GNB1Guar intracting parter of ALKC, S.Q4985CANXClanesinC, S.Q4985RCC2Protein BCC2C, S.Q4985RCC2Protein BC	Q8NC51	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	C,S
Old?4PKNT5Protein arginits N-methyltransforms 5WT, C, SQ60FH6MS12K13bersphosphakinase 2C5P11908PKP2Ribos-phosphakinase 2C5Q6FW1OTUB1Ubagint nhiseserase OTUB1C5Q6FW2IFO3ImportinsC5Q1565TRU15Pubytene checkpoint protein 2 homologC5Q15645TRU15Pubytene checkpoint protein 2 homologC5Q3XA7DCAFIELaudeneich repeartBighdes-interacting protein 1WT, C, SQ5185EIF231Laudeneich repeartBighdes-interacting protein 1C5Q69786MEAR7MTOR associtared protein MEAR7C5Q53585IDH3GIncitared departingmang NAD public 1C5Q54546BUB3Mitosic checkpoint protein BUB3C5Q5353IDH3GIncitared departingmang NAD public transformC5Q67946RCQPotein RC2C5Q79158RCGRCGRCGQ6745ZNFG0ZnG protein RC3C5Q79159Z3HC1Nuclear-interacting partner of ALKC5Q6745ZNFG0ZnG protein RC2C5Q6745ZNFG0ZnG protein RC2C5Q6745ZNFG0C6SiQ6745ZNFG1Saccitarity protein 1C5Q6745ZNFG1Radprin errotein BU7C5Q6745ZNFG0C6SiQ6745ZNFG1Radprin errotein G1(J/G(G)/G(T) unbuit beta-1C5Q6745ZNFG1Radprin erro	Q13185	CBX3	Chromobox protein homolog 3	WT, C <sub>s</sub> S
Q*60HisMSI2RNA-binding protein Musakin homolog 2WT, C,SP19080PRPS2Rhose-phosphate proposphate Ansaze 2C,SQ66F70IPO9Inportin-9C,SQ66F70IPO9Inportin-9C,SQ70K71DCAR16DDB1: and CUL4-associated factor 16C,SQ20K72LRAF1P1Laction-rick regar flighted-sinteracting protein 1WT,C,SQ5184IETS1Eakaryotic translation indiction factor 2 subani 1C,SQ69786MEAK7MTOR-associated protein MEAK7C,SQ49786MEAK7MTock associated protein MEAK7C,SQ51535IDF150Incitact dehydrogenesa [NAD] subarit gamam, nitochondrialC,SQ97858RC2Protein RC2C,SQ97858RC2Protein RC2C,SQ97859RC3ZNF03Zan finger protein SUBC,SQ97858RC2Protein RC2C,SQ97859RC3Zan finger protein SUBC,SQ97859RC3Zan finger protein SUBC,SQ97859RC3Zan finger protein SUBC,SQ97859RC4RABITPIRabit family-interacting protein G(I)/C(S)/G(T) subarit bera-1C,SQ97859RC3CASC,SQ97859RC4RABITPIRabit family-interacting protein 1C,SQ48750CASC,SC,SQ97854RABITPIRabit family-interacting protein 1C,SQ48754RABITPIRabit family-interacting protein 3WT,C,S <td< td=""><td>O14744</td><td>PRMT5</td><td>Protein arginine N-methyltransferase 5</td><td>WT, C<sub>p</sub>S</td></td<>	O14744	PRMT5	Protein arginine N-methyltransferase 5	WT, C <sub>p</sub> S
P11968PR52Rboc-phosphate prophosphate parcel photomiase 2C, SQP6FW1OTUB1Ubigatin chicecrares OTUB1C, SQP6FW1PC9Importin-9C, SQ15653TR1P13Pachrene checkpint poten 2 homologC, SQ23AZ4LRKHTP1Lacine-rich repert flipides-interacting poten 1WT, C, SQ64796MEAK7MTOR-associated factor 16C, SQ64796MEAK7MTOR-associated poten MUB3C, SQ45846BUB3Mitoric checkpoir poten SuB3C, SQ45846BUB3Bold-like protein MUB3C, SQ45846BUB3Bold-like protein 2C, SQ47356BOLA2Bold-like protein 2C, SQ4736BOLA2Bold-like protein 3C, SQ47358RCC2Protein RC2C, SQ47454ZNFG3Zne finger protein 3C, SQ47454ZNFG3Zne finger protein 3C, SQ47454ZNFG3Zne finger protein 53C, SQ47454ZNFG3Zne finger protein 18C, SQ47454ANB1Gaunine ancyltradrest rype Catalytic subunit fear-1C, SQ47545ZNFG3Zne finger protein 18C, SQ47544RAB1FP1Rab1 finnij-interacting protein 1C, SQ47545GANACaleratinC, SQ47546RAB97Histone-binding protein 2C, SQ47547TAC3Tandforming protein 2C, SQ47548RAD3C, SC, SQ47549 <td< td=""><td>Q96DH6</td><td>MSI2</td><td>RNA-binding protein Musashi homolog 2</td><td>WT, C<sub>r</sub>S</td></td<>	Q96DH6	MSI2	RNA-binding protein Musashi homolog 2	WT, C <sub>r</sub> S
QeFVP1OTUB1Ubiquitn hiseterse OTUB1C,SQeFVP2IPO9Importin-9C,SQ15645TRLP13Padryrene checkpoint protein 2 homolog.C,SQ2N474LCAF16DDB1-and CUL4-sociated factor 16C,SQ2N474L.R.KP114Leucine-rich repart flightess-interacting protein 1WT,C,SP05198IF2S1Eakaryotic translation initiation factor 2 subuni 1C,SQ49786MEAK7MTOR-associated protein MEAK7C,SQ49786MEAK7MTOR-associated protein MEAK7C,SQ5584B0L42BolA/like protein 2C,SQ49786NGC2Protein RCC2C,SQ49786KC24Protein RCC2C,SQ49786XLSC2Protein RCC2C,SQ49787XLSC3Zinc finger protein 053C,SQ4874RAB11FP1Histone-training partner of ALKC,SQ4874RAB11FP1Rab11 family-interacting protein 1BC,SQ4874RAB11FP1Rab11 family-interacting protein 1G(1)/G(S)/G(T) subunit bera-1C,SQ4875CANXCalnexinC,SQ48754RAB17Histone-binding protein RBP7C,SQ48754RAB17Histone-binding protein RBP7C,SQ48754RAB17Histone-binding protein 1BC,SQ48754RAB17Histone-binding protein 1ABP7C,SQ48754RAB17Histone-binding protein 1ABP7C,SQ48754RAB7Histone-binding protein 1ABP7C,SQ48754R	P11908	PRPS2	Ribose-phosphate pyrophosphokinase 2	C <sub>F</sub> S
Qx0670IPO9Importin-9C,SQ55645TKLP13PLedyrenc heckpoint protein 2 homologC,SQ9XX77DCAP16DDB1-and CUL-4-associated factor 16WT, C,SQ9X174LR,RP114Leucine-tch repart fliphdes-interacting protein 1WT, C,SQ61984EIP251Ealaryotic translation initiation factor 2 subanit 1C,SQ64986MEAK7MTOR-associated protein MEAK7C,SQ64986BUB3Mitoric checkpoint protein BUB3C,SQ55353IDH3GLocitrate dehydrogenase [NAD] subunit gamma, mitochondrialC,SQ91354BOLA2BoLAl-like protein 2C,SQ91355JDH3GLocitrate dehydrogenase [NAD] subunit gamma, mitochondrialC,SQ91364BOLA2BoLAl-like protein 2C,SQ91375CJB1GQualeer-interacting protein G(I)/G(S/C(T) subunit beta-1C,SQ91376ZM593Zine finger protein G(I)/G(S/C(T) subunit beta-1C,SQ6745ZM593Zine finger protein G(I)/G(S/C(T) subunit beta-1C,SQ4757GNB1Guanine muderide-binding protein G(I)/G(S/C(T) subunit beta-1C,SQ48757GNB1Guanine muderide-binding protein G(I)/G(S/C(T) subunit beta-1C,SQ48573MAP1Bab1 family-interact	Q96FW1	OTUB1	Ubiquitin thioesterase OTUB1	C <sub>r</sub> S
Q1564TRIP13Padwrene checkpoint protein 2 homologC,SQ9NNT7DCATH6DDB1 and CUL4-associated factor 16C,SQ32MZ4LRR FIP1Leucine-rich repear flightesi-interacting protein 1WT,C,SP05198EIP251Eukaryotic translation initiation factor 2 subunit 1C,SQ69206MEAK7MTOR-associated protein MEAK7C,SO43644BUB3Mitotic checkpoint protein BUB3C,SP35535DDH3GBol-Late protein activated protein BUB3C,SQ91258RC2Porcin RC2C,SQ91258RC2Porcin RC2C,SQ91258RC3DIA-100 matine nucleotido-choling protein 503C,SQ4645Z.NF903Zanc finger protein 503C,SQ47547HAT1Histone scapytransfrase type B ctalytic subunitC,SQ4654RABIFMitcroubule associated protein 1BC,SQ4654RABIFHalt1 family-interacting protein 30WT,C,SQ4654RABBTC,SSQ4654RABBTC,SSQ4656RBB7Histone-binding protein RBB7C,SQ4654RABBTC,SSQ4654TACC3Transforming acidic colid-containing protein 3WT,C,SQ4654TACC3Transforming acidic colid-containing protein 3WT,C,SQ4654TOM1Target of Mp protein 1C,SQ4654TOM1Target of Mp protein 3C,SQ7164DDX39AATP-dependent KAA helicate DDX39AC,S	Q96P70	IPO9	Importin-9	C <sub>r</sub> S
QPNAIPDCAF16DDBI- and CUL+associated factor 16C SQ2BVZ4LRR.FIP1Luccinc-rich repeat flightes-intracting protein 1WT, C SQ6P386MEAK7MTOR-associated protein MEAK7C SQ6P386MEAK7MTOR-associated protein MEAK7C SQ6P386BUB3Mitotic checkpoint protein BUB3C SQ9133K6BOLA2BoLA14be protein 2C SQ9133K6BOLA2BoLA14be protein 2C SQ9193ZC3HC1Nuclear-interacting partner of ALKC SQ9194ZC3HC1Nuclear-interacting protein 60(J/G(S)(GT) subunit bera-1C SQ6F45ZNF503Zinc finger protein 503C SQ6F45ZNF503Zinc finger protein 503C SQ6WKZ4RAB11FIP1Rab11 family-interacting protein 1C SQ6WKZ4RAB11FIP1Rab11 family-interacting protein 1C SQ6WKZ4RAB11FIP1Rab11 family-interacting protein 1C SQ6WX54RAB11FIP1Rab11 family-interacting protein 1C SQ6W754CANXCanexinWT, C SQ6W754TACC3Transforming activitic and and the factor 3 subunit AC SQ7131PM20D2Peptidase M20 domain-containing protein 3WT, C SQ6W754TACC3Transforming activitic and subunit AC SQ71247ElF3MEukaryotic translation initiation factor 3 subunit AC SQ71247ElF3MEukaryotic translation initiation factor 3 subunit AC SQ9WA3TACC3Transformi	Q15645	TRIP13	Pachytene checkpoint protein 2 homolog	<u>C</u> ,S
Q224/24LRR FIPLaudier icht repeat flightes-interacting protein 1VT, CSQ6P286MEAX7MTOR-associated protein MEAX7CSQ6P286MEAX7MTOR-associated protein MEAX7CSQ6P286BUB3Mitotic checkpoint protein BUB3CSQ915853IDH3GIsocitrate delydrogenae [NAD] subunit gamma, mitochondrialCSQ91586BOLA2BolAite protein 2CSQ91587RCC2Protein RCC2CSQ91588RCC2Protein RCC2CSQ91694ZAF503Zan Engerprotein 503CSQ92575GNB1Gaanine nucleotide-binding protein G(I)/G(S/G(T) subunit beta-1CSQ92729HAT1Histone acceptransferas trype B catalytic subunitCSQ48273GNB1Gaanine nucleotide-binding protein BCSQ48744RAB11FIP1Rab11 fmilly-interacting protein 1CSQ48754CANXCalnexinCSQ48744RAB11FIP1Rab11 fmilly-interacting protein 2CSQ48744CANXCalnexinCSQ48754CANXCalnexinCSQ48754TACC3Transforming acidic cold-containing protein 2CSQ7845TACC3Transforming acidic cold-containing protein 2CSQ97845TACC3Transforming acidic cold-coll-containing protein 2CSQ97845TACC3Transforming acidic cold-coll-containing protein 3WT, CSQ97845TACC3Transforming acidic cold-coll-containing protein 2CSQ9784	Q9NXF7	DCAF16	DDB1- and CUL4-associated factor 16	<u>C</u> <u>\$</u>
P05198EIF281EuLaryotic translation initiation factor 2 subunit 1C SQ6P986MEAK7MTOR associated portein MEAK7C SQ45864BUB3Mitotic checkyoint protein BUB3C SP1553IDH3GIsocitrate dehydrogenase [NAD] subunit gamma, mitochondrialC SQ9P286BOLA2BolA-like protein 2C SQ9P287R CC2Protein RCC2C SQ9090CC3HC1Nuclear-interacting partner of ALKC SQ96745ZNF503Zinc finger protein 503C SQ64745ZNF503Zinc finger protein 503C SQ64745RAD1Histone accetyntrasferase trype B catalytic subunitC SQ64756R BBP7Histone accetyntrasferase trype B catalytic subunitC SQ64756R BBP7Histone-binding protein RBP7C SQ64756R BBP7Histone-binding protein RBBP7C SQ76756R BBP7Histone-binding protein RBBP7C SQ7874CALAPKanadaptinC SQ7874TOAC3Transforming acdic coll-containing protein 3WT, C SQ7874TOAC1Transforming accidic coll-containing protein 3WT, C SQ79742EIF3LEakaryotic translation initiation factor 3 subunit IC SQ79745TOAC3Transforming accidic coll-containing protein 3WT, C SQ79745TOAC3Transforming accidic coll-containing fractor 3 subunit IC SQ97242EIF3LEakaryotic translation initiation factor 3 subunit IC SQ9	Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	WT, C, S
QAPP96MEAX/M IOK associated protein MEAX/C SQ48584BUB3M Notic checkpoint protein BUB3C SQ91386BOLA2BolA-like protein 2C SQ91386BOLA2BolA-like protein 2C SQ91386BOLA2BolA-like protein 2C SQ91387RCC2Protein RCC2C SQ9198RCC2Protein RCC2C SQ96785ZNF903Zinc finger protein 603C SQ96785ZNF903C SC SQ96785RNB1Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1C SQ48724RABIIPIPIHabil f family-interacting partner of ALKC SQ48724RABIIPIPIHabil family-interacting partner of an BPC SQ48724RABIIPIPIHabil family-interacting protein G(I)/G(S)/G(T) subunit beta-1C SQ48724RABIPIPIHabil family-interacting protein 1BC SQ48724CANXC CalnexinC SQ48731PM20D2Peptidase M20 donain-containing protein 2C SQ4754TACC3Transforming acidic colle-coli-containing protein 3WT, C SQ9754TACC3Transforming acidic colle-coli-containing protein 3WT, C SQ97240EIF3LEukaryotic translation initiation factor 3 subunit MC SQ97241EIF3MEukaryotic translation initiation factor 3 subunit MC SQ97242EIF3LEukaryotic translation initiation factor 3 subunit MC SQ97243EIF3LEukaryotic translation i	P05198	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	<u> </u>
OH384         DOBS         Mitotic Recepting protein BCBS         CS           951555         IDH3G         lackitrat delydrogenase (NAD) subunit gamma, mitochondrial         CS           QP1386         BOLA2         BolA-like protein 2         CS           QP1387         RCC2         Protein RCC2         CS           QP2588         RCC2         Protein RCC2         CS           QP6454         ZNF503         Zinc finger protein 503         CS           QP6454         ZNF503         Zinc finger protein 503         CS           Q64747         RAT1         Histone acceptransferrase type B catalytic subunit         CS           Q64782         RAB11FIP1         Rab11 family-interacting protein 18         CS           Q64782         RAB11FIP1         Rab11 family-interacting protein 18         CS           Q16576         RBB7         Histone-binding protein 18         CS           Q16576         RBB7         Histone-binding protein 2         CS           Q18751         PM2DD2         Peptidase M20 domain-containing protein 3         WT, CS           Q976A5         TACC3         Transforming acidic coil-containing protein 3         WT, CS           Q972A2         EFB3.         Eukaryotic translation inititation factor3 subunit L         CS </td <td>Q6P9B6</td> <td>MEAK/</td> <td>M I OR-associated protein MEAK/</td> <td><u> </u></td>	Q6P9B6	MEAK/	M I OR-associated protein MEAK/	<u> </u>
Ph153         IDPLS3         IDPLS4         IDPLS4         IDPLS4         IDPLS4           QP1356         BOLA.2         BoLA.1ke protein 2         C \$           QP1258         RCC.2         Protein RCC.2         C \$           QP1356         ZG3HC1         Nuclear-interacting partner of ALK         C \$           QP1575         ZNF503         Zin finger protein 503         C \$           QP2547         GNB1         Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1         C \$           QP26475         ZNF503         Zin finger protein 1         C \$           QP2647         RAB11FIP1         Rab11 family-interacting partner of nLK         C \$           QP4852         MAP1B         Microtubule-associated protein 1         C \$           Q6676         RBB7         Histone-binding protein 7BBP7         C \$           Q16576         RBB7         Histone-binding protein 7BBP7         C \$           Q18751         M20D2         Peptidas M20 domain-containing protein 2         C \$           Q18751         M20D2         Peptidas M20 domain-containing protein 3         WT, C \$           Q18751         M20D2         Peptidas M20 domain-containing protein 3         WT, C \$           Q18751         M20D2         Peptidas M20 dom	D51552	BUB3	Mitotic checkpoint protein BUB3	C,S
QP1258         RCC2         Protein RCC2         C_S           Q9P258         RCC2         Protein RCC2         C_S           Q9F254         ZNF503         Zinc finger protein 503         C_S           Q9F455         ZNF503         Zinc finger protein 503         C_S           Q9F258         RCC2         RCS7         GNB1         Guarine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1         C_S           Q6WK24         RAB11FIP1         Rab11 family-interacting protein 1         C_S         C_S           Q6WK24         RAB11FIP1         Rab11 family-interacting protein 1         C_S         C_S           Q6WK24         RAB17FIP1         Rabone-binding protein RBBP7         C_S         C_S           Q16576         RBBP7         Histone-binding protein RBBP7         C_S         C_S           Q18751         PM20D2         Peptidase M20 domain-containing protein 2         C_S         C_S           Q81YS1         PM20D2         Peptidase M20 domain-containing protein 3         WT, C_S         QG           Q976A5         TACC3         Transforming acidic coile-containing protein 3         WT, C_S         QG           Q97124         EIF3L         Eukaryotic translation initiation factor 3 subunit L         C_S         QG	C9H3K6	BOL A 2	Bol A like protein 2	<u> </u>
Q1450         ROCK         Interface of ALK         Op           Q9[019         ZC3HC1         Nuclear-interacting partner of ALK         C,5           Q96145         ZNF503         Zine finger protein 503         C,5           P62873         GNB1         Guanine nucleotide-binding protein GI/J/G(5)/G(T) subunit beta-1         C,5           Q64729         HAT1         Histone acetyltransferase type B catalyric subunit         C,5           Q648XZ4         RABITFIP1         Rab11 family-interacting protein 1         C,5           Q648XZ4         RABITFIP1         Rab11 family-interacting protein 1B         C,5           Q16576         RBB7         Histone-binding protein RBB7         C,5           Q16576         RBB7         Histone-binding protein RBB7         C,5           Q16576         RBB7         Histone-binding protein 1B         WT, C,5           Q16576         RBB7         Histone-binding protein 2         C,5           Q1573         TACC31         Transforming acidic colic-coli-containing protein 30         WT, C,5           Q81YS1         PM2002         Petpidase M20 domain-containing protein 3         WT         C,5           Q956A5         TACC3         Transforming acidic colic-coli-containing protein 30         WT, C,5         Q95	Q9P258	BCC2	Protein RCC2	<u> </u>
DysidDotsidInteract interactionC, S90%F45ZNF503Zinc finger protein 503C, S914929HAT1Histone accelyltransferase type B catalytic subunitC, S014929HAT1Histone accelyltransferase type B catalytic subunitC, S047829MAP1BMicrotubule-associated protein 1BC, S047821MAP1BMicrotubule-associated protein 1BC, S047823CANXCalactinWT, C, S04783CANXCalactinWT, C, S040857X0M4SLC4A1APKanadaptinC, S040857X0M4SLC4A1APKanadaptinC, S040857X0M4SLC4A1APKanadaptinC, S040857X0M4SLC4A1APKanadaptinC, S040857TACC3Transforming acidic colled-coli-containing protein 2C, S047645TACC3Transforming acidic colled-coli-containing protein 3WT, C, S04714EHF3MEukaryotic translation initiation factor 3 subunit MC, S0712147EIF3MEukaryotic translation initiation factor 3 subunit LC, S000148DDX39AATP-dependent Kinase 4C, S02061PCMT1Protein-L-isoapartate(D-aspartate) O-methyltransferaseWT, C, S0497462EIF3LEukaryotic translation initiation factor 3 subunit LC, S02041WDR77Methylosome protein 50WT, C, S049645AURA7Methylosome protein 50WT, C, S04965AURKAAurora kinase AWT049	C91019	ZC3HC1	Nuclear-interacting partner of ALK	C S
QC150Defining of protein StatisticCQC2373GNB1Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1C,SQ6WKZ4RAB11FIP1Rab11 family-interacting protein 1C,SQ6WKZ4RAB11FIP1Rab11 family-interacting protein 1C,SQ6WKZ4RAB11FIP1Rab11 family-interacting protein 1C,SQ16576RBBP7Histone-binding protein RBBP7C,SQ16576RBBP7Histone-binding protein RBBP7C,SQ16576RDBP7Histone-binding protein RBBP7C,SQ30X57X0M4SILCA1A1PKanadaptinC,SQ4IYS1PM20D2Peptidase M20 domain-containing protein 2C,SQ9Y6A5TACC3Transforming acidic coile-coil-containing protein 3WT,C,SQ9Y6A5TACC3Transforming acidic coile-coil-containing protein 3WT,C,SQ9Y6A5TAC3Transforming acidic coile-coil-containing protein 3WT,C,SQ9Y2A2EIF3LEukaryotic translation initiation factor 3 subunit L <t< td=""><td>096F45</td><td>ZNF503</td><td>Zinc finger protein 503</td><td>C S</td></t<>	096F45	ZNF503	Zinc finger protein 503	C S
OldOldOldOld04929HAT1Histone acetyltransferase type Brathylic subunitC\$049224RAB11FP1Rab11 family-interacting protein 1C\$046821MAP1BMicrotubule-associated protein 1BC\$04687RBBP7Histone-binding protein RBBP7C\$04687RBBP7Histone-binding protein RBBP7C\$04687CANXCalnexinWT, C\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$04087X0M4SLC4A1APKanadaptinC\$041802CDK4Cyclin-dependent kinase 4C\$04087X0M4TACC3Transforming acidic colle-containing protein 3WT, C\$04084TOM1Target of Myb protein 1C\$C\$04084DD39AATP-dependent RNA helicase DDX39AC\$C\$040148DD39AATP-dependent RNA helicase DDX39AC\$P04048DDX39AATP-dependent RNA helicase DDX39AWTC\$04048DDX39AATP-dependent SWTC\$04049WDR77Methylosome protein 50WT, C\$S04146 <td< td=""><td>P62873</td><td>GNB1</td><td>Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1</td><td>C S</td></td<>	P62873	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	C S
Q6WKZ4RAB11FIP1Rab11 family-interacting protein 1CQ6WKZ4RAB11FIP1Rab11 family-interacting protein 1BCP46821MAP1BMicrotubule-associated protein 1BCQ16576RBBP7Histone-binding protein RBP7CQ16576RABP7Histone-binding protein RBP7CQ7824CANXCalaexinWT, CA0A087X0M4SLC4A1APKanadaptinCA0A087X0M4SLC4A1APKanadaptinCQ81YS1PM20D2Peptidase M20 domain-containing protein 2CQ9Y6A5TACC3Transforming acidic colled-col-containing protein 3WT, C, SQ9Y6A5TACC3Transforming acidic colled-col-containing protein 3WT, C, SQ9Y262EIF3MEukaryotic translation initiation factor 3 subunit MCQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LCQ90148DDX39AATP-dependent RNA helicase DDX39ACP2061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseCQ9RQA1WDR77Methylosome protein 50WT, C, SQ9RQA1WDR77Methylosome protein 50WT, C, SQ1474PRMT5Protein arginine N-methyltransferase 5WT, C, SQ1474PRMT5Protein arginine N-methyltransferase 5WT, C, SQ1474PRMT5Protein arginine N-methyltransferase 5WT, C, SQ9H3K6BOLA2BolA-like protein 2WTQ9H3K6BOLA2BolA-like protein 2WT <td>014929</td> <td>HAT1</td> <td>Histone acetyltransferase type B catalytic subunit</td> <td>C.S.</td>	014929	HAT1	Histone acetyltransferase type B catalytic subunit	C.S.
P46821MAP1BMicrotubule-associated protein 1BC,SQ16576RBBP7Histone-binding protein RBBP7C,SP27824CANXCalnexinWT,C,SA0A087X0M4SLC4A1APKanadaptinC,SQ81YS1PM20D2Peptidase M20 domain-containing protein 2C,SP11802CDK4Cyclin-dependent kinase 4C,SQ9Y6A5TACC3Transforming acidic coiled-coil-containing protein 3WT,C,S060784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX39AATP-dependent RNA helicase DDX39AC,SP2D061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SPRDX2 cysteine-dependent interactorsWT,C,SQ9EQA1WDR77Methylosome protein 50WT,C,SQ4F181CIAPIN1AnamorsinWTE9PGZ1CALD1CaldesmonWT,C,SO14965AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTQ4H3K6BOLA2BolA-like protein 2WTQ4H3K6PCLM3Perilipin-3WT,C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT,C,SP10301RRASRas-related protein R-RasWT	Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	CS
Q16576RBBP7Histone-binding protein RBBP7C,SP27824CANXCalnexinWT, C,SA0A087X0M4SL C4A1APKanadaptinC,SQ8IYS1PM2DD2Peptidase M20 domain-containing protein 2C,SQ8IYS1PM2DD2Peptidase M20 domain-containing protein 2C,SQ9Y6A5TACC3Transforming acidic coiled-coil-containing protein 3WT, C,S060784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX39AATP-dependent RNA helicase DDX39AC,SP2D61P CMT1Protein L-isoaspartate(D-enspartate) O-methyltransferaseC,SQ9RQA1WDR77Methylosome protein 50WT, C,SQ6FI81CIAPIN1AnamorsinWTEPSCZ1CALD1C cladesmonWT, C,SQ14744PRMT5Protein arginine N-methyltransferase 5WT, C,SQ14744PRMT5BolA-like protein 2WTQ9H3K6BOLA2BolA-like protein 2WTQ9H3K6BOLA2BolA-like protein 2WTQ9KQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,S	P46821	MAP1B	Microtubule-associated protein 1B	C S
P27824CANXCalnexinWT, C,SA0A087X0M4SLC AA1APKanadaptinC,SQ8IYS1PM20D2Peptidase M20 domain-containing protein 2C,SP11802CDK4Cyclin-dependent kinase 4C,SQ9Y6A5TACC3Transforming acidic coile-coil-containing protein 3WT, C,S060784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX39AATP-dependent RNA helicase DDX39AC,SP22061PCMT1Protein-L-isoaspartate(D-aspartate) - methyltransferaseC,SPRDX2 cysteine-dependent interactorsVT, C,SQ8181CIAPIN1AnamorsinWTQ9F263AURK77Methylosome protein 50WT, C,SQ6F181CIAPIN1AnamorsinWTQ9F264PRMT5Protein arginine N-methyltransferase 5WT, C,S014744PRMT5Protein arginine N-methyltransferase 5WT, C,S014745AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTQ9H3K6PLN3Perlipin-3WT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	Q16576	RBBP7	Histone-binding protein RBBP7	C.S.
A0.0087X0M4SLC4A1APKanadaptinC,SQ8IYS1PM20D2Peptidase M20 domain-containing protein 2C,SP11802CDK4Cyclin-dependent kinase 4C,SQ9Y6A5TACC3Transforming acidic coiled-coil-containing protein 3WT, C,S060784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y6A5DX39AATP-dependent RNA helicase DDX39AC,S000148DDX39AATP-dependent RNA helicase DDX39AC,S20501PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SPRDX2 cysteine-dependent metatorsQ9BQA1WDR77Methylosome protein 50WT, C,SQ9FI81CIAPIN1AnamorsinWTE9PGZ1CALD1CaldesmonWT, C,S014744PRMT5Protein arginine N-methyltransferase 5WT, C,S014965AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTP48507GCLMGlutamate-cysteine ligase regulatory subunitWTQ8NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	P27824	CANX	Calnexin	WT, C.S
Q8IYS1PM20D2Peptidase M20 domain-containing protein 2C,SP11802CDK4Cyclin-dependent kinase 4C,SQ9Y6A5TACC3Transforming acidic coiled-coil-containing protein 3WT, C,SO60784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX39AATP-dependent RNA helicase DDX39AC,SP22061P CMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SP8DX2 cysteine-depenterVTQ9BQA1WDR77Q9BQA1WDR77Methylosome protein 50WT,C,SQ9F181CIAPIN1AnamorsinWTE9PG21CALD1CaldesmonWT,C,SO14744PRMT5Protein arginine N-methyltransferase 5WT,C,SO14965AURKAAurora kinase AWTQ9H366BOLA2BolA-like protein 2WTP48507GCLMGlutamater-cystein ligas regulatory subunitWTQ60664PLIN3Perilipin-3WT,C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT,C,SP10301RRASRas-related protein R-RasWT	A0A087X0M4	SLC4A1AP	Kanadaptin	C,S
P11802CDK4Cyclin-dependent kinase 4C,SQ9Y6A5TACC3Transforming acidic coiled-coil-containing protein 3WT, C,SO60784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX39AATP-dependent RNA helicase DDX39AC,SP22061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SP22061PCMT1Protein 50WT, C,SQ9BQA1WDR77Methylosome protein 50WT, C,SQ6F181CIAPIN1AnamorsinWTE9PGZ1CALD1CaldesmonWT, C,S014965AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTQ9H3K6BOLA2BolA-like protein 2WTQ9H3X6GCLMGlutamatecystein ligase regulatory subunitWT060664PLIN3Perilipin-3WT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	C,S
Q9Y6A5TACC3Transforming acidic coiled-coil-containing protein 3WT, C,S060784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX39AATP-dependent RNA helicase DDX39AC,SP22061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SPRDX2 cysteine-dependemt interactorsWT, C,SQ9BQA1WDR77Methylosome protein 50WT, C,SQ9EGZ1CALD1CaldesmonWT, C,S014744PRMT5Protein arginine N-methyltransferase 5WT, C,S014965AURKAAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTQ9H3K6PCL1N3Perilipin-3WT060664PLIN3Perilipin-3WT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	P11802	CDK4	Cyclin-dependent kinase 4	C,S
060784TOM1Target of Myb protein 1C,SQ7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX 39AATP-dependent RNA helicase DDX39AC,S22061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SPRDX2cysteine-depentent interactorsWT,C,SQ9BQA1WDR77Methylosome protein 50WT,C,SQ9FG21CALD1CaldesmonWT,C,S014744PRMT5Protein arginine N-methyltransferase 5WT,C,S014965AURKAAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTQ9H3K6BOLA2BolA-like protein 2WTQ9NQX3GPHNGephyrin [Includes: Molybodopterin adenylyltransferaseWT,C,SP10301RRASRas-related protein R-RasWT	Q9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	WT, C <sub>s</sub>
Q7L2H7EIF3MEukaryotic translation initiation factor 3 subunit MC,SQ9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX 39AATP-dependent RNA helicase DDX39AC,SP22061P CMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SPRDX2 cysteine-depent interactorsWT, C,SQ9BQA1WDR77Methylosome protein 50WT, C,SQ9FG21CALD1CaldesmonWT, C,SD14744PRMT5Protein arginine N-methyltransferase 5WT, C,SO14745AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTP48507GCLMGlutamate-cysteine ligase regulatory subunitWTO60664PLIN3Perilipin-3WT, C,SP10301RRASRas-related protein R-RasWT	O60784	TOM1	Target of Myb protein 1	C <sub>c</sub> S
Q9Y262EIF3LEukaryotic translation initiation factor 3 subunit LC,S000148DDX 39AATP-dependent RNA helicase DDX 39AC,SP22061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,S <b>PRDX2 cysteine-dependent mittractors</b> WT, C,SQ9EQA1WDR77Methylosome protein 50WT, C,SQ6F181CIAD10AnamorsinWTE9PGZ1CALD1CaldesmonWT, C,S014744PRMT5Protein arginine N-methyltransferase 5WT, C,S014965AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WT060664PLIN3Perilipin-3WT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	Q7L2H7	EIF3M	Eukaryotic translation initiation factor 3 subunit M	C <sub>i</sub> S
000148DDX 39AATP-dependent RNA helicase DDX 39AC,SP22061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SPRDX2 cysteine-dependent interactorsQ9BQA1WDR 77Methylosome protein 50WT, C,SQ6F181CIAD1N1AnamorsinWTE9PGZ1CALD1CaldesmonWT, C,S014744PRMT5Protein arginine N-methyltransferase 5WT, C,S014965AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTP48507GCLMGlutamatecysteine ligase regulatory subunitWT060664PLIN3Perilipin-3WT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	Q9Y262	EIF3L	Eukaryotic translation initiation factor 3 subunit L	C <sub>r</sub> S
P22061PCMT1Protein-L-isoaspartate(D-aspartate) O-methyltransferaseC,SPRDX2 cysteine-dependent interactorsQ9BQA1WDR77Methylosome protein 50WT, C,SQ6F181CIAPIN1AnamorsinWTE9PGZ1CALD1CaldesmonWT, C,S014744PRMT5Protein arginine N-methyltransferase 5WT, C,S014965AUR&AAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WTP48507GCLMGlutamatecysteine ligase regulatory subunitWT060664PLIN3Perilipin-3WT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	O00148	DDX39A	ATP-dependent RNA helicase DDX39A	C <sub>r</sub> S
PRDX2 cysteine-dependent interactors           Q9BQA1         WDR77         Methylosome protein 50         WT, C,S           Q6F181         CIAPIN1         Anamorsin         WT           E9PGZ1         CALD1         Caldesmon         WT, C,S           014744         PRMT5         Protein arginine N-methyltransferase 5         WT, C,S           014765         AURKA         Aurora kinase A         WT           Q9H3K6         BOLA2         BolA-like protein 2         WT           P48507         GCLM         Glutamatecysteine ligase regulatory subunit         WT           060664         PLIN3         Perilipin-3         WT, C,S           Q9NQX3         GPHN         Gephyrin [Includes: Molybdopterin adenylyltransferase         WT, C,S           P10301         RRAS         Ras-related protein R-Ras         WT	P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	C <sub>z</sub> S
Q9BQA1WDR77Methylosome protein 50WT, C,SQ6F181CIAPIN1AnamorsinWTE9PGZ1CALD1CaldesmonWT, C,S014744PR.MT5Protein arginine N-methyltransferase 5WT, C,S014965AURKAAurora kinase AWTQ9H3K6BOLA2BolA-like protein 2WT060664PLIN3Perilipin-3WT, C,SQ9NQX3GPHNGephyrin [Includes: Molybdopterin adenylyltransferaseWT, C,SP10301RRASRas-related protein R-RasWT	PRDX2 cysteine-de	pendent interactors		
QeFI81     CIAPIN1     Anamorsin     WT       E9PGZ1     CALD1     Caldesmon     WT, C §       014744     PRMT5     Protein arginine N-methyltransferase 5     WT, C §       014965     AURKA     Aurora kinase A     WT       09H3K6     BOLA2     BolA-like protein 2     WT       046664     PLIN3     Perilipin-3     WT, C §       09NQX3     GPHN     Gephyrin [Includes: Molybdopterin adenylyltransferase     WT, C §       P10301     RRAS     Ras-related protein R-Ras     WT	Q9BQA1	WDR77	Methylosome protein 50	WT, C,S
E3PGZ1     CALD1     Caldesmon     WT, C, S       014744     PRMT5     Protein arginine N-methyltransferase 5     WT, C, S       014965     AURKA     Aurora kinase A     WT       09H3K6     BOLA2     BolA-like protein 2     WT       P48507     GCLM     Glutamatecystein ligase regulatory subunit     WT       060664     PLIN3     Perlipin-3     WT, C, S       09NQX3     GPHN     Gephyrin [Includes: Molybdopterin adenylyltransferase     WT, C, S       P10301     RRAS     Ras-related protein R-Ras     WT	Q6FI81	CIAPIN1	Anamorsin	WT
O14744         PRMT5         Protein arginine N-methyltransferase 5         WT, C, S           O14965         AURKA         Aurora kinase A         WT           Q9H3K6         BOLA2         BolA-like protein 2         WT           P48507         GCLM         Glutamatecysteine ligase regulatory subunit         WT           060664         PLIN3         Perilipin-3         WT, C, S           Q9NQX3         GPHN         Gephyrin [Includes: Molybdopterin adenylyltransferase         WT, C, S           P10301         RRAS         Ras-related protein R-Ras         WT	E9PGZ1	CALD1	Caldesmon	WT, C S
014965         AURKA         Aurora kinase A         WT           Q9H3K6         BOLA2         BolA-like protein 2         WT           P48507         GCLM         Glutamatecysteine ligase regulatory subunit         WT           O60664         PLIN3         Perilipin-3         WT, C,S           Q9NQX3         GPHN         Gephyrin [Includes: Molybdopterin adenylyltransferase         WT, C,S           P10301         RRAS         Ras-related protein R-Ras         WT	014744	PRMT5	Protein arginine N-methyltransferase 5	WT, C,S
Q9H38.6         BOLA2         BolA-like protein 2         WT           P48507         GCLM         Glutamatecysteine ligase regulatory subunit         WT           O60664         PLIN3         Perilipin-3         WT, C,S           Q9NQX3         GPHN         Gephyrin [Includes: Molybdopterin adenylyltransferase         WT, C,S           P10301         RRAS         Ras-related protein R-Ras         WT	014965	AURKA	Aurora kinase A	WT
P4850//     GCLM     Glutamatecysteine ligase regulatory subunit     WT       O60664     PLIN3     Perilipin-3     WT, C,S       Q9NQX3     GPHN     Gephyrin [Includes: Molybdopterin adenylyltransferase     WT, C,S       P10301     RRAS     Ras-related protein R-Ras     WT	Q9H3K6	BOLA2	BolA-like protein 2	WT
O60664         PLIN3         Perilipin-3         WT, C, S           Q9NQX3         GPHN         Gephyrin [Includes: Molybdopterin adenylyltransferase         WT, C, S           P10301         RRAS         Ras-related protein R-Ras         WT	P48507	GCLM	Glutamatecysteine ligase regulatory subunit	WT
QPNQX5         GPHN         Gephyrin [Includes: Molybdopterin adenylyltransferase         WT, C, S           P10301         RRAS         Ras-related protein R-Ras         WT	060664	PLIN3	Perilipin-3	WT, CS
P10501 KKAS Kas-related protein K-Kas WT	Q9NQX3	GPHN	Gephyrin [Includes: Molybdopterin adenylyltransferase	WT, CS
	P10301	RRAS	Kas-related protein R-Ras	WT

Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase	WT, C S
Q9UL15	BAG5	BAG family molecular chaperone regulator 5	WT
EZEVAD	M A D/	Micrombule associated protein	WTCS
L/LV/10	111111	Microtubile associated protein	w1,0,5
Q9BTE6	AARSD1	Alanyl-tRNA editing protein Aarsdl	WT
Q5T4K5	CRTC2	CREB-regulated transcription coactivator 2	WT
O8NC51	SER BP1	Plasminogen activator inhibitor 1 R NA-binding protein	WT.CS
R/DDF/	CNN2		w/r
B4DDr4	CNN2	Calponin	W I
Q9NXV2	KCTD5	BTB/POZ domain-containing protein KCTD5	WT
A0A0A0MRN5	OGFR	Opioid growth factor receptor	WT
098570	DDME1	Protein allocalitation and publications of 1	WTCS
0/13/0	FFWLLI	Protein phosphatase methylesterase 1	w1,C3
O00566	MPHOSPH10	U3 small nucleolar ribonucleoprotein protein MPP10	WT
P53985	SLC16A1	Monocarboxylate transporter 1	WT
P35520	CBS	Cystathionine beta-synthase	WTCS
0.01100/	DDV/F		
Q9H084	DDX4/	Probable A I P-dependent KNA helicase DDX4/	W I
P10599	TXN	Thioredoxin	WT, C,S
O96IZ0	PAWR	PRKC apoptosis WT1 regulator protein	WT
D/5995	MAD2K4	Dual encoidaire mitocon activited protein kinaco kinaco é	W/T
14)/8)	WITH 2K4		w 1
Q13428	TCOF1	Treacle protein	WT, C,S
P85037	FOXK1	Forkhead box protein K1	WT
P07355	ANXA2	Annexin A2	WT C S
0.05	EVE (EDD)		
Q13541	EIF4EBP1	Eukaryotic translation initiation factor 4E-binding protein 1	w1,C,S
Q9ULX6	AKAP8L	A-kinase anchor protein 8-like	WT
O95816	BAG2	BAG family molecular chaperone regulator 2	WT
09(007	MOCS2	Malub dantarin gunthaca astaluria gubunit	WT
0,000/	110032	Non-outpoint synthiase catalytic subunit	** 1 *****
Q9HA64	FN3KRP	Ketosamine-3-kinase	W F, C, S
Q15417	CNN3	Calponin-3	WT, C S
095104	SCAF4	SR-related and CTD-associated factor 4	WT.C.S
0152/5	DODDI		w1,0,0
Q15365	PCBP1	Poly(rC)-binding protein 1	W I
Q9P2B4	CTTNBP2NL	CTTNBP2 N-terminal-like protein	WT, C S
O12948	FOXC1	Forkhead box protein C1	WT, CS
00/E45	ZNIE502		WTCS
Q96F45	ZINF303	Zine ninger protein 505	w1,C <sub>2</sub> 5
015511	ARPC5	Actin-related protein 2/3 complex subunit 5	WT
Q9NUQ3	TXLNG	Gamma-taxilin	WT, C.S
O8WYA6	CTNNBI 1	Beta-catenin-like protein 1	WT
0000110	ATDOULU		W/T
090112	AIP6VIH	V-type proton A I Pase subunit H	W I
P52888	THOP1	Thimet oligopeptidase	WT, C,S
O16204	CCDC6	Coiled-coil domain-containing protein 6	WT, CS
G3X AG1	ZNIE512	7 inc finder protein \$12	WT
O MOI	2101312		wi
Q9H7E9	C8orf33	UPF0488 protein C8orf33	WT
Q14247	CTTN	Src substrate cortactin	WT, C.S
P82921	MR PS21	28S ribosomal protein S21, mitochondrial	WT
Depart	010711		WT OO
P32907	CAPZAI	r-actin-capping protein subunit alpha-1	w1,C <sub>2</sub> 5
P61758	VBP1	Prefoldin subunit 3	WT, C, S
P49790	NUP153	Nuclear pore complex protein Nup153	WT, CS
O8N806	LIBP 7	Dutative F3 ubiquitin protein ligace LIRP 7	WT
2011000	UBR/	Tutative Ly document proteining as control	wi
Q92945	KHSRP	Far upstream element-binding protein 2	WI
O00273	DFFA	DNA fragmentation factor subunit alpha	WT, C <sub>S</sub>
P63167	DYNLL1	Dynein light chain 1. cytoplasmic	WT
0125.42	ELE/ERD2	$\sigma$ -	WT C S
Q13342	EIF4EDP2	Eukaryotic translation initiation factor 4E-binding protein 2	w1,C3
Q9UNF1	MAGED2	Melanoma-associated antigen D2	w 1, C S
J3QQZ9	PNPO	Pyridoxal 5'-phosphate synthase	WT
E7EV99	ADD1	Alpha-adducin	WT, C S
AOA 1 BOOW 29	CPI	F2 ubiquitie protoin ligano CPI	WTCS
AUAIDUG W 38	CDL		w 1, C <sub>1</sub> 3
Q5QPM7	PSMF1	Proteasome inhibitor PI31 subunit	WT, C S
F5H8D7	XRCC1	DNA repair protein XRCC1	WT, C.S
P26599	PT'BP1	Polynyrinidine tract-hinding protein 1	WTCS
01/57/	DDD7		
Q165/6	KBBP/	Histone-binding protein KBBP/	W1,C5
Q06124	PTPN11	Tyrosine-protein phosphatase non-receptor type 11	WT, C,S
O9UHD1	CHOR DC1	Cysteine and histidine-rich domain-containing protein 1	WT.CS
0.0817.81	DM 20D2	Dentidaes M20 domain containing protein 2	WT C S
031131	FM20D2	Peptuase w/20 domain-containing protein 2	w1,C3
O60826	CCDC22	Coiled-coil domain-containing protein 22	WT, C <sub>s</sub>
Q5T6F2	UBAP2	Ubiquitin-associated protein 2	WT, C.S
A0A087WTM1	ROBO1	Roundabout homolog 1	WT.CS
058W70		Contractoria of 170 hDa	WTCS
Q38W/7	( LD170		w1,C3
	CEP170	Centrosoma piotem or 170 kDa	
Q7Z434	CEP170 MAVS	Mitochondrial antiviral-signaling protein	WT, C, S
Q7Z434 P49458	MAVS SRP9	Mitochondrial antiviral-signaling protein Signal recognition particle 9kDa protein	WT, C,S WT
Q7Z434 P49458 Q9Y3F4	CEPI70 MAVS SRP9 STR AP	Mitosomal protein or 170 kDa Mitosomal protein or 170 kDa Signal recognition particle 9 kDa protein Serine-throning kinase recentor-associated protein	WT, CS
Q7Z434 P49458 Q9Y3F4	CEP170 MAVS SRP9 STRAP	Mitochondrial antiviral-signaling protein Signal recognition particle 9 kDa protein Serine-theorine kinase receptor-associated protein	WT, C,S WT WT, C,S
Q7Z434 P49458 Q9Y3F4 Q6WKZ4	MAVS SRP9 STRAP RAB11FIP1	Mitochondrial antiviral-signaling protein Signal recognition particle 9 kDa protein Serine-threonine kinase receptor-associated protein Rab11 family-interacting protein 1	WT, C, S WT WT, C, S WT, C, S
Q7Z434 P49458 Q9Y3F4 Q6WKZ4 P22314	CEP170 MAVS SRP9 STRAP RAB11FIP1 UBA1	Mitochondrial antiviral-signaling protein Signal recognition particle 9 kDa protein Serine-threonine kinase receptor-associated protein Rab11 family-interacting protein 1 Ubiquitin-like modifier-activating enzyme 1	WT, C, S WT WT, C, S WT, C, S WT, C, S
Q7Z434 P49458 Q9Y3F4 Q6WKZ4 P22314 P49321	CEP170 MAVS SRP9 STRAP RAB11FIP1 UBA1 NASP	Mitochondrial antiviral-signaling protein Signal recognition particle 9 kDa protein Serine-threonine kinase receptor-associated protein Rab11 family-interacting protein 1 Ubiquitin-like modifier-activating enzyme 1 Nuclear autoantivenic sperm protein	WT, C, S WT WT, C, S WT, C, S WT, C, S WT
Q7Z434 P49458 Q9Y3F4 Q6WKZ4 P22314 P49321 O\$WWK2	CEP170 MAVS SRP9 STRAP RAB11FIP1 UBA1 NASP CKAP2	Mitochondrial antiviral-signaling protein Signal recognition particle 9 kDa protein Serine-threonine kinase receptor-associated protein Rab11 family-interacting protein 1 Ubiquitin-like modifier-activating enzyme 1 Nuclear autoantigenic sperm protein Cutaskidene accessing denzenic 2	WT, C, S WT WT, C, S WT, C, S WT, C, S WT WT
Q7Z434 P49458 Q9Y3F4 Q6WKZ4 P22314 P49321 Q8WWK9	CEP170 MAVS SRP9 STRAP RAB11FIP1 UBA1 NASP CKAP2	Mitochondrial antiviral-signaling protein Signal recognition particle 9 kDa protein Serine-threonine kinase receptor-associated protein Rab11 family-interacting protein 1 Ubiquitin-like modifier-activating enzyme 1 Nuclear autoantigenic sperm protein Cytoskeleton-associated protein 2	WT, C, S WT WT, C, S WT, C, S WT WT, C, S
Q7Z434 P49458 Q9Y3F4 Q6WKZ4 P22314 P49321 Q8WWK9 Q96F86	CEP170 MAVS SRP9 STRAP RAB111FIP1 UBA1 NASP CKAP2 EDC3	Mitochondrial antiviral-signaling protein         Signal recognition particle 9 kDa protein         Serine-threonine kinase receptor-associated protein         Rab11 family-interacting protein 1         Ubiquitin-like modifier-activating enzyme 1         Nuclear autoantigenic sperm protein         Cytoskeleton-associated protein 2         Enhancer of mRNA-decapping protein 3	WT, C,S WT WT, C,S WT, C,S WT, C,S WT WT, C,S WT, C,S

O00629	KPNA4	Importin subunit alpha-3	WT, C <sub>p</sub> S
Q68EM7	ARHGAP17	Rho GTPase-activating protein 17	WT
Q6PKG0	LARP1	La-related protein 1	WT, C, S
Q8N6M0	OTUD6B	Deubiquitinase OTUD6B	WT, C <sub>p</sub> S
Q93034	CUL5	Cullin-5	WT, C, S
Q96P47	AGAP3	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	WT
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	WT, C S
Q2NKX8	ERCC6L	DNA excision repair protein ERCC-6-like	WT, C S
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	WI, CS
Q92/83	CATADDA	Signal transducing adapter molecule 1	WT.CS
CO01P4	DP P C 2C	Dranscriptional repressor p66-alpha	WT CS
P40222	TYI NA	Alpha-tavilin	WT CS
P35237	SER PINB6	Sernin B6	WT CS
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2.	WT.CS
Q9BT25	HAUS8	HAUS augmin-like complex subunit 8	WT, CS
Q96D09	GPRASP2	G-protein coupled receptor-associated sorting protein 2	WT, C.S
Q9NVP1	DDX18	ATP-dependent RNA helicase DDX18	WT, C.S
A0MZ66	SHTN1	Shootin-1	WT, C S
P48634	PRRC2A	Protein PRRC2A	WT, C S
P30740	SERPINB1	Leukocyte elastase inhibitor	WT, C S
O60832	DKC1	H/ACA ribonucleoprotein complex subunit DKC1	C <sub>s</sub> S
O14974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	WT, C <sub>r</sub> S
Q13200	PSMD2	26S proteasome non-ATPase regulatory subunit 2	WT, C <sub>r</sub> S
Q8IWB7	WDFY1	WD repeat and FYVE domain-containing protein 1	WT, C <sub>r</sub> S
Q6UN15	FIP1L1	Pre-mRNA 3'-end-processing factor FIP1	C <sub>r</sub> S
Q9UHV9	PFDN2	Prefoldin subunit 2	WT, C <sub>s</sub> S
C9J0I9	ZC3HC1	Nuclear-interacting partner of ALK	WT, C, S
Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	WT, C S
Q92667	AKAP1	A-kinase anchor protein 1, mitochondrial	WT, C <sub>s</sub> s
P13797	PLS3	Plastin-3	WT, C S
Q0/666	KHDKB51	KH domain-containing, KNA-binding, signal transduction-associated protein 1	WI,CS
DEEDLE	A DA P	Largeting protein for XKIP2	w1,C,S
F9DCT1	TSN	Component 3 of promoter of BISC	WT CS
092769	HDAC2	Histone deacetylase 2	WT CS
000267	SUPT5H	Transcription elongation factor SPT5	C S
P46939	UTRN	Utrophin	C S
Q7Z6Z7	HUWE1	E3 ubiquitin-protein ligase HUWE1	WT, CS
Q92597	NDRG1	Protein NDRG1	CS
A4D1S0	KLRG2	Killer cell lectin-like receptor subfamily G member 2	WT, C S
Q9H3S7	PTPN23	Tyrosine-protein phosphatase non-receptor type 23	WT, C S
O95573	ACSL3	Long-chain-fatty-acidCoA ligase 3	C <sub>z</sub> S
Q6P4A7	SFXN4	Sideroflexin-4	C <sub>s</sub>
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	C <sub>z</sub> S
B1AK87	CAPZB	F-actin-capping protein subunit beta	WT, C <sub>r</sub> S
Q9NYZ3	GTSE1	G2 and S phase-expressed protein 1	WT, C <sub>r</sub> S
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	WT, C,S
G8JLH9	STAT3	Signal transducer and activator of transcription	C <sub>r</sub> S
Q9UN37	VPS4A	Vacuolar protein sorting-associated protein 4A	WI, CS
Q9H2U2	PPA2	Inorganic pyrophosphatase 2, mitochondrial	WI, CS
Q5JKA6	MIA3	Iransport and Goigi organization protein 1 nomolog	WT CS
075225	HAUSC	Gamma-giutamyicyciotransferase	 
Q/Z4II/ O9NYE7	DCAE14	DDR1 and CUL & associated factor 16	WT CS
02M1P5	KIF7	Kinesin-like protein KIF7	C S
Q2M11 ) 09Y266	NUDC	Nuclear migration protein nudC	WT.C.S
O14694	USP10	Ubiquitin carboxyl-terminal hydrolase 10	C S
Q7LBC6	KDM3B	Lysine-specific demethylase 3B	CS
075663	TIPRL	TIP41-like protein	WT, C S
E9PLA9	CAPRIN1	Caprin-1	WT, C.S
O00170	AIP	AH receptor-interacting protein	WT, C,S
Q14240	EIF4A2	Eukaryotic initiation factor 4A-II	WT, C S
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	WT, C <sub>s</sub> S
O15143	ARPC1B	Actin-related protein 2/3 complex subunit 1B	C <sub>r</sub> S
Q96T23	RSF1	Remodeling and spacing factor 1	C <sub>r</sub> S
O60493	SNX3	Sorting nexin-3	C,S
Q9UKX7	NUP50	Nuclear pore complex protein Nup50	C,S
Q92598	HSPH1	Heat shock protein 105 kDa	WT, C <sub>s</sub>
S4R3H4	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	C_S
Q8ND82	ZNF280C	Zinc finger protein 280C	<u>C</u> S
Q9UIG0	BAZIB	Tyrosine-protein kinase BAZ1B	<u>C</u> S
Q8N127	THOC2	THO complex subunit 2	C <sub>r</sub> S

015276	R A BEP1	Rah GTPase-binding effector protein 1	C.S.
P49903	SEPHS1	Selenide water dikinase 1	WTCS
08TA02	SMARCC2	SWI/SNF complex subunit SMAR CC2	WT CS
Q0111Q2	BCC2	Protein R CC2	WT CS
Q/12/0	DEMIDO	2(Spectrocomp non ATDaco resultant subunit 9	WT CS
<u>J3KN2</u>	PDUM1	265 proteasome non-AT Pase regulatory subunit /	w1,C3
D128(1	PDLIMI DD V AD 2 A	PDZ and LIM domain protein 1	<u>C</u> S
P13861	PRKARZA	CAMP-dependent protein kinase type II-alpha regulatory subunit	CS
Q5BKZ1	ZNF326	DBIRD complex subunit ZNF326	C <sub>2</sub> S
Q96KR1	ZFR	Zinc finger RNA-binding protein	C <sub>s</sub> S
Q9NPH2	ISYNA1	Inositol-3-phosphate synthase 1	WT, C <sub>s</sub>
P50213	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	C <sub>r</sub> S
O60343	TBC1D4	TBC1 domain family member 4	WT, C, S
P49588	AARS1	AlaninetRNA ligase, cytoplasmic	C S
A0A3B3ISG5	IDE	Insulin-degrading enzyme	C,S
O43815	STRN	Striatin	CS
A1X283	SH3PXD2B	SH3 and PX domain-containing protein 2B	CS
O6UWP7	LCLAT1	Lysocardiolipin acyltransferase 1	C S
095347	SMC2	Structural maintenance of chromosomes protein 2	C S
D78346	P DD30	R ibonuclease D protein cubunit n30	C S
P/3040	RFF 30	P = 1 = 1 C21 = 1 = 1 = 1 = 1	<u>C</u> 3
P63000	RACI	Ras-related C5 bortuinum toxin substrate 1	C,3
Q9NZB2	FAM120A	Constitutive coactivator of PPAR-gamma-like protein 1	<u>C</u> S
P49750	YLPM1	YLP motif-containing protein 1	CS
Q8N6T3	ARFGAP1	ADP-ribosylation factor GTPase-activating protein 1	C,S
Q9Y2R9	MRPS7	28S ribosomal protein S7, mitochondrial	C <sub>_</sub> S
E9PQV9	DCUN1D5	DCN1-like protein	C <sub>z</sub> S
Q9BXP5	SRRT	Serrate RNA effector molecule homolog	C S
Q8N3X1	FNBP4	Formin-binding protein 4	WT, C,S
O43143	DHX15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	WT, C.S
Q9Y5A9	YTHDF2	YTH domain-containing family protein 2	CS
099598	TSNAX	Translin-associated protein X	WT.C.S
P00387	CYB5R 3	NADH-cytochrome b5 reductase 3	C S
P52701	MSH6	DNA microatch renair protein Meb4	C S
00/002	DI DDD	Duri duru luk suk kan kan su	C5
D/2/77	PLPBP D DC27	Pyridoxal phosphate nomeostasis protein	<u>C</u> 3
P426//	RPS2/	40S ribosomal protein S2/	<u>C</u> S
Q14739	LBR	Delta(14)-sterol reductase LBR	CS
A0A024RCR6	BAG6	BCL2-associated athanogene 6	C <sub>.</sub> S
P51452	DUSP3	Dual specificity protein phosphatase 3	WT, C <sub>2</sub> S
Q8WVC2	RPS21	40S ribosomal protein S21	WT, C S
Q9Y295	DRG1	Developmentally-regulated GTP-binding protein 1	C,S
Q6IQ49	SDE2	Replication stress response regulator SDE2	WT, C, S
M0QY97	ZC3H4	Zinc finger CCCH domain-containing protein 4	C,S
Q04917	YWHAH	14-3-3 protein eta	C,S
P52788	SMS	Spermine synthase	CS
O96A33	CCDC47	Coiled-coil domain-containing protein 47	ĊŚ
P38159	RBMX	R NA-binding motif protein X chromosome	C.S.
D23588	FIF4B	Fukervotic translation initiation factor /B	C S
125500 A0A087WWD4	D DM15	P NA binding protoin 15	<u>C</u> S
A0A007W/T775	KDM13		<u>C</u> 3
A0A08/W1Z5	UBANI	UBX domain-containing protein 1	C,S
Q9UQE7	SMC3	Structural maintenance of chromosomes protein 3	W1, C, S
P46821	MAP1B	Microtubule-associated protein 1B	WT, C <sub>2</sub> S
O95801	TTC4	Tetratricopeptide repeat protein 4	C <sub>2</sub> S
Q9UJV9	DDX41	Probable ATP-dependent RNA helicase DDX41	C <sub>2</sub> S
O00487			
Q8N5F7	PSMD14	26S proteasome non-ATPase regulatory subunit 14	C <sub>s</sub> S
A0A0A0MRM8	PSMD14 NKAP	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein	C S C S
	PSMD14 NKAP MYO6	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6	C S C S C S
P49593	PSMD14 NKAP MYO6 PPM1F	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F	C_\$ C_\$ C_\$ C_\$
P49593 P25786	PSMD14 NKAP MYO6 PPM1F PSMA1	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1	C_S C_S C_S C_S C_S C_S
P49593 P25786 O43809	PSMD14 NKAP MYO6 PPM1F PSMA1 NUDT21	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5	C,S C,S C,S C,S C,S C,S C,S WT.C,S
P49593 P25786 O43809 O13547	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histope deacetylase 1	C,S C,S C,S C,S C,S WT,C,S WT C,S
P49593 P25786 O43809 Q13547 P56385	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1 ATPSMF	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e_mitochondrial	C,S C,S C,S C,S C,S WT,C,S C,S WT,C,S C,S
P49593           P25786           O43809           Q13547           P56385           H0VNUWS	PSMD14 NKAP MYO6 PPMIF PSMA1 NUDT21 HDAC1 ATP5ME DUT	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Dearwarding of strainbargh tot avaloatidehydrologo	C,S C,S C,S C,S C,S WT,C,S WT,C,S C,S WT,C,S C,S WT,C,S
P49593 P25786 O43809 Q13547 P56385 H0YNW5 P11902	PSMD14 NKAP MYO6 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDV4	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cuslin demondent kings 6	C,S C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S WT,C,S
P49593 P25786 O43809 Q13547 P56385 H0YNW5 P11802 P5502	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitione in our doublement ATPase	C,S C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S WT,C,S C,S
P49593 P25786 O43809 Q13547 P56385 H0YNW5 P11802 P55072 P25072	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase	C,S C,S C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593           P25786           O43809           Q13547           P56385           H0YNW5           P11802           P55072           P09936	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase Ubiquitin carboxyl-terminal hydrolase isozyme L1	C,S C,S C,S C,S WT,C,S WT,C,S C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S
P49593       P25786       O43809       Q13547       P56385       H0YNW5       P11802       P55072       P09936       P08240	PSMD14 NKAP MYO6 PPMIF PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase Ubiquitin carboxyl-terminal hydrolase isozyme L1 Signal recognition particle receptor subunit alpha	C,S C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S
P49593           P25786           O43809           Q13547           P56385           H0YNW5           P11802           P55072           P09936           P08240           P22695	PSMD14 NKAP MYO6 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase Ubiquitin carboxyl-terminal hydrolase isozyme L1 Signal recognition particle receptor subunit alpha Cytochrome b-c1 complex subunit 2, mitochondrial	C,S C,S C,S C,S C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593           P25786           O43809           Q13547           P56385           H0YNW5           P11802           P55072           P09336           P08240           P22695           Q13045	PSMD14 NKAP MYO6 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2 FLII	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5 <sup>-</sup> triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase Ubiquitin carboxy1-terminal hydrolase isozyme L1 Signal recognition particle receptor subunit alpha Cytochrome b-c1 complex subunit 2, mitochondrial Protein flightless-1 homolog	C,S C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593           P25786           O43809           Q13547           P56385           H0YNW5           P11802           P55072           P09936           P08240           P22695           Q13045           Q9C0C2	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2 FLII TNKS1BP1	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase Ubiquitin carboxyl-terminal hydrolase isozyme L1 Signal recognition particle receptor subunit alpha Cytochrome b-c1 complex subunit 2, mitochondrial Protein flightless-1 homolog 182 kDa tankyrase-1-binding protein	C,S C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593       P25786       O43809       Q13547       P56385       H0YNW5       P11802       P55072       P09336       P08240       P22695       Q13045       Q9C0C2       P98175	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2 FLII TNKS1BP1 RBM10	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase Ubiquitin carboxyl-terminal hydrolase isozyme L1 Signal recognition particle receptor subunit alpha Cytochrome b-c1 complex subunit 2, mitochondrial Protein flightless-1 homolog 182 kDa tankyrase-1-binding protein RNA-binding protein 10	C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593         P25786         O43809         Q13547         P56385         H0YNWS         P11802         P55072         P09936         P08240         P22695         Q13045         Q9C0C2         P98175         E9PLK3	PSMD14 NKAP MYO6 PPMIF PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2 FLII TNKS1BP1 RBM10 NPEPPS	26S proteasome non-ATPase regulatory subunit 14 NF-kappa-B-activating protein Unconventional myosin-6 Protein phosphatase 1F Proteasome subunit alpha type-1 Cleavage and polyadenylation specificity factor subunit 5 Histone deacetylase 1 ATP synthase subunit e, mitochondrial Deoxyuridine 5'-triphosphate nucleotidohydrolase Cyclin-dependent kinase 4 Transitional endoplasmic reticulum ATPase Ubiquitin carboxyl-terminal hydrolase isozyme L1 Signal recognition particle receptor subunit alpha Cytochrome b-c1 complex subunit 2, mitochondrial Protein flightless-1 homolog 182 kDa tankyrase-1-binding protein RNA-binding protein 10 Aminopeptidase	C,S C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593         P25786         O43809         Q13547         P56385         H0YNW5         P11802         P55072         P09936         P08240         P22695         Q13045         Q9C0C2         P98175         E9PLK3         O8WXF1	PSMD14 NKAP MYO6 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2 FLII TNKS1BP1 RBM10 NPEPPS PSPC1	26S proteasome non-ATPase regulatory subunit 14         NF-kappa-B-activating protein         Unconventional myosin-6         Protein phosphatase 1F         Proteasome subunit alpha type-1         Cleavage and polyadenylation specificity factor subunit 5         Histone deacetylase 1         ATP synthase subunit e, mitochondrial         Deoxyuridine 5'-triphosphate nucleotidohydrolase         Cyclin-dependent kinase 4         Transitional endoplasmic reticulum ATPase         Ubiquitin carboxyl-terminal hydrolase isozyme L1         Signal recognition particle receptor subunit alpha         Cytochrome b-c1 complex subunit 2, mitochondrial         Protein flightless-1 homolog         182 kDa tankyrase-1-binding protein         RNA-binding protein 10         Aminopeptidase         Paraspeckle component 1	C,S C,S C,S C,S C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593 P25786 O43809 Q13547 P56385 H0YNW5 P11802 P55072 P09936 P08240 P22695 Q13045 Q9C0C2 P98175 E9PLK3 Q8WXF1 P62191	PSMD14 NKAP MYO6 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2 FLII TNKS1BP1 RBM10 NPEPPS PSPC1 PSMC1	26S proteasome non-ATPase regulatory subunit 14         NF-kappa-B-activating protein         Unconventional myosin-6         Protein phosphatase 1F         Proteasome subunit alpha type-1         Cleavage and polyadenylation specificity factor subunit 5         Histone deacetylase 1         ATP synthase subunit e, mitochondrial         Deoxyuridine 5'-triphosphate nucleotidohydrolase         Cyclin-dependent kinase 4         Transitional endoplasmic reticulum ATPase         Ubiquitin carboxyl-terminal hydrolase isozyme L1         Signal recognition particle receptor subunit alpha         Cytochrome b-c1 complex subunit 2, mitochondrial         Protein flightless-1 homolog         182 kDa tankyrase-1-binding protein         RNA-binding protein 10         Aminopeptidase         Paraspeckle component 1         26S proteasome regulatory subunit 4	C,S C,S C,S C,S C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S
P49593 P25786 O43809 Q13547 P56385 H0YNW5 P11802 P55072 P09936 P08240 P22695 Q13045 Q9C0C2 P98175 E9PLK3 Q8WXF1 P62191 O967T9	PSMD14 NKAP MY06 PPM1F PSMA1 NUDT21 HDAC1 ATP5ME DUT CDK4 VCP UCHL1 SRPRA UQCRC2 FLII TNKS1BP1 RBM10 NPEPPS PSPC1 PSMC1 FGI N1	26S proteasome non-ATPase regulatory subunit 14         NF-kappa-B-activating protein         Unconventional myosin-6         Protein phosphatase 1F         Proteasome subunit alpha type-1         Cleavage and polyadenylation specificity factor subunit 5         Histone deacetylase 1         ATP synthase subunit e, mitochondrial         Deoxyuridine 5'-triphosphate nucleotidohydrolase         Cyclin-dependent kinase 4         Transitional endoplasmic reticulum ATPase         Ubiquitin carboxyl-terminal hydrolase isozyme L1         Signal recognition particle receptor subunit 2, mitochondrial         Protein flightless-1 homolog         182 kDa tankyrase-1-binding protein         RNA-binding protein 10         Aminopeptidase         Paraspeckle component 1         26S proteasome regulatory subunit 4         Fel nine homolog	C,S C,S C,S C,S WT,C,S WT,C,S WT,C,S C,S C,S C,S C,S C,S C,S C,S C,S C,S

Q9UPN7	PPP6R1	Serine/threonine-protein phosphatase 6 regulatory subunit 1	C <sub>r</sub> S
075533	SF3B1	Splicing factor 3B subunit 1	C <sub>r</sub> S
Q9BRP1	PDCD2L	Programmed cell death protein 2-like	WT, C <sub>r</sub> S
Q86V48	LUZP1	Leucine zipper protein 1	WT, C <sub>r</sub> S
Q15019	SEPTIN2	Septin-2	C <sub>r</sub> S
Q99504	EYA3	Eyes absent homolog 3	C <sub>s</sub>
Q9BWJ5	SF3B5	Splicing factor 3B subunit 5	C S
A6NGP5	JPT2	Jupiter microtubule-associated homolog 2	WT, C, S
Q9BTE3	MCMBP	Mini-chromosome maintenance complex-binding protein	<u>C</u> S
Q15046	KARS1	LysinetRNA ligase	CS
Q96GD0	PDXP	Pyridoxal phosphate phosphatase	<u> </u>
P61981	YWHAG	14-3-3 protein gamma	<u> </u>
Q12800	I FCP2	Alpha-globin transcription factor CP2	<u> </u>
Q06203	PPAI		CS
Q9H//3	DCTPP1 DDVCL2	Dihudamminidiana adatad matain 2	
D10176	DP13L2 DLCC1	1 phoenbatidelinosited 4 5 biophoenbate phoenbadiostoreses campa 1	WT CS
01/5/	PLCGI	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	w 1, C, S
Q14566	DSMD12	2(S protosomo non ATDece regulatory subunit 12	<u> </u>
D41214	FIED	Euloguatia translation initiation factor 2D	<u> </u>
LI2DDI2	LIPED1	Ubiguitin domain containing protein LIPED1	C
D20228	EIE3E	Eukarvotic translation initiation factor 3 subunit F	<u> </u>
09NZI 9	MAT2B	Methionine adenosultransferase 2 subunit beta	<u> </u>
P52732	KIF11	Kinesin-like protein KIF11	<u>_</u>
096P70	IPO9	Importin-9	<u>C</u> \$
014137	BOP1	R ibosome biogenesis protein BOP1	C S
O6NUK1	SLC25A24	Calcium-binding mitochondrial carrier protein SCaMC-1	C.S.
043765	SGTA	Small glutamine-rich tetratricopentide repeat-containing protein alpha	C S
016531	DDB1	DNA damage-binding protein 1	C S
O9Y230	RUVBL2	RuvB-like 2	C S
P06737	PYGL	Glycogen phosphorylase, liver form	C S
P05023	ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	CS
O14929	HAT1	Histone acetyltransferase type B catalytic subunit	WT, CS
A0A087WUX8	APOOL	MICOS complex subunit	C.S.
Q9Y6Y8	SEC23IP	SEC23-interacting protein	CS
P58546	MTPN	Myotrophin	C,S
E9PS17	SCYL1	N-terminal kinase-like protein	C,S
P20020	ATP2B1	Plasma membrane calcium-transporting ATPase 1	CS
O94992	HEXIM1	Protein HEXIM1	C,S
Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	WT, C.S
O75381	PEX14	Peroxisomal membrane protein PEX14	C S
Q15393	SF3B3	Splicing factor 3B subunit 3	C <sub>s</sub>
Q8IVM0	CCDC50	Coiled-coil domain-containing protein 50	C <sub>s</sub> S
P42771	CDKN2A	Cyclin-dependent kinase inhibitor 2A	WT, C <sub>r</sub> S
O94905	ERLIN2	Erlin-2	C <sub>r</sub> S
H0YDU8	PPP5C	Serine/threonine-protein phosphatase	C <sub>s</sub> S
K7EJQ8	HDHD2	Haloacid dehalogenase-like hydrolase domain-containing protein 2	C <sub>r</sub> S
O43242	PSMD3	26S proteasome non-ATPase regulatory subunit 3	C <sub>r</sub> S
Q9H936	SLC25A22	Mitochondrial glutamate carrier 1	C <sub>r</sub> S
P30041	PRDX6	Peroxiredoxin-6	C <sub>r</sub> S
P15374	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	C <sub>r</sub> S
P29373	CRABP2	Cellular retinoic acid-binding protein 2	C <sub>r</sub> S
P61106	RAB14	Ras-related protein Rab-14	C <sub>r</sub> S
P00338	LDHA	L-lactate dehydrogenase A chain	C S
Q9H6S0	YTHDC2	3'-5' RNA helicase YTHDC2	C <sub>r</sub> S
Q14C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	C <sub>F</sub> S
A0A0C4DGX4	CUL1	Cullin-1	C S
Q9UBE0	SAE1	SUMO-activating enzyme subunit 1	C <sub>r</sub> S
P22570	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial	C <sub>s</sub>
P31946	YWHAB	14-3-3 protein beta/alpha	<u>C</u> S
Q9UJZ1	STOML2	Stomatin-like protein 2, mitochondrial	<u> </u>
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	WT, C, S
Q9H9B4	SFXN1	Sideroflexin-1	CS
Q9H0U4	KAB1B	Kas-related protein Kab-1B	<u> </u>
P31153	MAT2A	S-adenosylmethionine synthase isoform type-2	<u> </u>
Q6P2Q9	PRPF8	Pre-mKNA-processing-splicing factor 8	CS
095684	CEP43	Centrosomal protein 43	<u>C_S</u>
B/Z7F3	KANBP3	Kan-binding protein 3	WT, C, S
P42574	CASP3	Caspase-3	C S
Q96EA4	SPDL1	Protein Spindly	WT, C, S
Q9UKG1	APPL1	DCC-interacting protein 13-alpha	C <sub>s</sub>
F5GZS6	SLC3A2	4F2 cell-surface antigen heavy chain	CS
P00492	HPRT'1	Hypoxanthine-guanine phosphoribosyltransferase	C <sub>r</sub> S

P06132	UROD	Uroporphyrinogen decarboxylase	C_S
Q9BXJ9	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	C <sub>r</sub> S
Q9Y265	RUVBL1	RuvB-like 1	C_S
P62333	PSMC6	26S proteasome regulatory subunit 10B	C_S
P12955	PEPD	Xaa-Pro dipeptidase	WT, C,S
P41250	GARS1	GlycinetRNA ligase	C.S
Q9NUP9	LIN7C	Protein lin-7 homolog C	CS
A0A087X054	HYOU1	Hypoxia up-regulated protein 1	CS
09Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	WT C S
Q9HBH5	RDH14	Ratinol debudrogenase 1/	C S
0/05/7	CMDS	CDD manager 4 ( dahudaataa	WT C S
06054/	GMD5	GDP-mannose 4,6 denydratase	w1,C,S
P35998	PSMC2	265 proteasome regulatory subunit /	<u>C</u> S
Q16512	PKN1	Serine/threonine-protein kinase N1	CS
Q8NFC6	BOD1L1	Biorientation of chromosomes in cell division protein 1-like 1	WT, C, S
O00165	HAX1	HCLS1-associated protein X-1	C <sub>2</sub> S
A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6	WT, C S
P61289	PSME3	Proteasome activator complex subunit 3	C <sub>r</sub> S
Q9Y3D0	CIAO2B	Cytosolic iron-sulfur assembly component 2B	C,S
Q86WA6	BPHL	Valacyclovir hydrolase	CS
Q9UBS4	DNAJB11	Dnal homolog subfamily B member 11	ĊŚ
E9PM 92	C11orf58	Small acidic protein	C.S.
09Y3B7	MR PL11	39S ribosomal protein L11 mitochondrial	C S
0/9426	CLVR 1	Putative ovidereductare CLVR 1	C S
Q4)A20	BLIKI		C_3
AUAU8/A2B5	BSG	Basigin	<u>C</u> 3
K7ELV2	SEH1L	Nucleoporin SEH1	C <sub>5</sub>
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	CS
Q14257	RCN2	Reticulocalbin-2	C <sub>2</sub> S
O00483	NDUFA4	Cytochrome c oxidase subunit NDUFA4	C <sub>2</sub> S
PRDX3 cysteine-depend	lent interactors		
B7WPG3	HNRNPLL	Heterogeneous nuclear ribonucleoprotein L-like	WT
Q14161	GIT2	ARF GTPase-activating protein GIT2	WT
Q9Y4B6	DCAF1	DDB1- and CUL4-associated factor 1	WT, C.S
Q92804	TAF15	TATA-binding protein-associated factor 2N	WT
O9UBE0	SAE1	SUMO-activating enzyme subunit 1	WT
E8W038	C17orf49	Chromosome 17 open reading frame 49	WT
O6PKG0	LARD1	La related protein 1	WT
Q01 K00	DDIAC		WT C S
Q15084	PDIA6	Protein disulfide-isomerase A6	WI,CS
Q92/85	DPF2	Zinc finger protein ubi-d4	WI,CS
P51148	RAB5C	Ras-related protein Rab-5C	W1, C <sub>5</sub>
Q9ULX3	NOB1	RNA-binding protein NOB1	WT, C, S
P04843	RPN1	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 1	WT
Q86WA6	BPHL	Valacyclovir hydrolase	WT, C,S
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	WT, C, S
O14828	SCAMP3	Secretory carrier-associated membrane protein 3	WT
Q5JRI1	SRSF10	Serine/arginine-rich-splicing factor 10	WT
G3V279	ERH	Enhancer of rudimentary homolog	WT
P10599	TXN	Thioredoxin	WT.CS
08N5K1	CISD2	CDGSH iron-sulfur domain-containing protein 2	WT CS
ADADADMEDO	DTDNO	Turesing protein photosphetase non recenter ture 9	WT
OOH(PO	DUV22	ATD dependent P NA balianse DHX22	WT CS
Q9H6K0	DRASS		wi,cs
V13271	LUDE')	The labor state of the second	w 1, C, 3
H/BXII	EST12	Extended synaptotagmin-2	w 1
H3BRY6	INTS14	Integrator complex subunit 14	WT
Q5TDH0	DDI2	Protein DD11 homolog 2	WT
P08240	SRPRA	Signal recognition particle receptor subunit alpha	WT
P27824	CANX	Calnexin	WT
P22695	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	WT
Q16718	NDUFA5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	WT, C,S
Q14697	GANAB	Neutral alpha-glucosidase AB	WT
075146	HIP1R	Huntingtin-interacting protein 1-related protein	WT, CS
O5VW32	BROX	BRO1 domain-containing protein BROX	WT.C.S
P05386	R PLP1	60S acidic ribosomal protein P1	WT.C.S
AGNDU8	C5orf51	UPE0600 protein CSorf51	WT CS
O(DEI)	D DI 7I 1	(OS ribosomal protein I.7 like 1	WT C S
200/1	NFL/LI	Description of the second seco	WT CS
P30041	PKDX6	Peroxiredoxin-6	w1,CS
Q9UKK9	NUD15	ADP-sugar pyrophosphatase	w1,C5
Q2M2I8	AAK1	AP2-associated protein kinase 1	WT, C.S
P57076	CFAP298	Cilia- and flagella-associated protein 298	WT, C <sub>z</sub> S
Q66PJ3	ARL6IP4	ADP-ribosylation factor-like protein 6-interacting protein 4	WT, C <sub>2</sub> S
Q15814	TBCC	Tubulin-specific chaperone C	WT, C, S
Q9NYK5	MRPL39	39S ribosomal protein L39, mitochondrial	WT, C <sub>2</sub> S
P78346	RPP30	Ribonuclease P protein subunit p30	WT, C S
D06132	UROD	Uroporphyrinogen decarboxylase	WTCS

P62081	RPS7	40S ribosomal protein S7	WT, C.S
Q9UJS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	WT
K7ERF1	EIF3K	Eukaryotic translation initiation factor 3 subunit K	WT
Q9H0E2	TOLLIP	Toll-interacting protein	WT
O5SY16	NOL9	Polynucleotide 5'-hydroxyl-kinase NOL9	WT.C.S
015269	SPTI C1	Serine palmitovltransferase 1	WT CS
019207	NI IRD2	Cutocolic Fe Schuter assembly factor NUBD2	WT CS
0917512	NOBE2	Cytosofic re-s cluster assembly factor NOBF2	WT CS
Q81V32	MCA1		
P50454	SERPINHI	Serpin H1	
Q9NP97	DYNLRB1	Dynein light chain roadblock-type 1	W1, C,S
Q9NS69	TOMM22	Mitochondrial import receptor subunit TOM22 homolog	WT, C, S
Q6UW78	UQCC3	Ubiquinol-cytochrome-c reductase complex assembly factor 3	C_S
A0A2R8YFH5	SEC23B	Protein transport protein SEC23	WT
Q9UHD2	TBK1	Serine/threonine-protein kinase TBK1	WT, C <sub>r</sub> S
P31040	SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	WT, C,S
Q8NBU5	ATAD1	ATPase family AAA domain-containing protein 1	WT, C <sub>s</sub> S
Q96AT9	RPE	Ribulose-phosphate 3-epimerase	WT, C.S
P35268	RPL22	60S ribosomal protein L22	WT, C.S
P19022	CDH2	Cadherin-2	WT, CS
F8VYE8	PPP1CC	Serine/threonine-protein phosphatase	WT, C S
O6IBS0	TWF2	Twinfilin-2	WT.C.S
Q60784	TOM1	Target of Myh protein 1	WT CS
D62873	CNB1	Guanine nucleotide hinding protein G(I)/G(S)/G(T) subunit beta 1	WT CS
012509	TI IDD2	Tubulin bate 2 shain	WT CS
Q13509	I UDD3	Tubuim bera-5 chain	
Q96EA4	SPDLI	Protein Spindly	
A0A0A0M1B8	WDR36	WD repeat-containing protein 36	w1, C.S
Q92990	GLMN	Glomulin	WT, C, S
Q9UL15	BAG5	BAG family molecular chaperone regulator 5	WT, C <sub>c</sub> S
O43815	STRN	Striatin	WT, C,S
Q9H0U4	RAB1B	Ras-related protein Rab-1B	WT, C,S
Q9UQR0	SCML2	Sex comb on midleg-like protein 2	WT, C,S
F5H008	VPS33B	Vacuolar protein sorting-associated protein 33B	WT, C S
Q9BSJ8	ESYT1	Extended synaptotagmin-1	WT, C,S
P14174	MIF	Macrophage migration inhibitory factor	WT, C.S
P51809	VAMP7	Vesicle-associated membrane protein 7	WT, C S
09NZ45	CISD1	CDGSH iron-sulfur domain-containing protein 1	WT, C S
O9BZX2	UCK2	Uridine-cytidine kinase 2	WTCS
OSTDH9	BLOC155	Biogenesis of lysosome-related organelles complex 1 subunit 5	WT CS
Q01D11	DDU2	2 (2 aming 2 and average) Whistiding synthese suburit 2	WT CS
Q75QC3	TIDD I	Z-(5-annino-5-carboxypropyr)nistidine synthase subunit 2	
0/5663	TIPKL WDD (1	11P41-like protein	C3
Q9GZS3	WDR61	WD repeat-containing protein 61	
075688	PPM1B	Protein phosphatase 1B	C <sub>z</sub> S
P35237	SERPINB6	Serpin B6	WT, C, S
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	WT, C,S
Q9NP61	ARFGAP3	ADP-ribosylation factor GTPase-activating protein 3	WT, C,S
H7C155	RAF1	Non-specific serine/threonine protein kinase	C <sub>r</sub> S
P54646	PRKAA2	5'-AMP-activated protein kinase catalytic subunit alpha-2	WT, C S
P26368	U2AF2	Splicing factor U2AF 65 kDa subunit	C,S
Q9HB71	CACYBP	Calcyclin-binding protein	WT, C.S
A0A087WU06	TUBGCP3	Gamma-tubulin complex component	WT, C S
O8N6M0	OTUD6B	Deubiquitinase OTUD6B	WT, C S
P62820	R A B1 A	Ras-related protein Rah-1A	C.S.
B4D181	NDUES1	NADH ubiquinone ovidoreductase 75 kDa subunit mitochondrial	WT CS
ORNERO	FFF1 AKNMT	eFF1 A lysine and N terminal methyltransferase	WT CS
D11802	CDV/	Cerelia dana dana biana d	WT CS
P11802	CDK4	Cyclin-dependent kinase 4	
Q9H974	QIR12	Queuine tRNA-ribosyltransferase accessory subunit 2	
P21964	COMT	Catechol O-methyltransterase	w1, CS
Q9P287	BCCIP	BRCA2 and CDKN1A-interacting protein	WT, C, S
Q9UGV2	NDRG3	Protein NDRG3	C_S
P62879	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	WT, C,S
H3BV80	RNPS1	RNA-binding protein with serine-rich domain 1	WT, C,S
Q8IYS1	PM20D2	Peptidase M20 domain-containing protein 2	WT, C <sub>s</sub> S
Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	WT, C <sub>r</sub> S
X6RM00	ERC1	ELKS/Rab6-interacting/CAST family member 1	WT, C.S
Q15738	NSDHL	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	C S
Q9Y679	AUP1	Lipid droplet-regulating VLDL assembly factor AUP1	WT. C S
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	WT CS
071.2H7	FIE3M	Fultration in initiation factor 3 suburit M	WT CC
D19/(0	DCAM1	Dhoonhoolyoorete mutees 1	WT CC
F 18667	PGAMI	r nospnogiycerate mutase i	w1,C5
Q96859	KANBP9	Kan-binding protein 9	<u> </u>
095295	SNAPIN	SNARE-associated protein Snapin	WT, C, S
Q15019	SEPTIN2	Septin-2	C S
Q96BW9	TAMM41	Phosphatidate cytidylyltransferase, mitochondrial	WT, C <sub>r</sub> S

Q9BTE1	DCTN5	Dynactin subunit 5	WT, C S
P18031	PTPN1	Tyrosine-protein phosphatase non-receptor type 1	WT, C,S
Q147X3	NAA30	N-alpha-acetyltransferase 30	C_S
Q9NQT5	EXOSC3	Exosome complex component RRP40	CS
M0R026	ILVBL	2-hydroxyacyl-CoA lyase 2	WT, C.S
Q96FW1	OTUB1	Ubiquitin thioesterase OTUB1	CS
Q9Y3D0	CIAO2B	Cytosolic iron-sulfur assembly component 2B	WT, CS
P29558	RBMS1	RNA-binding motif, single-stranded-interacting protein 1	CS
095551	TDP2	Tyrosyl-DNA phosphodiesterase ?	C.S.
050PM7	PSME1	Protessome inhibitor PI31 subunit	WT CS
OSVT66	MTARC1	Mitachondrial amidovine reducing component 1	CS
D20740	SED DINID1	I aukoauto alattasa inkihitar	WT CS
	LUICDU	L 2 hudermeluterete debuder ere ere mite der deid	WT CS
Q9H9P8	DVNGUUD		WI,CS
04323/	DINCILIZ	Cytoplasmic dynein 1 light intermediate chain 2	WI,CS
Q961U4	ABHD14B	Protein ABHD14B	WI,CS
H3BIA2	PPP4C	Serine/threonine-protein phosphatase	w1,C5
P19367	HK1	Hexokinase-1	C <sub>2</sub> S
Q53EL6	PDCD4	Programmed cell death protein 4	C <sub>2</sub> S
Q07820	MCL1	Induced myeloid leukemia cell differentiation protein Mcl-1	WT, C,S
Q8N6T3	ARFGAP1	ADP-ribosylation factor GTPase-activating protein 1	WT, C,S
O43809	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	WT, C,S
P17252	PRKCA	Protein kinase C alpha type	CS
A0A0A0MS29	MFF	Mitochondrial fission factor	WT
Q16698	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	WT, C,S
Q14318	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8	WT, C,S
P16435	POR	NADPHcytochrome P450 reductase	C S
G5EA06	MRPS27	28S ribosomal protein S27, mitochondrial	WT, C.S
P35520	CBS	Cystathionine beta-synthase	WT, CS
P52788	SMS	Spermine synthase	CS
P07355	ANXA2	Annexin A2	WT, C S
014126	DSG2	Desmoglein-?	CS
060566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	C.S.
016204	CCDC6	Coiled-coil domain-containing protein 6	C S
D117((	ADUS	Alashal dahudraganaga alasa 2	WT C S
O9V570	DDME1	Distain phasehatasa mathulastarasa 1	w1,C,5
Q/13/0	P DC25	406 sibasemul metri sent sent sent sent sent sent sent sent	<u>C</u> 5
P62831	RF323		UJ WT CC
P61106	RAB14	Kas-related protein Kab-14	WI,CS
Q8WVC2	KPS21	405 ribosomai protein 521	w1,C3
P45954	ACADSB	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	<u>C</u> S
P34896	SHM11	Serine hydroxymethyltransterase, cytosolic	C <sub>S</sub>
Q16543	CDC37	Hsp90 co-chaperone Cdc37	CS
Q07021	C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial	WT, C,S
P55072	VCP	Transitional endoplasmic reticulum ATPase	C_S
D6RA00	ENOPH1	Enolase-phosphatase E1	WT, C <sub>p</sub> S
Q9UL25	RAB21	Ras-related protein Rab-21	C <sub>r</sub> S
Q7L5D6	GET4	Golgi to ER traffic protein 4 homolog	C <sub>2</sub> S
Q5T749	KPRP	Keratinocyte proline-rich protein	WT, C S
Q9NQX3	GPHN	Gephyrin [Includes: Molybdopterin adenylyltransferase	C_S
Q96TC7	RMDN3	Regulator of microtubule dynamics protein 3	C <sub>r</sub> S
P09211	GSTP1	Glutathione S-transferase P	C S
O14744	PRMT5	Protein arginine N-methyltransferase 5	C <sub>r</sub> S
Q16576	RBBP7	Histone-binding protein RBBP7	C <sub>s</sub>
Q8IUF8	RIOX2	Ribosomal oxygenase 2	C_S
P60953	CDC42	Cell division control protein 42 homolog	CS
Q8TEX9	IPO4	Importin-4	C,S
Q8TC07	TBC1D15	TBC1 domain family member 15	C.S
O9Y266	NUDC	Nuclear migration protein nudC	CS
O9UI30	TRMT112	Multifunctional methyltransferase subunit TR M112-like protein	CS
Q96A49	SYAP1	Synapse-associated protein 1	WT C S
P21796	VDAC1	Voltage-dependent anion-selective channel protein 1	C.S.
D56182	R R D1	R ibosomal R NA processing protein 1 homolog A	C S
09(\$44	TDS2D V	EKC/KEODS complex suburis TDS2D K	WT C S
095831	A IFM 1	Anontosis.inducing factor 1 mitochondrial	
01/18/	ADR M1	Protestomal ubiquitin recentor A DR M1	C 5
Q10100	DDV	Troncasoniai uoiquittii teteptoi ADAMI	C 5
Q76KD3	CEMINI7	Lympnokine-activated kiner 1-cen-originated protein kinase	<u></u>
Q7F1840	GEMIN/	Collinears of DDD7 and the standard stand	US WE CO
Q9HD26	GUPC	Goigi-associated PDZ and colled-coll motif-containing protein	w1,C5
E9PJN0	ACO18	Acyl-coenzyme A thioesterase 8	w 1, C, S
Q15388	10MM20	Mitochondrial import receptor subunit TOM20 homolog	CS
Q8NDI1	EHBP1	EH domain-binding protein 1	C <sub>S</sub>
Q9NWV4	CZIB	CXXC motif containing zinc binding protein	WT, C,S
P02790	HPX	Hemopexin	C S
Q5T760	SRSF11	Serine/arginine-rich-splicing factor 11	C_S

Q9Y6Y8	SEC23IP	SEC23-interacting protein	C,S
O60825	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2	C,S
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	WT, C,S
P51553	IDH3G	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	C,S
Q8IXI1	RHOT2	Mitochondrial Rho GTPase 2	C <sub>r</sub> S
O75600	GCAT	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	WT, C, S
C9JAW5	C9JAW5	HIG1 domain-containing protein	WT, C S
P40616	ARL1	ADP-ribosylation factor-like protein 1	WT, C <sub>2</sub> S
Q7Z434	MAVS	Mitochondrial antiviral-signaling protein	WT, C <sub>2</sub> S
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	C <sub>r</sub> S
Q92667	AKAP1	A-kinase anchor protein 1, mitochondrial	WT, C, S
Q9UH62	ARMCX3	Armadillo repeat-containing X-linked protein 3	C <sub>r</sub> S
Q9BYN0	SRXN1	Sulfiredoxin-1	WT, C <sub>s</sub>
Q5SZR4	TDRKH	Tudor and KH domain containing, isoform CRA_a	WT, C,S
B3KUS5	USP30	Ubiquitin carboxyl-terminal hydrolase	WT, C,S
Q14498	RBM39	RNA-binding protein 39	C S
Q5VUJ6	LRCH2	Leucine-rich repeat and calponin homology domain-containing protein 2	C <sub>r</sub> S
Q9NQG6	MIEF1	Mitochondrial dynamics protein MID51	C <sub>r</sub> S
O60547	GMDS	GDP-mannose 4,6 dehydratase	C S
O95801	TTC4	Tetratricopeptide repeat protein 4	C <sub>r</sub> S
Q9BQA1	WDR77	Methylosome protein 50	C <sub>r</sub> S
Q14964	RAB39A	Ras-related protein Rab-39A	C <sub>r</sub> S
P49903	SEPHS1	Selenide, water dikinase 1	C <sub>r</sub> S
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	C <sub>r</sub> S
Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	C <sub>s</sub>
Q9BPZ2	SPIN2B	Spindlin-2B	C S
P20042	EIF2S2	Eukaryotic translation initiation factor 2 subunit 2	C <sub>s</sub>
B4E1N1	ARMC6	Armadillo repeat-containing protein 6	<u>C</u> S
P63151	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	<u>C</u> S
K7EJQ8	HDHD2	Haloacid dehalogenase-like hydrolase domain-containing protein 2	<u>C</u> S
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	<u>C</u> S
A0A0B4J1Z1	SKSF/	Serine/arginine-rich-splicing factor /	0.5
PRDX4 cysteine-d	lependent interactors		157/27
Q96ACI	FERM12	Fermitin family homolog 2	WI
Q98826	EKP44	PNA li li ne si b( li le le 2	W I
Q96DH6	M512	KNA-binding protein Musashi nomolog 2	W I
Q9IN W82	WDR/0	WD repeat-containing protein /0	WT
P09110 D22207	ACAA1 SCD2	S-ketoacyt-CoA thiolase, peroxisomal	WT
F2230/	SUC2A2	(T2 all surface articles hours do in	WT
CONDESO	TYNDCS	4F2 cell-surrace antigen neavy chain	WTCS
D(0176	TDI1	Triceenhaanhata icomatana	WT
P200/1	DP DV(	Deserviced avia	WT
O9BT72	DHPS/	Petoxitedoxiti-6	WT
Q98122	MP DS17	285 ribosomal protein \$17 mirochondrial	WTCS
096876	USD/7	Ubiquirin carboxyl terminal hydrolase /7	WT
01508/	DDI 44	Diquicin carboxyr-terminar nyufolase 4/	WT
013257	MAD2L1	Mitatic spindle assembly checkpoint pratein MAD2A	WT
01/739	IRP	Delte/14) starol reductose J BR	WT
Q14/3/	KTN1	Kinectin	WT
E9PGZ1	CALDI	Caldesmon	WT
O9UHV9	PFDN2	Prefaldin subunit 2	WT
C919K3	R PSA	40S ribosomal protein SA	WT
P26599	PTBP1	Polypyrimidine tract-binding protein 1	WT
096199	SUCL G2	SuccinateCoA ligase [GDP-forming] subunit beta mitochondrial	WT
Q66K74	MAPIS	Microtubule-associated protein 1S	WTCS
P34897	SHMT2	Serine hydroxymethyltransferase, mitochondrial	WT
P10599	TXN	Thioredoxin	WT
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	WT.C.S
P62249	RPS16	40S ribosomal protein S16	WT, CS
13L1P8	SLC25A11	Mitochondrial 2-oxoglutarate/malate carrier protein	WT.C.S
O9Y4B6	DCAF1	DDB1- and CUL4-associated factor 1	WT
P15880	RPS2	40S ribosomal protein S2	WT
O15372	EIF3H	Eukaryotic translation initiation factor 3 subunit H	WT
P34949	MPI	Mannose-6-phosphate isomerase	WT
Q93034	CUL5	Cullin-5	WT
Q92783	STAM	Signal transducing adapter molecule 1	WT, C.S
P05388	RPLP0	60S acidic ribosomal protein P0	WT
P06576	ATP5F1B	ATP synthase subunit beta, mitochondrial	WT
P42345	MTOR	Serine/threonine-protein kinase mTOR	WT
P06733	ENO1	Alpha-enolase	WT
P18077	RPL35A	60S ribosomal protein L35a	WT
Q9HCD5	NCOA5	Nuclear receptor coactivator 5	WT
<b>~</b>			

Q9BSJ8	ESYT1	Extended synaptotagmin-1	WT, C <sub>s</sub>
P30154	PPP2R1B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	WT, C,S
Q96C36	PYCR2	Pyrroline-5-carboxylate reductase 2	WT
B4DJ81	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	WT, C <sub>.</sub> S
D6RA00	ENOPH1	Enolase-phosphatase E1	WT, C <sub>2</sub> S
O43809	NUDT21	Cleavage and polyadenylation specificity factor subunit 5	WT, C <sub>2</sub> S
Q13347	EIF3I	Eukaryotic translation initiation factor 3 subunit I	WT
P49411	TUFM	Elongation factor Tu, mitochondrial	WT, C <sub>2</sub> S
Q5SW79	CEP170	Centrosomal protein of 170 kDa	WT, C <sub>z</sub> S
Q9P2J5	LARS1	LeucinetRNA ligase, cytoplasmic	WT
P62906	RPL10A	60S ribosomal protein L10a	WT
Q9UQR0	SCML2	Sex comb on midleg-like protein 2	WT, C <sub>2</sub> S
Q16513	PKN2	Serine/threonine-protein kinase N2	WT, C <u>S</u>
P13489	RNH1	Ribonuclease inhibitor	WT, C,S
A0A087WY71	AP2M1	AP-2 complex subunit mu	WT, C,S
P18858	LIG1	DNA ligase 1	WT, C <u>S</u>
014974	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	WT, C, S
Q8IUI8	CRLF3	Cytokine receptor-like factor 3	C,S
F5H6E2	MYOIC	Unconventional myosin-Ic	w1,CS
Q12904	AIMPI	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	w1,C,S
Q0/020	RPL18	60S ribosomal protein L18	<u> </u>
Q8WX93	PALLD	Palladin	CS
Q14152	EIF3A CANAD	Eukaryotic translation initiation factor 3 subunit A	wit, C,S
Q1469/	GANAB	Neutral alpha-giucosidase AB	w1,C,S
Q14318	FKBP8	Peptidyl-prolyl cis-trans isomerase FKBP8	<u>C</u> \$
Q7DWF3	SMARCA4	KNA-binding protein 4	WT CS
AUA2K81/32	MARCA4	Iranscription activator BKG1	w1,C,S
075592	MYCPD2	F2 ubiquitie protein ligace MVCPD2	<u> </u>
0/3592	MICDP2	ES ubiquitin-protein ligase MTCBP2	<u> </u>
Q07666	U F2	Interfoliast differentiation-associated protein AFINAK	<u> </u>
Q12905 D30520	ADSS2	A developmente contractor 2	<u> </u>
090002	TNKS1BD1	182 kDa tankurasa 1 binding protein	
Q7C0C2 D8/103	SP SE3	Serine/arginine rich chliging factor 3	 
08TCG1	CIP2A	Protein CIP2 A	C\$
QUICCI OPRVP2	GNI 3	Guanine nucleotide-binding protein-like 3	C\$
A0A0B4I171	SR SF7	Serine/arginine-rich-splicing factor 7	WT C S
E7EPN9	PR R C2C	Protein PR RC2C	C.S.
016543	CDC37	Hsp20 co-chaperone Cdc37	C.S.
O13618	CUL3	Cullin-3	C \$
07KZ85	SUPT6H	Transcription elongation factor SPT6	CS
Q92974	ARHGEF2	Rho guanine nucleotide exchange factor 2	CS
Q9Y2R4	DDX52	Probable ATP-dependent RNA helicase DDX52	C.S.
Q99567	NUP88	Nuclear pore complex protein Nup88	CS
P49593	PPM1F	Protein phosphatase 1F	C,S
P27824	CANX	Calnexin	C,S
Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	C S
P29372	MPG	DNA-3-methyladenine glycosylase	C,S
A0A087X054	HYOU1	Hypoxia up-regulated protein 1	C.S
P11802	CDK4	Cyclin-dependent kinase 4	C <sub>.</sub> S
Q12797	ASPH	Aspartyl/asparaginyl beta-hydroxylase	WT, C <sub>2</sub> S
O00469	PLOD2	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	C <sub>s</sub> s
Q9NVP1	DDX18	ATP-dependent RNA helicase DDX18	C <sub>s</sub> s
PRDX5 cysteine-de	pendent interactors		
Q15388	TOMM20	Mitochondrial import receptor subunit TOM20 homolog	WT
Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	WT
Q9H2P9	DPH5	Diphthine methyl ester synthase	WT
Q53GQ0	HSD17B12	Very-long-chain 3-oxoacyl-CoA reductase	WT
P63167	DYNLL1	Dynein light chain 1, cytoplasmic	WT
Q5T760	SRSF11	Serine/arginine-rich-splicing factor 11	WT
Q16822	PCK2	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	WT
Q16698	DECR1	2,4-dienoyl-CoA reductase, mitochondrial	WT
E9PGT1	TSN	Component 3 of promoter of RISC	WT
Q92990	GLMN	Glomulin	WT
Q9NT62	ATG3	Ubiquitin-like-conjugating enzyme ATG3	WT
Q99598	TSNAX	Translin-associated protein X	WT
A0A0B4J1Z1	SRSF7	Serine/arginine-rich-splicing factor 7	WT
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	WT
Q15/50	IABI	1 Gr-Deta-activated kinase 1 and MAP3K/-binding protein 1	W I
Q91266	NUDC	Nuclear migration protein nudC	W T
Q9BW92	THOP:	1 nreoninetKNA ligase, mitochondrial	W I
1 22000	THOPT	i mnet ongopeptidase	W 1
09H773	DCTDD1	dCTP pyrophosphetase 1	W/T

Q9P2N5	RBM27	RNA-binding protein 27	WT
Q6WKZ4	RAB11FIP1	Rab11 family-interacting protein 1	WT
F5GZS6	SLC3A2	4F2 cell-surface antigen heavy chain	WT
E9PJN0	ACOT8	Acyl-coenzyme A thioesterase 8	WT
Q9NQX3	GPHN	Gephyrin [Includes: Molybdopterin adenylyltransferase	WT
Q9GZU8	PSME3IP1	PSME3-interacting protein	WT
A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6	WT
Q12931	TRAP1	Heat shock protein 75 kDa, mitochondrial	WT
B7Z7F3	RANBP3	Ran-binding protein 3	WT
Q9UL15	BAG5	BAG family molecular chaperone regulator 5	WT
Q15061	WDR43	WD repeat-containing protein 43	WT
Q8NBU5	ATAD1	ATPase family AAA domain-containing protein 1	WT
Q13185	CBX3	Chromobox protein homolog 3	WT
P30041	PRDX6	Peroxiredoxin-6	WT
P26599	PTBP1	Polypyrimidine tract-binding protein 1	WT, CS
P141/4 01/020	MIF	Macrophage migration inhibitory factor	WI
014929 00POA1	HAII WDB 77	Histone acetyltransferase type B catalytic subunit	WI
Q7BQA1 09V570	DDME1	Destrip phoenhatese methylosterese 1	WT
01/579	CODE	Costomer subunit englon	WT
O5T6F2	LIBAP2	Ubiquirin-associated protein 2	WT
090002	TNKS1BP1	182 kDa tankyrase-1-binding protein	WT
Q9BS18	FSYT1	Fytended synantotaomin-1	WT
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	WT
O9Y6A5	TACC3	Transforming acidic coiled-coil-containing protein 3	WT
O09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	WT
H7BZM7	ZPR1	Zinc finger protein ZPR1	WT
P12955	PEPD	Xaa-Pro dipeptidase	WT
P22234	PAICS	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	WT, C.S
O60664	PLIN3	Perilipin-3	WT
Q9BRS2	RIOK1	Serine/threonine-protein kinase RIO1	WT
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	WT
C9J9K3	RPSA	40S ribosomal protein SA	WT
Q14C86	GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	WT, C,S
Q96RL1	UIMC1	BRCA1-A complex subunit RAP80	WT
O43815	STRN	Striatin	WT
Q9NQP4	PFDN4	Prefoldin subunit 4	WT
P15880	RPS2	40S ribosomal protein S2	WT
Q9HB71	CACYBP	Calcyclin-binding protein	WT, C <sub>z</sub> S
P40222	TXLNA	Alpha-taxilin	WT, C <sub>r</sub> S
Q15276	RABEP1	Rab GTPase-binding effector protein 1	WT
Q9UNM6	PSMD13	26S proteasome non-ATPase regulatory subunit 13	WT
Q66PJ3	ARL6IP4	ADP-ribosylation factor-like protein 6-interacting protein 4	WT
Q9H0E2	TOLLIP	Toll-interacting protein	WT
Q8NFC6	BODILI	Biorientation of chromosomes in cell division protein 1-like 1	WT, C,S
Q04446	GBEI	1,4-alpha-glucan-branching enzyme	WT
Q8N3X1	FNBP4	Pormin-binding protein 4	WI,CS
Q05655	ATDSDO	ATD suptace subusit O miteshandrial	WI CS
05IR 44	MIA3	Transport and Colgi organization protein 1 homolog	
D/330/	CDD2	Clucerol 3 phoenhate debudrocenace mitochondrial	WTCS
09V3F4	STR AD	Sector 5-phosphate denythogenase, initoenondrian Sector 5-phosphate denythogenase, initoenondrian	WT
016531	DDB1	DNA damage.hinding protein 1	WT
H7C128	BRD8	Bromodomain-containing protein 8	WT.CS
P05386	R PLP1	60S acidic ribosomal protein P1	WT
096A49	SYAP1	Synapse-associated protein 1	WTCS
P51665	PSMD7	26S proteasome non-ATPase regulatory subunit 7	WT
O32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	WT
08NC51	SER BP1	Plasminogen activator inhibitor 1 RNA-binding protein	WT.C.S
A0A0A0MR02	VDAC2	Outer mitochondrial membrane protein porin 2	WT, CS
O8N6M0	OTUD6B	Deubiquitinase OTUD6B	WT
O9UI12	ATP6V1H	V-type proton ATPase subunit H	WT
O95801	TTC4	Tetratricopeptide repeat protein 4	WT, C_S
Q9BSD7	NTPCR	Cancer-related nucleoside-triphosphatase	WT
Q9BTY7	HGH1	Protein HGH1 homolog	WT
E7EVA0	MAP4	Microtubule-associated protein	WT
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	WT
A0A087WUT6	EIF5B	Eukaryotic translation initiation factor 5B	WT
E7EV99	ADD1	Alpha-adducin	WT
E9PLA9	CAPRIN1	Caprin-1	WT
Q9H2U1	DHX36	ATP-dependent DNA/RNA helicase DHX36	WT
Q9BQ69	MACROD1	ADP-ribose glycohydrolase MACROD1	WT
P22570	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial	WT

P43686	PSMC4	26S proteasome regulatory subunit 6B	WT, C_S
Q02952	AKAP12	A-kinase anchor protein 12	WT
P62195	PSMC5	26S proteasome regulatory subunit 8	WT
P31689	DNAJA1	DnaJ homolog subfamily A member 1	WT, C_S
Q2TAM5	RELA	RELA protein	WT, C.S
P25398	RPS12	40S ribosomal protein S12	WT
P62333	PSMC6	26S proteasome regulatory subunit 10B	WT
P56385	ATP5ME	ATP synthase subunit e, mitochondrial	WT
A0A0C4DGQ6	RPRD1A	Regulation of nuclear pre-mRNA domain-containing protein 1A	WT, C.S
P04843	RPN1	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 1	WT
Q10713	PMPCA	Mitochondrial-processing peptidase subunit alpha	WT, C,S
P46821	MAP1B	Microtubule-associated protein 1B	WT
F8W1A4	AK2	Adenylate kinase 2, mitochondrial	WT
Q6PID6	TTC33	Tetratricopeptide repeat protein 33	WT, C,S
Q15645	TRIP13	Pachytene checkpoint protein 2 homolog	WT
O00483	NDUFA4	Cytochrome c oxidase subunit NDUFA4	WT, C_S
P78371	CCT2	T-complex protein 1 subunit beta	WT, C,S
P07355	ANXA2	Annexin A2	WT, C,S
Q96IZ0	PAWR	PRKC apoptosis WT1 regulator protein	WT, C,S
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	WT, C S
E9PGZ1	CALD1	Caldesmon	WT, C,S
C9J4Z3	RPL37A	60S ribosomal protein L37a	WT, C,S
Q5QPM7	PSMF1	Proteasome inhibitor PI31 subunit	C <sub>z</sub> S
Q9NZL9	MAT2B	Methionine adenosyltransferase 2 subunit beta	WT, C,S
P85037	FOXK1	Forkhead box protein K1	WT, C <sub>s</sub> S
Q9NX63	CHCHD3	MICOS complex subunit MIC19	CS
A0A024R442	A0A024R442	>tr A0A024R442 A0A024R442_HUMAN Aspartyl aminopeptidase, isoform CRA_b OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>sp Q9ULA0 DNPEP_HUMAN Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1;>tr E7ETB3 E7ETB3_HUMAN Aspartyl aminopeptidase, iso	WT, C <sub>r</sub> S
P13667	PDIA4	Protein disulfide-isomerase A4	C <sub>r</sub> S
Q96HS1	PGAM5	Serine/threonine-protein phosphatase PGAM5, mitochondrial	C <sub>z</sub> S
O95831	AIFM1	Apoptosis-inducing factor 1, mitochondrial	C <sub>r</sub> S
A0A075B6R9	IGKV2D-24	Probable non-functional immunoglobulin kappa variable 2D-24	CS
Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	C <sub>r</sub> S
E5KLJ9	OPA1	Dynamin-like 120 kDa protein, form S1	C <sub>r</sub> S
P30740	SERPINB1	Leukocyte elastase inhibitor	CS
Q6DKK2	TTC19	Tetratricopeptide repeat protein 19, mitochondrial	WT, C <sub>s</sub> S
P36551	CPOX	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	WT, C <sub>s</sub> S
O00165	HAX1	HCLS1-associated protein X-1	WT, C <sub>s</sub>
0%DH6	MSI2	R NA hinding protein Musschi homolog 2	CS

	motif	score	fold increase		
1	W.CC.	319.4	15.3		
2	.CC.	315.7	7.6		
3	.CCG	315.7	5.2	86	VCS
4	CCG	315.3	4.8	87	VRC
5	.HCC.	315.2	7.5	88	LCT
6	.CCI	311.7	4.5	89	LCT
7	.CN	311.7	4.7	90	VCE
8	KCC.	311.6	3.7	91	FCD
9	.CCQ	310.5	3.6	92	A CI
10	.CD.C	17.2	3.2	93	C TS
11	CD.C.	16.4	3.3	94	D CE
12	LLCL.	16.2	2.7	95	VCI
13	.CV.C	14	2.8	96	KCL
14	.ACC.	13	2.9	97	C SS
15	LCL.	12.3	1.6	98	VCI
16	F.Q.C	11.6	2.6	99	ICG
17	.CG.C	11.3	2.7	100	AL.C
18	GCC.	10.1	2.8	101	L.CV
19	V.K.C	9.8	1.9	102	.VCT
20	LFC	9.1	1.9	103	ICD
21	FYC	9.1	3	104	TCL
22	E.CL.	8.8	1.7	105	G.CD
23	.LCD.	8.6	1.9	106	.LCK
24	.IC.E	8.3	1.9	107	.LCY
25	L.N.C	8	1.8	108	VCS
26	VVC	7.9	1.9	109	CC.
27	CIN	7.9	2.8	110	.LCL
28	ICY.	7.6	2.4	111	FLC
29	L.E.C	7.5	1.6	112	.V.SC
30 27	.CC	7.4	1.6	113	.IC.D
31	.GCC.	7	2.5	114	LCA.
32 22	.vCA.	7	1.6	115	SCT
33	GC.V	6.9	1.8	116	L.V.C
34	.ECK	6.8	1.8	117	.LCI
35	LCL.	6.8	1.6	118	.LCE
30	IFC	6.7	2.2	119	YC
31	F.IC	6./	2.2	120	G.C.L
38	. YCL.	0.3	2.3	121	WC
39 40	.vCP	6.2	1.8	122	CW.
40	LAC	6	1.0	123	HC
41	C VI	5.0	2	124	CY
42	LAC	5.8	16	125	I.C
11	VCI	5.8	1.0	126	CF
45 45	V C V	5.7	2.1	127	FC
46	LOC	57	17	128	.MC
47	HC A	5.6	2.3	129	VC
48	VCR	5.6	2.1	130	CM
49	CN.N.	5.6	2.9	131	Cv
50	CFQ	5.5	2.3	132	C.L
51	A.CY	5.5	2.4	133	Cw
52	.ICG.	5.4	1.8	134	
53	VCL.	5.3	1.6	135	
54	I.CV	5.3	2	137	C V
55	FCV.	5.2	2	138	CW
56	CVL	5.2	1.8	130	YC
57	CS.F.	5.2	2.4	140	FC
58	FCP.	5	2.1	141	IC
59	.YCL	5	2.1	142	.LC
60	LCV.	4.9	1.6	143	CR
61	IC.A	4.9	1.9	144	SC
62	DCI	4.9	2.6	145	CI
63	.VCR.	4.8	1.7	146	CS
64	VCI	4.8	1.8	147	CP
65	1CI.	4.8	2	148	.PC
66	ACA.	4.8	2	149	C.W
07	.S.AC	4.7	1.9	150	.VC
08 60	SCS	4.6	1.9	151	.FC
70 70	AL.C	4.0	2.2	152	CH.
70 71	LLC	4.5	1.0	153	F.C
/1	L.LC.I.	4.5	1.5	154	CI
12	лСI Т. СС	4.5	1./	155	.QC
13 74	1C.S	4.5	1.0	156	CS
74 75	DC D	4.3	1.0	157	CL
15 76	FC V	4.5	2.2	158	Q.C
70 77	GIC	4.4	2.1 1 º	159	PC
78	G V C	4.4	1.0	160	CT
70 70	6.1.C	4.4	1.9	161	CF.
77 80	CPV	4.5	2	162	C.V
0U Q1	L CI	4.5	22	163	CV.
01 87	V C A	4.5	2.2	164	CA
02 83	VC.A.	4.5	2.4	165	IC
	LCI.	7.4	2	166	CE
84	CRI	12	2		

		Table S6. Amino aci	d motifs in CP-S-	S-C <sub>R</sub> -mediated interactors
		motif	score	fold increase
		1CCG	322.2	9.4
		2 .CCG	322	9.4
4.2		3CP.C.	313.4	7.1
4.2	2.1	A CPC	312.0	6.8
4.1	1.7	4 .Cr.C	211.2	0.8
4.1	1.9	5 VC.C	311.5	5.2
4.1	2.1	6CCK	310.6	4.5
4	1.9	7 .CCK	18.7	4.6
4	2	8CC.	15.2	2.1
4	17	9 LLC	11.5	1.9
4	1.7	10 .C.C	9.9	1.9
4	2.1		9.4	2.3
3.9	1.9	12 VIC	7.9	2.0
3.9	1.8	12 VLC	7.5	2.1
3.9	2	13	7.7	4
3.9	2.1	14R.CL.	7.3	2.1
3.8	1.8	15V.C.V	7.1	2
3.8	1.8	16 LCF.	6.9	2
3.8	2	17 .VCV	6.3	2
2.0	17	18V.CG.	6.3	2.1
3.0	1.7	19 LCN	6.1	2
3.7	1./	20 TCV	57	21
3.7	1.9	21 ACI	5.4	2.1
3.7	1.6	21A.C.L	5.4	2.2
3.7	1.9	22LCL.	5.5	2.1
3.7	1.8	23 ICG	5.2	1.9
3.6	1.8	24ICD	5.1	2.4
3.6	1.8	25V.CL	5.1	1.9
3.5	1.0	26CP.I.	5	2.3
2.4	1.4	27 FLC	4.9	1.9
5.4	1.4	28RCL.	4.9	1.9
3.4	1.8	29 VIC	4.8	21
3.4	1.7	27 .VI.C 20 I.C.V	4.0	2.1
3.4	1.8	50 .L.CV.	4./	1.0
3.3	1.5	31 LFC	4.6	1.9
3.3	1.7	32 ICL.	4.5	1.8
3.2	1.6	33 .TCL	4.5	2.1
3.2	17	34 VC.D	4.2	2.1
2	1.7	35 .AS.C	4.1	1.6
20	1.7	36 .V.CL	4.1	1.8
2.9	1.2	37 I.C.D	4	19
2.9	1.7	28 L C.V	2.0	1.7
2.5	1.4	36 LC.V	5.9	1./
2.1	1.3	39 L.D.C	3.9	1.8
2.1	1.3	40C.V.L	3.7	1.9
2	1.2	41 .LCV	3.7	1.9
2	1.2	42 AAC	3.6	1.7
1.0	1.2	43 .AC.L	3.6	1.7
1.0	1.2	44 LAC	3.6	2.1
1.9	1.2	45 CL L	3.5	17
1.9	1.3	46 VC S	3.4	1.8
1.9	1.2	40 V C	2.2	1.0
1.9	1.4	47 AL.C	5.5	1.8
1.9	1.3	48 .LC.L	3.2	1.8
1.9	1.3	49FC	2.6	1.3
1.8	1.4	50C.T	2.6	1.4
1.8	12	51YC	2.5	1.3
1.8	1.3	52CL	2.4	1.3
1.0	1.5	53C.I	2.3	1.2
1.7	1.2	54IC	2.2	1.2
1.7	1.2	55 HC	22	13
1./	1.3	56 V.C	2.2	1.4
1.7	1.2	57 L C	2.2	1.4
1.7	1.2	57 IC	2.1	1.2
1.7	1.2	58 .LC	2.1	1.3
1.7	1.2	59WC	2	1.5
1.7	1.3	60VC	2	1.3
17	13	61C.F	1.9	1.3
17	13	62C.V	1.9	1.2
17	1.5	63 .HC	1.9	1.4
1./	1.4	64 .FC	1.9	1.3
1./	1.5	65 C.S	19	1.2
1.7	1.6	66 E.C	1.9	1.2
1.6	1.4	67 V C	1.7	1.2
1.6	1.2	07 VC	1.8	1.2
1.6	1.2	68V.C	1.8	1.2
1.6	1.3	69 .YC	1.8	1.3
16	12	70CP	1.6	1.2
16	12	71CD	1.6	1.4
1.5	1.2	72 GC	1.5	1.2
1.0	1.2	73C.A	1.4	1.2
1.0	1.2	74 C N	14	13
1.6	1.2		1.7	* 1.2'
1.6	1.4			
1.6	1.5			
1.6	1.5			
1.5	1.2			
1.5	1.3			
15	13			
1.5	1.5			
1.5	1.5			
1.4	1.5			
1.4	1.4			
1.3	1.3			
1.3	1.3			

# REFERENCES

- 3. Winterbourn, C.C.; Hampton, M.B. Thiol Chemistry and Specificity in Redox Signaling. Free Radical Bio Med 2008, 45, 549 561,

- Oxidation and Activation of a Stress-Activated MAP Kinase. *Mol Cell*
- 10. Jarvis, R.M.; Hughes, S.M.; Ledgerwood, E.C. Peroxiredoxin 1 Func-
- 11. Sobotta, M.C.; Liou, W.; cker, S.S. ouml; Talwar, D.; Oehler, M.;
- D. Oxidative Protein Folding by an Endoplasmic Reticulum-Lo-
- Biol 2018, 14, 148-155, doi:10.1038/nchembio.2536.

- ing Value Imputation for Label-Free LC-MS Analysis. Bmc Bioinfor-

- A Worldwide Hub of Protein Knowledge. Nucleic Acids Res 2018, 47,

- 29. Peskin, A.V.; Meotti, F.C.; Kean, K.M.; Göbl, C.; Peixoto, A.S.; Pace,

# THE BIOCHEMICAL CHARACTERIZATION OF TIPRL AS A REDOX-SENSITIVE PROTEIN

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redox signaling; cysteine oxidation; mTOR signaling

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**KEYWORDS** hosphatases, odimerization



# THE BIOCHEMICAL **CHARACTERIZATION OF TIPRL AS A REDOX-SENSITIVE PROTEIN**

#### ABSTRACT

# INTRODUCTION

A few other proteins have been described to regulate PP2A activity. For example, a4 and TIPRL (TOR signaling pathway In order to function correctly and maintain homeostasis, cells regulator-like; TOR: Target of rapamycin) were suggested to must respond to their ever-changing environment. Cells do be two of five PP2A modulators, serving to prevent aspecific phosphatase activity until the PP2A trimeric holoenzyme this by sensing changes in their environment and transducing these signals into a cellular response. The correct integration is assembled [12]. Unlike in yeast where the TIPRL homoand amplification of different signals is crucial for the correct log Tip41 induces PP2A activity (Sit4 in yeast) by blocking functioning of cells. For example, elevated ROS levels or low the binding of a4 orthologue and Sit4 inhibitor Tap42 [13], reducing power can create a more oxidizing local redox state, human TIPRL function is more ambiguous. Several publiwhich leads to oxidative modifications on specific cysteines cations report the formation of a ternary complex between including reversible disulfide bonds. These modifications may TIPRL, α4 and PP2A, suggesting that the mutually exclusive lead to structural changes, thereby altering protein function interaction between a4 and TIPRL or PP2A is not conserved and modifying signaling outcome. An example of this is the from yeast to humans [14,15]. Furthermore, while TIPRL transient burst of H<sub>2</sub>O<sub>2</sub> induced upon growth factor recepstimulates PP2A activity in yeast, mammalian TIPRL has tor activation through NADPH-dependent oxidases (NOXs) been reported to inhibit PP2A-C catalytic activity, thereby [1,2], which reversibly oxidizes a cysteine in the active site of positively regulating mTOR signaling and downstream tarprotein tyrosine phosphatases (PTPs) and the lipid phosgets [14-17]. Furthermore, TIPRL has recently been suggestphatase PTEN [3,4]. The ROS-induced oxidation of these ed in another PP2A-independent process by interacting with phosphatases leads to their inactivation and allows protein and subsequent activation of eukaryotic initiation factor  $2\alpha$ phosphorylation cascades to take place, required for sustained (eIF2a) [18]. growth factor signaling [5,6].

The protein TIPRL was identified as prone to cysteine oxida-Interestingly, protein phosphatase 2A (PP2A) is also reported tion in two mass-spectrometry-based screens for cysteine-deto be a redox regulated phosphatase. Several studies reported pendent protein-protein interaction performed in our labo-PP2A thiol oxidation, resulting in the inhibition of PP2A ratory [19]. Here we further explore the function and redox catalytic activity [7–9], although details and implications regulation of TIPRL in human cells in relation to mTORC of these modifications need to be further elucidated. PP2A and PP2A dependent signaling. We provide evidence that enzymes constitute a large family of Ser-Thr phosphatases, TIPRL is highly sensitive to changes in the cellular redox with widespread functions in many cellular processes. The state. Under more oxidizing conditions, it is readily oxidized PP2A holoenzyme consists of the assembly of a catalytic C on C14 and C87. This leads to the formation of three different TIPRL homodimers, linked though a disulfide between C14subunit (A or B isoform), one of two scaffolding subunits (subunit A) and a wide variety of regulatory subunits (subunit C14, C87-C87 or C14-C87. Although the biological function B, 26) that fine-tunes the substrate specificity, localization and of this cysteine-dependent control of TIPRL is not yet clear, phosphatase activity [10]. Together, there are more than 100 our preliminary results suggest a role for redox-sensitive hopossibilities for the formation of the ternary PP2A complex. modimerization of TIPRL in its regulation of PP2A-C and This is one of the reasons that PP2A is involved in practically downstream PP2A targets mTORC1 and PKB. any signaling pathway and mediates 30-50% of Ser-Thr dephosphorylation events [11].



#### Figure 1. TIPRL is a redox-sensitive protein.

(A-B) Colony formation assay in doxycycline-inducible TIRPL knockout cells, showing that TIPRL is essential in protecting cells from redox stress. Both treatment with glucose oxidase (GO) as well as paraquat (PQ) lead to a decrease in colony outgrowth in TIPRL deficient cells. Re-expression of TIPRL can reverse the reduced colony outgrowth. (C) Oxidizing conditions (i.e. H<sub>2</sub>O<sub>2</sub> exposure) induce a mass shift of a fraction of TIPRL. Parallel reducing and non-reducing SDS-PAGE and western blot analysis (WB) of Flag-TIPRL immunoprecipitations (IP). Cells were incubated with 200 µM of H<sub>2</sub>O<sub>2</sub> for 15 minutes where indicated. Under non-reducing conditions, a fraction of TIPRL shows a H<sub>2</sub>O<sub>2</sub>-induced HMW band pattern (blue arrows). This band pattern is lost when samples were incubated with 10 mM DTT for 10 minutes prior to washing, or when samples are analyzed under reducing conditions (lower panel). (D) Endogenous TIPRL shows a HMW band pattern under oxidizing conditions (indicated by a smear). Cells were transfected with scrambled control (Scr) or TIPRL RNAi and incubated with 200 µM H<sub>2</sub>O, for 15 minutes. Cells were lysed in non-reducing sample buffer and whole cell lysates were analyzed. Panels are from different exposures of the same membrane. (E) Cysteines (yellow) in the crystal structure of TIPRL (PDB ID: 5D9G). Residues 1-15 were removed for crystallization and are added manually, indicated in grey. The four cysteines 14, 75, 87 and 249 are indicated in yellow. (F) The TIPRL HMW band pattern is cysteine-dependent. Wild-type TIPRL and TIPRLAC were immunoprecipitated and analyzed under reducing and non-reducing conditions. (G) The H<sub>2</sub>O<sub>2</sub>-induced, cysteine-dependent HMW band pattern is induced within 1 minute of H<sub>2</sub>O<sub>2</sub>, treatment, and diminishes after 30 minutes of H,O, treatment (h). The HMW shift of TIPRL is induces H,O, concentrations as low as 5 µM. Cells were incubated with different concentrations of H<sub>2</sub>O<sub>2</sub> for 10 minutes prior to lysis.

# RESULTS

#### **TIPRL is a Redox-Sensitive Protein**

We identified TIPRL as prone to cysteine oxidation in multi-(Figure 1D), suggesting that the HMW complexes also occur ple mass-spectrometry-based screens for redox sensitive proat endogenous TIPRL protein levels. teins. If oxidation of TIPRL is important in mediating the response to changes in the cellular redox state, loss of TIPRL We next set out to identify which cysteines are involved in could affect cell viability when cells are exposed to an oxithe formation of the disulfide induced mass shifts of TIPRL. TIPRL contains 4 cysteines (14, 75, 87, 249), of which C14 dative challenge. To investigate this, we deleted the TIPRL gene from RPE cells using Crispr-Cas9, and introduced a and C87 are surface exposed in an extended loop (Figure 1E). doxycycline-inducible TIPRL expression construct. We then A cysteine-free mutant of TIPRL (TIPRL  $\Delta C$ , in which its challenged cells with prolonged exposure to  $H_2O_2$  generated four cysteines were replaced with serines) no longer shift up by extracellular Glucose Oxidase (GOx), or treatment with on non-reducing SDS-PAGE, confirming that the HMW the redox cycler paraquat (PQ) which generates superoxide. bands indeed represent disulfide-dependent complexes con-Cells that are knockout for TIPRL show strongly reduced taining TIPRL (Figure 1F). colony outgrowth when challenged with these compounds. Re-expression of TIPRL can rescue this phenotype, indicat-A time course of exposure to peroxide indicates that the oxiing that it indeed stems from loss of TIPRL (Figure 1A-B). dation of TIPRL occurs rapidly (within one minute) as well Flow cytometry experiments demonstrate that loss of colony as transiently (Figure 1G-H. Furthermore, we show that the outgrowth is not caused by differences in cell death (prelimoxidation of TIPRL occurs upon exposure to peroxide levels inary, data not shown), suggesting that a ROS-induced susas low as 10 µM (Figure 1I). tained cell cycle arrest might underlie the impaired outgrowth Together, these findings suggest that TIPRL is highly sensiupon loss of TIPRL expression. These data suggest, for the first time, that TIPRL is important in resolving redox stress. tive to oxidation and readily forms cysteine-dependent HMW complexes upon exposure to low levels of peroxide.

The observation that TIPRL is required for resistance to oxidants further led credence that TIPRL could be a bona fide **TIPRL Forms Disulfide-Dependent Homodimers Upon Oxidation** hit in the aforementioned mass spectrometry screens for potentially redox-regulated proteins. To test if TIPRL is indeed To dissect the nature of the HMW cysteine-dependent coma redox-sensitive protein (i.e. whether it undergoes reversible plexes containing TIPRL, we performed a diagonal SDS-PAGE on immunoprecipitated TIPRL (Figure 2A). With cysteine oxidation) we expressed and immunoprecipitated Flag-TIPRL before analysis under parallel reducing and non-rethis technique, immunoprecipitated samples are separated under non-reducing conditions in the first dimension, folducing conditions. Exposure to H<sub>2</sub>O<sub>2</sub> induces a mass shift of lowed by a second dimension under reducing conditions. a fraction of TIPRL, as indicated by bands that migrate well above the MW of TIPRL (Figure 1C, blue arrows). There are Non-covalently bound proteins run in the diagonal in the five clearly visible bands; an intense triplet of bands at around second dimension, whereas covalent disulfide-dependent complex members run below the diagonal. As can be seen 75, 85 and 100 kDa and two bands at 50 and 60 kDa. These from the diagonal SDS-PAGE for wild-type TIPRL (for both TIRPL-containing complexes likely contain intermolecular disulfides judged by the large mass-shift and their reversibility the SimplyBlue-stained gel, top panel and Figure \$1, and upon treatment with the reducing agent DTT prior to washing Flag-stained western blot, lower panel), the shifted HMW

(right lane). Furthermore, endogenous TIPRL also displays a H<sub>2</sub>O<sub>2</sub>-induced high molecular weight (HMW) band pattern (indicated by a smear), which is lost upon TIPRL knockdown

bands indeed contain TIPRL, visible as distinct spots at the height of Flag-TIPRL below the diagonal (Figure 2B and S1). This indicates that the HMW bands indeed contain TIPRL. For Flag-TIPRL $\Delta C$  these spots could indeed not be detected. However, no evidence of other proteins present in the complex was found below the diagonal at the predicted positions. This suggests that the HMW bands of TIPRL represent different cysteine-dependent TIPRL homo-oligomers.

To investigate this possibility further, Flag- and hemagglutinin (HA)-tagged TIPRL were co-expressed, followed by an IP for Flag-TIPRL and analysis under non-reducing and reducing conditions. HA-TIPRL is co-immunoprecipitated with Flag-TIPRL, indicating an interaction (Figure 2C). Like Flag-TIPRL, HA-TIPRL shows a H<sub>2</sub>O<sub>2</sub>-induced massshift under non-reducing conditions. The typical three-band pattern runs at (approximately) the same MW and could therefore be in the same complex. HA-TIPRL also binds to Flag-TIPRL independent of cysteines or H<sub>2</sub>O<sub>2</sub> treatment, suggesting that TIPRL may already exist as complexes prior to disulfide formation.

To estimate the stoichiometry of the oligomeric TIPRL complexes, TIPRL-expressing cell lysates were fractionated on a size exclusion column (SEC), followed by immunoprecipitation and western blotting. The distinct HMW complexes of TIPRL elute from the column in one fraction, suggesting that these complexes have a similar molecular weight, about 40 kDa bigger than monomeric TIPRL (Figure 2D). These findings suggest that oxidized TIPRL can be found as homodimers of different shapes, potentially involving different disulfides.

To investigate which cysteines are involved in the formation of the different TIPRL homodimers we designed several TIPRL cysteine mutants (Figure 3A). These include the cysteine-free mutant of TIPRL (TIPRL $\Delta C$ ) that was described above. In addition, we generated four TIPRL mutants in which one of the four cysteines (Figure 3B) is mutated to a serine, and four mutants that contain only one of the four cysteines (e.g.

TIPRL 14C contains a cysteine at position 14 and serines at positions 75, 87 and 249). There are several conclusions we can draw from IP experiments under parallel non-reducing and reducing conditions using these mutants.

First of all, the lower band of the HMW triplet is completely dependent on cysteine 14, as it is absent in the TIPRL-C14S pulldown, but detectable in the TIPRL-14C pulldown (Figure 3C). Similarly, the upper band of the triplet seems dependent on cysteine 87. Both cysteine 75 and 249 are not required for any HMW band. The middle band of the HMW triplet requires the presence of both cysteines 14 and 87, as evidenced by co-expressing TIPRL-14C or TIPRL-87C. Indeed, in these conditions we observe the formation of all three HMW bands (Figure 3D). Therefore, it seems like TIPRL forms at least three different disulfide-mediated homodimers involving C14 and C87: C14-C14, C87-C87 and C14-C87. Differences in migratory behavior of these homodimers could potentially be explained by the differential accessibility of SDS around the disulfide.

Closer inspection of the molecular packing of the TIPRL crystal structure as published in ref. [17] provides further evidence for the formation of homodimers. The N-terminal deletion, containing C14, was predicted to be a potential flexible region (Figure 3D, hypothetical N-terminus in grey), which could promote availability for homodimerization [17]. The crystal structure contains no evidence of a disulfide between C14-C87. The asymmetric unit of the TIPRL crystal structure seems to form a dimer through the N-terminal interface (containing C14), but this is not likely the case in cells, since the N-terminal residues of the purified protein are not native to TIPRL. Interestingly, a C87-C87-mediated disulfide between two TIPRL molecules was also modeled in the crystal packing of TIPRL, with a distance of 2.03 Å (Figure 3E), thereby confirming C87-C87-mediated homodimerization in vitro.

Together, our observations shows that TIPRL forms three different reversible disulfide-mediated homodimers upon exposure to H<sub>2</sub>O<sub>2</sub>, involving C14 and C87.



Figure 2. TIPRL forms disulfide-dependent homodimers upon oxidation. (A) Schematic overview of diagonal (2D) SDS-PAGE. Immunoprecipitated samples are run under non-reducing conditions, so disulfide-mediated complexes migrate at their combined MW. The entire lane is excised and incubated in reducing sample buffer before running the second dimension, where disulfide-mediated complex members migrate at their own MW. Proteins migrating at their own MW in both the first and the second dimensions are shown on a diagonal, whereas disulfide-mediated complexes migrate below the diagonal in the second dimension. (B) TIPRL homodimerizes. The HMW bands indeed contain TIPRL, visible as distinct spots at the height of Flag-TIPRL below the diagonal. The absence of binding partners suggests that intermolecular disulfide bond formation between TIPRL and other proteins is not likely. (C) HMW HA-TIPRL co-immunoprecipitates with Flag-TIPRL, indicating homodimerization. Flag-TIPRL and Flag-TIPRLAC (green) were co-expressed with HA-TIPRL (red), immunoprecipitated and analyzed under non-reducing conditions. (D) Size exclusion chromatography (SEC) of TIPRL. Flag-TIPRL expressing cells were treated with 200 µM of H<sub>2</sub>O<sub>2</sub> for 15 minutes and their cell lysates were separated on a size-exclusion column. Flag-TIPRL was immunoprecipitated from the resulting 52 fractions, and analyzed under non-reducing conditions. Flag-TIPRL HMW bands were quantified from the resulting western blots (graph). HMW TIPRL are eluted from the column in one fraction, suggesting that TIPRL-containing complexes in all these bands have a similar molecular weight.

#### **Functional Characterization of Redox-Dependent TIPRL Homodimerization**

We next aimed to study whether cysteine-dependent homodimerization of TIPRL plays a role in the observed resistance to oxidants (Figure 1A). To this end, we stably expressed

doxycycline-incudible TIPRL and TIPRLAC in TIPRL knockout RPE cells and challenged these with prolonged exposure to H<sub>2</sub>O<sub>2</sub> produced by GOx. No difference was found in colony outgrowth between wild-type and mutant TIPRL, suggesting that the ability of TIPRL to resolve redox stress is



#### Figure 3. TIPRL forms three different disulfide-dependent homodimers upon oxidation.

(A) Schematic overview of TIPRL cysteine mutants that were used in our experiments. C, cysteine, S, serine. (B) HMW TIPRL is cysteine-specific. Different TIPRL cysteine mutants (see a) were used in immunoprecipitation and analysis under non-reducing conditions. The lower band of the HMW triplet is completely dependent on C14, the upper on C87, the middle on both C14 and C87. (C) Combining expression of TIPRL containing only C14 and only C87, respectively, results in the formation of all three disulfide-mediated HMW homodimeric complexes of TIPRL: C14-C14, C87-C87 and C14-C87. (D) Crystal packing of TIPRL (PDB ID: 5D9G), showing the N-terminal dimer interface in the asymmetric unit. Residues 1-15 were removed for crystallization and are added manually, indicated in grey. C14 is indicated in yellow. (E) Crystal packing of TIPRL (PDB ID: 5D9G), showing the C87-C87-mediated disulfide between two TIPRL molecules. C87 is indicated in yellow.

not dependent on its oxidation and subsequent dimerization (Figure 4A and S2).

The functional role of TIPRL in human cells is largely unclear. In order to see whether the interactome of TIPRL depends It is, however, possible that not the binding but the ability of on its redox modifications we compared the interactome of TIPRL to inhibit PP2A-C is affected by oxidation of TIPRL. wildtype (WT) and TIPRLAC under oxidizing conditions To this end, we measured PP2A-C activity in combination in a label-free MS/MS-based approach. With this approach, with TIPRL or TIPRLAC and in basal and oxidizing condiwe identify proteins that are significantly enriched in a H<sub>2</sub>O<sub>2</sub>tions in a preliminary experiment (Figure 4E). Indeed, overand cysteine-dependent manner (Figure 4B and Table 1-2). expression of TIPRL inhibits PP2A-C phosphatase activity, Interestingly, many of these are known redox-sensitive proteins, as was described before. As controls, the PP2A-C inhibitor involved in the cellular ROS detoxification system, including okadaic acid (OA) lowers PP2A-C activity, but activity is not thioredoxin (TRX) and peroxiredoxin 1, 2 and 5 (PRDX1, affected by oxidizing conditions. Like wild-type TIPRL, cys-PRDX2 and PRDX5). We confirmed the complex formation teine-free TIPRL is also able to inhibit PP2A-C. Interestingwith PRDX2 (general discussion). Other notable H<sub>2</sub>O<sub>2</sub>-inly, more oxidizing conditions enhance the ability of TIPRL duced, cysteine-dependent interactors of TIPRL are DJ1, to inhibit PP2A-C, but not in the cysteine-free mutant of SUMO, GAPDH and CDK4. However, experiments analyz-TIPRL. Although differences are small and this experiment ing a possible functional role for these interactions have been needs to be repeated, this would suggest that oxidized TIPRL is more efficient at inhibiting PP2A-C than non-oxidized or inconclusive up to date. We also identified known interactors of TIPRL such as IGBP1 (a4), but their interaction with TIPRL TIPRL $\Delta C$  is. We confirmed this by testing phosphatase acseems not H<sub>2</sub>O<sub>2</sub>-induced (data not shown). tivity of phosphatases bound to TIPRL. Although we might also measure activity of other phosphatases in this assay, we again see lower phosphatase activity in samples containing oxidized TIPRL compared to those with reduced or cysteine-free TIPRL (Figure 4F, preliminary data). An interesting observation is that although less PP2A-C is co-immunoprecipitated in samples with TIPRL $\Delta C$  due to lower expression, more phosphatase activity is measured compared to wild-type TIPRL. Therefore, our results might be an underestimation of the effect of TIPRL oxidation on PP2A-C activity.

Interestingly, PP2A-C (PPP2CB) is significantly enriched in binding to wild-type TIPRL as compared to TIPRL $\Delta C$ (Table 1), suggesting a role for oxidation and subsequent homodimerization of TIPRL in its regulation of PP2A-C. TIPRL binding to PP2A-C has been shown to inhibit the catalytic activity of the phosphatase [14-17], thereby positively regulating mTORC1 targets S6K and 4EBP1. We tested whether the absence of cysteines affects TIPRL binding to PP2A in an IP experiment (Figure 4C], but we observed no difference in the ability of TIPRL or TIPRL  $\Delta C$  to interact It has been shown that TIPRL facilitates amino acid-regulated mTORC1 signaling by inhibiting PP2A-C [15]. with PP2A-C. Similarly, the interaction between TIPRL and PP2A-C is not affected by oxidizing conditions. Since not all Combined with our previous results, this implies that oxi-TIPRL homodimerizes under oxidizing conditions we might dized TIPRL is more efficient at inhibiting PP2A-C in this underestimate the effect of oxidation in these experiments, context, leaving the mTORC1 target S6K phosphorylated. we investigated whether homodimerized TIPRL (HMW) Indeed, preliminary experiments show that TIPRL overexis able to interact with PP2A-C. Indeed, HMW homodipression results in sustained phosphorylation of S6K at T389, merized TIPRL is co-immunoprecipitated with PP2A-C which seems dependent on TIPRL cysteines since TIPRL $\Delta C$ does not show this effect (Figure 4G, preliminary data). In under non-reducing conditions (Figure 4D). These experi-

ments suggest, in contrast to the mass spectrometry data, that oxidation and homodimerization of TIPRL do not affect its ability to bind PP2A-C. this line, reducing the cellular environment by treating cells with  $\beta$ -mercaptoethanol limits the ability of TIPRL to sustain p-S6K phosphorylation (Figure 4H, preliminary data). Interestingly, H2O2 treatment completely diminishes S6K phosphorylation at T389, even when amino acids are added.

A major target of PP2A is PKB (Akt), which is dephosphorylated and inactivated at both T308 and S473 by PP2A [20-24]. Since TIPRL seems to inhibit PP2A activity, we examined whether TIPRL positively affects the phosphorylation status of PKB. Surprisingly, re-expression of TIPRL in TIPRL knockout cells lowers the phosphorylation of PKB at both T308 and S473 (Figure 4I-J, preliminary data). Inhibition of PP2A with OA does not abolish the observed dephosporylation of p-PKB, suggesting that the inhibitory effect of TIPRL on PKB does not involve the inactivation of PP2A (Figure 4J, preliminary data). Likewise, inhibition of mTORC1 by treatment with rapamycin does not affect this, which suggests mTORC1 activity is not required for TIPRL-dependent PKB inhibition.

Next, we wondered whether the inhibitory effect of TIPRL on PKB phosphorylation might be affected by oxidation of TIPRL. To this end, we treated TIPRL knockout cells and TIPRL expressing cells with H2O2. Oxidizing conditions seem to efficiently induce phosphorylation of PKB at both T308 and S473. Interestingly, the inhibitory effect of TIPRL on PKB phosphorylation that we observed under basal conditions is no longer present in more oxidizing conditions (Figure 4J, preliminary data). In summary, our preliminary data shows that the oxidation of TIPRL enhances its inhibitory effect on PP2A-C leading to more efficient inhibition of dephosphorylation of the mTORC1 target S6K. Furthermore, we observe an inhibitory effect of TIPRL on PKB (measured by phosphorylation at T308 and S473), although the oxidation of TIPRL itself does not seem to play a role in this. Of note, these data are preliminary and follow-up studies have to be done in order to confirm these findings.

#### DISCUSSION

The reversible oxidation of cysteines, which is indispensable for redox signaling, allows for the rapid respond to changes in the local redox environment, thereby integrating the cellular redox status with other signaling pathways. Cysteine oxidation can lead to reversible disulfide bond formation and subsequent structural rearrangements to modify signaling output. In this chapter, we describe TOR signaling pathway regulator-like (TIPRL) as a novel redox-sensitive protein, which is potentially involved in the control of PP2A and its downstream effects.

TIPRL rapidly forms disulfide-dependent homodimers via two of its cysteines, C14 and C87 upon treatment with low levels of H<sub>2</sub>O<sub>2</sub>, (Figure 1). For comparison, TIPRL oxidation occurs at H<sub>2</sub>O<sub>2</sub> concentrations similar to those required for peroxiredoxin dimerization in tissue culture [25], both for ectopically expressed and endogenous TIPRL (Figure 1D).

Using mutational analysis, we show that three different homodimers can be formed with similar stoichiometry: C14-C14 C87-C87 and C14-C87. Interestingly, both C14 and C87 are surface exposed in an extended loop (Figure 1E). Closer inspection of the published crystal structure of TIPRL revealed that the C87-C87-mediated disulfide was also modeled in the crystal packing of TIPRL, with a distance of 2.03 Å (Figure 3E), which was not described by the authors [17]. In addition, TIPRL has been identified in several screens for redox-sensitive proteins [26-29]. Furthermore, recombinant TIPRL that is kept in reducing buffer in vitro rapidly turns over DTT present in the buffer (T. Madl, data not shown), suggesting that TIPRL cysteines are oxidized readily, or that TIPRL itself has an enzymatic redox acivity. On top of that, TIPRL maintains its structure upon oxidation in NMR spectroscopy and small-angle X-ray scattering experiments (T. Madl, data not shown). However, considerable caution should be taken when interpreting the results of these in vitro and NMR experiments, and they were variable and inconclusive.



Figure 4. Functional characterization of TIPRL homodimerization. (figure legend continues on next page)

(A) Cysteine oxidation and homodimerization of TIPRL does not affect its ability to resolve redox stress. Colony formation assay in doxycycline-inducible TIRPL and TIPRLAC cells with a TIPRL knockout background. TIPRL proficient cells are protected from GOx-induced redox stress. Removal of cysteines does not affect this. (B) Scatter plot of the mass spectrometry data, showing the log, fold change of proteins within indicated conditions. Colored dots represent proteins with a p-value < 0.05 as calculated using inference of protein differential abundance by probabilistic dropout analysis (proDA). Horizontal dotted lines are positioned at log, fold change of 1 and -1 (i.e. a 2-fold change). For the identity of specific TIPRL interactors see Tables 1-2. (C) Both Flag-TIPRL and Flag-TIPRLΔC interact with PP2A-C to a similar extent. Treatment with H<sub>2</sub>O<sub>2</sub> does not affect this interaction. An IGG immunoprecipitation is used as a control. (D) Disulfide-dependent homodimers of TIPRL also interact with PP2A-C. PP2A-C was immunoprecipitated from cells expressing Flag-TIPRL and analysed under parallel reducing and non-reducing conditions. Total cell lysates are also shown (right panel, input) to indicate the MW of homodimerized TIPRL under non-reducing conditions. (E) Preliminary data. TIPRL inhibition of PP2A-C activity is increased under oxidizing conditions in a TIPRL cysteine-dependent manner. PP2A-C was immunoprecipitated from Flag-TIPRL and TIPRLΔC-expressing cells, which were treated as indicated with okadaic acid (OA) and H,O, (the last two samples were treated on-bead). Immunoprecipitates were incubated on-bead with phosphorylated peptide and dephosphorylation (i.e. the release of PPi) was measured by colorimetric malachite green. Corresponding western blots show IP efficiency for PP2A-C and expression levels of Flag-TIPRL. Dotted lines indicate rearrangement of the same western blot. A typical experiment from a biological duplicate is shown. (F) Preliminary data. Phosphatases interacting with wild-type TIPRL show lower phosphatase activity is compared to those interacting with TIPRL $\Delta C$ . This effect is cysteine-dependent. Overexpressed Flag-TIPRL and TIPRL $\Delta C$  were immunoprecipitated from cells treated with H<sub>2</sub>O<sub>2</sub> prior to lysis and phosphatase activity was measured using a malachite green detection method. Of note, less PP2A-C is co-immunoprecipitated in samples with TIPRLAC due to lower expression, but more phosphatase activity is measured compared to wild-type TIPRL. n=1. (G) Preliminary data. TIPRL, but not TIPRLΔC overexpression results in sustained phosphorylation of (both endogenous and GST- overexpressed) S6K at T389 when cells are deprived of amino acids. Cells were starved from amino acids and growth factors for 1h, after which amino acids (AA) were replenished for 15 minutes and total cell lysates were analyzed on western blot. The antibody staining for endogenous p-S6K shows unspecific bands in non-starved cells, likely caused by the presence of BSA. (H) Preliminary data. Reducing the cellular environment reduces the ability of TIPRL to sustain p-S6K phosphorylation. Cells were treated with 100 µM β-mercaptoethanol during amino acid starvation. Dotted lines indicate rearrangement of the same western blot. The ratio of S6K phosphorylation in starved cells compared to AA addback represents the fraction of S6K phosphorylation that is retained upon amino acid starvation. (I) Preliminary data. TIPRL reduces the phosphorylation of PKB at S473. TIPRL expression was induced by doxycyclin treatment in TIPRL knockout cells for the indicated times. Cells were incubated with 10 nM of okadaic acid (OA) to inhibit PP2A for the indicated times. (J) Preliminary data. Both TIPRL and TIPRLAC expression inhibit the phosphorylation of T308 and S473 in PKB, independent of mTORC1. Cells were treated with 50 nM rapamycin for indicated times. Oxidizing conditions, induced by treating cells with 200 µM of H<sub>2</sub>O<sub>2</sub> for 10 minutes, induces phosphorylation of PKB.

Another prerequisite for reversible redox signaling is that the oxidation of cysteine thiols is transient, i.e. goes down after a period of time. Since not all TIPRL homodimers are reduced simultaneously (Figure 1H), it is possible that their reduction is enzymatically regulated. This idea is supported by the cysteine-dependent, H2O2-induced binding of thioredoxin (TRX) to TIPRL as shown in our mass spectrometry data (Table 2 and Figure 4B). Similar to observations such as the reduction of the disulfide-dependent complex between FOXO4 and p300 [30], it is possible that TXN in involved in actively reducing TIPRL disulfides, a process that requires the formation of a temporary mixed disulfide intermediate between TXN and TIPRL.

In addition to TXN, several peroxiredoxin isoforms (PRDX1, 2 and 5) seem to interact with TIPRL in a  $H_2O_2$ -induced, cysteine-dependent manner, as observed in our mass spectrometry experiment (Table 2). Peroxiredoxins are dedicated  $H_2O_2$  scavengers, and are up to a million times more reactive with H<sub>2</sub>O<sub>2</sub> than other known redox sensitive proteins. More importantly, they are also known to actively participate in the oxidation of proteins through redox relays. Further experiments need to be done to test whether peroxiredoxins are responsible for the oxidation of TIPRL through a redox relay. If this is the case, this would explain the high reactivity of TIPRL cysteines towards  $H_2O_2$ .

The oxidation-induced homodimerization of TIPRL occurs under near-physiological oxidizing conditions, suggesting a biological role for TIPRL oxidation. A number of studies have focused on a role for TIPRL in the inhibition of PP2A-C, although a precise role is unclear. For example, it has been suggested that TIPRL mediates binding between PP2A-C and its targets [31], but TIPRL overexpression was also reported to inhibit PP2A-C catalytic activity towards several TIPRL has been considered (and named after) an mTOR targets, among which S6K and an ATM/ATR target [15,16] regulating protein because its yeast homolog, Tip41, inhibits The activity of TIPRL-bound PP2A-C was shown to be in-TOR signaling by sequestration of the  $\alpha$ 4 ortholog Tap42. hibited *in vitro*, and does not associate with the structural In contrast, however, human TIPRL has been reported to A- or regulatory B-subunits that are required for PP2A holopositively stimulate mTORC1 in response to amino acids [15]. enzyme formation [14,15]. More recently, this was supported We found that TIPRL overexpression results in sustained phosphorylation of S6K at T389, which seemed dependent by the TIPRL protein structure, which provides evidence that TIPRL blocks the PP2A-C active site as well as the binding on TIPRL oxidation since TIPRLAC did not prevent dephosphorylation (Figure 4G, preliminary data). Interestingly, surface for the regulatory B-subunit [17]. In line with this, TIPRL was suggested to be one of five PP2A modulators, H<sub>2</sub>O<sub>2</sub> treatment completely diminishes S6K phosphorylation serving to prevent aspecific phosphatase activity until the at T389, even when amino acids are added (Figure 4H). This PP2A trimeric holoenzyme is assembled [12]. Complemenis in disagreement with observations that treating cells with tary to this, we find that TIPRL expression as well as binding oxidizing agents increases S6K phosphorylation, even when inhibits the activity of PP2A-C (Figures 4E-F). mTORC1 is inactivated by depleting cells from amino acids or treatment with rapamycin [32]. The molecular details un-

Our results also suggest that in addition to the association derlying this discrepancy need to be further elucidated. between PP2A-C and TIPRL, oxidation and subsequent homodimerization of TIPRL might affect the inhibitory effect As discussed above, PP2A-C is a phosphatase with an exof TIPRL on PP2A. Oxidizing conditions seem to further tensive number of targets which is functionally involved in a inhibit PP2A in a TIPRL cysteine-dependent manner, an obdiverse array of signaling pathways, sometimes in seemingly servation that is lost when expressing the cysteine-free mutant of TIPRL. The cysteine-free mutant of TIPRL is, however, still able to bind and inhibit PP2A in a redox-independent manner. and inactivated at both T308 and S473 by PP2A [20-24]. Likely not all PP2A-C is bound by TIPRL and not all TIPRL is dimerized under more oxidizing conditions, so specific efphorylation of PKB. Surprisingly, TIPRL seems to negafects of oxidized-TIPRL-bound PP2A-C might be diluted by free PP2A-C and reduced TIPRL in these assays. In addition, TIPRL might not only affect PP2A-C catalytic activity, but instead regulate its activity towards specific targets. In line with this, examining the effects of TIPRL oxidation on the general phospho-proteome could provide evidence as to site, are both affected, already suggests this is regulated more whether TIRPL oxidation indeed inhibits PP2A-C activity upstream of mTORC2 and PDK1.

opposite manners. If PP2A-C catalytic activity were directly affected by its association with oxidized TIPRL, other targets downstream of PP2A-C would also be affected. A major target of PP2A is PKB (Akt), which is dephosphorylated We tested whether TIPRL can induce the sustained phostively affect PKB phosphorylation at both T308 and S473, but this seemed not mediated though PP2A-C, suggesting a PP2A-independent role for TIPRL in the regulation of PKB. The notion that S473, an mTORC2 phosphorylation site [33], as well as T308, a PDK1-dependent phosphorylation in cells, and if so to what extent. It is important to keep in mind that PP2A thiols are also thought to be subject to oxi-When cells are also exposed to H<sub>2</sub>O<sub>2</sub> to induce TIPRL oxidation, leading to inhibition of PP2A catalytic activity [7–9], dation and homodimerization, PKB is strongly phosphoryalthough we did not observe evidence for this in our experilated at T308 and S473. This is consistent with findings that ments (Figures 4E-F). the PTEN phosphatase, well-known for its inhibition of the PI3K/PKB pathway, can also be oxidized and subsequently

#### inhibited [4]. Interestingly, the inhibitory effect of TIPRL on PKB phosphorylation that we observed under basal conditions is absent under oxidizing conditions (Figure 4J, preliminary data). Thus, H<sub>2</sub>O<sub>2</sub> treatment seems to overrule the inhibitory effect of TIPRL on PKB phosphorylation.

Activation of PKB normally promotes glucose uptake and glycolysis. Indeed, inducible expression of TIPRL lowers both the basal glycolytic rates as well as the glycolytic capacity. However, again this seems not dependent on the ability of TIPRL to form disulfide-dependent homodimers, since re-expression of TIPRLAC affects glycolytic function in a similar manner (Figure \$3, preliminary data). Furthermore, the relative contribution to cellular bioenergetics of mitochondrial respiration and glycolysis (measured by %OCR/ECAR, data not shown) indicate a relative increase of mitochondrial activity in RPE cells expressing TIPRL, independent of cysteines.

Of note, PP2A is not the only phosphatase that seems to interact with TIPRL. Our mass spectrometry data suggest that, among others, related phosphatases PPP4 (catalytic and regulatory subunit), PPP6 (catalytic and regulatory subunits) and PPP1 (regulatory subunit) bind to TIPRL in a cysteine-dependent manner (Table 1). These interactions were also reported by others [16,34,35], and they suggest a more widespread role for TIPRL in the regulation of phosphatases. Future studies should therefore also focus on the effects of these interactions in order to elucidate the effect of TIPRL on these phosphatases.

Our results suggest that rather than affecting PP2A-C catalytic activity in general, the oxidation of TIPRL may affect pathways downstream of PP2A-C in different manners. However, we were so far unable to link the observed redox-dependent dimerization of TIPRL to newly discovered TIPRL-dependent phenotypes like oxidant-induced loss of viability or changes in metabolism. Further studies should aim at further elucidating a role for redox regulation of TIPRL.

# MATERIALS AND METHODS

#### Cell Lines and Culturing

HEK293T were cultured in bicarbonate-buffered DMEM, supplemented with 10% FBS (Bodinco BDC-40506-C05), 2 mM L-glutamine (Lonza, BE17-605E) and 100 U/mL penicillin-streptomycin (Lonza, DE17-602E) and kept at 37°C and under a 6% CO<sup>2</sup> atmosphere. Transfections of HEK293T cells were carried out using PEI (Sigma-Aldrich, P3640) or Fugene-HD reagent (Promega, E2311) following the manufacturer's instructions. After two days, cells were harvested for further analysis. During amino acid starvation, cells were washed with PBS twice before they were incubated in amino acid free bicarbonate-buffered DMEM (Gibco) for 60 minutes. Amino acids (Bio Whitacker) were added back in the amino acid free medium for 15 minutes prior to lysis. CRISPR knockout lines were a kind gift of J. van den Berg and J. Nieuwenhuis. In short, 200k cells were plated with an siRNA for p53. After 8h, cells were transfected with pX330 (addgene plasmid ID 42230) and TIA-2A-Blast selection plasmids. Cells were selected with blasicidin and monoclonal knockout lines were verified by western blotting. Doxycylcin-inducible TIRPL or TIPRLAC cells were transduced with lentivirus containing pINDUCER20-TIPRL or -TIPRL DC and monoclonally selected for stable transduction using G418. TIPRL expression was confirmed by sequencing and western blotting.

For colony outgrowth assays, 1000 cells were seeded in a 6-wells plate. After allowing them to adhere for 4 hours, treatments were started as indicated. At 10 days post seeding, cells were fixed in methanol and stained with 0.5% crystal violet in 25% methanol. Plates were dried before imaging.

#### **Plasmids and Reagents**

Human TIPRL with att recombination sites were cloned from cDNA using the following primers: 5'-GGGG-ACAAGTTTGTACAAAAAAGCAGGCTTGAT-GATGATCCACGGCTTCCAG-3', R 5'-GGGGAC-CACTTTGTACAAGAAAGCTGGGTATTCC ACTTGTGTACTTTTTTGTG-3'. Using Gateway technology (Invitrogen) entry clones were generated. The peroxidatic and resolving cysteine mutants of PRDX1-5 were created by site-directed mutagenesis PCR using the following primers: C14S\_F\_5'-GGGATTTCTCTTTCGGGCCCT-3', C14S\_R\_5'-AGGGCCCGAAAGAGAAATCCC-3', C75S F 5'- TGCGTTAAGATCCGTAAACAACTAC-3', C75S\_R\_5'-GTAGTTGTTTACGGATCTTAACGCA-3', C87S\_F\_5'- AAAGTGGCCTCAGCTGHAAGAGT-3', C87S R 5'- ACTCTTCAGCTGAGGCCACTTT-3', C249S\_F\_5'-GGGATTTCTCTTTCGGGCCCT-3', C249S\_R\_5'-AGGGCCCGAAAGAGAAATCCC-3', and verified by sequencing.

Gateway technology (Life Technologies) was used to create N-terminally tagged Flag-His, HA- and doxycylcin-inducible expression vectors (backbones pCDNA3 and pIN-DUCER20, Addgene #44012) from the resulting TIPRL cysteine mutant entry clones. The GST-S6K construct was a the FUJIFILM Luminescent Image Analyser LAS-3000. kind gift from Fried Zwartkruis. TIPRL sgRNA sequences are 5'-GACCCACATCATGAAGTCGG-3' and 5'-CAT-2D Diagonal Electrophoresis CATGAAGTCGGCGGATG-3' TIPRL knockdown was Immunoprecipitates were separated in the first dimension on a 10% SDS-PAGE gel and total protein content was stained performed using smartpool RNAi oligos from Dharmacon (261726). β-mercaptoethanol was used in a concentration of using SimplyBlue. Gel lanes were cut out and incubated with 100 µM. Rapamycin was purchased from Biomol and used at 2x Laemmli sample buffer containing  $\beta$ -mercaptoethanol for 50 nM, okadaic acid was used at 500 nM unless stated other-30' at room temperature. In the second dimension, reduced wise. 30% H<sub>2</sub>O<sub>2</sub> (Sigma 31642) was freshly diluted to a stock gel lanes were loaded on a second 10% SDS-PAGE gel at a right of 10 or 100 mM in H<sub>2</sub>O for every experiment. Unless stated angle to the first dimension. Detection of proteins was done otherwise, H<sub>2</sub>O<sub>2</sub> treatments were 200 for 10 minutes. using SimplyBlue stain and using western blotting.

#### **Co-Immunoprecipitations and Western Blotting**

For the identification of TIPRL interactors the lysate of After treatment as indicated, cells were lysed using a buffer containing 50 mM Tris-HCl pH 7.5, 1% TX100, 1.5 mM 4x20cm dishes were used for each pulldown on 75 ml of Flag-MgCl2, 5 mM EDTA, 100 mM NaCl, NaF, Leupeptin and M2 beads similar to the immunoprecipitation experiments Aprotinin. 100 mM iodoacetamide was added to the lysis described above. All immunoprecipitations were performed buffer to prevent post-lysis cysteine oxidation and to inacusing three biological replicates. After washing, beads were tivate disulfide reducing enzymes. After centrifugation at resuspended with 8M urea in 1M ammonium bicarbonate 14000 rpm for 10 min, 5% of the supernatant was kept as (ABC), reduced and alkylated in 10 mM TCEP and 40 mM input and the remaining supernatant was used for immunochloroacetamide (CAA) for 30 minutes at RT. After fourfold precipitation with anti-Flag-M2 affinity gel (Sigma A222). dilution with 1M ABC, proteins were digested overnight on-After a 2 h incubation whilst gently mixing, immunoprecipbead with 250 ng Trypsin/LysC (Promega V5071) per sample

itates were washed 4 times with lysis buffer containing 1 M NaCl and samples were boiled for 5 min in sample buffer with or without the reducing agent  $\beta$ -mercaptoethanol. Samples were separated on a 10% polyacrylamide gel and transferred to immobilon-FL membranes (using standard protocols) before staining and antibody detection.

Antibodies that were used are Flag M2 (Sigma F3165), HA (12CA5, monoclonal from hybridoma cell lines and SC805), TIPRL (Abcam), S6K and pS6K (Cell signaling, CS2708 and CSS9205), PKB and p-PKB (Cell signaling, CS2920, CS4060 and CS13038), GST (SC138), anti-tubulin (Merck Millipore CP06), PP2A-C (Abcam ab188253). Detection of fluorescent secondary antibodies was performed using the LI-COR Biosciences Odyssey Infrared Imaging System or the Amersham Typhoon NIR Plus Biomolecular Imager (GE Healthcare), detection of secondary HRP-antibodies was performed on

#### Mass Spectrometry

at 37°C. Samples were cleaned up with in-house-made C18 stagetips.

Mass spectrometry was performed as previously described [19]. Peptides were separated on a 30-cm pico-tip column (75  $\mu$ m ID, New Objective) and were packed in-house with 3  $\mu$ m aquapur gold C-18 material (Dr. Maisch) using a 140-min gradient (7–80% ACN 0.1% FA), delivered by an easy-nLC 1000 (LC120, Thermo Scientific), and electro-sprayed directly into an Orbitrap Fusion Tribrid Mass Spectrometer (Thermo Scientific). Raw files were analyzed with the Max-Quant software version 1.5.2.8 with oxidation of methionine, alkylation with N-ethylmaleimide and carbamidomethylation set as variable modifications. The Human protein database of UniProt was searched with both the peptide as well as the protein false discovery rate set to 1%. Downstream analysis was done using R version 4.0.2.

#### **Data Analysis**

A SummarizedExperiment object was created using LFQ data from the MaxQuant proteinGroups file and corresponding protein information. Proteins were filtered for reverse hits and standard contaminants. Next, we selected proteins that were identified with three or more unique peptides and were measured in at least one sample in 2 or more replicates. Data was  $log_2$ -transformed and normalized using quantile normalization, which ensures overall intensity differences due to IP efficiency differences between samples are equalized while maintaining identical statistical distributions. ProDA model fitting was performed using sample names as design input and the number of proteins in the data as the number of subsamples. To test for differential protein abundance, the proDa fit object was used for comparing wild-type against mutant TIPRL or H<sub>2</sub>O<sub>2</sub>-treated against control conditions.

#### Size Exclusion Chromatography

20 million Flag-TIPRL transfected 293T cells were lysed in 1 ml of lysis buffer containing 100 mM iodoacetamide (desctibed abovetion). Lysates were cleared by sonication and centrifugation and subsequently fractionated in 52 fractions (1 ml per minute, 2 ml per fraction) on a HiLoad 16/60 Superdex 200 prep grade column (GE Healthcare) using lysis buffer without iodoacetamide as flow buffer. Upon fractionation, IPs were performed as described above. For quantification, band intensity was measured in ImageJ. The relative intensity was calculated per band and per fractions relative to the total protein intensity per band (e.g. the intensities of the monomeric TIPRL band in all fractions were added up), and the percentage of total per fraction was plotted. The peak of each data line (indicated with the vertical lines) represents the fraction in which the respective band was enriched the most.

#### **PP2A Activity Assays**

The activity of the catalytic PP2A-subunit was assayed according manufacturers protocol using the PP2A Immunoprecipitation Phosphatase Assay Kit (Upstate). In short, transfected 293T cells were lysed in phosphatase lysis buffer (20 mM imidazole-HCL, 2 mM EDTA, 2 mM EGTA pH 7.0 containing, aprotinin, leupeptin and 1 mM PMSF) and homogenized by sonication. PP2A-C or Flag-TIPRL was immunoprecipitated and washed with TBS and Ser/Thr assay buffer. Beads were incubated with phosphorylated peptide whilst shaking, and dephosphorylation (release of phosphate) was assayed by incubating the supernatant (taken of the beads) with a Malachite Green Phosphate Detection Solution. Absorbance values were measured at 655 nm and compared to the standard curve to determine the amount of released phosphate per sample.

#### SUPPLEMENTAL MATERIALS AND METHODS

#### Seahorse Flux Analysis

Extracellular consumption rates (ECAR) and oxygen consumption rates (OICR were measured using a Seahorse Bioscience XFe24 Analyzer in in mpH (milli pH) per min and pmol O2 per min, respectively. Cells were treated with doxycycline. After 24h, 40k cells were seeded in fibronectin-coated XF24 cell culture microplates (Seahorse Bioscience) and grown for 24h. Culture medium was replaced 1h before measurements and incubated at 37 °C. For the glycolysis stress test, culture medium was replaced by Sea-horse XF Base medium, supplemented with 2 mM L-glutamine and 26 µL NaOH (1M). During the test 10 mM glucose, 5 mM oligomycin and 100 mM 2-deoxyglucose (Sigma-Aldrich) were injected to each well after 18, 36 and 65 min, respectively. For the mitochondrial stress test, culture medium was replaced by Seahorse XF Base medium (Seahorse Bioscience), supplemented with 10 mM glucose (Sigma-Aldrich), 10 mM pyruvate (Sigma-Aldrich), 2 mM L-glutamine (Sigma-Aldrich), and 27 µL NaOH (1M). During the measurements, 1  $\mu$ M oligomycin, 1  $\mu$ M FCCP and µM of rotenone and antimycin A (all Sigma-Aldrich) were injected to each well after 18, 45 and 63cmin, respectively. After injections, plates were mixed for 4 minutes and measurements of 2 min were performed in triplicates, The first measurements after oligomycin injections were preceded by 5 min mixture time, followed by 8 min pause for the mitochondrial stress test and 5 min mixture time followed by 10 min pause for the glycolysis stress test. OCR and ECAR values per group were normalized to the total amount of protein present per well.

# 3 I BIOCHEMICAL CHARACTERIZATION OF TIPRL

# **TABLES**

#### Table 1. MSMS data corresponding to Figure 4B: Cysteine- and H2O2dependent interactors of TIPRL and TIPRL $\Delta C$

Table 1. M	MSMS data corresponding to Figure 4B:	Cysteine- and H2O2-dependent interactors of TIPRL and TIPRLAC		
gene	uniprot ID	protein	log ratio	p-value
Q92945-2	rs for TIPKLAC, H <sub>2</sub> O <sub>2</sub> vs. untreated ? KHSRP	Far upstream element-binding protein 2	4.8	< 0.001
Q06830	PRDX1	Peroxiredoxin-1	4.3	<0.001
E9PHK9 06P2F9	TCOF1 FDC4	Treacle protein Enhancer of mRNA_decamping protein 4	3.8	0.004
P10599	TXN	Thioredoxin	3.3	<0.001
P32119	PRDX2	Peroxiredoxin-2	3.1	0.002
Q90F45 Q4VCS5	AMOT	Angiomotin	2.8	<0.012
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	2.7	0.001
P49790 09P258	NUP153 RCC2	Nuclear pore complex protein Nup153 Protein RCC2	2.6	0.001
P05204	HMGN2	Non-histone chromosomal protein HMG-17	2.2	0.012
P26599	PTBP1	Polypyrimidine tract-binding protein 1	1.5	0.008
Q81V96 H0Y5D5	CIZ1	Cipl-interacting zinc finger protein	13	0.011
Q6PL18	ATAD2	ATPase family AAA domain-containing protein 2	1.2	0.013
E7ETK8 P12270	AARS	AlaninetRNA ligase, cytoplasmic Nucleoprotein TPR	1.2	0.021
interacto	rs for H <sub>2</sub> O <sub>2</sub> -treated TIPRL, wild-type	vs. $\Delta C$	1.0	
P32119	PRDX2	Peroxiredoxin-2	5.7	<0.001
P30044-2	PRDX5 PRDX1	Peroxiredoxin-5, mitochondrial Peroxiredoxin-1	5.0	0.001
P10599	TXN	Thioredoxin	3.3	<0.001
095685	PPP1R3D	Protein phosphatase 1 regulatory subunit 3D	3.2	0.012
C9J5L7	TNRC6B	Trinucleotide repeat-containing gene 6B protein	2.8	0.001
Q9UHD1	CHORDC1	Cysteine and histidine-rich domain-containing protein 1	2.7	< 0.001
Q96H99 E7EVA0	CTTN MAP4	Src substrate cortactin Microtubule-associated protein	2.7	0.011
Q9H3K6	BOLA2	BolA-like protein 2	2.3	0.006
Q8TEQ6	GEMIN5	Gem-associated protein 5	2.2	<0.001
E9PH12	WAPAL	Prefoldin subunit 2 Wings apart-like protein homolog	2.2	0.012
E9PBS1	PAICS	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (Fragment)	2.1	0.006
Q32Q12 F7FTK8	NME1-NME2	Nucleoside diphosphate kinase	2.1	0.039
E7EMC7	SQSTM1	Sequestosome-1	1.9	0.002
F8WA86	CNN3	Calponin-3	1.9	0.035
090EG4	ZNF629	Zinc finger protein 629	1.8	0.001
000743-2	2 PPP6C	Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit	1.7	0.015
C9JRJ5	LIMD1	LIM domain-containing protein 1	1.6	0.008
P60510	PPP4C	Serine/threonine-protein phosphatase 4 regulatory subunit 2 Serine/threonine-protein phosphatase 4 catalytic subunit	1.6	0.008
B4DP17	CNBP	Cellular nucleic acid-binding protein	1.6	0.035
Q5JSZ5-: P11802	5 PRRC2B CDK4	Protein PRRC2B Cyclin.dependent kinsse 4	1.6	0.039
A8K8U5	ттк	Dual specificity protein kinase TTK	1.5	0.008
015084	ANKRD28	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	1.5	0.048
P13639 09UPN7	PPP6R1	Elongation factor 2 Serine/threonine-protein phosphatase 6 regulatory subunit 1	1.4	0.005
060566	BUB1B	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	1.4	0.035
F2Z3M7	PPP6R2 TPIM21	Serine/threonine-protein phosphatase 6 regulatory subunit 2	1.4	0.045
Q5W0B1	RNF219	RING finger protein 219	13	0.028
P48507	GCLM	Glutamatecysteine ligase regulatory subunit	1.3	0.046
BIAHBI DA6781	MCM5 PPS0	DNA replication licensing factor MCM5 405 ribosomal protein S9	1.2	0.016
Q9H7E2-	3 TDRD3	Tudor domain-containing protein 3	1.1	0.008
014646-2	2 CHD1	Chromodomain-helicase-DNA-binding protein 1	1.1	0.008
095239	KIF4A PCBPI	Chromosome-associated kinesin KIF4A Poly(C)-binding protein 1	1.1	0.010
C9J4Z3	RPL37A	60S ribosomal protein L37a	1.0	0.019
P62714	PPP2CB	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	1.0	0.029
interacto	ora for wild-type TIPRI. H.O. vs. untr	ested	1.0	0.049
P32119	PRDX2	Peroxiredoxin-2	8.2	< 0.001
Q06830	PRDX1	Peroxiredoxin-1	6.0	<0.001
P10599	TXN	Thioredoxin	5.0	<0.001
P30044-2	PRDX5	Peroxiredoxin-5, mitochondrial	4.1	0.005
E/ETK8 E9PHK9	AARS TCOFI	AlannetRNA ligase, cytoplasmic Treacle protein	3.8	<0.001
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	3.1	< 0.001
B4DI60	PLS3	Plastin-3	2.9	0.001
Q9P258	RCC2	Protein RCC2	2.8	0.024
P49790	NUP153	Nuclear pore complex protein Nup153	2.6	0.003
Q6P2E9 E7EVA0	EDC4 MAP4	Enhancer of mRNA-decapping protein 4 Microtubule-associated protein	2.6	0.025
B5MDQ0	ERCC6L	DNA excision repair protein ERCC-6-like	2.5	0.042
Q99497	PARK7	Protein DJ-1	2.4	0.001
Q90HD1 Q96H99	CTTN	Src substrate cortactin	2.2	0.001
095239	KIF4A	Chromosome-associated kinesin KIF4A	2.1	0.001
P35659 P26599	DEK	Protein DEK Polynyrimidine tract-hinding protein 1	2.0	0.029
Q4VCS5	AMOT	Angiomotin	1.8	0.004
B4DP17	CNBP	Cellular nucleic acid-binding protein	1.8	0.020
P11802	CDK4	Cyclin-dependent kinase 4	1.7	0.002
E9PBS1	PAICS	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (Fragment)	1.7	0.025
Q81EQ6 008945	GEMIN5 SSRP1	Gem-associated protein 5 FACT complex subunit SSRP1	15	0.005
A8K8U5	ТТК	Dual specificity protein kinase TTK	1.4	0.036
P11387	TOP1	DNA topoisomerase 1 EACT complex subunit SPT16	1.3	0.019
Q15637-4	4 SF1	Splicing factor 1	1.2	0.027
P35520	CBS	Cystathionine beta-synthase	1.2	0.021
B7WNZ6 B877N4	PKRC2C SUMO1	Protein PRRC2C Small ubiquitin-related modifier 1	1.1	0.006
BIAJY7	PSMD10	26S proteasome non-ATPase regulatory subunit 10	1.1	0.047
P78371	CCT2	T-complex protein I subunit beta	1.0	0.016
interacto	rs for untreated TIPRL, wild-type vs.	AC Peroviredovin-1	27	<0.001
P10599	TXN	Thioredoxin	1.6	0.006
Q9NY27	PPP4R2	Serine/threonine-protein phosphatase 4 regulatory subunit 2	1.6	0.008
015084 09UPN7	PPP6R1	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A Serine/threonine-protein phosphatase 6 regulatory subunit 1	1.0	0.042
P60510	PPP4C	Serine/threonine-protein phosphatase 4 catalytic subunit	1.5	0.044
E7EMC7 E7EPE0	SQSTM1 ZCCHC17	Sequestosome-1 Nucleolar protein of 40 kDa	1.4	0.008
000743-2	2 PPP6C	Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit	1.3	0.048
Q14126	DSG2	Desmoglein-2	1.2	0.036
014040-2	CHD1	Cinomodomani-neticase-DiNA-biliding protein 1	1.1	0.024

Table 2. List of cysteine- and  $H_2O_2$ -dependent interactors of TIPRL

uninno	t ID gono	protoin
1 02(50)	TID gene	protein Debase in it is to set the line set of a l
1 P2039	PIBPI	Polypyrimidine tract-binding protein 1
2 QOP2E	9 EDC4	Ennancer of mKNA-decapping protein 4
5 Q8WW	K9 CKAP2	Cytoskeleton-associated protein 2
4 Q9Y5B	9 SUPI16H	FACI complex subunit SP116
5 P3565	9 DEK	Protein DEK
6 P1138	TOPI	DNA topoisomerase 1
7 Q1563	/ SF1	Splicing factor 1
8 B8ZZN	6 SUMOI	Small ubiquitin-related modifier 1
9 E9PHI	79 TCOF1	Treacle protein
10P49790	9 NUP153	Nuclear pore complex protein Nup153
11 P04400	6 GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
12 Q0894	5 SSRP1	FACT complex subunit SSRP1
13 Q9294	5 KHSRP	Far upstream element-binding protein 2
14P35520	O CBS	Cystathionine beta-synthase
15 B5MD	Q0 ERCC6L	DNA excision repair protein ERCC-6-like
16Q9P25	8 RCC2	Protein RCC2
17 P7837.	I CCT2	T-complex protein 1 subunit beta
18Q4VCS	5 AMOT	Angiomotin
19 B7WN	Z6 PRRC2C	Protein PRRC2C
20 B4DP1	7 CNBP	Cellular nucleic acid-binding protein
21 BIAJY	7 PSMD10	26S proteasome non-ATPase regulatory subunit 10
22 Q96H9	9 CTTN	Src substrate cortactin
23 09523	9 KIF4A	Chromosome-associated kinesin KIF4A
24 A8K8U	/5 TTK	Dual specificity protein kinase TTK
25 E9PBS	1 PAICS	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole su
26 09 H3F	6 BOLA2	BolA-like protein 2
27 P11802	2 CDK4	Cyclin-dependent kinase 4
28 E7EVA	0 MAP4	Microtubule-associated protein
29 E7ETK	8 AARS	AlaninetRNA ligase, cytoplasmic
30 09949	7 PARK7	Protein DL1
31 P3004	4 PRDX5	Peroxiredoxin-5 mitochondrial
32.B4DI6	0 PLS3	Plastin-3
33.08TEC	06 GEMIN5	Gem-associated protein 5
34.0911H	DI CHORDC	Cysteine and histidine-rich domain-containing protein 1
35 P1050	TXN	Thioredoxin
36 P32110	PRDY2	Perovinedovin_?
27 00683	0 000001	Paroviradovin 1



panel) and non-reducing (upper panel) SDS-PAGE. SDS-PAGE gels were stained for total protein using Simply blue stain.

ccinocarboxamide synthetase (Fragment)

# SUPPLEMENTARY FIGURES AND LEGENDS



Figure S1. Simply blue-stained SDS-PAGE gel as was used for the experiment shown in Figure 2B (right lane). Cells expressing Flag-TIPRL were exposed to 200 µM of H,O, for 10 minutes and cells lysates were separated under reducing (lower





Cysteine oxidation and homodimerization of TIPRL does not affect its ability to resolve redox stress. Colony formation assay in doxycycline-inducible TIRPL and TIPRL  $\Delta C$  cells with a TIPRL knockout background. TIPRL proficient cells are protected from GOx-induced redox stress. Removal of cysteines does not affect this.



Figure S3. TIPRL decreases glycolytic capacity in a cysteine-independent manner. ECAR (extracellular acidification rate) was determined in a glycolysis stress test and OCR (oxygen consumption rate) was determined in a mitochondrial stress test by Seahorse analysis of doxycyclin-inducible TIPRL or TIPRLΔC cells. TIRPL expression lowers both the basal glycolytic rates and maximal glycolysis. (n=3, mean and SD are plotted)

# REFERENCES

- Spencer, N.Y.; Engelhardt, J.F. The Basic Biology of Redoxosomes in Cytokine-Mediated Signal Transduction and Implications for Disease-Specific Therapies. *Biochemistry-us* 2014, 53, 1551–1564, doi:10.1021/bi401719r.
- Mahadev, K.; Motoshima, H.; Wu, X.; Ruddy, J.M.; Arnold, R.S.; Cheng, G.; Lambeth, J.D.; Goldstein, B.J. The NAD(P)H Oxidase Homolog Nox4 Modulates Insulin-Stimulated Generation of H2O2 and Plays an Integral Role in Insulin Signal Transduction. *Mol Cell Biol* 2004, 24, 1844–1854, doi:10.1128/mcb.24.5.1844-1854.2004.
- Tanner, J.J.; Parsons, Z.D.; Cummings, A.H.; Zhou, H.; Gates, K.S. Redox Regulation of Protein Tyrosine Phosphatases: Structural and Chemical Aspects. *Antioxid Redox Sign* 2011, 15, 77–97, doi:10.1089/ ars.2010.3611.
- Lee, S.-R.; Yang, K.-S.; Kwon, J.; Lee, C.; Jeong, W.; Rhee, S.G. Reversibl Inactivation of the Tumor Suppressor PTEN by H2O2 \*. *J Biol Chem* 2002, 277, 20336–20342, doi:10.1074/jbc.m111899200.
- Frijhoff, J.; Dagnell, M.; Godfrey, R.; Östman, A. Regulation of Protein Tyrosine Phosphatase Oxidation in Cell Adhesion and Migration. *Antioxid Redox Sign* **2014**, *20*, 1994–2010, doi:10.1089/ars.2013.5643.
- Czech, M.P.; Lawrence, J.C.; Lynn, W.S. Evidence for the Involvement of Sulfhydryl Oxidation in the Regulation of Fat Cell Hexose Transport by Insulin. *Proc National Acad Sci* 1974, *71*, 4173–4177, doi:10.1073/ pnas.71.10.4173.
- Sommer, D.; Coleman, S.; Swanson, S.A.; Stemmer, P.M. Differential Susceptibilities of Serine/Threonine Phosphatases to Oxidative and Nitrosative Stress. *Arch Biochem Biophys* 2002, 404, 271–278, doi:10.1016/ s0003-9861(02)00242-4.
- Foley, T.D.; Kintner, M.E. Brain PP2A Is Modified by Thiol-Disulfide Exchange and Intermolecular Disulfide Formation. *Biochem Bioph Res Co* 2005, *330*, 1224 1229, doi:10.1016/j.bbrc.2005.03.108.
- Foley, T.D.; Petro, L.A.; Stredny, C.M.; Coppa, T.M. Oxidative Inhibition of Protein Phosphatase 2A Activity: Role of Catalytic Subuni Disulfides. *Neurochem Res* 2007, *32*, 1957–1964, doi:10.1007/s11064 007-9394-x.
- Eichhorn, P.J.A.; Creyghton, M.P.; Bernards, R. Protein Phosphatase
   2A Regulatory Subunits and Cancer. *Biochimica Et Biophysica Acta Bba - Rev Cancer* 2009, *1795*, 1–15, doi:10.1016/j.bbcan.2008.05.005.
- Arnold, H.K.; Sears, R.C. A Tumor Suppressor Role for PP2A-B56a through Negative Regulation of c-Myc and Other Key Oncoproteins. *Cancer Metast Rev* 2008, *27*, 147–158, doi:10.1007/s10555-008-9128-9.
- Sents, W.; Ivanova, E.; Lambrecht, C.; Haesen, D.; Janssens, V. The Biogenesis of Active Protein Phosphatase 2A Holoenzymes: A Tightly Regulated Process Creating Phosphatase Specificity. *Febs J* 2013, 280, 644–661, doi:10.1111/j.1742-4658.2012.08579.x.

 Jacinto, E.; Guo, B.; Arndt, K.T.; Schmelzle, T.; Hall, M.N. TIP41 Interacts with TAP42 and Negatively Regulates the TOR Signaling Pathway. *Mol Cell* 2001, *8*, 1017–1026, doi:10.1016/s1097-2765(01)00386-0

- 14. Smetana, J.H.C.; Zanchin, N.I.T. Interaction Analysis of the Heterotrimer Formed by the Phosphatase 2A Catalytic Subunit, A4 and the Mammalian Ortholog of Yeast Tip41 (TIPRL). *Febs J* 2007, 274, 5891 5904, doi:10.1111/j.1742-4658.2007.06112.x.
- 15. Nakashima, A.; Tanimura-Ito, K.; Oshiro, N.; Eguchi, S.; Miyamoto, T.; Momonami, A.; Kamada, S.; Yonezawa, K.; Kikkawa, U. A Positive Role of Mammalian Tip41-like Protein, TIPRL, in the Amino-Acid Dependent MTORC1-Signaling Pathway through Interaction with PP2A. *Febs Lett* **2013**, *587*, 2924 2929, doi:10.1016/j. febslet.2013.07.027.
- 16. McConnell, J.L.; Gomez, R.J.; McCorvey, L.R.A.; Law, B.K.; Wadzinski, B.E. Identification of a PP2A-Interacting Protein That Functions as a Negative Regulator of Phosphatase Activity in the ATM/ ATR Signaling Pathway. *Oncogene* **2007**, *26*, 6021 6030, doi:10.1038/ sj.onc.1210406.
- 17. Scorsato, V.; Lima, T.B.; Righetto, G.L.; Zanchin, N.I.T.; Brandão-Neto, J.; Sandy, J.; Pereira, H.D.; Ferrari, Á.J.R.; Gozzo, F.C.; Smetana, J.H.C.; et al. Crystal Structure of the Human Tip41 Orthologue, TIPRL, Reveals a Novel Fold and a Binding Site for the PP2Ac C-Terminus. *Sci Rep-uk* **2016**, *6*, 30813, doi:10.1038/srep30813.
- 18. Jeon, S.-J.; Ahn, J.-H.; Halder, D.; Cho, H.-S.; Lim, J.-H.; Jun, S.Y.; Lee, J.-J.; Yoon, J.-Y.; Choi, M.-H.; Jung, C.-R.; et al. TIPRL Potentiates Survival of Lung Cancer by Inducing Autophagy through the EIF2a-ATF4 Pathway. *Cell Death Dis* **2019**, *10*, 959, doi:10.1038/ s41419-019-2190-0.
- Putker, M.; Madl, T.; Vos, H.R.; Ruiter, H. de; Visscher, M.; Berg, M.C.W. van den; Kaplan, M.; Korswagen, H.C.; Boelens, R.; Vermeulen, M.; et al. Redox-Dependent Control of FOXO/DAF-16 by Transportin-1. *Mol Cell* **2013**, *49*, 730 742, doi:10.1016/j. molcel.2012.12.014.
- 0. Andjelković, M.; Jakubowicz, T.; Cron, P.; Ming, X.F.; Han, J.W.; Hemmings, B.A. Activation and Phosphorylation of a Pleckstrin Homology Domain Containing Protein Kinase (RAC-PK/PKB) Promoted by Serum and Protein Phosphatase Inhibitors. *Proc National Acad Sci* **1996**, *93*, 5699–5704, doi:10.1073/pnas.93.12.5699.
- Meier, R.; Thelen, M.; Hemmings, B.A. Inactivation and Dephosphorylation of Protein Kinase Bα (PKBα) Promoted by Hyperosmotic Stress. *Embo J* 1998, *17*, 7294–7303, doi:10.1093/emboj/17.24.7294.
- 22. Chen, D.; Fucini, R.V.; Olson, A.L.; Hemmings, B.A.; Pessin, J.E. Osmotic Shock Inhibits Insulin Signaling by Maintaining Akt/Protein Kinase B in an Inactive Dephosphorylated State. *Mol Cell Biol* **1999**, *19*, 4684–4694, doi:10.1128/mcb.19.7.4684.

- Ivaska, J.; Nissinen, L.; Immonen, N.; Eriksson, J.E.; Kähäri, V.-M Heino, J. Integrin A2β1 Promotes Activation of Protein Phosphatas 2A and Dephosphorylation of Akt and Glycogen Synthase Kinas 3β. *Mol Cell Biol* **2002**, *22*, 1352–1359, doi:10.1128/mcb.22.5.1352 1359.2002.
- 24. Resjö, S.; Göransson, O.; Härndahl, L.; Zolnierowicz, S.; Manganiello V.; Degerman, E. Protein Phosphatase 2A Is the Main Phosphatas Involved in the Regulation of Protein Kinase B in Rat Adipocytes *Cell Signal* **2002**, *14*, 231–238, doi:10.1016/s0898-6568(01)00238-8
- Morgan, B.; Laer, K.V.; Owusu, T.N.E.; Ezeriņa, D.; Pastor-Flores, D Amponsah, P.S.; Tursch, A.; Dick, T.P. Real-Time Monitoring of Bass H2O2 Levels with Peroxiredoxin-Based Probes. *Nat Chem Biol* 2016 *12*, 437 443, doi:10.1038/nchembio.2067.
- 26. Xiao, H.; Jedrychowski, M.P.; Schweppe, D.K.; Huttlin, E.L.; Yu, Q Heppner, D.E.; Li, J.; Long, J.; Mills, E.L.; Szpyt, J.; et al. A Quanti tative Tissue-Specific Landscape of Protein Redox Regulation durin Aging. *Cell* **2020**, doi:10.1016/j.cell.2020.02.012.
- 27. Weerapana, E.; Wang, C.; Simon, G.M.; Richter, F.; Khare, S.; Dillor M.B.D.; Bachovchin, D.A.; Mowen, K.; Baker, D.; Cravatt, B.F. Quant tative Reactivity Profiling Predicts Functional Cysteines in Proteomer *Nature* **2010**, *468*, 790 795, doi:10.1038/nature09472.
- 28. Wang, H.; Chen, X.; Li, C.; Liu, Y.; Yang, F.; Wang, C. Sequence-Base Prediction of Cysteine Reactivity Using Machine Learning. *Biochem. try-us* **2018**, *57*, 451 460, doi:10.1021/acs.biochem.7b00897.
- 29. Löwe, O.; Rezende, F.; Heidler, J.; Wittig, I.; Helfinger, V.; Brandes, R.P. Schröder, K. BIAM Switch Assay Coupled to Mass Spectrometry Iden tifies Novel Redox Targets of NADPH Oxidase 4. *Redox Biol* 2019, 21 101125, doi:10.1016/j.redox.2019.101125.
- 30. Dansen, T.B.; Smits, L.M.M.; Triest, M.H. van; Keizer, P.L.J. d Leenen, D. van; Koerkamp, M.G.; Szypowska, A.; Meppelink, A.; Bret kman, A.B.; Yodoi, J.; et al. Redox-Sensitive Cysteines Bridge P300 CBP-Mediated Acetylation and FoxO4 Activity. *Nat Chem Biol* 200 5, 664 672, doi:10.1038/nchembio.194.
- 31. Song, I.S.; Jun, S.Y.; Na, H.J.; Kim, H.T.; Jung, S.Y.; Ha, G.H.; Par Y.H.; Long, L.Z.; Yu, D.Y.; Kim, J.M.; et al. Inhibition of MKK7–JN by the TOR Signaling Pathway Regulator-Like Protein Contributes Resistance of HCC Cells to TRAIL-Induced Apoptosis. *Gastroentercogy* **2012**, *143*, 1341 1351, doi:10.1053/j.gastro.2012.07.103.
- Sarbassov, D.D.; Sabatini, D.M. Redox Regulation of the Nutrient-Se sitive Raptor-MTOR Pathway and Complex. *J Biol Chem* 2005, 28 39505 39509, doi:10.1074/jbc.m506096200.
- 33. Sarbassov, D.D.; Guertin, D.A.; Ali, S.M.; Sabatini, D.M. Phospho ylation and Regulation of Akt/PKB by the Rictor-MTOR Comple *Science* 2005, *307*, 1098 1101, doi:10.1126/science.1106148.
- 34. Rosales, K.R.; Reid, M.A.; Yang, Y.; Tran, T.Q.; Wang, W.-I.; Lowma X.; Pan, M.; Kong, M. TIPRL Inhibits Protein Phosphatase 4 Activi and Promotes H2AX Phosphorylation in the DNA Damage Response *Plos One* **2015**, *10*, e0145938, doi:10.1371/journal.pone.0145938.

35. Gingras, A.-C.; Caballero, M.; Zarske, M.; Sanchez, A.; Hazbun, T.R.; Fields, S.; Sonenberg, N.; Hafen, E.; Raught, B.; Aebersold, R. A Novel, Evolutionarily Conserved Protein Phosphatase Complex Involved in Cisplatin Sensitivity\* S. *Mol Cell Proteomics* 2005, *4*, 1725–1740, doi:10.1074/mcp.m500231-mcp200.





# CYSTEINE OXIDATION TRIGGERS AMYLOID FIBRIL FORMATION OF THE TUMOR SUPPRESSOR P16<sup>INK4A</sup>

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# INTRODUCTION

A number of observations spurred us to hypothesize that oxidation of p16<sup>INK4A</sup> C72 could play a role in the regulation of The CDKN2A gene-product p16<sup>INK4A</sup> is an important cell-cyp16<sup>INK4A</sup> activity at the molecular level. Firstly, several studies cle regulator and acts as a tumor suppressor. It inhibits the have implicated a role for increased ROS in the oncogene-induced accumulation of p16<sup>INK4A</sup> [10], but cysteine oxidation D-type cyclin-dependent kinases CDK4 and CDK6 and hence prevents the downstream phosphorylation of the retas the underlying mechanism has thus far not been considinoblastoma (Rb) pocket protein [1]. This prevents release ered nor excluded. Secondly, we identified p16<sup>INK4A</sup> as prone to of E2 promoter binding factor 1 (E2F1), which is otherwise cysteine oxidation in a large mass-spectrometry based screen required for the transcriptional regulation of proteins that for redox sensitive proteins [11]. Here, we provide evidence regulate entry into S-phase of the cell cycle [2]. Accumulation that p16<sup>INK4A</sup> itself is indeed sensitive to cysteine oxidation. We find that p16<sup>INK4A</sup> is readily oxidized both *in vitro* and in of p16<sup>INK4A</sup> is observed upon exposure of cells to several stresscultured human cells to form a disulfide-dependent homodors such as oxidative stress and is one of the earliest markers of oncogenic transformation [3]. The loss of p16<sup>INK4A</sup> function, imer, and the oxidizing conditions required are well within or loss of Rb downstream of CDK4/6, are some of the most the physiological range. Surprisingly, disulfide-dependent dimerization of p16<sup>INK4A</sup> subsequently leads to the rapid forfrequently observed mutations in tumors [4]. Additionally, p16<sup>INK4A</sup> plays an important role in aging, as clearance of mation of  $\beta$ -amyloid fibril structures, a state that has not been p16<sup>INK4A</sup>-expressing senescent cells has been shown to prolong previously described for p16<sup>INK4A</sup>. This transition subsequentlifespan in mice [5,6]. ly leads to loss of CDK4/6 inhibitory capacity. Redox signaling-induced reversible disulfides have not previously been The molecular basis of p16<sup>INK4A</sup>-mediated CDK4/6 inhibishown to induce  $\beta$ -amyloid fibrils in other proteins and hence tion is well established. p16<sup>INK4A</sup> is a small, globular all-a-headds to the repertoire of redox dependent protein regulation.

lical protein, that tightly binds into one side of the catalytic cleft of the CDK4/6 kinases. It efficiently distorts the cyclin D binding site, thereby blocking formation of the active CDK4/6-cyclin D complex, therefore preventing Rb phosphorylation [7,8]. Of particular relevance for this study, the single cysteine residue (C72) present in  $p16^{INK4A}$  is located on its surface and points away from the CDK4/6 kinase in the bound state; the residue is fully solvent accessible.

To test whether p16<sup>INK4A</sup> forms disulfide-dependent complexes under oxidizing conditions, immunoprecipitation followed by non-reducing SDS-PAGE was performed. Oxidation was Reversible cysteine oxidation is the lynchpin in redox signalinduced using a concentration series of either hydrogen peroxing, a form of signal transduction that is regulated by the celide or the thiol-specific oxidant diamide (tetramethylazodicarlular redox state. A more oxidizing cellular redox state, either boxamide) that ranged from subtoxic (5  $\mu$ M) to mildly toxic (250  $\mu$ M) in HEK293T cells. Flag-p16<sup>INK4A</sup> readily formed due to elevated reactive oxygen species or a lack of reducing power, leads to oxidative modification of specific cysteine-thiintermolecular disulfide-dependent complexes (Figure 1A), ols to form reversible disulfide (S-S) bridges. These oxidative as judged by the large mobility shift under non-reducing modifications can lead to structural rearrangements and can conditions, that was abolished when the samples were reboth negatively and positively regulate protein function (for duced prior to SDS-PAGE (last lanes). Note that only the Flag-p16<sup>INK4A</sup> disulfide-dependent dimer band is observed a review see [9]). and that its intensity increases upon exposure to increasing

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# RESULTS

#### p16<sup>INK4A</sup> is Oxidized to Form Disulfide Dependent Homodimers in Human Cells



#### Figure 1. p16<sup>INK4A</sup> forms intermolecular disulfides upon exposure to oxidants.

(A) Analysis of Immuno-precipitated Flag-p16<sup>INK4A</sup> by non-reducing SDS-PAGE and Western Blot shows that part of the Flag-p16<sup>INK4A</sup> migrates at about double the molecular weight upon 5 minutes treatment with low amounts of the thiol-specific oxidant diamide (left panel) or H,O, (right panel). Reduction (R) prior to SDS-PAGE abolishes the shift in molecular weight, indicating that it is indeed due to an intermolecular disulfide (see also Figure S2A, S2B for confirmation that the high molecular weight form of p16<sup>INK4A</sup> is an S-S-dependent homodimer). (B) S-S-dependent p16<sup>INK4A</sup> homodimerization upon 200 µM diamide (left) or 200 µM H<sub>2</sub>O<sub>2</sub> (right) occurs rapidly, coincides with accumulation of p16<sup>INK4A</sup> protein levels and oxidation as well as accumulation are fully dependent on C72. (C) Endogenous p16<sup>INK4A</sup> and over-expressed Flag-p16<sup>INK4A</sup> accumulate in response to 200 µM diamide with similar kinetics. Note that p16<sup>INK4A</sup>C72A does not accumulate whereas endogenous p16<sup>INK4A</sup> does, suggesting that endogenous p16<sup>INK4A</sup> levels are also regulated by cysteine-oxidation. (IP: immunoprecipitation, WB: Western Blot). All Western blots shown in Figure 1 are typical results of several repeats ( $n^3$ 3 for all experiments).

oxidant concentration. We did not observe a "smear", which would be if p16<sup>INK4A</sup> were to undergo random, nonspecific crosslinking to proteins. We then created p16<sup>INK4A</sup> mutants in which the only cysteine was replaced by alanine (C72A) or

serine (C72S). We opted to use p16<sup>INK4A</sup> C72A for our further experiments in human cells in order to circumvent the potential effects of the introduction of a novel phosphorylation site in the C72S mutant. The C72A mutant is still functional as

Concomitantly with its oxidation, p16<sup>INK4A</sup> protein abuna cell-cycle inhibitor and hence the mutation does not grossly affect protein function per se (Figure S1). To explore whether dance increased, and this was again dependent on its single the observed intermolecular disulfide-dependent complexes cysteine residue. Protein levels already increased after a few are Flag-p16<sup>INK4A</sup> homodimers, co-IP experiments were perminutes of diamide treatment, excluding a role for gene formed using combinations of wild-type (WT) p16<sup>INK4A</sup> and transcription but suggestive of a role for decreased protein C72A with short (Flag) and long (mCherry) N-terminal tags. breakdown. The accumulation is best observed using reducing SDS-PAGE because all p16<sup>INK4A</sup> then migrates in a single Under non-reducing conditions, bands could be observed corresponding to disulfide-dependent dimers of Flag-p16<sup>INK4A</sup>band (Figures 1B and 1C). The increased p16<sup>INK4A</sup> protein S-S-Flag-p16<sup>INK4A</sup> and of mCherry-p16<sup>INK4A</sup>-S-S-Flag-p16<sup>INK4A</sup> levels rapidly returned to basal upon diamide wash-out with fresh media (Figure 1C). Endogenous p16<sup>INK4A</sup> levels follow (Figure S2A) after Flag pull down. Furthermore, diagonal the same trend as Flag-p16<sup>INK4A</sup> indicating that endogenous electrophoresis showed that after reduction (2<sup>nd</sup> dimension) Flag-p16<sup>INK4A</sup> drops out of the diagonal as a single dot, wherep16<sup>INK4A</sup> is also regulated through cysteine oxidation. Taken together, both the increase in  $p16^{{\scriptscriptstyle\rm INK4A}}$  levels as well as the as a heterodimer would have revealed a second Simply Blue stained protein with similar intensity dropping out of the dioxidation are dependent on C72. agonal (Figure S2B, see also Figure 2A in Chapter 3). To test the dynamics of the intermolecular disulfide-dependent C72 of p16<sup>INK4A</sup> is Readily Oxidized In Vitro dimerization of p16<sup>INK4A</sup>, a time course of oxidant treatment To study the reactivity of the p16<sup>INK4A</sup> cysteine residue directwas performed, using p16<sup>INK4A</sup> C72A as a control. The oxidaly, we expressed and purified the isotope-labeled recombinant tion of p16<sup>INK4A</sup> was rapid, peaked after 10 minutes, was fully protein and confirmed its correct folding by solution nuclear dependent on the only cysteine and was resolved upon boiling magnetic resonance (NMR) spectroscopy. Upon treatment in reducing sample buffer (Figure 1B). of the purified protein with oxidized glutathione (GSSG), we



#### Figure 2. In vitro oxidation of p16INK4A.

(A), H<sub>12</sub>N HSQC solution NMR spectrum of recombinant p16<sup>INK4A</sup> in the reduced state (magenta) and after S-glutathionylation (yellow). Amino acids with large chemical shift changes are labeled. (B) Cartoon representation of the p16<sup>INK4A</sup> structure. A color gradient from white (unaffected) to red (strongly affected) shows the influence of S-glutathionylation on the chemical shift. (C) The redox potential of C72 is 198.3 ± 1.7 mV, as determined from intensity changes of four well-separated amino acids by titration of the reduced protein with oxidized glutathione.

observed chemical shift changes that occurred most strongly in proximity to the cysteine residue of p16<sup>INK4A</sup> (Figures 2A and 2B, Figure S3). These changes were reversed by addition of the reducing agent DTT, confirming the involvement of reversible cysteine oxidation. Mass spectrometric analysis of the intact protein showed that p16<sup>INK4A</sup> was S-glutathionylated (S-GSHylated) after treatment with GSSG (Figure S4). S-GSHylation of the protein does not change its monomeric state or overall fold, as indicated by identical peak line shapes and unchanged elution times in size exclusion chromatography. By titrating the reduced p16<sup>INK4A</sup> sample with increasing GSSG in a GSH/GSSG redox buffer we determined the redox potential of C72 using the Nernst equation <sup>17</sup> to be -198.3 +/- 1.7 meV (Figure 2C).

To study the structural role of the cysteine residue, we used the p16<sup>INK4A</sup>C72S mutant, which is the most structurally conservative mutation, differing only by replacement of the sulfhydryl group with a hydroxyl group. This mutant showed monomeric behavior during purification and largely identical chemical shifts as compared to the wild-type protein (Figure \$5), indicating that the mutation does not affect p16<sup>INK4A</sup> protein structure per se. Addition of GSSG to this mutant did not show any indications of interaction or covalent modification. Collectively, these experiments indicate that the p16<sup>INK4A</sup> C72 can be directly oxidized in vitro at physiologically occurring redox states.

#### Disulfide-Dependent Homo-Dimerization of p16<sup>INK4A</sup> **Triggers Aggregation**

The use of GSSG as an oxidant resulted in p16<sup>INK4A</sup> S-GSHylation in vitro, whereas experiments in human cells showed S-S-linked homodimerization (Figure 1) upon treatment with diamide or  $H_2O_2$ , even though both these agents lead to increased GSSG in cells. We therefore assessed whether H<sub>2</sub>O<sub>2</sub> and diamide can directly oxidize p16<sup>INK4A</sup> in vitro. SDS-PAGE analysis revealed that disulfide-linked protein homodimers are also formed in vitro, similar to the pattern observed in the experiments in human cells (Figure S6A). Comparison of size exclusion chromatography traces of reduced and oxidized

samples show that oxidation of p16<sup>INK4A</sup> causes a shift to high molecular mass, with the oxidized sample eluting in the void volume of the column (Figure S6B). In contrast to oxidation by GSSG, the addition of either  $H_2O_2$  (Figure 3A) or diamide (Figures S6C and S6D) led to strong NMR chemical shift changes that indicated protein unfolding and aggregation. This indicates the formation of a multimeric species and the absence of monomeric p16<sup>INK4A</sup>. Characterization of reduced and oxidized WT p16<sup>INK4A</sup> by Circular Dichroism (CD) spectroscopy revealed a transition to a less structured species, with some alpha-helical characteristics remaining (Figure S7A). Small-angle X-ray scattering (SAXS) on the oxidized samples indicates that the aggregates are larger than the detection limit of about 400 nm diameter (Figure S7B). S-Glutathionylation of p16<sup>INK4A</sup> C72 would abolish its reactivity towards diamide or  $H_2O_2$ . To exclude that the observed aggregation of p16<sup>INK4A</sup> stems from modifications other than C72, we also performed solution NMR spectroscopy on the S-glutathionylated p16<sup>IN-</sup> K4A (GS-p16<sup>INK4A</sup>), as well as on the p16<sup>INK4A</sup> C72A mutant, treated with diamide or  $H_2O_2$ . No chemical shift changes were observed and the monomeric, S-glutathionylated protein sample as well as the p16<sup>INK4A</sup> C72A mutant were stable in presence of oxidizing agents (Figure S8). Together, these experiments indicate the formation of an aggregated  $p16^{INK4A}$ species upon intermolecular disulfide bond formation in vitro.

#### Disulfide-Linked Homodimers of p16<sup>ink4a</sup> Form β-Amvloid Fibrils

Based on the indications of aggregation, transmission electron microscopy (EM) was employed to study the nature of the p16<sup>INK4A</sup> aggregates that formed upon oxidation. Interestingly, we found that the oxidized p16<sup>INK4A</sup> samples produced fibrillar structures (Figure 3B). One prominent group of fibrillar proteins are amyloid fibrils, which are characterized by a cross-β sheet core structure, meaning that  $\beta$ -strands run perpendicular to the fibril long axis [12,13]. To determine if p16<sup>INK4A</sup> fibrils are amyloid, we used the amyloid-specific dyes Thioflavin T (ThT) and Congo Red [14-16]. ThT assays showed an increase in fluorescence, which is characteristic for amyloids, when bound to oxidized p16<sup>INK4A</sup> (Figure 3C), while Congo



Figure 3, p16<sup>1NK+A</sup> forms amyloid fibrils under oxidizing conditions. (A) <sup>1</sup>H, <sup>15</sup>N HSQC solution NMR spectra of recombinant p16<sup>1NK+A</sup> before (magenta) and after (yellow) oxidation with 50 mM H<sub>2</sub>O<sub>2</sub> for 10 h at room temperature. The collapse of the peaks to the center of the spectrum suggests formation of unstructured or aggregated protein. (B) Negative-stained transmission electron micrographs of diamide-treated p16<sup>INK4A</sup> showing the presence of amyloid fibrils. Right panel is at higher magnification, arrows highlight the twisted morphology which is typical of amyloid fibrils. (C) Fibril formation of p16<sup>INK4A</sup> monitored by thioflavin-T fluorescence measurement. Error bars represent standard deviation from four measurements. (D) Fibril formation of p16<sup>INK4A</sup> monitored by Congo red absorption. The absorption maximum shifts when bound to oxidized p16<sup>INK4A</sup>, indicating the presence of amyloid fibrils. (E) Amide I region of the attenuated-total-reflectance Fourier-transform infrared spectra of p16<sup>INK4A</sup> monomer and fibrils. Peak maxima indicate that the structure contains primarily a-helix for monomers and cross-b sheet for fibrils.

Red absorbance measurements showed the red shift and in-Additionally, we recorded solid state NMR spectra on a uniformly <sup>13</sup>C-labeled p16<sup>INK4A</sup> sample to confirm the secondary creased absorbance characteristic of amyloid binding (Figure 3D). Fourier-transform infrared spectroscopy can distinguish structure of the aggregated state. Samples were prepared using cross  $\beta$ -sheets found in amyloid fibrils from  $\beta$ -sheets found in the same conditions that were used for other experiments inglobular monomeric proteins [17,18]; in line with the dye-bindcluding electron microscopy, to ensure that results are coming data, p16<sup>INK4A</sup> fibrils had a maximum at 1620 cm<sup>-1</sup>, which parable between experiments. In <sup>13</sup>C-<sup>13</sup>C correlation spectra, falls within the typical amyloid  $\beta$ -sheet region, confirming the only amino acid residues within a structured core are visible amyloid structure of the fibrils (Figure 3E). We performed a (Figure S9). The spectrum shows relatively few peaks comcomputational analysis using four fibril prediction algorithms pared to the 156 residues of full-length p16, suggesting that [19–22] and all suggested a high propensity for  $\beta$ -amyloid foronly specific parts of the sequence form the structural core mation in the region from residue no. 91-99 (Figure S9A). of the amyloid fibrils. This is also indicated by the absence of certain residue types from the spectrum, for example isoleu-



#### Figure 4. C72 is important for fibrillar morphology and ThT binding.

(A) Negative-stain transmission electron micrographs of p16<sup>INK4A</sup> treated with 200 µM hydrogen peroxide (left) and 200 µM diamide (right). Top: WT p16<sup>INK4A</sup>. Middle: p16<sup>INK4A</sup> C72S. Bottom: GS-p16<sup>INKA</sup>. (B) Thioflavin-T fluorescence kinetics assay of p16<sup>INK4A</sup> samples (WT, C72S and GS) with 200 µM diamide addition (top) 200 µM H<sub>2</sub>O<sub>2</sub> addition (middle) and without oxidizing agents (bottom). Three replicates were measured per sample and each are separately plotted.

cine (Figure S9B). Many of the peaks could be assigned to their amino-acid type due to their distinctive  $C\alpha$  and  $C\beta$  peak positions, which allowed for determination of the secondary structure. Nearly all assigned peaks have peak positions that are characteristic for  $\beta$ -sheet or random coil (Figure S9C), confirming that  $p16^{INK4A}$  aggregates have a  $\beta$ -sheet core and are therefore amyloid. These findings emphasize the dramatic structural rearrangement from the monomeric eight-a-helical bundle that is devoid of  $\beta$ -sheets.

#### Intermolecular p16<sup>INK4A</sup> Disulfide Bond Formation is **Essential for Amyloid Fibril Assembly**

We further investigated the role of oxidation of the cysteine residue in fibril formation by comparing the p16<sup>INK4A</sup> WT protein to p16<sup>INK4A</sup>C72S. Electron microscopy revealed that

upon treatment with as little as 200  $\mu$ M H<sub>2</sub>O<sub>2</sub> or diamide, WT samples formed large fibrillar structures (Figure 4A, top panels). There was no discernable difference between the morphology of fibrils formed with diamide or hydrogen peroxide treatment, or when higher concentrations of oxidizing agent were used. p16<sup>INK4A</sup>C72S samples displayed a very different morphology, instead forming unordered, amorphous aggregates, as well as a small amount of short fibrillar species (Figure 4A, middle panels).

Glutathionylated-p16<sup>INK4A</sup> (GS-p16<sup>INK4A</sup>) samples were also analyzed by electron microscopy, and were found to form large, granular aggregates without any fibrils upon treatment with either H<sub>2</sub>O<sub>2</sub> or diamide (Figure 4A, bottom panels). Although aggregates are seen by electron microscopy, the solution NMR spectra of GS-p16<sup>INK4A</sup> indicate the sample is in the solubilized pellet fraction and subsequent trapping of p16<sup>INK4A</sup> on the filter membrane, and both were dependent largely soluble and monomeric (Figure \$7), suggesting that the aggregates seen by electron microscopy constitute only a on C72. Reduction of the protein lysates with DTT prior to small proportion of the total GS-p16<sup>INK4A</sup> protein. washing abolished trapping, suggesting that the aggregation was reversible (Figure 5B). Clearance of p16<sup>INK4A</sup> aggregates We next investigated the influence of intermolecular disulfide was observed over time after diamide treatment. After 120 bond formation on the kinetics of fibril formation, by measuring the time- and oxidation-dependence of p16<sup>INK4A</sup> WT,

minutes the aggregates were largely resolved (Figure 5C), reminiscent of turnover of the disulfide-linked homodimer p16<sup>INK4A</sup> C72S and GS-p16<sup>INK4A</sup> variants using the ThT assay in Figure 1C. (Figure 4B). Upon treatment of WT p16<sup>INK4A</sup> with oxidizing agents, the sample fluorescence rapidly increased as ThT-posi-We also studied whether oxidation induced the aggregation of endogenous p16<sup>INK4A</sup>, for which the expression levels are gentive fibrils were formed, with maximum signal being achieved erally lower than those of transfected Flag-p16<sup>INK4A</sup>. We found within 2 hours upon 200 µM diamide treatment (Figure 4B, top) and more than 16 hours for 200  $\mu$ M H<sub>2</sub>O<sub>2</sub> treatment that endogenous p16<sup>INK4A</sup> also forms disulfide-linked dimers (Figure 4B, middle), while no fibrils were formed in the abupon oxidation and that part of these accumulate in the insolusence of oxidizing agents (Figure 4B, bottom). The C72S ble pellet fraction (Figure 5D). Similar amounts of endogenous p16<sup>INK4A</sup> are found in the solubilized pellet fraction in the presmutant displayed only a very slight increase in fluorescence over time, and this was not affected by the presence or absence ence and absence of transfected Flag-p16<sup>INK4A</sup>, suggesting that of oxidizing agents. GS-p16<sup>INK4A</sup> did not form ThT-positive endogenous p16<sup>INK4A</sup> levels are sufficient to form homodimers aggregates under any condition. The amyloids formed in and aggregates (see reducing IP panels). The phase-transition vitro were reversible: boiling in non-reducing sample buffer from monomeric to the amyloid form of p16<sup>INK4A</sup> would likely for five minutes prior to SDS-PAGE resulted mainly in detecchange its biochemical properties and protein-protein intertion of the S-S-dependent dimers (Figure \$10). The EM and actions. To test this, the interactomes of immunoprecipitated Flag-p16<sup>INK4A</sup> and Flag-p16<sup>INK4A</sup>C72A were investigated and ThT-kinetics data emphasize that the amorphous aggregates observed by EM for the  $p16^{INK4A}C72S$  and  $GS-p16^{INK4A}$  are compared by label-free quantitative mass spectrometry. Under not amyloid, both by morphology and by dye-binding properbasal conditions the interactomes were largely identical, but this ties. Therefore, we conclude that the intermolecular disulfide changed dramatically upon diamide treatment (Figure S11). bond formation of p16<sup>INK4A</sup> through C72 is critical for the Diamide-treated WT p16<sup>INK4A</sup> indeed showed a large number formation of  $p16^{INKA4}$  amyloid fibrils. of binding partners not identified in diamide-treated p16<sup>INK4A</sup> C72A pull-downs. The interaction with CDK4 and CDK6 p16<sup>INK4A</sup> Cysteine Oxidation Triggers its Aggregation was not affected by diamide treatment or the C72A mutation. in Cultured Cells Proteins that form amyloids are known to bind to chaperones Having shown that p16<sup>INK4A</sup> forms amyloid fibrils upon oxidaand indeed several Heat Shock Proteins (HSPs) were found to interact with WT p16<sup>INK4A</sup> upon diamide treatment, again intion in vitro, we investigated to what extent this behavior was conserved in cultured human cells. HEK293T cells expressing dicative of aggregate formation.

Flag-tagged p16<sup>INK4A</sup> WT and p16<sup>INK4A</sup> C72A mutant were exposed to diamide and processed for a filter trap assay: an p16<sup>INK4A</sup> Cysteine Oxidation Restores CDK4/6 Kinase Activity assay that is commonly used to detect amyloids in cell extracts We then investigated how the  $p16^{INK4A}$  function as a CDK4/6 (Scheme top of Figure 5A). Exposure to diamide prior to lysis rapidly led to accumulation of the p16<sup>INK4A</sup> homodimer inhibitor would be affected by amyloid formation. CDK4/6



#### Figure 5. p16<sup>INK4A</sup> Aggregates in Live Cells in Response to Oxidation.

(A) Set up for the filter trap assay for the detection of aggregates in cell lysates. (B) Results for the filter trap assay. Note that the majority of p16<sup>INK4A</sup> in the pellet is in the form of-S-S homodimers after lysis. p16<sup>INK4A</sup>, but not p16<sup>INK4A</sup>C72A, was trapped on the filter membrane upon treatment with 200 µM diamide and trapping was prevented by pretreatment with DTT. Equal amounts of p16<sup>INK4A</sup> and p16<sup>INK4A</sup> C72A were used as input for the filter trap assay. Note that the input for the filter trap assay runs mainly as a S-S-dependent dimer after boiling in non-reducing SDS-PAGE sample buffer. R: reducing, NR: non-reducing. (C) Aggregates of p16<sup>INK4A</sup> peak around 30 minutes and are then cleared over time. (D) Endogenous p16<sup>INK4A</sup> also forms S-S-linked dimers that (partially) form aggregates in the insoluble pellet fraction. Note that also mixed S-Slinked dimers of endogenous and overexpressed p16<sup>INK4A</sup> can be observed in lanes where Flag-p16<sup>INK4A</sup> was transfected. n.i: IP with non-immune serum as a control. p16(r): rabbit anti-p16<sup>INK4A</sup>, p16(m): mouse anti-p16<sup>INK4A</sup>, EV: empty vector, Red: reducing, Non-Red: non-reducing. All experiments were performed at least 3 times. Representative experiments are shown.

was co-immunoprecipitated with Flag-tagged p16<sup>INK4A</sup>, and fragment was regained when cells were exposed to diamide prior to lysis, despite the increased amount of p16<sup>INK4A</sup> that in vitro kinase assays were performed using a GST-tagged was pulled down. The reactivation was strictly dependent on Rb fragment as a substrate (scheme Figure 6A). These experiments revealed that oxidation of WT  $p16^{{\scriptscriptstyle\rm INK4A}}$  or p16<sup>INK4A</sup> C72. Taken together, these observations suggest that the amyloid form of  $p16^{\rm INK4A}$  still interacts with CDK4/6 but p16<sup>INK4A</sup>C72S did not greatly affect the binding to CDK4/6 (Figure 6A), which agrees with our observations in the MS in a manner that does not lead to kinase inhibition. experiments (Figure S11). The in vitro kinase assay showed that p16<sup>INK4A</sup>-associated CDK4/6 was, as expected, inactive To test how p16<sup>INK4A</sup> oxidation and aggregation impacts on under basal conditions. CDK4/6 activity towards the GST-Rb the total CDK4/6 activity we performed qPCR analysis



Figure 6. Oxidation of p16<sup>INK4A</sup> impairs its inhibitory function towards CDK4/6. (A) In vitro CDK4/6 kinase assay on WT p16<sup>INK4</sup>A pulldowns shows that the oxidation of p16<sup>INK4A</sup> C72 impairs its inhibitory function. Note that oxidation or mutation of C72 does not affect the amount of CDK4/6 that is co-immunoprecipitated. (R: Reducing, NR: Non-reducing). All Western blots shown in Figure 6 are typical results of several repeats (n=3 for all experiments). (B) qPCR analysis showing the expression of WT p16<sup>INK4A</sup> or p16<sup>INK4A</sup> C72A (top) in COLO-829 cells upon induction of expression from the respective pINDUCER20-p16INK4A construct. CCNE2 expression (bottom) is strongly repressed both by WT p16<sup>INK4A</sup> and p16<sup>INK4A</sup> C72A. Diamide treatment relieves this repression only in the WT p16<sup>INK4</sup> expressing cell line. Note that the inducible system is somewhat leaky, which could explain induction of CCNE2 in the p16<sup>INK4A</sup> WT cells by diamide in the absence of doxycycline. The mean plus SEM is displayed from n=5 biological replicates. \* p<0.05, \*\* p<0.01, pairwise comparison using a two-sided t-test comparing cells carrying the inducible WT p16<sup>INK4</sup> or p16<sup>INK4A</sup> C72A construct in each condition.



on the expression of Cyclin E2 (CCNE2), which is a transcriptional target of E2F1 and hence should be upregulated by active CDK4/6. CCNE2 (Figure 6B, lower panel) was strongly repressed upon the doxycycline-induced p16<sup>INK4A</sup> or p16<sup>INK4A</sup> C72A expression (Figure 6B, top panel) in otherwise p16<sup>INK4A</sup> deficient COLO829 melanoma cells. CCNE2 transcription was partially restored upon diamide treatment, but not in the cells expressing the p16<sup>INK4A</sup> C72A redox-insensitive variant. The induction of CCNE2 by diamide in the absence of doxycycline in the p16<sup>INK4A</sup> WT cell line is likely due to the fact that the inducible system is somewhat leaky. Although we did find evidence that CDK4/6 is indeed reactivated upon oxidation of p16<sup>INK4A</sup>, and that this partially relieves E2F1 repression, we did not find evidence of perturbation of the S-phase checkpoint in cell-cycle analysis experiments using flow cytometry and video time-lapse microscopy (data not shown). This might be explained by the notion that substantial amounts of monomeric p16<sup>INK4A</sup> persist under conditions where we find aggregated p16<sup>INK4A</sup> in the insoluble pellet fraction of our lysates. The observed reactivation of CDK4/6 might therefore not be strong enough for full re-entry of the cell cycle under the tested conditions, but we cannot exclude that this might occur in other situations. Furthermore, treatment with oxidizing agents also affects the cell cycle through several other pathways, possibly obscuring p16<sup>INK4A</sup> oxidation dependent effects.

#### **Evolutionary Analysis of the Redox Sensitive Cyste**ine in p16<sup>INK4A</sup>

Aggregation and inactivation of a tumor suppressor protein may seem a maladaptive response to oxidizing conditions, although we cannot exclude that it may support another currently unknown biological function. Conservation of evolutionarily-acquired cysteines at the surface of proteins can be indicative for a role in redox signaling, whereas the loss of acquired cysteines may indicate the cysteine hampers protein function [11,23]. We therefore investigated to what extent p16<sup>INK4A</sup> C72 is conserved throughout evolution. The genes encoding p16<sup>INK4A</sup> (CDKN2A) and p15<sup>INK4B</sup> (CDKN2B) are the product of a gene duplication that occurred somewhere in

evolution around the time that the mammalian branch of the evolutionary tree was formed [24] (see Figure S12A for reference). Strikingly, C72 in the human protein is not conserved in any of the protein sequences of the CDKN2 orthologues in fish, birds, reptiles and amphibians. Yet, this cysteine is present in both p16<sup>INK4A</sup> and p15<sup>INK4B</sup> in almost all mammalian species for which sequence information is available in the ENSEMBL database [25], suggesting that acquisition of this cysteine occurred just before or coincided with the gene duplication of the ancestral CDKN2 gene (Figure 7A, B). Further investigation of the protein sequences of the p16<sup>INK4A</sup> and p15<sup>INK4B</sup> orthologues revealed that the cysteine homologous to the human p16<sup>INK4A</sup>-C72 was substituted later in evolution in several branches of mammalian species including some primates, rodentia and perissodactyla (see Figures 7A, 7B and **S12B**). The latter could indicate that redox regulation of the acquired cysteine homologous to human p16<sup>INK4A</sup> C72 is not absolutely required for a  $p16^{INK4A}$  function and that C72 might be slightly deleterious and displays a weak purifying selection.

#### DISCUSSION

Amyloid fibrils are structures that can be formed by a wide variety of protein sequences [26]. These fibrils share common features, including an unbranched fibrillar morphology and a cross- $\beta$  sheet core structure. Amyloids were previously thought to be largely disease-related, especially involved in neurodegenerative diseases, but there are increasing numbers of amyloid fibrils discovered that have a physiological function. Several mammalian examples have been reported in recent years, including the melanosome protein pMeL, amyloids involved in hormone storage, and the RIPK proteins, whose fibril formation appears to trigger necroptotic signaling pathways [27–30]. In this work we show that  $p16^{INK4A}$  can form fibrils under physiological conditions and in cell-based models, and that the formation is triggered by oxidation of the single cysteine residue and homodimerization. We presented evidence that p16<sup>INK4A</sup> can form aggregates that have



# p15<sup>INK</sup> 2

brate evolution. Note that ENSEMBL [25] assigns some non-mammalian orthologues to ammalian species had branched off [24]. Sequences are named by ENSEMBL ID [25]. The to human p16<sup>INK4A</sup> C72 are indicated on yellow background, other cysteines are in yellow anches of mammals have lost the cysteine homologous to human p16<sup>INK4A</sup> C72. See Figure 1 nomologous to h eral distant branch served at the point of a served at the point of the point gue p15<sup>1</sup> (**B**) C74 in its paralogue 1 to yield these paralogue luplication to yiel and in bold. Cyst and (**B**) of an p (A) Conservation of C72 ii either p16<sup>INK4A</sup> or p15<sup>INK4B</sup> v human orthologues are ind text. The darker the magen S12 for a schematic tree of v
the typical features of amyloid fibrils, including binding of diagnostic dyes, presence of cross-ß sheet structure, and typical dimensions found in EM. The critical dependence of a disulfide cross-linked dimer as a subunit has not been observed so far and highlights the role of the cellular redox state as an important regulator of fibril formation.

The role of cysteine chemistry in amyloid formation has been discussed in detail previously [31]. Most commonly, disulfide bonds are found to stabilize a soluble, usually monomeric, form of the protein, preventing its un- or misfolding and aggregation. In many cases, blocking of disulfide bond formation by mutagenesis or chemistry generates proteins that are more prone to amyloid formation, such as has been demonstrated for lysozyme [32], SOD1 [33,34], insulin [35] and prion protein [36,37]. In contrast, oxidation of the single cysteine of p16<sup>INK4A</sup> is important for the transition of the monomeric protein to form amyloid fibrils, and modification of the cysteine by mutagenesis or S-glutathionylation prevents its amyloid formation. Proteins in which disulfide bonds have been postulated to be involved in stabilization of amyloid fibrils include the prion protein and RIPK fibrils, however disulfide bond formation itself is not required for conversion to amyloid in either of these cases [36-38].

Several properties of p16<sup>INK4A</sup> fibrils fit with those expected for functional amyloids, including their rapid formation (instead, disease-related amyloids can take days to form fibrils) [39,40], and their lack of clear polymorphism (no evidence of peak doubling in the solid-state NMR spectrum) [41,42]. We have shown that p16<sup>INK4A</sup> fibrils can be formed *in vitro* under relatively mild oxidizing conditions at physiological pH. In contrast to many other amyloid-forming proteins, p16<sup>INK4A</sup> does not require harsh treatments, such as extreme pH, high temperatures, high pressure or organic solvents, that are frequently used to destabilize folded proteins in order to convert them to amyloid fibrils in a practical time scale. One striking difference in the properties of p16<sup>INK4A</sup> amyloid fibrils, compared to classical disease-linked amyloids like amyloid-  $\beta$ and  $\alpha$ -synuclein, is the apparent reversibility of the fibrillar state. Typical amyloids are highly stable and are not disaggregated by SDS buffers and do not run into SDS-PAGE gels [26,43,44]. Our results show that SDS is able to disaggregate p16<sup>INK4A</sup> fibrils into dimers, and that reducing-agent treatment further returns p16<sup>INK4A</sup> to a monomeric state. This was shown for both recombinantly-produced p16<sup>INK4A</sup> amyloid in *vitro*, as well as p16<sup>INK4A</sup> amyloid formed in a cellular model. Furthermore, we find that p16<sup>INK4A</sup> amyloids are transiently formed and do not persist in the cellular environment as judged by the filter trap assay. Clearance of the amyloids in cells could in principle proceed through degradation or disaggregation into monomers. There does not seem to be a clear increase of the monomeric form upon disappearance of the aggregates, which could suggest that the aggregates are being degraded rather than disaggregated. A recent study showed that p16<sup>INK4A</sup> also forms aggregates upon inhibition of autophagy [45], which is in line with this notion. The observation that p16<sup>INK4A</sup> amyloids are reversible and can be cleared from cells potentially adds to an emerging pattern of lability of amyloid fibrils that have functional roles in the cell. For example, RIPK1/3, and the phase-separating proteins FUS and hnRNPA2 are all reported to form functional amyloid fibrils, and are apparently SDS soluble [35,38]. This may be a hallmark for functional fibrils, which must be regulated and removed when the function is no longer needed. In contrast, highly stable, persistent aggregates may have toxic properties, such as in the case of Tau or TDP-43 aggregates, which are pathogenically related to various neurodegenerative diseases [46,47].

It is now generally accepted that the cellular redox environment contributes to various signaling pathways and that H<sub>2</sub>O<sub>2</sub> can act as a secondary messenger molecule [9]. Cysteine residues are frequently found to be modified in large-scale analysis of the cysteinome and thousands of proteins are affected by redox regulation [48,49]. Redox potentials vary widely between cell types and specific compartments, ranging from -374 mV for the strongly reducing NADPH/NADP+ redox couple in the liver cytosol to -180 mV from the GSH/GSSG couple in the oxidizing endoplasmic reticulum of B-cells [50].

In addition, the average redox potential varies greatly between Taken together, the presented work shows that redox signaling cell cycle stages [51]. The redox potential of -198 mV that we can trigger the formation of amyloid fibrils from an otherwise found for the oxidation of C72 of p16<sup>INK4A</sup> is well within the alpha-helical protein. Conversion of a protein from a soluphysiological range. One difference between *in vitro* and cell ble, monomeric and an insoluble, beta-amyloid fibrillar phase culture oxidation of p16<sup>INK4A</sup> is that *in vitro* p16<sup>INK4A</sup> could be dependent on the cellular redox state has not been reported stably GSH-ylated whereas in cell cultures we only observed before. This could pose a more general mechanism in amyloid the disulfide-bonded homodimer. This might seem surprisformation, as was recently shown for redox-dependent liqing, because there is ample GSH available in the cell and addiuid-liquid phase-separation [55]. It also adds to the repertoire tion of micromolar ranges of diamide will likely react to form of structural alterations known to occur in response to redox GSSG. Therefore, it may be unlikely that in cells diamide and signaling. H<sub>2</sub>O<sub>2</sub> oxidize p16<sup>INK4A</sup> directly, but rather that its oxidation is the result of a redox relay or disulfide exchange mechanism, MATERIALS AND METHODS as has been proposed for other redox-sensitive proteins [52]. However, we cannot exclude that transient GSH-ylation of p16<sup>INK4A</sup> occurs in cells. Of note, tumor cells have been Cell Lines, Plasmids, Antibodies and Compounds frequently reported to exhibit a more oxidizing milieu [53]. Cells (HEK293T, COLO829) were cultured in DMEM This could mean that p16<sup>INK4A</sup> would be more often in the low glucose supplemented with FCS (10%), L-glutamine dimerized and aggregated state, which could contribute to (2mM) and Penicillin-Streptomycin (100 Units-0.1mg per reactivation of CDK4/6 in tumors that express p16<sup>INK4A</sup>. One ml medium) (all from Lonza). Cells were transfected using might argue that p16<sup>INK4A</sup> inactivation by oxidizing condi-PEI (Sigma Aldrich) or X-tremeGENE 9 (Roche) according tions would be an inadequate response, that would be lost to manufacturer's instruction. through evolutionary pressure. Evolutionary analysis indeed shows that the cysteine homologous to human p16<sup>INK4A</sup>C72 The vector containing the truncated form ( $\Delta 1$ –8) of wild was acquired recently: near or coinciding with the appeartype p16<sup>INK4A</sup> was a gift from R. Medema [56]. The cysteine mutant of p16<sup>INK4A</sup> was created by site-directed pcr mutagenance of mammals and was then substituted again multiple esis. mCherry- (backbone pLV-CMV-bc) and Flag-His-tagged times in several branches of mammalian evolution. However, this analysis would have to be further extended to be able to (backbone pCDNA3) and doxycycline-inducible (backbone reject a potential beneficial biological role for p16<sup>INK4A</sup> amypINDUCER20, Addgene #44012) p16<sup>INK4A</sup> constructs loid formation, for instance to temporarily reactivate CDK4/6 were created using gateway technology (Life Technologies). in cells with high p16<sup>INK4A</sup> levels. Whether and how this COLO-829 melanoma cells stably expressing doxycyline-inindeed could also contribute to tumor progression remains ducible constructs were transduced with lentivirus containing pINDUCER20-p16<sup>INK4A</sup> or -p16<sup>INK4A</sup>C72A. Cells were selectto be established. Our pull-down experiments indicate that oxidation of p16<sup>INK4A</sup> leads to loss of its inhibitory activity ed for stable transduction using geneticin and p16<sup>INK4A</sup> extowards CDK4/6 but that oxidized p16<sup>INK4A</sup> and CDK4/6 pression was confirmed by qPCR and western blotting. Substill bind. We speculate that the CDK4/6 interaction that we sequently, cells were transduced with lentivirus containing observe is of a different nature, which could underlie loss of the FUCCI cell cycle probes mAG-hGeminin(1/110) / pCinhibition of CDK4/6 upon oxidation of p16<sup>INK4A</sup>. Amyloid SII-EF (#RDB15268) and Fucci-G1 phase probe mKO2-hCdt1(30/120) / pCSII-EF (#RDB15267) (RIKEN BioResource formation-dependent inactivation of tumor suppressor proteins has been described before for p53 and also in this case Center), which were a kind gift from A. Miyawaki [57]. Cells amyloid formation was reversible [54].

were selected for stable transduction using zeocin and made monoclonal by limiting dilution.

The following antibodies were used in this study: Flag (M2 F3165 Sigma Aldrich), p16<sup>INK4A</sup> (10883 Proteintech), p16<sup>INK4A</sup> (ab16123 Abcam), CDK4 (C-22 Santa Cruz), CDK6 (C-21 Santa Cruz), tubulin (CP06 Merck Millipore), Phospho-Rb Ser807/811 (9308 Cell Signaling). Solutions/compounds not mentioned elsewhere: 35% hydrogen peroxide (Merck).

# **Co-immunoprecipitation, SDS-PAGE and Western** Blotting

Immuno-precipitation of endogenous p16 was done with rabbit anti-p16<sup>INK4A</sup> (10883 Proteintech) using three 10 cm dishes of HEK293T cells per sample. Transfection was performed two days prior to sample preparation. Cells were scraped in 100 mM N-ethyl-maleimide in PBS (37 °C) to prevent post-lysis oxidation and collected by centrifugation at 1200 rpm for 3 minutes. Cells were lysed in a standard lysis buffer containing 50 mM Tris pH 7.5, 1% triton X-100, 1.5 mM MgCl<sub>2</sub>, 5 mM EDTA, 100 mM NaCl supplemented with Aprotinin, Leupeptin and NaF. 100 mM iodoacetamide was added to to prevent post-lysis oxidation of cysteines. The cell lysates were subsequently centrifuged at 14000 rpm for 10 min. 50 µl of the supernatant was kept as input. For immunoprecipitation of endogenous p16<sup>INK4A</sup> the pellet was resuspended in lysis buffer, sonicated and supplemented with 125U of benzonase and incubated for 1hr at 37 degrees. The remaining supernatant (and where indicated also the resolubilized pellet) was used for immunoprecipitation with the indicated antibody coupled to protein A-Agarose (Roche) or in case of transfected Flag-tagged constructs with anti-Flag M2 Affinity gel (Sigma Aldrich). After 2 h of incubation, beads were washed 3 times with standard lysis buffer supplemented with extra NaCl (1 M final concentration). After washing, samples were split into two parts, and sample buffer with or without a reducing agent (b-mercaptoethanol) was added. Samples were boiled for 5 min and separated on a 15% polyacrylamide gel. For Western Blotting, proteins were transferred to immobilon-FL membranes. For diagonal electrophoresis, non-reducing samples were separated on a 15% polyacrylamide gel, after which the entire protein containing lane was excised, reduced, and separated on a new 15% polyacrylamide gel. For visualization of diagonal electrophoresis proteins were stained by SimplyBlue.

### Filter Trap Assay

HEK293T cells were transfected with Flag-p16<sup>INK4A</sup>, Flagp16<sup>INK4A</sup> C72A or GFP as a control. After two days, cells were scraped in 100 mM N-ethyl-maleimide in PBS (37°C) to prevent post-lysis oxidation and collected by centrifugation at 1200 rpm for 3 minutes. Lysis buffer (50 mM Tris pH 7.5, 1% v/v Triton X-100, 1.5 mM MgCl<sub>2</sub>, 5 mM EDTA, 100 mM NaCl, Protease inhibitors (Aprotinin + Leupeptin), NaF, 100 mM Iodoacetamide) added for 10 minutes followed by centrifugation for 15 minutes at 14000 rpm in an Eppendorf microfuge. The pellet was resuspended in benzonase buffer (50 mM Tris-HCL pH 8.0, 1 mM MgCl<sub>2</sub>) and 125U of benzonase was added followed by incubation for 1hr at 37 degrees. The reaction was stopped by adding 2x termination buffer (40 mM EDTA, 0.2 % SDS, with or without 10 mM DTT). Protein content was measured using the BCA kit and 50 micrograms of protein per sample were loaded on a Bio Dot apparatus (Biorad) equipped with a 0.2 micron pore size nitrocellulose membrane soaked in buffer B (10 mM Tris-HCL pH 8.0, 150 mM NaCl, 2 % SDS) on top of two Whatmann paper filters soaked in Buffer A (10 mM Tris-HCL pH 8.0, 150 mM NaCl, 1 % SDS), after pre-washing the membrane with 100 µl of buffer A. Samples were pulled through the membrane using vacuum, followed by washing thrice with 100 µl of buffer A. The nitrocellulose membrane was further processed as for Western Blotting to detect trapped p16<sup>INK4A</sup>.

### Kinase Assay

The kinase assays in this study were performed with immunoprecipitated Flag-p16<sup>INK4A</sup> or Flag-p16<sup>INK4A</sup>C72A and the attached binding-partners. Beads were washed three times with standard lysis buffer followed by two washes with kinase buffer containing 25 mM Tris pH 7.5 and 10 mM MgCl<sub>2</sub>. The beads were subsequently incubated for 30 min at 30 °C

minimal medium containing <sup>15</sup>NH<sub>4</sub>Cl as the only nitrogen source. The protein synthesis was induced by addition of 0.5 mM isopropyl-1-thio-D-galactopyranoside (IPTG) at an  $OD_{600}$  of 0.8 and cells were harvested after 14 h of induction at 19 °C. Cells were resuspended in purification buffer (110 mM potassium acetate, 20 mM HEPES [4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid], pH 8.0, 2 mM MgCl<sub>2</sub>, 2 mM β-mercaptoethanol (BME), 5% (v/v) glycerol and 20 mM imidazole) and ultrasonicated for lysis. The solution was applied to a gravity Ni-NTA agarose (QIAGEN) column following the manufacturer's instructions. After washing with purification buffer including 20 mM imidazole, the protein was eluted by using purification buffer including 200 mM imidazole and further purified by gel chromatography on an ÄKTA pure system equipped with a HiLoad 16/600 Superdex 75 pg column (GE Healthcare) running with purification buffer. The fractions containing the protein were pooled, incubated with 0.2 mg TEV protease overnight at 4 °C while dialyzed against purification buffer using a dialysis membrane with 5 kDa molecular weight cut-off (ZelluTrans, Roth). On the following day, the protein solution was applied to the Ni-NTA agarose column again to remove the cleaved tag, remaining undigested protein and the His, -tagged TEV protease. The eluate was then buffer exchanged into purification buffer where BME was substituted with 1 mM DTT using dialysis. The protein solution was aliquoted, frozen in liquid nitrogen and stored at -80 °C. Solution NMR spectroscopy showed that no differences were observed after the freezing and thawing of the samples.

in 20 µl kinase buffer supplemented with 1 mM DTT, 1 µg human GST-Rb (48-378 Sigma Aldrich) as substrate and 0.2 mM ATP. Directly after the assay beads were boiled for 5 min in reducing sample buffer and loaded on a 15% polyacrylamide gel followed by Western Blotting. RNA Extraction, cDNA Synthesis and qPCR Doxycylcine-inducible p16<sup>INK4A</sup> expressing Colo-829 cells were plated, and 24h before harvesting doxycline was added to induce expression of p16<sup>INK4A</sup> or p16<sup>INK4A</sup>C72A. Cells were treated as indicated. Cells were washed once with PBS and collected in RLT buffer. RNA was extracted using the RNeasy kit (Qiagen) according to the manufacturer's instructions. 1 ug RNA was used as input for cDNA synthesis using the iScript cDNA synthesis kit (Biorad). qPCR was performed with FastStart SYBR Green Master mix (Roche) using the CFX96 Touch Real-Time PCR Detection System. Relative gene expression was calculated using the  $\Delta\Delta$ Ct method [58] by normalization to HNRNPA1. Statistics were done with Graphpad Prism 8. Primer sequences: *p16<sup>INK4A</sup>* forward (5'-CAACGCACCGAATAGTTACG-3'), p16<sup>INK4A</sup> reverse (5'-ACCAGCGTGTCCAGGAAG-3'), CCNE2 forward (5'-GGGGGGATCAGTCCTTGCATT-3'), CCNE2 reverse (5'-TCCCCAGCTTAAATCAGGCA-3'), HNRNPA1 forward (5'-GGAAGCTACAGGTTACAACA-3'), HNRNPA1 reverse (5'-AGTCACAAATACAGTCCTCG-3'). **Protein Expression and Purification** An Escherichia coli codon-optimized gene of Homo sapiens

p16<sup>INK4</sup> (UniProt ID: P42771) was cloned into a modified version of pETM-11 that includes a 6xHis, a protein A tag Solution NMR Spectroscopy and a tobacco etch virus (TEV) protease cleavage site, leaving The protein stock was freshly buffer exchanged into NMR an additional glycine residue at the N-terminal cleavage site. buffer (4 mM HEPES, 5 mM EDTA, pH 7.5) before measure-For a glycerol stock solution, competent *E. coli* BL21 (DE3) ment. Samples for protein characterization contained 1 mM cells were transformed with the p16<sup>INK4</sup> harboring gene and DTT (dithiothreitol) whereas samples for redox-experiments inoculated in minimal medium in the presence of kanamydid not. The protein concentration was 0.15 mM and concin (50  $\mu$ g/l). After overnight incubation at 37 °C the cell tained 7% (vol/vol)  $^{2}$ H<sub>2</sub>O for the lock signal. Solution  $^{1}$ H<sup>15</sup>N suspension was mixed with glycerol to 50% (v/v) glycerol HSQC NMR spectra were measured on an Avance III 600 and stored at -80 °C. Uniformly <sup>15</sup>N-labeled protein sam-Bruker NMR spectrometer equipped with a cryogenic triple ples were prepared from this stock by growing the cells in resonance probe with gradients in the z-direction. The recycle

delay of the redox experiments performed (S-glutathionylation and hydrogen peroxide addition) was set to 1 s with a spectral window of 11/34 ppm in <sup>1</sup>H/<sup>15</sup>N dimensions, 2048 points in the direct <sup>1</sup>H dimension, 128 complex data points in the indirect <sup>15</sup>N dimension, and with 8 or 16 scans per increment. Spectra were processed with the NMRPipe package [59] and analyzed by CcpNmr Analysis [60].

For determination of the S-glutathionylation redox potential, the concentration of GSSG in the sample buffer was gradually increased (0.2; 1.0; 2.3; 3.3; 3.9; 5.9; 7.8; 8.8; 9.8; 11.7 mM) by titrating from a 65 mM pH corrected stock solution while the concentration of the reduced form of GSH was kept constant at 4 mM. At each concentration point, a <sup>1</sup>H<sup>15</sup>N HSQC NMR spectrum was recorded immediately after addition of the oxidation agent. For assignment of the S-GSHylated protein, HNCA and CBCACONH spectra were acquired. Determination of the redox potential was performed following the protocol of Piotukh et al. [61]. In summary, peak intensities of well isolated peaks (N71, C72, D74, T79) of the oxidized form were normalized to a non-affected asparagine side chain resonance and plotted against the redox potential of the buffer. This potential was determined from the standard half-cell potential of the glutathione redox couple (-240 mV at pH 7.0, 25 °C) after pH corrections [50]. The data were fitted to the sigmoidal decay function (equation 1):

$$y = A_2 + \frac{(A_1 - A_2)}{1 + e^{\frac{x - x_0}{dx}}}$$
, (eq. 1)

where A, and A, are the initial and final plateaus of the function, dx is the slope and x<sub>0</sub> refers to the desired parameter of the redox potential.

For oxidized samples of p16<sup>INK4</sup>, a final concentration of 50 mM hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>, from a 30% solution diluted with NMR buffer) or 100 µM diamide (from a freshly prepared 10 mM stock solution in H<sub>2</sub>O) was added to the <sup>15</sup>N-labeled protein solution. <sup>1</sup>H<sup>15</sup>N HSQC NMR spectra were acquired after the addition of the oxidizing agent in subsequent manner. After 10 h, no spectral changes were observed for WT protein anymore and the sample was applied to a size exclusion column (HiLoad 10/300 Superdex 75 pg column, GE Healthcare) and the dimeric fraction of about 50% of the total protein was pooled. The protein was applied to SDS gel electrophoresis in the presence and absence of BME.

# **CD** Spectroscopy

Far-UV CD experiments were recorded on a J-715 spectrapolarimeter (Jasco, Tokyo, Japan). Spectra were acquired at room temperature with a response time of 1 s and a step resolution of 0.3 nm. Five scans were averaged and the signal was background corrected by subtraction of the buffer signal. The CD spectra were obtained from a 1  $\mu M$  p16  $^{\rm INK4A}$  sample before and after oxidation with 200 µM hydrogen peroxide for 8 hours at room temperature and data were converted to molar ellipticity. Samples were freshly prepared and transferred into a 10 mM sodium phosphate buffer at pH 7.4 in the absence of reducing agents.

### Small-Angle X-ray Scattering Measurements

SAXS data was recorded on an in-house SAXS instrument (SAXSess mc2, Anton Paar, Graz, Austria) equipped with a Kratky camera, a sealed X-ray tube and a two-dimensional Princeton Instruments PI•SCX:4300 (Roper Scientific) CCD camera. Measurements were performed with 90 min exposure time (540 frames of 10 s each) of three concentrations of 2.5 mg/ml, 1.25 mg/ml and 0.625 mg/ml in NMR buffer. The sample of reduced  $p16^{\rm INK4A}$  was measured immediately after purification and buffer exchange. The oxidized sample of p16<sup>INK4A</sup> was treated overnight with  $50 \text{ mM H}_2\text{O}_2$  at room temperature. Next day, the sample was applied to size exclusion chromatography and the peak from 9-10 ml elution volume was pooled (see Figure S6B) and concentrated. Individual frames of the 90 min exposure were compared and no radiation damage was observed. A range of momentum transfer of  $0.012 < s < 0.63 \text{ Å}^{-1}$ was covered (s =  $4\pi \sin(\theta)/\lambda$ , where  $2\theta$  is the scattering angle and  $\lambda = 1.5$  Å is the X-ray wavelength). SAXS data were analyzed with the package ATSAS version 2.8.1 [62]. Desmearing of the oxidized sample could not be performed because the scattering curve showed strong aggregation.

### **Thioflavin-T Fluorescence Assay**

Samples of  $p16^{INK4A}$  (20  $\mu$ M) were prepared in buffer (4 mM HEPES, pH 7.5) with 20 µM ThT. Three replicates were measured for each sample. Samples were subjected to 1 mm orbital shaking for 2 min of every 5 min, in a 96-well, half-area, using a Tecan GENios microplate reader.

Approximately 10 mg (150 µM) of <sup>13</sup>C-<sup>15</sup>N labeled p16<sup>INK4A</sup> fluorescence plate (Corning) and measurements were taken fibrils were prepared in p16<sup>INK4A</sup> buffer by addition of 50 every 5 min. Samples were excited at 440 nm and fluorescence emission was measured at 480 nm. Measurements were made mM H<sub>2</sub>O<sub>2</sub> and incubation at 37 °C overnight. The sample was packed into a 3.2 mm MAS rotor by ultracentrifugation. Spectra were recorded on a Bruker Avance III 750 MHz spec-Negative-stain Transmission Electron Microscopy trometer (Bruker BioSpin) equipped with a 3.2 mm triple-res-Protein samples were prepared by incubation of  $p16^{{\rm INK4A}}$ onance MAS probe. A proton-driven spin diffusion (PDSD) samples with or without oxidizing agents for 6-24 h at RT. spectrum [64] was recorded at 16.5 kHz MAS, with 50 ms Copper grids with 300 meshes coated with formvar/carbon mixing time, at a set temperature of 273 K, with 352 scans film (Electron Microscopy Sciences, Hatfield, USA) were and 22 ms and 8 ms acquisition time in the direct and indirect glow-discharged in argon atmosphere for 30 s at 3 mA. Grids dimensions, respectively. Experiments were acquired using were floated on a 5 µl drop of a 50 µM protein sample and Topspin 3.2 (Bruker Biospin) and analysed using CCPN incubated for 60 s. Grids were washed once with water, and Analysis 2 [60]. The secondary chemical shift was calculated as  $[\delta(C\alpha_{observed}) - \delta(C\alpha_{random coil})] - [\delta(C\beta_{observed}) - \delta(C\beta_{random coil})]$ then floated on 5  $\mu$ l of uranyl acetate solution (2% w/v) for 30 s. Micrographs were taken on either a JEOL JEM 100CX with random coil chemical shifts taken from [65]. transmission electron microscope or a JEOL JEM 1400 Plus transmission electron microscope (JEOL, Tokyo, Japan). Sample Preparation for Mass Spectrometry

HEK293T cells were transfected with Flag-p16<sup>INK4A</sup> or Flag-p16<sup>INK4A</sup> C72A. After two days, half of the dishes (3 full **Prediction of Aggregation-Prone Regions** Four different aggregation prediction programs, TANGO 15cm dishes per sample) were treated for 10 minutes with di-[19], PASTA [20], Zyggregator [63] and Aggrescan [21] were amide (250 µM) (Sigma Aldrich) and subsequently harvested used to identify putative regions responsible for the beta-agfor immunoprecipitation with Flag beads as described before. gregation of p16<sup>INK4A</sup> using the default settings. After washing 2x with 1 M salt buffer and 3x with PBS to remove all soap, proteins were eluted from the beads by two times 5 minutes incubation with 75  $\mu l$  0.1 M glycine pH 2. **Congo-Red Absorbance** Absorbance spectra were measured on samples of  $p16^{\rm INK4A}$ The protein containing supernatant was transferred to a  $(20 \,\mu\text{M})$  with Congo red  $(20 \,\mu\text{M})$  in p16<sup>INK4A</sup> buffer. Spectra new tube and incubated for 20 minutes with 10 mM DTT were recorded from 400-650 nm, with a resolution of 2 nm, and 2 M Urea (dissolved in 100 mM Tris pH 7.5), followed on a Tecan Infinite 200Pro microplate reader in a 96-well, by 10 minutes incubation with iodoacetamide (50 mM). To half-area, fluorescence plate (Corning). digest the proteins, 0.25 µg trypsin (Promega) was added per sample and samples were incubated ON at 25 °C. The next day C18-stagetips were used for filtering and loading of the Fourier-Transform Infrared Spectroscopy p16<sup>INK4A</sup> (80  $\mu$ M) samples were treated with 50 mM H<sub>2</sub>O<sub>2</sub> protein digest.

overnight in p16<sup>INK4A</sup> buffer, then dialysed against water overnight. Spectra were recorded on a JASCO FT/IR-4100

FT-IR spectrometer with attenuated total reflectance (ATR) attachment. The samples were measured with 128 scans at a resolution of 2 cm<sup>-1</sup> at room temperature.

### Solid-State NMR Spectroscopy

### **Mass Spectrometry and Data Analysis**

The mass spectrometry was performed as previously described [11].

For the analysis MaxQuant software version 1.5.1.0 [66] was used. During the analysis, oxidation of methionine, alkylation of cysteines with iodoacetamide were set as variable modification. Proteins were identified by the IPI human V3.68 database and the relative amounts of protein in the separate experiments, the Intensity Based Absolute Quantification (IBAQ) [67], as well as the label free quantification [68] were calculated.

Further analysis was done using R version 3.4.0. The used code and description is currently being uploaded to GitHub. Proteins identified with two or more unique peptides were filtered for reverse hits, decoy hits and standard contaminants and samples that show aberrant clustering or low protein count were excluded. Subsequently the IBAQ data was Log2 transformed and normalized for IP efficiency. For p-value calculations, left-censored missing data was first imputed using a stochastic minimal value approach. Imputation was performed by random draws from a Gaussian distribution centered in the 10<sup>-4</sup> quantile of the known data with a standard deviation that is same as the observed values [69]. A standard t-test was performed on the imputed data and p-values were adjusted for multiple testing using the Benjamini-Hochberg correction.

# Mass Spectrometry of GS-p16<sup>INK4A</sup>

The intact mass of p16<sup>INK4A</sup> before and after oxidation by GSSG was obtained from LC-MS analysis, that was performed on recombinantly expressed protein (see protein expression and purification section). The sample was desalted using 10 kDa Amicon Ultra-0.5 centrifugal filter devices prior to measurement. 150 pmol of protein were injected into an Agilent 1200 system (Vienna, Austria) coupled to an LTQ-FT mass spectrometer (Thermo Fisher Scientific, Waltham, MA, USA). Separation was carried out on a monolithic PepSwift® column (500 µm x 5 cm Monolithic PS - DVB) at a flow rate of 20 µl/min using the following gradient, where solvent A is 0.05 % trifluoroacetic acid in water and solvent B is 0.05

% trifluoroacetic acid in acetonitrile: 0-5 min: 10 % B; 5-55 min: 10-100 % B; 55-65 min: 100 % B, 65-80 min: 10 % B. The sample was ionized in the electrospray source and analyzed using FT-MS operated in positive ion mode applying full scan MS (m/z 300 to 2000) with a resolution of 400,000. Acquired data were processed with the software Protein Deconvolution 2.0 SP2 (Thermo Fisher Scientific) using a S/N threshold of 5 and a relative abundance threshold of 20 %.

# Flow Cytometry

Cell cycle analysis was performed using a combination of the FUCCI [57] system and DNA content staining. COLO-829 cells expressing the FUCCI constructs as well as pINDUC- $ER20\mbox{-}p16\mbox{}^{\rm INK4A}$  or  $p16\mbox{}^{\rm INK4A}$  C72A were seeded and treated with doxycycline and LEE-011 for the indicated times and samples. Nocodazole was added 16h before harvest to capture cycling cells in mitosis to distinguish transient G1 from G1/G0 arrested cells. Cell culture medium was collected and cells were washed in PBS before trypsinization. Cells were fixed for 10 minutes at room temperature with 2% formalin in PBS. After 2 washes with PBS, cells were permeabilized with 70% ethanol for 30 minutes. Cells were resuspended in PBS with 0.1% BSA with DAPI and RNAse to stain the DNA. mKO2-hCtd1(30/120), mAG-hGeminin(1/110) and DAPI were measured using a BD FACSCelesta Flow Cytometer (BD Bioscience).

### **Evolutionary Analysis**

Amino acid sequences of vertebrate orthologues of human  $p16^{\rm INK4A}$  and  $p15^{\rm INK4B}$  were downloaded from the ENSEMBL database [25]. Alignment and visualization of conservation was performed using JalView 2.10.1 software [70], with the Clustal plugin with default settings.

# Data Availability

The datasets generated and/or analyzed in the current study are available from the corresponding authors upon reasonable request. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [71] partner repository with the dataset identifier PXD012353 and can be accessed using username: reviewer89417@ebi.ac.uk and password: fQ0pzPhh.

# SUPPLEMENTARY FIGURES AND LEGENDS



Figure S1. p16<sup>INK4A</sup> C72 is dispensable for its role in cell cycle arrest. (A) Cell-cycle profiling of COLO-829 cells expressing doxycycline inducible pINDUCER20-p16<sup>INK4A</sup> wildtype or p16<sup>INK4A</sup>C72A as well as the FUCCI cell cycle indicator system. Cells were trapped overnight in mitosis using Nocodazole to make G1/G0-arrested cells more obvious from those that were still cycling. The CDK4/6 inhibitor LEE011 was added to estimate to what extent CDK4/6 inhibition can induce cell cycle arrest in this cell line. The C72A mutation leaves the cell-cycle inhibitor function of p16<sup>INK4A</sup> intact. (B) The graph shows the pooled results for the percentage of cells in G1/G0 phase of the cell cycle quantified from two experiments with at two or three replicates each. We conclude that p16<sup>INK4A</sup>C72A is still able to induce a cell cycle arrest. (C) The FACS plots and histograms show typical results for each of the conditions.



# Figure S2. SDS-PAGE analysis of p16<sup>INK4A</sup>.

(A) mCherry-p16<sup>INK4A</sup> co-immunoprecipitates with Flag-p16<sup>INK4A</sup> in a disulfide-dependent manner. Dimers consisting of both two Flag-p16<sup>INK4A</sup> molecules or one Flag-p16<sup>INK4A</sup> and one mCherry-p16<sup>INK4A</sup> molecule can be detected. (**B**) Diagonal electrophoresis (non-reducing SDS-PAGE followed by reducing SDS-PAGE) shows that the high-molecular weight form of Flag-p16<sup>INK4A</sup> separates in a single dot under the diagonal, confirming that the disulfide-containing high-molecular weight species of p16<sup>INK4A</sup> consists of only p16<sup>INK4A</sup> protein. Collectively, and because p16<sup>INK4A</sup> has only one cysteine, these data must mean that the slow-migrating species of p16<sup>INK4A</sup> detected under non-reducing conditions are indeed p16<sup>INK4A</sup> homo-dimers. The experiments shown are typical results of at least two independent experiments. See also Figure 2A in Chapter 3.



Figure S3. Overlap of <sup>1</sup>H<sup>13</sup>C HSQC spectra in the reduced (magenta) and glutathionylated state (yellow). disappears and the oxidized C $\beta$  resonance appears at the position labeled as (2).





Figure S4. Mass spectrometry analysis of reduced and glutathionylated p16<sup>INK4A</sup>. (figure legend continues on next page)

# The magenta peak labeled as (1) is the reduced C72 CB resonance. After titration with glutathione to the end point, the resonance

	1190.9791	1282.5873	1389.3942	1515.5094 1500	16 1600	67.0640 	185	4.3757 1900	1973.6119
32	0547								
	1212.774	8 1305.993	33 1414.8	190 1543.25	606	1697.7000		1885.8595	i
0	1200	1300	1400	1500	1600	1700	1800	1900	

(A) Deconvoluted mass spectra of p16<sup>INK4A</sup> treated with GSSG shows a mass-shift of 305 Da which is in agreement with the modification of p16^{INK4A} C72 with disulfide-linked glutathione (i.e. S-GSHylated p16^{INK4A}). (**B**) m/z spectra of the LC-MS analysis of recombinant p16<sup>INK4A</sup> before and after S-GSHylation. The mass-spectrometric analysis to determine whether p16<sup>INK4A</sup> was indeed S-GSHylated upon GSSG treatment was performed once.



Figure S5. 1H15N HSQC solution NMR spectra of WT p16INK4A (blue) and p16INK4A C72S (orange).



Figure S6. Analysis of oxidized p16<sup>INK4A</sup>. (figure legend continues on next page)

(A) SDS-PAGE of wild-type p16<sup>1NK4A</sup> after hydrogen peroxide oxidation in the presence (left) and absence of the reducing agent BME in the sample buffer. A typical result is shown of at least 10 replicate experiments.

(B) Size exclusion chromatography of WT p16<sup>INK4A</sup> before (magenta) and after (yellow) overnight oxidation with 50 mM hydrogen

Overlap of <sup>1</sup>H<sup>15</sup>N HSQC solution spectra of WT p16<sup>INK4A</sup> oxidized with H<sub>2</sub>O<sub>2</sub> (magenta) and diamide (yellow).



Figure S7. CD spectroscopy and SAXS curves of reduced and oxidized p16<sup>INK4A</sup> samples. (A) CD spectra of reduced (magenta) and oxidized (yellow) p16<sup>INK4A</sup>. The experiment was performed twice and a typical result is shown. (B) Scattering curves of reduced (magenta) and oxidized (yellow) p16<sup>INK4A</sup>. Curves recorded using 2.5 mg/ml protein are presented. The oxidized sample displays typical characteristics of an aggregated protein state and could not be desmeared for detailed data analysis. The experiments were performed three times with varying concentrations showing the same trend and a single representative is shown.







# Figure S8. Effect of oxidizing agents on GS-p16<sup>INK4A</sup> and p16<sup>INK4A</sup> C72S.

(A) Overlap of <sup>1</sup>H<sup>15</sup>N HSQC solution spectra of reduced (magenta) and H<sub>2</sub>O<sub>2</sub> treated (yellow) GS-p16<sup>1NK4A</sup>. (B) Overlap of <sup>1</sup>H<sup>15</sup>N HSQC solution spectra of reduced (magenta) and diamide treated (yellow) GS-p16<sup>INK4A</sup>. (C) Overlap of <sup>1</sup>H<sup>15</sup>N HSQC solution spectra of reduced (magenta) and GSSG treated (yellow) p16<sup>INK4A</sup> C72S. (**D**) Overlap of <sup>1</sup>H<sup>15</sup>N HSQC solution spectra of reduced (yellow) and H,O, treated (magenta) p16<sup>1NK4A</sup> C72S. (E) Overlap of <sup>1</sup>H<sup>15</sup>N HSQC solution spectra of reduced (magenta) and diamide treated (yellow) p16<sup>INK4A</sup>C72S.



Figure S9. Prediction of p16<sup>INK4A</sup> aggregation-prone regions. (A) Four b-aggregation prediction algorithms predict that residues 90 to 99 of  $p16^{INK4A}$  have high aggregation propensity. (B)  $^{13}C^{13}C$ solid state NMR spectrum of p16<sup>INK4A</sup> fibrils showing the full aliphatic region. Crosses mark positions where peaks would be expected to arise from isoleucine residues. There are three isoleucines in the full p16<sup>INK4A</sup> sequence, suggesting that these residues are absent from the folded b-sheet core of p16<sup>INK4A</sup> fibrils. Peaks that correspond to amino acid types with distinct shifts are labeled. Boxes indicate the average shift expected for both secondary-structure types of proline and valine, within one standard deviation. (C) <sup>13</sup>C Secondary chemical shifts of uniquely assigned amino acid types showing the presence of  $\beta$ -sheet secondary structural elements. Horizontal lines indicate average values for secondary chemical shifts of alpha-helix (blue) and β-sheet (yellow), and regions are shaded to one standard deviation.



Figure S10. SDS-PAGE of p16<sup>INK4A</sup> samples before and after ThT fibril formation assay.

Samples were taken before and after the ThT kinetics assay (see Figure 4B) and analyzed by SDS-PAGE. WT p16<sup>INK4A</sup>, p16<sup>INK4A</sup>C72S and GS-p16<sup>INK4A</sup> were allowed to form fibrils in the absence or presence of oxidizing agents (H<sub>2</sub>O<sub>2</sub> or diamide). Samples for gel analysis were incubated is SDS loading buffer with or without reducing agent (DTT). Dimer bands can be seen in non-reduced samples of oxidized WT p16<sup>INK4A</sup>. Similar experiments (with slightly different loading and conditions) were performed at least 4 times. A typical result is shown.



Figure S11. MS/MS analysis of the p16<sup>INK4A</sup> interactome upon oxidation. Diamide treatment (200 µM) induces large changes in the interaction profile of WT p16<sup>INK4A</sup> and this largely depends on C72. (A) Comparison of the interactomes of WT p16<sup>INK4A</sup> with or without diamide treatment. (B) Comparison of the interactomes of p16<sup>IN-</sup> <sup>K4A</sup> C72A with or without diamide treatment. (C) Comparison of the interactomes of WT p16<sup>INK4A</sup> and p16<sup>INK4A</sup> C72A without diamide treatment. (D) Comparison of the interactomes of WT p16<sup>INK4A</sup> and p16<sup>INK4A</sup> C72A with diamide treatment. Note that the interaction with CDK4 and CDK6 is not altered by diamide treatment nor C72 dependent and that equal amounts of WT p16<sup>INK4A</sup> and p16<sup>INK4A</sup> C72A were pulled down. Several chaperone proteins can be found to interact upon oxidation. Log-transformed median IBAQ values are plotted, green colors represent proteins with adjusted p-values smaller than 0.05. Marginal plots represent the total number of significant proteins. N=6 biological replicates for WT  $p_{16}^{INK4A}$  and  $p_{16}^{INK4A}$  C72A, N=5 for  $p_{16}^{INK4A}$  + diamide and N=4 for p16<sup>INK4A</sup> C72A + diamide.





### Figure S12. Evolutionary trees of vertebrate and mammalian evolution for reference.

(A) Evolutionary tree of vertebrate evolution for reference. LVCA: Last Vertebrate Common Ancestor. (B) Evolutionary tree of mammalian evolution for reference. LMCA: Last Mammalian Common Ancestor. Branches indicated in yellow color indicate branches in which some species have lost the cysteine homologous to human p16<sup>INK4A</sup> C72. Note that for some branches very few sequence information is available and that it cannot be excluded that also in the branches indicated in black color species might have lost the C homologous to human p16<sup>INK4A</sup> C72. Note that evolutionary trees in (A) and (B) are not to scale.

# REFERENCES

- Sherr, C.J. Cancer Cell Cycles. *Science* 1996, 274, 1672–1677, doi:10.112 science.274.5293.1672.
- Johnson, D.G.; Schwarz, J.K.; Cress, W.D.; Nevins, J.R. Expression Transcription Factor E2F1 Induces Quiescent Cells to Enter S Pha-*Nature* 1993, *365*, 349–352, doi:10.1038/365349a0.
- Burd, C.E.; Sorrentino, J.A.; Clark, K.S.; Darr, D.B.; Krishnamurthy, Deal, A.M.; Bardeesy, N.; Castrillon, D.H.; Beach, D.H.; Sharples N.E. Monitoring Tumorigenesis and Senescence In Vivo with a P. INK4a -Luciferase Model. *Cell* 2013, *152*, 340–351, doi:10.1016, cell.2012.12.010.
- Forbes, S.A.; Beare, D.; Boutselakis, H.; Bamford, S.; Bindal, N.; Tatt J.; Cole, C.G.; Ward, S.; Dawson, E.; Ponting, L.; et al. COSMIC: Se matic Cancer Genetics at High-Resolution. *Nucleic Acids Res* 2017, 4: D777–D783, doi:10.1093/nar/gkw1121.
- Baker, D.J.; Wijshake, T.; Tchkonia, T.; LeBrasseur, N.K.; Childs, B.G Sluis, B. van de; Kirkland, J.L.; Deursen, J.M. van Clearance of P16Ir k4a-Positive Senescent Cells Delays Ageing-Associated Disorder: *Nature* 2011, 479, 232–236, doi:10.1038/nature10600.
- 6. Childs, B.G.; Durik, M.; Wijers, M.E.; Sieben, C.J.; Zhong, J.; Saltnes R.A.; Jeganathan, K.B.; Verzosa, G.C.; Pezeshki, A.; Khazaie, K.; et a Naturally Occurring P16Ink4a-Positive Cells Shorten Healthy Life pan. *Nature* 2016, *530*, 184 189, doi:10.1038/nature16932.
- Russo, A.A.; Tong, L.; Lee, J.-O.; Jeffrey, P.D.; Pavletich, N.P. Struc tural Basis for Inhibition of the Cyclin-Dependent Kinase Cdk by the Tumour Suppressor P16INK4a. *Nature* 1998, *395*, 237 243 doi:10.1038/26155.
- 8. Stepanova, L.; Leng, X.; Parker, S.B.; Harper, J.W. Mammalian P50Cdc3 Is a Protein Kinase-Targeting Subunit of Hsp90 That Binds and Stabi lizes Cdk4. *Gene Dev* 1996, *10*, 1491–1502, doi:10.1101/gad.10.12.1491
- Holmström, K.M.; Finkel, T. Cellular Mechanisms and Physiologica Consequences of Redox-Dependent Signalling. *Nat Rev Mol Cell Bi* 2014, 15, 411–421, doi:10.1038/nrm3801.
- Vurusaner, B.; Poli, G.; Basaga, H. Tumor Suppressor Genes and ROS Complex Networks of Interactions. *Free Radical Bio Med* 2012, 52 7–18, doi:10.1016/j.freeradbiomed.2011.09.035.
- Putker, M.; Madl, T.; Vos, H.R.; Ruiter, H. de; Visscher, M.; Berg M.C.W. van den; Kaplan, M.; Korswagen, H.C.; Boelens, R.; Vermeu len, M.; et al. Redox-Dependent Control of FOXO/DAF-16 by Trans portin-1. *Mol Cell* 2013, *49*, 730 742, doi:10.1016/j.molcel.2012.12.014
- Sunde, M.; Serpell, L.C.; Bartlam, M.; Fraser, P.E.; Pepys, M.B.; Blak C.C.F. Common Core Structure of Amyloid Fibrils by Synchrotro X-Ray Diffraction11Edited by F. E. Cohen. *J Mol Biol* 1997, 27. 729–739, doi:10.1006/jmbi.1997.1348.

- Chiti, F.; Dobson, C.M. Protein Misfolding, Functional Amyloid, and Human Disease. *Annu Rev Biochem* 2006, *75*, 333–366, doi:10.1146/ annurev.biochem.75.101304.123901.
- LeVine, H. Quantification of β-Sheet Amyloid Fibril Structures with Thioflavin T. *Methods Enzymol* 1999, 309, 274–284, doi:10.1016/ s0076-6879(99)09020-5.
- Klunk, W.E.; Pettegrew, J.W.; Abraham, D.J. Quantitative Evaluation of Congo Red Binding to Amyloid-like Proteins with a Beta-Pleated Sheet Conformation. *J Histochem Cytochem Official J Histochem Soc* 1989, *37*, 1273–1281, doi:10.1177/37.8.2666510.
- Nilsson, M.R. Techniques to Study Amyloid Fibril Formation in Vitro. *Methods* 2004, *34*, 151–160, doi:10.1016/j.ymeth.2004.03.012.
- 17. Zandomeneghi, G.; Krebs, M.R.H.; McCammon, M.G.; Fändrich, M. FTIR Reveals Structural Differences between Native B-sheet Proteins and Amyloid Fibrils. *Protein Sci* 2004, *13*, 3314–3321, doi:10.1110/ ps.041024904.
- Sarroukh, R.; Goormaghtigh, E.; Ruysschaert, J.-M.; Raussens, V. ATR-FTIR: A "Rejuvenated" Tool to Investigate Amyloid Proteins. *Biochimica Et Biophysica Acta Bba - Biomembr* 2013, *1828*, 2328–2338, doi:10.1016/j.bbamem.2013.04.012.
- Fernandez-Escamilla, A.-M.; Rousseau, F.; Schymkowitz, J.; Serrano, L. Prediction of Sequence-Dependent and Mutational Effects on the Aggregation of Peptides and Proteins. *Nat Biotechnol* 2004, *22*, 1302– 1306, doi:10.1038/nbt1012.
- Walsh, I.; Seno, F.; Tosatto, S.C.E.; Trovato, A. PASTA 2.0: An Improved Server for Protein Aggregation Prediction. *Nucleic Acids Res* 2014, *42*, W301–W307, doi:10.1093/nar/gku399.
- 21. Conchillo-Solé, O.; Groot, N.S. de; Avilés, F.X.; Vendrell, J.; Daura, X.; Ventura, S. AGGRESCAN: A Server for the Prediction and Evaluation of "Hot Spots" of Aggregation in Polypeptides. *Bmc Bioinformatics* 2007, 8, 65, doi:10.1186/1471-2105-8-65.
- Tartaglia, G.G.; Pawar, A.P.; Campioni, S.; Dobson, C.M.; Chiti,
   F.; Vendruscolo, M. Prediction of Aggregation-Prone Regions in Structured Proteins. *J Mol Biol* 2008, *380*, 425–436, doi:10.1016/j.
   jmb.2008.05.013.
- 23. Marino, S.M.; Gladyshev, V.N. Cysteine Function Governs Its Conservation and Degeneration and Restricts Its Utilization on Protein Surfaces. *J Mol Biol* 2010, 404, 902–916, doi:10.1016/j.jmb.2010.09.027.
- 24. Regneri, J.; Klotz, B.; Wilde, B.; Kottler, V.A.; Hausmann, M.; Kneitz, S.; Regensburger, M.; Maurus, K.; Götz, R.; Lu, Y.; et al. Analysis of the Putative Tumor Suppressor Gene Cdkn2ab in Pigment Cells and Melanoma of Xiphophorus and Medaka. *Pigm Cell Melanoma R* 2019, 32, 248–258, doi:10.1111/pcmr.12729.
- Zerbino, D.R.; Achuthan, P.; Akanni, W.; Amode, M.R.; Barrell, D.; Bhai, J.; Billis, K.; Cummins, C.; Gall, A.; Girón, C.G.; et al. Ensembl 2018. *Nucleic Acids Res* 2018, *46*, D754–D761, doi:10.1093/nar/gkx1098.

- Chiti, F.; Dobson, C.M. Protein Misfolding, Amyloid Formation, and Human Disease: A Summary of Progress Over the Last Decade. *Annu Rev Biochem* 2016, *86*, 1–42, doi:10.1146/annurev-biochem-061516-045115.
- 27. Fowler, D.M.; Koulov, A.V.; Alory-Jost, C.; Marks, M.S.; Balch, W.E. Kelly, J.W. Functional Amyloid Formation within Mammalian Tissue *Plos Biol* 2006, 4, e6, doi:10.1371/journal.pbio.0040006.
- 28. Li, J.; McQuade, T.; Siemer, A.B.; Napetschnig, J.; Moriwaki, K.; Hsiao, Y.-S.; Damko, E.; Moquin, D.; Walz, T.; McDermott, A.; et al. The RIP1/RIP3 Necrosome Forms a Functional Amyloid Signaling Complex Required for Programmed Necrosis. *Cell* 2012, *150*, 339–350, doi:10.1016/j.cell.2012.06.019.
- 29. Maji, S.K.; Perrin, M.H.; Sawaya, M.R.; Jessberger, S.; Vadodaria, K.; Rissman, R.A.; Singru, P.S.; Nilsson, K.P.R.; Simon, R.; Schubert, D.; et al. Functional Amyloids As Natural Storage of Peptide Hormones in Pituitary Secretory Granules. *Science* 2009, *325*, 328–332, doi:10.1126/ science.1173155.
- Zhang, S.; Tang, M.; Luo, H.; Shi, C.; Xu, Y. Necroptosis in Neurodegenerative Diseases: A Potential Therapeutic Target. *Cell Death Dis* 2017, 8, e2905–e2905, doi:10.1038/cddis.2017.286.
- Li, Y.; Yan, J.; Zhang, X.; Huang, K. Disulfide Bonds in Amyloidogenesis Diseases Related Proteins. *Proteins Struct Funct Bioinform* 2013, *81*, 1862–1873, doi:10.1002/prot.24338.
- 32. Mossuto, M.F.; Bolognesi, B.; Guixer, B.; Dhulesia, A.; Agostini, F.; Kumita, J.R.; Tartaglia, G.G.; Dumoulin, M.; Dobson, C.M.; Salvatella, X. Disulfide Bonds Reduce the Toxicity of the Amyloid Fibrils Formed by an Extracellular Protein\*\*. *Angewandte Chemie Int Ed Engl* 2011, *50*, 7048–7051, doi:10.1002/anie.201100986.
- 33. Chattopadhyay, M.; Durazo, A.; Sohn, S.H.; Strong, C.D.; Gralla, E.B.; Whitelegge, J.P.; Valentine, J.S. Initiation and Elongation in Fibrillation of ALS-Linked Superoxide Dismutase. *Proc National Acad Sci* 2008, *105*, 18663–18668, doi:10.1073/pnas.0807058105.
- 34. Furukawa, Y.; Kaneko, K.; Yamanaka, K.; O'Halloran, T.V.; Nukina, N. Complete Loss of Post-Translational Modifications Triggers Fibrillar Aggregation of SOD1 in the Familial Form of Amyotrophic Lateral Sclerosis\*. J Biol Chem 2008, 283, 24167–24176, doi:10.1074/jbc. m802083200.
- 35. Kato, M.; Han, T.W.; Xie, S.; Shi, K.; Du, X.; Wu, L.C.; Mirzaei, H.; Goldsmith, E.J.; Longgood, J.; Pei, J.; et al. Cell-Free Formation of RNA Granules: Low Complexity Sequence Domains Form Dynamic Fibers within Hydrogels. *Cell* 2012, *149*, 753–767, doi:10.1016/j. cell.2012.04.017.
- 36. Maiti, N.R.; Surewicz, W.K. The Role of Disulfide Bridge in the Folding and Stability of the Recombinant Human Prion Protein\*. *J Biol Chem* 2001, 276, 2427–2431, doi:10.1074/jbc.m007862200.
- Honda, R. Role of the Disulfide Bond in Prion Protein Amyloid Formation: A Thermodynamic and Kinetic Analysis. *Biophys J* 2018, *114*, 885–892, doi:10.1016/j.bpj.2017.12.031.

- 38. Mompeán, M.; Li, W.; Li, J.; Laage, S.; Siemer, A.B.; Bozkurt, G.; Wu, H.; McDermott, A.E. The Structure of the Necrosome RIPK1-RIPK3 Core, a Human Hetero-Amyloid Signaling Complex. *Cell* 2018, *173*, 1244-1253.e10, doi:10.1016/j.cell.2018.03.032.
- Ono, K.; Takahashi, R.; Ikeda, T.; Yamada, M. Cross-seeding Effects of Amyloid B-protein and A-synuclein. *J Neurochem* 2012, *122*, 883–890, doi:10.1111/j.1471-4159.2012.07847.x.
- 40. Ehrnhoefer, D.E.; Bieschke, J.; Boeddrich, A.; Herbst, M.; Masino, L. Lurz, R.; Engemann, S.; Pastore, A.; Wanker, E.E. EGCG Redirects Amyloidogenic Polypeptides into Unstructured, off-Pathway Oligomers. *Nat Struct Mol Biol* 2008, *15*, 558–566, doi:10.1038/nsmb.1437
- Deshmukh, M.; Evans, M.L.; Chapman, M.R. Amyloid by Design: In trinsic Regulation of Microbial Amyloid Assembly. *J Mol Biol* 2018 *430*, 3631–3641, doi:10.1016/j.jmb.2018.07.007.
- 42. Murray, D.T.; Kato, M.; Lin, Y.; Thurber, K.R.; Hung, I.; McKnight, S.L.; Tycko, R. Structure of FUS Protein Fibrils and Its Relevance to Self-Assembly and Phase Separation of Low-Complexity Domains. *Cell* 2017, *171*, 615-627.e16, doi:10.1016/j.cell.2017.08.048.
- 43. Makin, O.S.; Atkins, E.; Sikorski, P.; Johansson, J.; Serpell, L.C. Molecular Basis for Amyloid Fibril Formation and Stability. *P Natl Acad Sci Usa* 2005, *102*, 315–320, doi:10.1073/pnas.0406847102.
- 44. Baldwin, A.J.; Knowles, T.P.J.; Tartaglia, G.G.; Fitzpatrick, A.W.; Devlin, G.L.; Shammas, S.L.; Waudby, C.A.; Mossuto, M.F.; Meehan, S.; Gras, S.L.; et al. Metastability of Native Proteins and the Phenomenon of Amyloid Formation. *J Am Chem Soc* 2011, *133*, 14160–14163, doi:10.1021/ja2017703.
- 65. Coryell, P.R.; Goraya, S.K.; Griffin, K.A.; Redick, M.A.; Sisk, S.R.; Purvis, J.E. Autophagy Regulates the Localization and Degradation of P16INK4a. *Aging Cell* 2020, *19*, e13171, doi:10.1111/acel.13171.
- Hanger, D.P.; Anderton, B.H.; Noble, W. Tau Phosphorylation: The Therapeutic Challenge for Neurodegenerative Disease. *Trends Mol Med* 2009, *15*, 112–119, doi:10.1016/j.molmed.2009.01.003.
- 47. Capitini, C.; Conti, S.; Perni, M.; Guidi, F.; Cascella, R.; Poli, A.D.; Penco, A.; Relini, A.; Cecchi, C.; Chiti, F. TDP-43 Inclusion Bodies Formed in Bacteria Are Structurally Amorphous, Non-Amyloid and Inherently Toxic to Neuroblastoma Cells. *Plos One* 2014, *9*, e86720, doi:10.1371/journal.pone.0086720.
- Reest, J. van der; Lilla, S.; Zheng, L.; Zanivan, S.; Gottlieb, E. Proteome-Wide Analysis of Cysteine Oxidation Reveals Metabolic Sensitivity to Redox Stress. *Nat Commun* 2018, *9*, 1581 16, doi:10.1038/ s41467-018-04003-3.
- 49. Yang, J.; Carroll, K.S.; Liebler, D.C. The Expanding Landscape of the Thiol Redox Proteome\*. *Mol Cell Proteomics* 2016, 15, 1–11, doi:10.1074/mcp.o115.056051.
- Schafer, F.Q.; Buettner, G.R. Redox Environment of the Cell as Viewed through the Redox State of the Glutathione Disulfide/Glutathione Couple. *Free Radical Bio Med* 2001, *30*, 1191–1212, doi:10.1016/ s0891-5849(01)00480-4.

- 51. Menon, S.G.; Goswami, P.C. A Redox Cycle within the Cell Cycle: Ring in the Old with the New. Oncogene 2007, 26, 1101 1109, doi:10.1038/ sj.onc.1209895.
  63. Tartaglia, G.G.; Vendruscolo, M. The Zyggregator Method for Predicting Protein Aggregation Propensities. Chem Soc Rev 2008, 37, 1395–1401, doi:10.1039/b706784b.
- 52. Stöcker, S.; Maurer, M.; Ruppert, T.; Dick, T.P. A Role for 2-Cys Peroxiredoxins in Facilitating Cytosolic Protein Thiol Oxidation. *Nat Chem Biol* 2018, *14*, 148–155, doi:10.1038/nchembio.2536.
  53. Gorrini, C.; Harris, J.S.; Mak, T.W. Modulation of Oxidative Stress
- 53. Gorrini, C.; Harris, I.S.; Mak, T.W. Modulation of Oxidative Stress as an Anticancer Strategy. *Nat Rev Drug Discov* 2013, *12*, 931 947, doi:10.1038/nrd4002.
  54. Lee, A.S.: Galea, C.: DiGiammatino, F.L.: Jun, B.: Murti, G.: Ribeiro,
  55. Galea, C.: DiGiammatino, F.L.: Jun, B.: Murti, G.: Ribeiro,
  56. Wang, Y.; Jardetzky, O. Probability-based Protein Secondary Structure Identification Using Combined NMR Chemical-shift Data. *Protein Sci* 2002, *11*, 852–861, doi:10.1110/ps.3180102.
- 54. Lee, A.S.; Galea, C.; DiGiammarino, E.L.; Jun, B.; Murti, G.; Ribeiro, R.C.; Zambetti, G.; Schultz, C.P.; Kriwacki, R.W. Reversible Amyloid Formation by the P53 Tetramerization Domain and a Cancer-Associated Mutant. *J Mol Biol* 2003, *327*, 699–709, doi:10.1016/s0022-2836(03)00175-x.
  54. 2002, *11*, 852–861, doi:10.1110/ps.3180102.
  66. Cox, J.; Mann, M. MaxQuant Enables High Peptide Identification Rates, Individualized p.p.b.-Range Mass Accuracies and Proteome-Wide Protein Quantification. *Nat Biotechnol* 2008, *26*, 1367– 1372, doi:10.1038/nbt.1511.
- 55. Kato, M.; Yang, Y.-S.; Sutter, B.M.; Wang, Y.; McKnight, S.L.; Tu, B.P. Redox State Controls Phase Separation of the Yeast Ataxin-2 Protein
   via Reversible Oxidation of Its Methionine-Rich Low-Complexity Domain. Cell 2019, 177, 711-721.e8, doi:10.1016/j.cell.2019.02.044.
   67. Schwanhäusser, B.; Busse, D.; Li, N.; Dittmar, G.; Schuchhardt, J.; Wolf, J.; Chen, W.; Selbach, M. Global Quantification of Mammalian Gene Expression Control. Nature 2011, 473, 337–342, doi:10.1038/ nature10098.
- 56. Medema, R.H.; Herrera, R.E.; Lam, F.; Weinberg, R.A. Growth Suppression by P16ink4 Requires Functional Retinoblastoma Protein. Proc National Acad Sci 1995, 92, 6289–6293, doi:10.1073/pnas.92.14.6289.
  57. Sakaue-Sawano, A.; Kurokawa, H.; Morimura, T.; Hanyu, A.; Hama, H.: Osawa, H.: Kashiwagi, S.: Fukami, K.: Miyata, T.: Miyoshi, H.: et
  68. Luber, C.A.; Cox, J.; Lauterbach, H.; Fancke, B.; Selbach, M.; Tschopp, J.; Akira, S.; Wiegand, M.; Hochrein, H.; O'Keeffe, M.; et al. Quantitative Proteomics Reveals Subset-Specific Viral Recognition in Dendritic Cells. Immunity 2010, 32, 279–289, doi:10.1016/j. immuni.2010.01.013.
- 57. Sakaue-Sawano, A.; Kurokawa, H.; Morimura, T.; Hanyu, A.; Ham H.; Osawa, H.; Kashiwagi, S.; Fukami, K.; Miyata, T.; Miyoshi, H.; al. Visualizing Spatiotemporal Dynamics of Multicellular Cell-Cyc Progression. *Cell* 2008, *132*, 487 498, doi:10.1016/j.cell.2007.12.033
- Livak, K.J.; Schmittgen, T.D. Analysis of Relative Gene Expression D: Using Real-Time Quantitative PCR and the 2–ΔΔC T Method. *Methods of solution and the 2–40*.
- 59. Delaglio, F.; Grzesiek, S.; Vuister, G.W.; Zhu, G.; Pfeifer, J.; Bax, A NMRPipe: A Multidimensional Spectral Processing System Base on UNIX Pipes. *J Biomol Nmr* 1995, *6*, 277–293, doi:10.1007 bf00197809.
- 60. Vranken, W.F.; Boucher, W.; Stevens, T.J.; Fogh, R.H.; Pajon, A.; Llina M.; Ulrich, E.L.; Markley, J.L.; Ionides, J.; Laue, E.D. The CCPN Dat Model for NMR Spectroscopy: Development of a Software Pipelin *Proteins Struct Funct Bioinform* 2005, *59*, 687–696, doi:10.1002 prot.20449.
- 61. Piotukh, K.; Kosslick, D.; Zimmermann, J.; Krause, E.; Freund, C Reversible Disulfide Bond Formation of Intracellular Proteins Prober by NMR Spectroscopy. *Free Radical Bio Med* 2007, *43*, 1263–1270 doi:10.1016/j.freeradbiomed.2007.06.010.
- 62. Franke, D.; Petoukhov, M.V.; Konarev, P.V.; Panjkovich, A.; Tuukkaner A.; Mertens, H.D.T.; Kikhney, A.G.; Hajizadeh, N.R.; Franklin, J.M Jeffries, C.M.; et al. ATSAS 2.8: A Comprehensive Data Analysis Suit for Small-Angle Scattering from Macromolecular Solutions. *J App Crystallogr* 2017, *50*, 1212–1225, doi:10.1107/s1600576717007786.

- Chich, J.-F.; David, O.; Villers, F.; Schaeffer, B.; Lutomski, D.; Huet S. Statistics for Proteomics: Experimental Design and 2-DE Differ ential Analysis. *J Chromatogr B* 2007, *849*, 261–272, doi:10.1016/j jchromb.2006.09.033.
- 70. Waterhouse, A.M.; Procter, J.B.; Martin, D.M.A.; Clamp, M.; Barton, G.J. Jalview Version 2—a Multiple Sequence Alignment Editor and Analysis Workbench. *Bioinformatics* 2009, 25, 1189–1191, doi:10.1093/ bioinformatics/btp033.
- 71. Vizcaíno, J.A.; Csordas, A.; del-Toro, N.; Dianes, J.A.; Griss, J.; Lavidas,
   I.; Mayer, G.; Perez-Riverol, Y.; Reisinger, F.; Ternent, T.; et al. 2016
   Update of the PRIDE Database and Its Related Tools. *Nucleic Acids Res* 2016, 44, D447–D456, doi:10.1093/nat/gkv1145.

# CROSSTALK BETWEEN REDOX SIGNALING AND PROTEIN AGGREGATION



# **CROSSTALK BETWEEN REDOX SIGNALING AND PROTEIN AGGREGATION**

# ABSTRACT

# INTRODUCTION

Both the loss of proteostasis and ROS production as a consequence of mitochondrial dysfunction are among the hall-**Protein Folding** marks of aging [1]. While there is plenty of evidence that these Proteins are synthesized as linear peptide chains on ribosomes two hallmarks are tightly intertwined, their cause and effect and must fold into 3D structures to execute their biological relationships remain unclear. This might be partly due to the functions. Protein folding is driven for a large part by the fact that ROS, in the form of  $H_2O_2$ , itself plays a dual role. spontaneous burial of nonpolar amino acids in the folding While at lower levels H<sub>2</sub>O<sub>2</sub> acts as a second messenger in redox core, but also guided by hydrogen bonds, van der Waals- and signaling, which is absolutely required for physiology and for electrostatic interactions. The many weak, noncovalent and lifespan extension in model systems [2], at higher levels  $H_2O_2$ often distant (in sequence) interaction possibilities compliand other ROS could lead to random damage including for cate the conformational possibilities. The stability of natively instance protein unfolding and aggregation, and the latter folded proteins depends on local environmental factors such has been proposed to accelerate the aging process [3–10]. But as pH and temperature. there is also evidence of functional redox signaling dependent protein aggregation, for instance providing a means to (tem-Most (~70%) protein folding takes place at the ribosome porarily) inactivate or alter function of proteins. Redox-deduring translation. Several mechanisms are in place to ensure pendent protein aggregation is also often reversible. But there correct folding: the sequential folding of domains emerging are also many examples of protein aggregation-induced enfrom the ribosome, the spatial restrictions of the ribosomal hanced ROS production, which may eventually contribute exit channel, the rate of translation as well as the ribosome-asto cellular dysfunction and cell death. sociated chaperones RAC and NAC (ribosome-associated

An hypothesis that could unite both H<sub>2</sub>O<sub>2</sub> as a signaling molecule and ROS as a driver of age-related protein aggregation was posed by Hekimi et al. [2]. It proposes that age-related damage triggers stress-response pathways that could depend on redox signaling and hence produce H<sub>2</sub>O<sub>2</sub> (either directly or indirectly through O2<sup>--</sup> followed by dismutation) as a second messenger in an attempt to regain homeostasis. Over time,

when more damage accumulates,  $H_2O_2$  produced to further Proteins need to overcome considerable energy barriers to boost this stress response surpasses levels that are merely reach their final, stable conformation, inherently leading involved in signaling, leading to a build-up H<sub>2</sub>O<sub>2</sub> and ROS to accumulation of folding intermediates (Figure 1) [13]. associated damage. This eventually would lead to a vicious Examples of slow steps in protein folding include disulfide cycle in which ROS-dependent damage triggers a redox sigbond formation and prolyl isomerization [14]. Partially folded naling-dependent stress-response, leading to a further increase proteins are at high risk of misfolding and aggregation, due to in ROS. This hypothesis would also fit with the observations non-native interactions through for instance the exposure of that several types of aggregates can trigger ROS production. hydrophobic residues [15,16]. Other reasons for faulty protein accumulation are mutations or polymorphisms, translation In this review we will focus on examples of the interplay beerrors and the structurally dynamic characteristic of proteins. tween redox signaling and protein aggregation. We review the Misfolded conformations are quasi-stable, making them more

current knowledge and try to illuminate possible relationships between redox signaling and proteostasis.

complex and nascent-chain associated complex, respectively) [11,12]. More downstream of the ribosome, the HSP70 system of chaperones prevents undesirable domain interactions. Moreover, HSP70 functions as a binding interface for other chaperones like HSP90 and chaperonins, which aid in de novo folding by recognizing exposed hydrophobic residues and promoting ATP-dependent refolding.



### Figure 1. Energy landscape in proteostasis

Newly synthesized peptides sample different conformations during protein folding, on their way downhill to the most thermodynamically favorable state. Energetically trapped, partially unfolded or sub-optimally folded intermediates may accumulate as they need to cross energy barriers to reach their native, low energy state. Non-native interactions may lead to protein aggregation, thereby interfering with the protein folding process. The proteostasis network can assist in lowering energy barriers and preventing non-native interactions. As indicated by the yellow circles,  $H_2O_2$ -mediated redox signaling or ROS-dependent damage helps to overcome the transition state between intermediates of the proteostasis network.

prone to aggregation when proteostasis control systems are saturated. The latter happens increasingly during aging [17]. The high plasticity of partially folded intermediates is in contrast to extremely structured aggregates like amyloid fibrils.

Another hallmark of aging, the failure to maintain proteostasis, presents itself as an accumulation of misfolded proteins and aggregates. Like folding, aggregation is predominantly driven by hydrophobic interactions, which is why aggregation prone regions (APRs) in proteins are generally distinguished by their high hydrophobicity, low net charge and high  $\beta$ -sheet propensity [18,19]. During aggregation, the hydrophobic interactions are mostly intermolecular, and therefore aggregation is concentration dependent. Due to the similarity between the composition of APRs and protein regions driving hydrophobic core formation during folding, aggregation and folding pathways constantly compete. Aggregation has long been considered only as a sign of degeneration and dysfunction. However, despite strong selective pressure against protein aggregation, numerous APRs remain in the proteome, which is in line with the notion that protein aggregation can play a functional or regulatory role [20,21]. The number of possible conformations for aggregation intermediates is large, and they need to overcome free energy barriers on their way to mature aggregates. This means that aggregation intermediates are energetically trapped and thus accumulate (**Figure** 1), allowing more non-native interactions to occur. Typically, these nonspecific interactions between polypeptides form a disordered assembly without a specified shape termed amorphous aggregates.

While most aggregates are amorphous, examples of more structured aggregate types are oligomeric aggregates and the extremely structured  $\beta$ -amyloid fibrils, and the latter are characterized by a cross- $\beta$ -structure (in which  $\beta$ -strands lie perpendicular to the fibril axis). Amyloid fibrillization consists of a slow lag phase directed by intermolecular interactions during which misfolded polypeptides congregate into nuclei and form oligomers containing  $\beta$ -sheets. During the subsequent exponential growth phase oligomers cluster further with these nuclei and grow rapidly into prefibrils and As mentioned previously, chaperones aid in de novo protein protofibrils with a cross-\beta-structure. During the final saturafolding by lowering energy barriers between folding intertion phase 2-6 protofibrils assemble into mature multistrand mediates. During aggregation, chaperones instead raise the amyloid fibrils which can adopt several polymorphic strucenergy barriers toward aggregation by preventing intermolectures by twisting or lateral association [22]. Amyloid fibrils ular interactions. Besides preventing aggregation, chaperones are one of the most thermodynamically stable and stiff protein play an important role in active disaggregation [34]. Recent arrangements known [23]. reports show that almost all types of aggregates are reversible [35,36]. The coordinated action of small HSPs (sHSPs), HSP40, HSP70 and HSP110 can even disaggregate amyloid Amyloids are a hallmark of (age-related) proteinopathies such as ALS, Alzheimer's, prion disease and cataract. Early studies fibrils by fragmentation and depolymerization into both mofocused on the mature aggregate deposits as toxic species. The nomeric and oligomeric species. The activity of chaperones is toxicity of amyloids is complex however, and several intertherefore twofold: on the one hand to prevent aggregation, on mediates and oligomers but also mature amyloid fibrils have the other to disaggregate (intermediate) aggregates.

now been linked to pathogenesis [11-13]. Some reports even suggest an inverse correlation between oligomer size and tox-One of the major protein degradation systems is the ubiquiicity of aggregates [24–27]. This complexity is also thought to tin-proteasome system (UPS). There are several constitutions be one of the reasons for clinical trial failures in proteinopaof the proteasome, but the 20S and 26S are most prominent. thies, with hardly any effective therapy available for treatment Ubiquitinated proteins and insoluble aggregates are pulled through the proteasomal ring-like structure, to be broken [13,28]. Adding to the complexity is the fact that many types of amyloids are shown to be functional with roles reported down by proteolysis. Not surprisingly, proteasomal dysfuncin chemical storage, structure, signaling and inactivation of tion is associated with aging and leads to the accumulation the soluble protein [29]. Another type of functional aggregaof aggregates [5–7,9,10], catalyzing a chain reaction in which tion is controlled by protein domains lacking rigid 3D strucaggregates block the proteasome which causes further dystures under physiological conditions, present in 15-30% of function [37]. proteins. These intrinsically disordered regions (IDRs) have a high conformational plasticity and susceptibility to modifi-A third mechanism by which cells can clear and recycle cellucations, enabling a multitude of interactions [30]. With these lar components is by autophagy. Many types of protein aggreinteractions, IDRs drive misfolding and aggregation of (pargates are cleared by autophagy, including tau, Aβ, α-synuclein, tially) disordered proteins as well as liquid-liquid phase sepahuntingtin, SOD1 and p16<sup>INK4A</sup> [38–43], with autophagy deration (LLPS), thereby forming membrane-less compartments fects leading to neurodegenerative disease [44,45]. which are important for the concentration and segregation of biochemical reactions [31]. However, LLPS condensates have Defects in and decreased activity of any of these proteostaalso been reported to catalyze amyloid fibrillization [32,33]. sis surveillance systems are associated with aging and prote-

### **Clearance of Protein Aggregates**

There are three quality control networks to ensure continuous surveillance of the proteome: (i) chaperones that mediate (re)folding, (ii) the ubiquitin-proteasome system (UPS) and (iii) autophagy to clear misfolded proteins and aggregates.

Defects in and decreased activity of any of these proteosta sis surveillance systems are associated with aging and prote inopathies, underpinning their importance in maintaining proteostasis.

# e Redox Signaling

Increased markers for ROS-induced damage and mitochondrial ROS generation have long been associated with age and neurodegenerative disorders, which has often been regarded as evidence for a causal link between oxidative damage and aging [46-54]. This is in contrast with the unexpected observation that increased ROS levels may extend lifespan in yeast and C. elegans [55,56], while increased ROS does not accelerate aging in mice [57]. The key to resolve this apparent paradox probably lies in the notion that ROS in the form of H<sub>2</sub>O<sub>2</sub> has become widely recognized as second messenger in so-called redox signaling, which has been shown to be involved in a plethora of cellular responses [46]. Central to redox signaling is the reversible oxidation/reduction of the nucleophilic thiol side chain of specific cysteine residues. Oxidation of cysteines in proteins commonly causes structural changes and functional interactions through disulfide bond formation, such as (hetero)dimerization, oligomerization, and even aggregation, and thereby provides an important molecular switch for protein activity or function. For a comprehensive review see [58].

Compared to superoxide anions and hydroxyl radicals, the other main cellular ROS, H<sub>2</sub>O<sub>2</sub>, has a relatively low reactivity and allows for specific rather than random oxidation of dedicated cysteines. Redox signaling starts with the production of H<sub>2</sub>O<sub>2</sub>: either directly (i.e. by DUOX enzymes or ERO1-dependent protein folding in the ER) or after dismutation of superoxide produced by leakage of electrons from complex I and III of the electron transport chain during mitochondrial respiration, or by NADPH-dependent oxidases (NOXs). For a comprehensive review on subcellular sources of ROS see [59].

Superoxide and H<sub>2</sub>O<sub>2</sub> are efficiently scavenged by antioxidant systems and the balance between ROS production and antioxidant capacity determines the redox state of cellular compartments [60,61]. When the amount of ROS surpasses the levels required for signaling, non-specific cellular damage (oxidative stress) can occur due to their high reactivity with biomolecules. Furthermore, H2O2 may be converted by more reactive species in the presence of transition metal ions, thereby changing its role from messenger to damaging agent. In line with this, it has been suggested that oxidative damage exists merely as a side product of cellular signaling, and that ROS are in fact part of the stress response to for instance proteotoxic

stress [2,62]. A good distinction between ROS as a signaling molecule versus ROS as oxidative stress has been proposed by Sies et al. [59]. Throughout this review we will try to use the term 'ROS' in case the exact species is unclear or in the case of random damage rather than signaling, whereas redox signaling and reversible cysteine oxidation are considered regulated processes downstream of  $H_2O_2$ .

Other amino acid side chains besides cysteine and methionine are also subject to oxidation. For example, Tyr and Trp phenoxyl radicals, carbonylated Lys/His/Cys, SNO-/SSG-modifications as well as lipid peroxidation and its aldehyde byproduct 4-hydroxynonenal (HNE) are all ROS-induced and have been associated with proteinopathies [63,64]. Collectively, the dual roles of  $H_2O_2/ROS$  in signaling and damage make it difficult to understand whether the increase in ROS in aging represents a causal link with oxidative damage, redox signaling or both. In this review we will focus mostly on the effects of reversible cysteine oxidation dependent redox signaling but will also include examples of how random oxidative damage affects protein aggregation.

# **REDOX SIGNALING AND** PROTEIN AGGREGATION

Protein aggregation can be affected or directly regulated by redox signaling or the cellular redox state. In general, cysteine oxidation results in structural changes, for instance through disulfide formation, that affect protein function [58]. These structural changes can also provide a molecular switch to partially unfold and subsequently aggregate. Interestingly, many proteins are predicted to contain conditionally disordered regions that could be redox sensitive and thereby facilitate the transition from disorder-to-order or order-to-disorder dependent on oxidation or reduction [65]. Similar to IDPs, this transition is driven by the multiplicity of possible interactions. Conversely, it is also known that misfolded proteins are more sensitive to oxidation, which has been suggested to tag proteins for proteolysis [66].

### **Functional Redox-Dependent Aggregation**

As mentioned earlier, several amyloid fibrils have functional roles in humans. Amyloid fibril formation can also be reversible [67,68] and reversible oxidation of cysteines can provide deposits, linking them to neuronal impairment [75-79]. the molecular switch that regulates fibrillization. For example, the tumor suppressor p16<sup>INK4A</sup> is readily oxidized on its only Conversely, there are also examples where cysteine oxidacysteine in an oxidizing environment, causing disulfide-linked tion prevents functional aggregation rather than trigger it. homodimerization and subsequent rapid but reversible  $\beta$ -am-For example, yeast ataxin2 spontaneously forms liquid-like yloid fibrillization. This redox-dependent change from a soldroplets that can convert to β-amyloid fibrils. Oxidation uble monomeric protein into insoluble but reversible  $\beta$ -amof ataxin1 regulates this process by melting the droplets, a yloid fibrils leads to the inactivation of the protein, allowing process that can be reversed by methionine sulfoxide reducreactivation of CDK4/6 proteins otherwise inactivated by tases [80]. Phase-separated ataxin2 is an inhibitor of TORC1 high p16<sup>INK4A</sup> expression [69]. These observations fit with the during respiratory growth, thereby stimulating autophagy. notion that redox signaling can regulate S-phase entry and Reactivation of TORC1 under oxidizing conditions though cellular proliferation [70,71]. regulation of ataxin2, in combination with nutrient starvation thereby allows coupling of mitochondrial function to Another illustration of redox-dependent functional protein TORC1-mediated metabolism [81].

aggregation is provided by tryptophan hydroxylase 2 (TPH2), the rate-limiting enzyme in serotonin neurotransmitter pro-This combination of findings suggests a more general mechduction. TPH2 aggregates upon oxidation of any out of 13 anism, where reversible redox-regulated protein aggregation cysteines and subsequent intra- and intermolecular disulfide directly dictates protein activity. It also has significant implibond formation, thereby reversibly inhibiting protein activity. cations for our understanding of aggregated proteins, which are not solely a waste product of misfolded proteins but rather TPH2 catalytic activity correlates directly with the number of cysteines that are oxidized [72,73]. Although the direct a temporary conformation linked to protein activity. purpose for redox regulation of serotonin biosynthesis is unknown, it provides a link between neurological function Cysteine Oxidation-Driven Protein Aggregation in Disease and redox signaling, a concept that is widely accepted in the molecular regulation of circadian rhythm [74]. Cysteine oxidation is also involved in toxic protein aggre-

gation. This is illustrated by the amorphous aggregation of In a similar way, redox status is linked to intracellular calcium  $\gamma$ -crystallins, known to cause cataract. Reduced antioxidant concentrations through oxidation-dependent protein aggrecapacity induces formation of an intramolecular disulfide gation of visinin-like protein-1 (VSNL1), a neuronal calcium bond between C32 and C41, which is both necessary and sensor important that can activate guanylyl cyclase (GC). sufficient to induce irreversible aggregation through destabili-Under low calcium concentrations, GC produces the second zation of the N-terminus [82,83]. This is especially interesting messenger cGMP that can activate calcium channels. When in an age-related context since the reducing capacity of the eye bound to calcium, structural rearrangements in VSNL1 make diminishes with age [84]. the C-terminal C187 available for reversible oxidation and subsequent homodimerization and aggregation. These di-Another detrimental type of aggregation is caused by mutasulfide-crosslinked aggregates are reversible upon treatment tions resulting in an uneven number of cysteines in the transwith reducing agents. As a result of aggregation, functional membrane receptor NOTCH3. NOTCH3 contains a highly

levels of VSNL1 are decreased, possibly providing a second mechanism to keep GC inactive besides calcium levels. Furthermore, VSNL1 aggregates are found in ALS-associated

conserved even number of cysteines forming disulfide bridges that maintain structural integrity. Any unpaired cysteine stimulates multimerization and aggregation through loss of a structural disulfides and exposure of an oxidation-prone cysteine that can form non-native disulfide [85,86]. Aggregated NOTCH3 accumulates in the vascular wall, leading to the rare systemic vasculopathology CASADIL.

Oxidation can also occur on other amino acids like methionine which can drastically alter protein structure. In this way, oxidation of a surface-exposed vital residue results in misfolding and aggregation. Several proteins follow this order of events. Examples include: GAPDH [87], y-synuclein [88],

interferon β1a [89], human growth hormone [90], κ-casein [91], FasL [92], transthyretin [93], apolipoprotein AI [94], AMPK [95], PrP [96] and huntingtin [97].

Interestingly, oxidation also triggers the aggregation of direct redox modulators. Cu,Zn-superoxide dismutase (SOD1) is an enzyme important for the dismutation of superoxide to  $H_2O_2$ and O<sub>2</sub>, and its misfolding and fibrillization plays a crucial role in the etiology of the familial form of amyotrophic lateral sclerosis (ALS). The enzymatic product of SOD1,  $H_2O_2$ , can directly oxidize the surface-exposed C111 in SOD1 which triggers its amyloid fibrillization. In a different manner, higher concentrations of H<sub>2</sub>O<sub>2</sub> overoxidize C111 to SO<sub>2/2</sub>H causing



### Figure 2. The proteostasis network

Cells employ several mechanisms to maintain proteins integrity and minimize non-native or harmful protein conformations. Mechanisms are in place for proteome quality control. Redox signaling participates in proteostasis by modulating the folding, misfolding, (dis)aggregation and the extent of toxicity of protein aggregates. References to examples of the various steps are indicated in numbers. Note that in some cases it is not clear from the literature what exact step in aggregation is affected, or whether multiple steps are affected, and in this case the reference is denoted at the first transition from native to partially unfolded.

amorphous aggregation [98-102]. Additionally, mutations causing conformational changes in SOD1 expose its four cysteines, making the structural disulfide bond between C57 and C146 accessible to reduction by the TRX and GSH-GRX systems [101]. Subsequent oxidation leads to the formation of non-native disulfides that cause formation of insoluble SOD1 multimers and aggregates. Contributing to the cytotoxicity of SOD1 aggregates, SOD1 oxidation has been shown to co-occur with cytoplasmic mislocalization and fibrillization of TAR-DNA-binding protein TDP-43, thereby inducing apoptosis [102].

Besides facilitating aggregation, cysteine oxidation can also prevent it. This is evident for human amylin (hIAPP), which forms a disulfide bridge between C2 and C7 upon oxidation. Oxidized hIAPP stabilizes an  $\alpha$ -helical structure at the N-terminus, protecting the peptide from amyloid formation and safeguarding its activity in insulin and glucagon secretion as well as reducing food intake and gastric emptying [103,104]. A similar mechanism has been published for  $\beta\mbox{-microglobulin}$ and endostatin, for which two disulfide bonds guard its native folded conformation [105-107].

In summary, the cellular redox environment and protein ag-Furthermore, oxidation does not only trigger aggregation. gregation show a strong association. With examples of protein Post-aggregation oxidation of proteins seems to be wideoxidation both inducing and preventing aggregation (summarized in Table 1), having functional as wells as pathological spread, changing the structural conformation of established consequences and occurring both before and after aggregaaggregates of proteins including huntingtin and \beta-microglobulin [106,107]. Besides providing an explanation for the abuntion, there seems no unifying role for protein oxidation in prodance of oxidative modifications found in aggregate deposits, tein aggregation. However, many proteins do seem to follow this finding suggests that insoluble aggregates are not inert the same sequence of events upon oxidation, which includes protein disposals but can still alter their structure and interaca partial unfolding and subsequent aggregation step. tions due to redox-dependent post-aggregation modifications. This view is supported by the concept that distinct struc-EFFECTS OF AGGREGATION tures of aggregated proteins also cause distinct phenotypes ON THE CELLULAR REDOX [108,109]. Targeting post-misfolding oxidation might also STATE offer therapeutic opportunities. For example, thiol-reactive compounds can force refolding and reactivation of mutant Protein aggregation can also modulate the cellular redox state, p53 tumor-suppressor (be it direct or indirect) [110,111], a concept that could be meaningful in proteinopathies. and, as mentioned, this could either be part of the proteotoxic stress response, cellular dysfunction as a result of the accu-

mulation of protein aggregates, or both. For example, based on thiol-disulfide redox couples and redox sensors it has been determined that under basal conditions mitochondria, the cytosol and nucleus are in a relatively reduced state as compared to the ER. This reverses radically when protein aggregation induces proteasomal dysfunction, resulting in a more oxidizing cytosol and reducing ER [60,113]. S-nitrosylation could be a possible contributor to this change due to the overactivation of the N-methyl-D-aspartate receptor (NMDAR, an inducer of neuronal nitric oxide synthase (nNOS)) or Aβ-dependent iNOS activation in neurons and glial cells of AD patients [114-116]. A shift to a more oxidizing cellular redox state upon proteotoxic stress is further supported by many reversible cysteine modifications that change in models for proteinopathies like AD [117,118].

A more direct explanation for the redox changes that occur upon aggregation can be found in the direct redox-dependent aggregation of redox modulators. As discussed above, SOD1 aggregation is directly triggered by oxidation of C111, thereby inactivating its function. This leads to the accumulation of superoxide at the expense of  $H_2O_2$ , where the former is more associated with random damage and the latter with redox signaling.

Another effect of aggregation on the cellular redox state is exemplified by the transmembrane AB protein precursor (ABPP), which is the precursor for the archetypical amyloidogenic  $A\beta$  peptide and the main component of amyloid plaques in brains of AD-patients. Interestingly, monomeric Aβ is suggested to have an antioxidant activity by hydrophilic chelation of transition metals, thereby preventing lipoprotein oxidation [119-122]. However, this chelation of metals also promotes the aggregation of A $\beta$ , and redox-active metal ions like Cu(II) and Fe(III) can catalyze the production of ROS when bound to aggregated Aβ. Aβ binding results in the reduction of the metal's oxidation state, which then converts O2 into H2O2, superoxide and hydroxyl radicals via Fenton chemistry [123-126]. Hence, the binding of AB to metals changes its properties from an antioxidant to a pro-oxidant

[120]. ROS-induced 0,0'-dityrosine covalent crosslinking then catalyzes further aggregation of A $\beta$  [127]. Interestingly, a similar interplay between metals and oligomers has been reported for a-synuclein [128], pointing potentially at a more general mechanism in which misfolded oligomeric proteins in conjunction with metal ions induce the production of ROS. Metal concentrations, aggregation as well as ROS production all increase with age and even without knowing the exact cause, the consequence is faster neurodegeneration [129].

Furthermore, many aggregates can directly cause mitochondrial dysfunction, resulting in metabolic stress, enhanced ROS production and eventually cell death. For example, amyloid oligomers are well-known for their permeabilization of membranes, which is considered a main toxicity event. A rapid influx of intracellular Ca<sup>2+</sup> as well as the direct permeabilization of the mitochondrial membrane causes an increase in mitochondrial ROS production [130-133].

When unfolded proteins accumulate in the ER, a condition called ER stress triggers the unfolded protein response (UPR) in an attempt to restore homeostasis. Protein aggregates like oligomeric A<sup>β</sup> have been shown to trigger ER stress and the UPR [134,135]. Prolonged ER stress is known to evoke intracellular ROS production at the ER through several mechanisms. These include overactivation of Ero1 oxidoreductases through a futile cycle of forming and repairing mismatched disulfides, thereby producing H2O2 and oxidizing GSH, respectively [132,136,137]. In addition, ER stress causes superoxide production though activation of NOXs and the release of Ca<sup>2+</sup> which increases electron leakage from mitochondria (for a review see [138]). Hence, since ROS are both a trigger and a consequence of ER stress, this further aggravates the imbalance accompanying ER stress [139].

# **REDOX REGULATION OF** AGGREGATE CLEARANCE

Redox control of the UPS is complex, with studies claiming both inhibitory and activating effects. In general, the 20S, but not 26S proteasome is thought to specifically degrade oxidized proteins [150-152]. Elevated ROS and mitochondrial dysfunction shift the proteasome population from 26S to 20S, thereby adapting to the proteolytic need for clearance of oxidized substrates [153]. In support of this, proteasomal degradation has been shown to be stimulated >10-fold upon exposure to H<sub>2</sub>O<sub>2</sub> or superoxide, while simultaneously abolishing 26S-mediated degradation [154-156]. The proteasome is also subject to direct redox modifications. For example, the 20S proteasome can be glutathionylated, resulting in its opening and activation [156,157]. Thus, under oxidizing conditions the 20S proteasome is stimulated to clear oxidized substrates, but this shift away from 26S permits the accumulation of otherwise misfolded proteins. This, however, has been debated by the notion that a high NAD+/NADH ratio, correlating with an oxidizing cellular state, opens and activates the 26S proteasome [158,159]. Also, the lipid peroxidation byproduct HNE was found to inhibit proteasomal activity for the breakdown of oxidized proteins [160,161]. In summary, oxidizing conditions result in a shift to the 20S proteasome, accompanied by a possible decrease in 26S activity. This might favor the accuinteraction between the cellular redox state and the proteavicious cycle of protein oxidation and aggregation [162,163].

To cope with the challenges caused by protein aggregation, cells are equipped with several mechanisms aimed at the clearance of misfolded proteins and aggregates, which themselves are also shown to be redox-regulated, adding another level of the complex interdependency of proteostasis and ROS. Besides their role in folding of newly synthesized proteins, molecular chaperones are also part of this cellular disaggregation machinery. There are many types of chaperones, but a general initial step seems to be the initial coverage of aggregates with HSP70 [140]. An example of the redox regulation of HSPs is through the reversible oxidation of MGE1, a mitochondrial nucleotide exchange factor of HSP70, on M155. The consequential structural change from an active homodimer to monomer leads to MGE1 amyloid formation, which prevents activation of HSP70. Interestingly, oxidized MGE1 is suggested to increases binding affinity of the inactive HSP70 for unfolded substrates. As HSP70 is essential in protein folding and proteostasis, MGE1 might act as an initial sensor of protein aggregation, priming the chaperone system for resolution of protein aggregates [141,142]. Peroxiredoxins are more unconventional chaperones. With their abundance and exceptional reactivity to H<sub>2</sub>O<sub>2</sub>, peroxiredoxins are important H2O2 scavengers. Their highly conserved active site consists of 2 catalytic cysteine residues. Besides their antioxidant activity, peroxiredoxins are known for their ability to oxidize protein thiols by a redox relay as

mulation of non-oxidized misfolded proteins. Moreover, the some is bidirectional. Blockage of the proteasome for instance, leads to an increase in ROS, which in its turn might cause a well as for their chaperone activity [143]. Assembled as a high molecular weight complex, peroxiredoxins can form ring-It has been suggested that both aggregation and cellular like chaperone structures with holdase activity that bind and redox state are coupled through their regulation of autophaprevent aggregation of unfolded proteins [144,145]. Among gy [164]. Autophagy is thought to be activated in more oxiothers, hyperoxidation of the peroxiredoxin catalytic cystedizing conditions [165–168], although this might not always ine particularly stimulates an oligomeric chaperone structure, be straightforward as glutathione reductase loss, resulting in whereas glutathionylation inhibits it [146-149]. Thereby peroxidizing conditions, was recently shown to suppress autooxiredoxins can sense high and low ROS levels and switch phagy and enhance aggregation [169]. The recruitment of ubiquitinylated substrates to autophagosomes is mediated

their function accordingly from antioxidant and redox signaling mediator to chaperone.

by receptors like SQSTM1/p62. Interestingly, components of the autophagy system have also been found to aggregate in a redox-dependent manner themselves. For example, oxidation of p62 at C105/113 in the N-terminal disordered region causes oligomerization and subsequent aggregation of p62. This stimulates autophagy in response to ROS, possibly in an attempt to maintain cellular homeostasis [170]. In addition, aggregated p62 occupies the NRF2-binding site in KEAP1, allowing stabilization of NRF2. NRF2 nuclear translocation causes expression of antioxidant- and stress response genes, among which p62 itself [171]. Redox-dependent p62 aggregation therefore ensures a robust stress response involving both autophagy and antioxidant response. Accordingly, mutations perturbing the redox-sensitivity of the NRF2 pathway are linked to ALS. Of note, mutant KRAS induced lung tumors in mice have been shown to depend on the NRF2 pathway for their survival and outgrowth [172], likely because it facilitates antioxidant- and autophagy-dependent clearance of cancer-associated proteotoxic and metabolic stress.



Taken together, protein aggregation has been shown to modulate ROS levels in several ways. Some of the increases in ROS production upon the gradual accumulation of aggregates might therefore be an attempt to regain homeostasis through modulation of the stress response. This eventually reaches a turning point when ROS reaches toxic levels and triggers a stress-response on its own [2]. The notion that oxidation by ROS can facilitate protein aggregation and that amyloids themselves can trigger ROS production could in principle also constitute a feed forward loop in which a small change in either ROS or protein aggregation could rapidly lead to a toxic cellular catastrophe, making redox-regulated protein aggregation an irreversible process [173]. But extensive random damage induced by ROS production either from an overactive stress response or from gross cellular dysfunction resulting in for instance lipid peroxidation might also have an evolutionary benefit and serve to actively eliminate damaged cells through the induction of ferroptosis [174].

# CONCLUSIONS

In this review, we have discussed the reciprocal regulation of redox signaling and protein aggregation. In short, oxidation of specific residues causes conformational changes and causes partial unfolding of a protein. This exposes residues that can participate in non-native interactions. Further structural rearrangements drive the oligomerization and subsequent formation of insoluble aggregates. We can distinguish two types of cysteine residues here: structural residues that form disulfide bonds for correct protein folding, and cysteines that can be reversibly oxidized which serve as important signaling switches. When reversible disulfide bond formation changes the protein structure such that it directly corresponds to protein function, it can be both a structural and a regulatory residue. Although the underlying processes seem somewhat

### Figure 3. Redox regulation of proteostasis

Redox signaling modulates proteostasis in many ways. Among its roles are the regulation of protein folding, unfolding/aggregation, toxicity reduction and damage response.

similar, the functional consequences of redox-dependent a stress-response in order to regain homeostasis might change protein aggregation are not. Besides simply resulting in toxic our view of proteinopathies. protein aggregates, oxidative aggregation can result in reversible (in)activation of a protein which allows regulation. Why aggregation is so much more prominent in aged individ-This can alter protein function and may serve as a protective uals is not entirely clear. The age-dependent increase of aggregation, oxidation and mitochondrial dysfunction, together or pro-survival mechanism. Although little is known about functional aggregation, it is thought that most aggregates are with a decline in multiple aggregation clearance systems could actually reversible, benefiting the regulatory possibilities. This cumulatively cause a destabilizing environment from which is also reflected in the suggestion that insoluble aggregates are protein aggregates can no longer recover [175,176]. The dinot inert protein disposals but can still alter its structure and verse effects of oxidative aggregation on proteins suggests that morphology according to redox-dependent post-aggregation in order to regulate proteins by oxidative aggregation, reversmodifications and that distinct structures of aggregated proibility of the process is essential in some cases. Little is known teins also cause distinct phenotypes. about reversibility of oxidized aggregates. For example, when the reducing capacity of a cell is restored, can the aggregates On the other hand, there is the hypothesis that ROS-induced fall apart into functional monomers again by reduction of the aggregation might be a cellular strategy to clear the more toxic oxidative modifications? It is also not clear if and how cellular soluble aggregates. Many of the examples we discussed in this systems to clear protein aggregates such as the proteasome and review support this; they are part of a positive feedback system autophagy can distinguish between 'functional' aggregates in which high ROS levels promote aggregation and the agthat are a temporary, regulated protein state, and toxic protein gregates themselves promote ROS production. In this way, aggregates that need clearance

redox signaling creates a bistable switch between functional proteins and insoluble aggregates without the accumulation PERSPECTIVES of toxic intermediates. Therefore, modulating ROS levels to promote rather than inhibit aggregation could be a more sensible therapeutic approach. Importance of the field: Both redox signaling and cor-

Almost all processes involved in protein aggregation are redox regulated (Figure 3). However, it is hard to determine whethand ROS production as a consequence of mitochondrial dysfunction have been described as hallmarks of aging. er altered redox signaling is a cause or consequence of protein aggregation. Often times it seems like it is both: altered redox This becomes especially clear in proteinopathies, where signaling favors aggregation, but the mutual amplification of both aberrant redox signaling and protein aggregation are the systems also provides a feed forward loop, consequently associated with severe neurodegenerative problems. altering the cellular redox state. One clue might lie in the hy-Summary of the current thinking: Collectively, these pothesis stating that  $H_2O_2$  is produced as a signaling molecule studies outline complex relationship between ROS, redox in response to damage, such as an accumulation of aggregates. signaling and proteostasis, where cause and consequence A gradual increase in aggregation is accompanied by an inare often hard to differentiate. Whereas protein oxidation creased H<sub>2</sub>O<sub>2</sub> production, which intensifies over time. Evencan trigger aggregation, increases in H<sub>2</sub>O<sub>2</sub> production tually, the H<sub>2</sub>O<sub>2</sub> might reach toxic levels, which itself may upon the gradual accumulation of aggregates might be a lead to damage. Understanding whether H<sub>2</sub>O<sub>2</sub> is produced as stress-response by itself. A small change in redox state or aggregation can in this way rapidly lead to a feed-forward

rect protein folding are essential for maintaining healthy cellular homeostasis. Accordingly, loss of proteostasis loop, making redox-regulated protein aggregation an irreversible process.

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**Future directions:** Going forward, it is important to better understand whether or not H2O2 is produced as a signal in response to proteotoxic stress in order to restore homeostasis, and whether increased H2O2 levels promote aggregation as a cellular strategy to clear the more toxic oligomeric aggregates. Understanding the multifaceted mechanisms regulating protein aggregation will pave the way for novel therapeutic windows to combat proteinopathies.

Protein	Abbreviation	Normal function	Involved Residue (Cys)	Modification	Consequence(s)	Type of Aggregation	Related Pathologies	Reference
AMP-activated protein kinase	AMPK-alpha	Energy metabolism	C130 and C174	disulfde	Inactivation	soluble aggregates	Cardiopathologies, energy starvation	[95]
Apolipoprotein A-I	APOA1	Cholesterol transport	methionines	methionine oxidation	Partial unfolding, fibrillization and inactivation	amyloid	APOA1 amyloidoses and atherosclerosis	[94]
APP/Amyloid-β	Aβ	Unknown	M35	methionine oxidation	Required for pro-oxidative activity	amyloid	Alzheimer's	[119]
Ataxin-2	ATXN2	TORC1 inhibition	methionines	methionine oxidation	Oxidation reverses aggregation, fuctional regulation of activity	LLPS, amyloid	Spinocerebellar atrophy, ALS	[80]
Cellular prion protein	PrP <sup>c</sup> and PrP <sup>sc</sup>	Synaptic function	C179 and C214	disulfde exchange	Reduction of PrP <sup>C</sup> induces agrgegation of PrP <sup>SC</sup> polymer	amyloid	Transmissable spongiform encelopathies	[96]
Cyclin-dependent kinase inhibitor 2A	p16 <sup>INK4A</sup>	Cell cycle regulation, senescence	C72	homodimerization	Inactivation	amyloid	Cancer	[69]

# TABLES

Table 1. Summary of redox-regulated protein aggregates

Endostatin	COL18A1	Angiogenesis inhibition	C33, C135, C165 and C173	disulfde	Prevents aggregation	amyloid	Alzheimer's	[105]
Fas ligand	FasL	Apoptosis, inflammation	methionines	methionine oxidation	Multimerization and aggregation, enhanced biological activity	unknown	Acute lung injury	[92]
Glyceraldehyde- 3-phosphate dehydrogenase	GAPDH	Glycolysis	M46	methionine oxidation, disulfdes	Local conformational change promotes disulfde crosslinking and aggregation	amyloid	Alzheimer's, motor neuron disease	[87]
Growth hormone (recombinant)	hGH	(Therapeutic protein production)	M14 and M125	methionine oxidation	Lower stability	unknown	GH deficiency	[06]
human Islet Amyloid Polypeptide	hIAPP	Insulin/glucagon secretion, gastric emptying	C2 and C7	disulfde	Prevents aggregation	amyloid	Type 2 diabetes	[103]
Huntingtin	HT'T	Unknown	M8	post-aggregation methionine oxidation	Controls interaction between aggregates	amyloid	Huntington disease	[106]
			C115 and C119	disulfde mediated oligomerization	Oxidation-dependent soluble toxic oligomers, slower clearance	soluble oligomeric aggregates		[97]
Interferon-\$1a (recombinant)	IFN β1a	(Therapeutic protein production)	many residues (M, H, F, W, Y)	crosslinking	Lower stability	unknown		[89]

CROSS-TALK BETWEEN REDOX SIGNALLING AND PROTEIN AGGREGATION

Table 1. Continue	ų.							
Protein	Abbreviation	Normal function	Involved Residue (Cys)	Modification	Consequence(s)	Type of Aggregation	Related Pathologies	Reference
Mitochondrial GrpE protein homolog	MGE1	Proteostasis, HSP70 cochaperone	M155	methionine oxidation	Inactive HSP70 but targeting it to unfolded proteins	amyloid	Myopathies	[141]
Sequestosome-1	SQSTM1/p62	Autophagy	C105 and C113	disulfde mediated oligomerization	More autophagy, cell survival	insoluble aggregates, LLPS	ALS	[170]
Superoxide dismutase 1	SOD1	Dismutation of superoxide	C111	disulfde-linked dimerization	Oligomerization and subsequent fibril formation	oligomeric, amyloid and amorphous	ALS	[102]
Transthyretin	T'TR	Thyroid hormone binding	C10, M1 and M13	cysteine solfonic acid, methionine sulfoxide	Tetramer dissociation and aggregation	amyloid	Senile systemic amyloidosis	[93]
Tryptophan hydroxylase 2	TPH2	Serotonin biosynthesis	any out of 13 cysteines	disulfde, crosslinking	Misfolding, intra- and intermolecular disulfde bond formation, protein inactivation	unknown, disulfde crosslinked oligomers	Parkinson's	[72]
Vinisin-like protein 1	VSNL1	Calcium sensing	C187	disulfde-linked homodimerization	Reduced levels of functional protein	amyloid, disulfde crosslinked oligomers	ALS, AD	[75]
y-synuclein	SNCG	Neurofilament network integrity	M38 and Y39	oxidation-dependent oligomerization	Aggregation and seeding for <i>a</i> -synuclein aggregation	amyloid	Parkinson's	[88]
β2-microglobulin	β2M	MHCI light chain	C25 and C80	disulfde reduction, disulfide exchange, post aggregation oxidation	Aggregation, post-aggregation stabilization	amyloid	Hæmodialysis-related amyloidosis	[107]
$\gamma$ -crystallins	CRYG	Lens transparency	C32 and C41	intramolecular disulfde	Destabilizes its N-terminal domain, stabilizes an intermediate which is prone to aggregation	amorphous	Cataract	[82]
ĸ-casein	CSN3	Milk protein	M95 and M106	methionine oxidation	Increased aggregation, increased toxicity	amyloid	Corpora amylacea	[91]

# REFERENCES

- López-Otín, C.; Blasco, M.A.; Partridge, L.; Serrano, M.; Kroemer, The Hallmarks of Aging. *Cell* 2013, *153*, 1194–1217, doi:10.1016 cell.2013.05.039.
- 2. Hekimi, S.; Lapointe, J.; Wen, Y. Taking a "Good" Look at Free Radica in the Aging Process. *Trends Cell Biol* 2011, *21*, 569–576, doi:10.1016, tcb.2011.06.008.
- Hipp, M.S.; Kasturi, P.; Hartl, F.U. The Proteostasis Network and Its D cline in Ageing. *Nat Rev Mol Cell Bio* 2019, *20*, 421–435, doi:10.1038 s41580-019-0101-y.
- Walther, D.M.; Kasturi, P.; Zheng, M.; Pinkert, S.; Vecchi, G.; Ciryan P.; Morimoto, R.I.; Dobson, C.M.; Vendruscolo, M.; Mann, M.; et a Widespread Proteome Remodeling and Aggregation in Aging C. Ele gans. *Cell* 2015, *161*, 919–932, doi:10.1016/j.cell.2015.03.032.
- Matsui, H.; Ito, H.; Taniguchi, Y.; Inoue, H.; Takeda, S.; Takahashi, F. Proteasome Inhibition in Medaka Brain Induces the Features of Pa kinson's Disease. *J Neurochem* 2010, *115*, 178–187, doi:10.1111/j.147. 4159.2010.06918.x.
- 6. Kitajima, Y.; Tashiro, Y.; Suzuki, N.; Warita, H.; Kato, M.; Tateyama, M. Ando, R.; Izumi, R.; Yamazaki, M.; Abe, M.; et al. Proteasome Dy function Induces Muscle Growth Defects and Protein Aggregation *Cell Sci* 2014, *127*, 5204–5217, doi:10.1242/jcs.150961.
- 7. Wang, R.; Zhao, J.; Zhang, J.; Liu, W.; Zhao, M.; Li, J.; Lv, J.; Li, Y. Effect of Lysosomal and Ubiquitin-Proteasome System Dysfunction on the Abnormal Aggregation of α-Synuclein in PC12 Cells. *Exp Ther Me* 2015, *9*, 2088–2094, doi:10.3892/etm.2015.2432.
- Koga, H.; Kaushik, S.; Cuervo, A.M. Protein Homeostasis and Aging The Importance of Exquisite Quality Control. *Ageing Res Rev* 201 10, 205–215, doi:10.1016/j.arr.2010.02.001.
- Visscher, M.; Henau, S.D.; Wildschut, M.H.E.; Es, R.M. van; Dhondt, I Michels, H.; Kemmeren, P.; Nollen, E.A.; Braeckman, B.P.; Burgerin B.M.T.; et al. Proteome-Wide Changes in Protein Turnover Rates i C. Elegans Models of Longevity and Age-Related Disease. *Cell Repor* 2016, *16*, 3041 3051, doi:10.1016/j.celrep.2016.08.025.
- Kumar, V.; Singh, D.; Singh, B.K.; Singh, S.; Mittra, N.; Jha, R.R.; Pa D.K.; Singh, C. Alpha-Synuclein Aggregation, Ubiquitin Protease System Impairment, and l-Dopa Response in Zinc-Induced Parkins ism: Resemblance to Sporadic Parkinson's Disease. *Mol Cell Bioch* 2018, 444, 149–160, doi:10.1007/s11010-017-3239-y.
- 11. Wilson, D.N.; Beckmann, R. The Ribosomal Tunnel as a Functional J vironment for Nascent Polypeptide Folding and Translational Stalli *Curr Opin Struc Biol* 2011, *21*, 274–282, doi:10.1016/j.sbi.2011.01.0
- Balchin, D.; Hayer-Hartl, M.; Hartl, F.U. In Vivo Aspects of Prot Folding and Quality Control. *Science* 2016, *353*, aac4354, doi:10.112 science.aac4354.

- Brockwell, D.J.; Radford, S.E. Intermediates: Ubiquitous Species on Folding Energy Landscapes? *Curr Opin Struc Biol* 2007, *17*, 30–37, doi:10.1016/j.sbi.2007.01.003.
- Braakman, I.; Hebert, D.N. Protein Folding in the Endoplasmic Reticulum. *Csh Perspect Biol* 2013, *5*, a013201, doi:10.1101/cshperspect. a013201.
- Weids, A.J.; Ibstedt, S.; Tamás, M.J.; Grant, C.M. Distinct Stress Conditions Result in Aggregation of Proteins with Similar Properties. *Sci Rep-uk* 2016, *6*, srep24554, doi:10.1038/srep24554.
- Uversky, V.N.; Fink, A.L. Conformational Constraints for Amyloid Fibrillation: The Importance of Being Unfolded. *Biochimica Et Biophysica Acta Bba - Proteins Proteom* 2004, *1698*, 131–153, doi:10.1016/j. bbapap.2003.12.008.
- Gupta, R.; Kasturi, P.; Bracher, A.; Loew, C.; Zheng, M.; Villella, A.; Garza, D.; Hartl, F.U.; Raychaudhuri, S. Firefly Luciferase Mutants as Sensors of Proteome Stress. *Nat Methods* 2011, *8*, 879–884, doi:10.1038/nmeth.1697.
- Bouziane, H.; Chouarfia, A. Sequence- and Structure-Based Prediction of Amyloidogenic Regions in Proteins. *Soft Comput* 2019, 1–24, doi:10.1007/s00500-019-04087-z.
- 19. Chiti, F.; Stefani, M.; Taddei, N.; Ramponi, G.; Dobson, C.M. Rationalization of the Effects of Mutations on Peptide and Protein Aggregation Rates. *Nature* 2003, *424*, 805, doi:10.1038/nature01891.
- Monsellier, E.; Chiti, F. Prevention of Amyloid-like Aggregation as a Driving Force of Protein Evolution. *Embo Rep* 2007, *8*, 737–742, doi:10.1038/sj.embor.7401034.
- Levy, E.D.; De, S.; Teichmann, S.A. Cellular Crowding Imposes Global Constraints on the Chemistry and Evolution of Proteomes. *Proc National Acad Sci* 2012, *109*, 20461–20466, doi:10.1073/ pnas.1209312109.
- Annamalai, K.; Gührs, K.; Koehler, R.; Schmidt, M.; Michel, H.; Loos, C.; Gaffney, P.M.; Sigurdson, C.J.; Hegenbart, U.; Schönland, S.; et al. Polymorphism of Amyloid Fibrils In Vivo. *Angewandte Chemie Int Ed* 2016, *55*, 4822–4825, doi:10.1002/anie.201511524.
- Knowles, T.P.; Fitzpatrick, A.W.; Meehan, S.; Mott, H.R.; Vendruscolo, M.; Dobson, C.M.; Welland, M.E. Role of Intermolecular Forces in Defining Material Properties of Protein Nanofibrils. *Science* 2007, *318*, 1900–1903, doi:10.1126/science.1150057.
- Sengupta, U.; Nilson, A.N.; Kayed, R. The Role of Amyloid-β Oligomers in Toxicity, Propagation, and Immunotherapy. *Ebiomedicine* 2016, 6, 42–49, doi:10.1016/j.ebiom.2016.03.035.
- 25. Lambert, M.P.; Barlow, A.K.; Chromy, B.A.; Edwards, C.; Freed, R.; Liosatos, M.; Morgan, T.E.; Rozovsky, I.; Trommer, B.; Viola, K.L.; et al. Diffusible, Nonfibrillar Ligands Derived from Aβ1–42 Are Potent Central Nervous System Neurotoxins. *Proc National Acad Sci* 1998, 95, 6448–6453, doi:10.1073/pnas.95.11.6448.

- Glabe, C.G. Common Mechanisms of Amyloid Oligomer Pathogenesis in Degenerative Disease. *Neurobiol Aging* 2006, *27*, 570–575, doi:10.1016/j.neurobiolaging.2005.04.017.
- 27. Soeda, Y.; Saito, M.; Maeda, S.; Ishida, K.; Nakamura, A.; Kojima, S.; Takashima, A. Methylene Blue Inhibits Formation of Tau Fibrils but Not of Granular Tau Oligomers: A Plausible Key to Understanding Failure of a Clinical Trial for Alzheimer's Disease. *J Alzheimer's Dis* 2019, *Preprint*, 1–10, doi:10.3233/jad-181001.
- 28. Mijnders, M.; Kleizen, B.; Braakman, I. Correcting CFTR Folding Defects by Small-Molecule Correctors to Cure Cystic Fibrosis. *Curr Opin Pharmacol* 2017, 34, 83–90, doi:10.1016/j.coph.2017.09.014.
- 29. Otzen, D.; Riek, R. Functional Amyloids. *Csh Perspect Biol* 2019, a033860, doi:10.1101/cshperspect.a033860.
- Uversky, V.N.; Oldfield, C.J.; Dunker, A.K. Intrinsically Disordered Proteins in Human Diseases: Introducing the D2 Concept. *Annu Rev Biophys* 2008, *37*, 215–246, doi:10.1146/annurev.biophys.37.032807.125924.
- Banani, S.F.; Lee, H.O.; Hyman, A.A.; Rosen, M.K. Biomolecular Condensates: Organizers of Cellular Biochemistry. *Nat Rev Mol Cell Bio* 2017, 18, 285–298, doi:10.1038/nrm.2017.7.
- 32. Peskett, T.R.; Rau, F.; O'Driscoll, J.; Patani, R.; Lowe, A.R.; Saibil, H.R. A Liquid to Solid Phase Transition Underlying Pathological Huntingtin Exon1 Aggregation. *Mol Cell* 2018, *70*, 588-601.e6, doi:10.1016/j.molcel.2018.04.007.
- 33. Ambadipudi, S.; Biernat, J.; Riedel, D.; Mandelkow, E.; Zweckstetter, M. Liquid–Liquid Phase Separation of the Microtubule-Binding Repeats of the Alzheimer-Related Protein Tau. *Nat Commun* 2017, *8*, 275, doi:10.1038/s41467-017-00480-0.
- Wentink, A.; Nussbaum-Krammer, C.; Bukau, B. Modulation of Amyloid States by Molecular Chaperones. *Csh Perspect Biol* 2019, *11*, a033969, doi:10.1101/cshperspect.a033969.
- Gao, X.; Carroni, M.; Nussbaum-Krammer, C.; Mogk, A.; Nillegoda, N.B.; Szlachcic, A.; Guilbride, D.L.; Saibil, H.R.; Mayer, M.P.; Bukau, B. Human Hsp70 Disaggregase Reverses Parkinson's-Linked α-Synuclein Amyloid Fibrils. *Mol Cell* 2015, *59*, 781–793, doi:10.1016/j. molcel.2015.07.012.
- 36. Cereghetti, G.; Saad, S.; Dechant, R.; Peter, M. Reversible, Functional Amyloids: Towards an Understanding of Their Regulation in Yeast and Humans. *Cell Cycle* 2018, *17*, 1545–1558, doi:10.1080/1538410 1.2018.1480220.
- Thibaudeau, T.A.; Anderson, R.T.; Smith, D.M. A Common Mechanism of Proteasome Impairment by Neurodegenerative Disease-Associated Oligomers. *Nat Commun* 2018, *9*, 1097, doi:10.1038/s41467-018-03509-0.
- Caccamo, A.; Ferreira, E.; Branca, C.; Oddo, S. P62 Improves AD-like Pathology by Increasing Autophagy. *Mol Psychiatr* 2016, *22*, 865, doi:10.1038/mp.2016.139.

- 39. Cho, M.-H.; Cho, K.; Kang, H.-J.; Jeon, E.-Y.; Kim, H.-S.; Kwon, H.-J.; Kim, H.-M.; Kim, D.-H.; Yoon, S.-Y. Autophagy in Microglia Degrades Extracellular β-Amyloid Fibrils and Regulates the NLRP3 Inflammasome. *Autophagy* 2014, *10*, 1761–1775, doi:10.4161/auto.29647.
- Cuervo, A.M.; Stefanis, L.; Fredenburg, R.; Lansbury, P.T.; Sulzer, D. Impaired Degradation of Mutant α-Synuclein by Chaperone-Mediated Autophagy. *Science* 2004, *305*, 1292–1295, doi:10.1126/science.1101738.
- 41. Ravikumar, B.; Duden, R.; Rubinsztein, D.C. Aggregate-Prone Proteins with Polyglutamine and Polyalanine Expansions Are Degraded by Autophagy. *Hum Mol Genet* 2002, *11*, 1107–1117, doi:10.1093/ hmg/11.9.1107.
- 42. Yung, C.; Sha, D.; Li, L.; Chin, L.-S. Parkin Protects Against Misfolded SOD1 Toxicity by Promoting Its Aggresome Formation and Autophagic Clearance. *Mol Neurobiol* 2016, *53*, 6270–6287, doi:10.1007/ s12035-015-9537-z.
- Coryell, P.R.; Goraya, S.K.; Griffin, K.A.; Redick, M.A.; Sisk, S.R.; Purvis, J.E. Autophagy Regulates the Localization and Degradation of P16INK4a. *Biorxiv* 2019, 521682, doi:10.1101/521682.
- 44. Chen, Y.; Liu, H.; Guan, Y.; Wang, Q.; Zhou, F.; Jie, L.; Ju, J.; Pu, L.; Du, H.; Wang, X. The Altered Autophagy Mediated by TFEB in Animal and Cell Models of Amyotrophic Lateral Sclerosis. *American journal* of translational research 2015, 7, 1574–1587.
- i5. Bordi, M.; Berg, M.J.; Mohan, P.S.; Peterhoff, C.M.; Alldred, M.J.; Che, S.; Ginsberg, S.D.; Nixon, R.A. Autophagy Flux in CA1 Neurons of Alzheimer Hippocampus: Increased Induction Overburdens Failing Lysosomes to Propel Neuritic Dystrophy. *Autophagy* 2016, *12*, 2467– 2483, doi:10.1080/15548627.2016.1239003.
- Stadtman, E.R. Protein Modification in Aging. J Gerontology 1988, 43, B112–B120, doi:10.1093/geronj/43.5.b112.
- Evans, A.R.; Gu, L.; Guerrero, R.; Robinson, R.A.S. Global CPILOT Analysis of the APP/PS-1 Mouse Liver Proteome. *Proteom - Clin Appl* 2015, 9, 872–884, doi:10.1002/prca.201400149.
- Abdul, H.M.; Sultana, R.; Clair, D.K.S.; Markesbery, W.R.; Butterfield, D.A. Oxidative Damage in Brain from Human Mutant APP/PS-1 Double Knock-in Mice as a Function of Age. *Free Radic Biology Medicine* 2008, *45*, 1420–1425, doi:10.1016/j.freeradbiomed.2008.08.012.
- Sinclair, A.J.; Bayer, A.J.; Johnston, J.; Warner, C.; Maxwell, S.R.J. Altered Plasma Antioxidant Status in Subjects with Alzheimer's Disease and Vascular Dementia. *Int J Geriatr Psych* 1998, *13*, 840–845, doi:10.1002/(sici)1099-1166(1998120)13:12<840::aidgps877>3.0.co;2-r.
- Smith, M.A.; Rottkamp, C.A.; Nunomura, A.; Raina, A.K.; Perry, G. Oxidative Stress in Alzheimer's Disease. *Biochimica Et Biophysica Acta Bba - Mol Basis Dis* 2000, *1502*, 139–144, doi:10.1016/s0925-4439(00)00040-5.

- Gu, L.; Robinson, R.A.S. High-Throughput Endogenous Measur ment of S -Nitrosylation in Alzheimer's Disease Using Oxidized Cy teine-Selective CPILOT. *Analyst* 2016, *141*, 3904 3915, doi:10.103 c6an00417b.
- Robinson, R.A.S.; Cao, Z.; Williams, C. Oxidative Stress in CD90 T-Cells of AβPP/PS-1 Transgenic Mice. *J Alzheimer's Dis* 2013, 3, 661–666, doi:10.3233/jad-130665.
- Sohal, R.S.; Sohal, B.H. Hydrogen Peroxide Release by Mitocho dria Increases during Aging. *Mech Ageing Dev* 1991, *57*, 187–20 doi:10.1016/0047-6374(91)90034-w.
- 54. Asensi, M.; Sastre, J.; Pallardo, F.V.; Lloret, A.; Lehner, M.; Asunci J.G.; Viña, J. [23] Ratio of Reduced to Oxidized Glutathione as In cator of Oxidative Stress Status and DNA Damage. *Methods Enzy* 1999, 299, 267–276, doi:10.1016/s0076-6879(99)99026-2.
- 55. Raamsdonk, J.M.V.; Hekimi, S. Deletion of the Mitochondrial Superide Dismutase Sod-2 Extends Lifespan in Caenorhabditis Elegans. *I Genet* 2009, 5, e1000361, doi:10.1371/journal.pgen.1000361.
- 56. Mesquita, A.; Weinberger, M.; Silva, A.; Sampaio-Marques, B.; Almeid B.; Leão, C.; Costa, V.; Rodrigues, F.; Burhans, W.C.; Ludovico, Caloric Restriction or Catalase Inactivation Extends Yeast Chron logical Lifespan by Inducing H2O2 and Superoxide Dismutase A tivity. *Proc National Acad Sci* 2010, *107*, 15123–15128, doi:10.107/ pnas.1004432107.
- 57. Pérez, V.I.; Remmen, H.V.; Bokov, A.; Epstein, C.J.; Vijg, J.; Richar son, A. The Overexpression of Major Antioxidant Enzymes Does N Extend the Lifespan of Mice. *Aging Cell* 2009, *8*, 73–75, doi:10.111 j.1474-9726.2008.00449.x.
- Holmström, K.M.; Finkel, T. Cellular Mechanisms and Physiologic Consequences of Redox-Dependent Signalling. *Nat Rev Mol Cell E* 2014, 15, 411–421, doi:10.1038/nrm3801.
- Sies, H.; Berndt, C.; Jones, D.P. Oxidative Stress. Annu Rev Bioch 2017, 86, 715–748, doi:10.1146/annurev-biochem-061516-045037.
- Go, Y.-M.; Jones, D.P. Redox Compartmentalization in Eukaryot Cells. *Biochimica Et Biophysica Acta Bba - Gen Subj* 2008, *1780*, 1273 1290, doi:10.1016/j.bbagen.2008.01.011.
- Kaludercic, N.; Deshwal, S.; Lisa, F.D. Reactive Oxygen Species an Redox Compartmentalization. *Front Physiol* 2014, *5*, 285, doi:10.338 fphys.2014.00285.
- 62. Wang, Y.; Hekimi, S. Mitochondrial Dysfunction and Longevity in An mals: Untangling the Knot. *Science* 2015, *350*, 1204–1207, doi:10.1120 science.aac4357.
- 63. Cheignon, C.; Tomas, M.; Bonnefont-Rousselot, D.; Faller, P.; Hureau C.; Collin, F. Oxidative Stress and the Amyloid Beta Peptide in Alz heimer's Disease. *Redox Biol* 2018, *14*, 450–464, doi:10.1016/redox.2017.10.014.

- l t 5 A 1 I t
- tion to Stressors by Systemic Protein Amyloidogenesis. Dev Cell 239, 155–168, doi:10.1016/j.devcel.2016.09.002.
  68. Saad, S.; Cereghetti, G.; Feng, Y.; Picotti, P.; Peter, M.; Dechar Reversible Protein Aggregation Is a Protective Mechanism to Encell Cycle Restart after Stress. Nat Cell Biol 2017, 19, 1202–2014
- 69. Göbl, C.; Morris, V.K.; Dam, L. van; Visscher, M.; Polderman, P.E.; Hartlmüller, C.; Ruiter, H. de; Hora, M.; Liesinger, L.; Birner-Gruenberger, R.; et al. Cysteine Oxidation Triggers Amyloid Fibril Formation of the Tumor Suppressor P16INK4A. *Redox Biol* 2019, 101316, doi:10.1016/j.redox.2019.101316.
- 70. Pervaiz, S.; Clement, M.-V. Superoxide Anion: Oncogenic Reactive Oxygen Species? *Int J Biochem Cell Biology* 2007, *39*, 1297–1304, doi:10.1016/j.biocel.2007.04.007.
- 71. Hoffman, A.; Spetner, L.M.; Burke, M. Ramifications of a Redox Switch within a Normal Cell: Its Absence in a Cancer Cell. *Free Radical Bio Med* 2008, *45*, 265–268, doi:10.1016/j.freeradbiomed.2008.03.025.
- 72. Kuhn, D.M.; Sykes, C.E.; Geddes, T.J.; Jaunarajs, K.L.E.; Bishop, C. Tryptophan Hydroxylase 2 Aggregates through Disulfide Cross-linking upon Oxidation: Possible Link to Serotonin Deficits and Non-motor Symptoms in Parkinson's Disease. *J Neurochem* 2011, *116*, 426–437, doi:10.1111/j.1471-4159.2010.07123.x.
- Kuhn, D.M.; Geddes, T.J. Peroxynitrite Inactivates Tryptophan Hydroxylase via Sulfhydryl Oxidation. *J Biol Chem* 1999, 274, 29726– 29732, doi:10.1074/jbc.274.42.29726.
- 74. Bothwell, M.Y.; Gillette, M.U. Circadian Redox Rhythms in the Regulation of Neuronal Excitability. *Free Radical Bio Med* 2018, *119*, 45–55, doi:10.1016/j.freeradbiomed.2018.01.025.
- 75. Liebl, M.P.; Kaya, A.M.; Tenzer, S.; Mittenzwei, R.; Koziollek-Drechsler, I.; Schild, H.; Moosmann, B.; Behl, C.; Clement, A.M. Dimerization of Visinin-like Protein 1 Is Regulated by Oxidative Stress and Calcium and Is a Pathological Hallmark of Amyotrophic Lateral Sclerosis. *Free Radical Bio Med* 2014, *72*, 41 54, doi:10.1016/j.freeradbiomed.2014.04.008.

- 121. Atwood, C.S.; Obrenovich, M.E.; Liu, T.; Chan, H.; Perry, G.; Smith, M.A.; Martins, R.N. Amyloid-β: A Chameleon Walking in Two Worlds: A Review of the Trophic and Toxic Properties of Amyloid-β. *Brain Res Rev* 2003, *43*, 1–16, doi:10.1016/s0165-0173(03)00174-7.
- 122. Baruch-Suchodolsky, R.; Fischer, B. Aβ 40, Either Soluble or Aggregated, Is a Remarkably Potent Antioxidant in Cell-Free Oxidative Systems. *Biochemistry-us* 2009, 48, 4354–4370, doi:10.1021/bi802361k.
- 123. Huang, X.; Atwood, C.S.; Hartshorn, M.A.; Multhaup, G.; Goldstein, L.E.; Scarpa, R.C.; Cuajungco, M.P.; Gray, D.N.; Lim, J.; Moir, R.D.; et al. The Aβ Peptide of Alzheimer's Disease Directly Produces Hydrogen Peroxide through Metal Ion Reduction. *Biochemistry-us* 1999, *38*, 7609–7616, doi:10.1021/bi990438f.
- 124. Hensley, K.; Carney, J.M.; Mattson, M.P.; Aksenova, M.; Harris, M.; Wu, J.F.; Floyd, R.A.; Butterfield, D.A. A Model for Beta-Amyloid Aggregation and Neurotoxicity Based on Free Radical Generation by the Peptide: Relevance to Alzheimer Disease. *Proc National Acad Sci* 1994, *91*, 3270–3274, doi:10.1073/pnas.91.8.3270.
- 125. Smith, D.G.; Cappai, R.; Barnham, K.J. The Redox Chemistry of the Alzheimer's Disease Amyloid β Peptide. *Biochimica Et Biophysica Acta Bba - Biomembr* 2007, *1768*, 1976–1990, doi:10.1016/j. bbamem.2007.02.002.
- 126. Barnham, K.J.; Ciccotosto, G.D.; Tickler, A.K.; Ali, F.E.; Smith, D.G.; Williamson, N.A.; Lam, Y.-H.; Carrington, D.; Tew, D.; Kocak, G.; et al. Neurotoxic, Redox-Competent Alzheimer's β-Amyloid Is Released from Lipid Membrane by Methionine Oxidation. *J Biol Chem* 2003, 278, 42959–42965, doi:10.1074/jbc.m305494200.
- 127. Atwood, C.S.; Perry, G.; Zeng, H.; Kato, Y.; Jones, W.D.; Ling, K.-Q.; Huang, X.; Moir, R.D.; Wang, D.; Sayre, L.M.; et al. Copper Mediates Dityrosine Cross-Linking of Alzheimer's Amyloid-β †. *Biochemistry-us* 2004, 43, 560–568, doi:10.1021/bi0358824.
- 128. Deas, E.; Cremades, N.; Angelova, P.R.; Ludtmann, M.H.R.; Yao, Z.; Chen, S.; Horrocks, M.H.; Banushi, B.; Little, D.; Devine, M.J.; et al. Alpha-Synuclein Oligomers Interact with Metal Ions to Induce Oxidative Stress and Neuronal Death in Parkinson's Disease. *Antioxid Redox Sign* 2016, *24*, 376–391, doi:10.1089/ars.2015.6343.
- 129. Lovell, M.A.; Robertson, J.D.; Teesdale, W.J.; Campbell, J.L.; Markesbery, W.R. Copper, Iron and Zinc in Alzheimer's Disease Senile Plaques. *J Neurol Sci* 1998, *158*, 47–52, doi:10.1016/s0022-510x(98)00092-6.
- 130. Hashimoto, M.; Rockenstein, E.; Crews, L.; Masliah, E. Role of Pro tein Aggregation in Mitochondrial Dysfunction and Neurodegenera tion in Alzheimer's and Parkinson's Diseases. *Neuromol Med* 2003, 4 21–35, doi:10.1385/nmm:4:1-2:21.
- 131. Schubert, D.; Behl, C.; Lesley, R.; Brack, A.; Dargusch, R.; Sagara, Y.; Kimura, H. Amyloid Peptides Are Toxic via a Common Oxidative Mechanism. *Proc National Acad Sci* 1995, *92*, 1989–1993, doi:10.1073/ pnas.92.6.1989.

- 132. Brookes, P.S.; Yoon, Y.; Robotham, J.L.; Anders, M.W.; Sheu, S.-S. Calcium, ATP, and ROS: A Mitochondrial Love-Hate Triangle. *Am J Physiol-cell Ph* 2004, 287, C817–C833, doi:10.1152/ajpcell.00139.2004.
- 33. Curtain, C.C.; Ali, F.; Volitakis, I.; Cherny, R.A.; Norton, R.S.; Beyreuther, K.; Barrow, C.J.; Masters, C.L.; Bush, A.I.; Barnham, K.J. Alzheimer's Disease Amyloid-β Binds Copper and Zinc to Generate an Allosterically Ordered Membrane-Penetrating Structure Containing Superoxide Dismutase-like Subunits. *J Biol Chem* 2001, 276, 20466–20473, doi:10.1074/jbc.m100175200.
- 134. Casas-Tinto, S.; Zhang, Y.; Sanchez-Garcia, J.; Gomez-Velazquez, M.; Rincon-Limas, D.E.; Fernandez-Funez, P. The ER Stress Factor XBP1s Prevents Amyloid-Beta Neurotoxicity. *Hum Mol Genet* 2011, 20, 2144–2160, doi:10.1093/hmg/ddr100.
- 135. Gerakis, Y.; Hetz, C. Emerging Roles of ER Stress in the Aetiology and Pathogenesis of Alzheimer's Disease. *Febs J* 2017, 285, 995–1011, doi:10.1111/febs.14332.
- 136. Haynes, C.M.; Titus, E.A.; Cooper, A.A. Degradation of Misfolded Proteins Prevents ER-Derived Oxidative Stress and Cell Death. *Mol Cell* 2004, 15, 767–776, doi:10.1016/j.molcel.2004.08.025.
- 137. Peng, T.; Jou, M. Oxidative Stress Caused by Mitochondrial Calcium Overload. *Ann Ny Acad Sci* 2010, *1201*, 183–188, doi:10.1111/j.1749-6632.2010.05634.x.
- 38. Santos, C.X.C.; Tanaka, L.Y.; Wosniak, J.; Laurindo, F.R.M. Mechanisms and Implications of Reactive Oxygen Species Generation During the Unfolded Protein Response: Roles of Endoplasmic Reticulum Oxidoreductases, Mitochondrial Electron Transport, and NADPH Oxidase. *Antioxid Redox Sign* 2009, *11*, 2409–2427, doi:10.1089/ars.2009.2625.
- 139. Malhotra, J.D.; Kaufman, R.J. Endoplasmic Reticulum Stress and Oxidative Stress: A Vicious Cycle or a Double-Edged Sword? *Antioxid Redox Sign* 2007, *9*, 2277–2294, doi:10.1089/ars.2007.1782.
- 140. Mogk, A.; Bukau, B.; Kampinga, H.H. Cellular Handling of Protein Aggregates by Disaggregation Machines. *Mol Cell* 2018, *69*, 214–226, doi:10.1016/j.molcel.2018.01.004.
- 41. Karri, S.; Singh, S.; Paripati, A.K.; Marada, A.; Krishnamoorthy, T.; Guruprasad, L.; Balasubramanian, D.; Sepuri, N.B.V. Adaptation of Mge1 to Oxidative Stress by Local Unfolding and Altered Interaction with Mitochondrial Hsp70 and Mxr2. *Mitochondrion* 2018, 46, 140– 148, doi:10.1016/j.mito.2018.04.003.
- 142. Miyata, Y.; Rauch, J.N.; Jinwal, U.K.; Thompson, A.D.; Srinivasan, S.; Dickey, C.A.; Gestwicki, J.E. Cysteine Reactivity Distinguishes Redox Sensing by the Heat-Inducible and Constitutive Forms of Heat Shock Protein 70. *Chem Biol* 2012, *19*, 1391–1399, doi:10.1016/j.chembiol.2012.07.026.
- 143. Stöcker, S.; Maurer, M.; Ruppert, T.; Dick, T.P. A Role for 2-Cys Peroxiredoxins in Facilitating Cytosolic Protein Thiol Oxidation. Nat Chem Biol 2017, 14, doi:10.1038/nchembio.2536.

- 144. Weids, A.J.; Grant, C.M. The Yeast Peroxiredoxin Tsa1 Protects against Protein-Aggregate-Induced Oxidative Stress. *J Cell Sci* 2014, *127*, 1327– 1335, doi:10.1242/jcs.144022.
  145. Teixeira, F.; Tse, E.; Castro, H.; Makepeace, K.A.T.; Meinen, B.A.;
  156. Silva, G.M.; Netto, L.E.S.; Simões, V.; Santos, L.F.A.; Gozzo, F.C.; Demasi, M.A.A.; Oliveira, C.L.P.; Bicev, R.N.; Klitzke, C.F.; Sogayar, M.C.; et al. Redox Control of 20S Proteasome Gating. *Antioxid Redox Sign* 2012, *16*, 1183–1194, doi:10.1089/ars.2011.4210.
- 145. Teixeira, F.; Tse, E.; Castro, H.; Makepeace, K.A.T.; Meinen, B.A.; Borchers, C.H.; Poole, L.B.; Bardwell, J.C.; Tomás, A.M.; Southworth, D.R.; et al. Chaperone Activation and Client Binding of a 2-Cysteine Peroxiredoxin. *Nat Commun* 2019, *10*, 659, doi:10.1038/s41467-019-08565-8. *Sign* 2012, *16*, 1183–1194, doi:10.1089/ars.2011.4210.
  157. Jung, T.; Höhn, A.; Grune, T. The Proteasome and the Degradation of Oxidized Proteins: Part III—Redox Regulation of the Proteasomal System. *Redox Biol* 2014, *2*, 388–394, doi:10.1016/j.redox.2013.12.029.
  158. Tsverkov, P.: Myers, N.: Eliav, R.: Adamovich, Y.: Hagai, T.: Adler.
- 146. Jang, H.H.; Kim, S.Y.; Park, S.K.; Jeon, H.S.; Lee, Y.M.; Jung, J.H.; Le S.Y.; Chae, H.B.; Jung, Y.J.; Lee, K.O.; et al. Phosphorylation and Concomitant Structural Changes in Human 2-Cys Peroxiredoxin Isotype Differentially Regulate Its Peroxidase and Molecular Chaperone Funtions. *Febs Lett* 2006, *580*, 351–355, doi:10.1016/j.febslet.2005.12.03
- 147. Saccoccia, F.; Di Micco, P.; Boumis, G.; Brunori, M.; Koutris, Miele, A.E.; Morea, V.; Sriratana, P.; Williams, D.L.; Bellelli, A.; et Moonlighting by Different Stressors: Crystal Structure of the Cha erone Species of a 2-Cys Peroxiredoxin. *Structure* 2012, *20*, 429–43 doi:10.1016/j.str.2012.01.004.
- 148. Park, J.W.; Piszczek, G.; Rhee, S.G.; Chock, P.B. Glutathionylatic of Peroxiredoxin I Induces Decamer to Dimers Dissociation with Concomitant Loss of Chaperone Activity. *Biochemistry-us* 2011, 5 3204–3210, doi:10.1021/bi101373h.
- 149. Barranco-Medina, S.; Lázaro, J.-J.; Dietz, K.-J. The Oligomeric C formation of Peroxiredoxins Links Redox State to Function. *Febs I* 2009, 583, 1809 1816, doi:10.1016/j.febslet.2009.05.029.
- 150. Shringarpure, R.; Grune, T.; Davies, K.J.A. Protein Oxidation and 2 Proteasome-Dependent Proteolysis in Mammalian Cells. *Cell Mol L Sci Cmls* 2001, *58*, 1442–1450, doi:10.1007/pl00000787.
- 151. Shringarpure, R.; Grune, T.; Mehlhase, J.; Davies, K.J.A. Ubiqui Conjugation Is Not Required for the Degradation of Oxidized P teins by Proteasome. *J Biol Chem* 2003, *278*, 311–318, doi:10.1074/j m206279200.
- 152. Grune, T.; Merker, K.; Sandig, G.; Davies, K.J.A. Selective Degradat of Oxidatively Modified Protein Substrates by the Proteasome. *Bioch Bioph Res Co* 2003, 305, 709–718, doi:10.1016/s0006-291x(03)00809
- 153. Livnat-Levanon, N.; Kevei, É.; Kleifeld, O.; Krutauz, D.; Segref, Rinaldi, T.; Erpapazoglou, Z.; Cohen, M.; Reis, N.; Hoppe, T.; et Reversible 26S Proteasome Disassembly upon Mitochondrial Stre *Cell Reports* 2014, 7, 1371–1380, doi:10.1016/j.celrep.2014.04.030.
- 154. Davies, K.J.; Goldberg, A.L. Oxygen Radicals Stimulate In Proteolysis and Lipid Peroxidation by Independent Mech Erythrocytes. *J Biological Chem* 1987, *262*, 8220–8226.
- 155. Reinheckel, T.; Ullrich, O.; Sitte, N.; Grune, T. Differential Impa ment of 20S and 26S Proteasome Activities in Human Hematopoie K562 Cells during Oxidative Stress. *Archives of Biochemistry and E physics* 2000, *377*, 65–68.

- 158. Tsvetkov, P.; Myers, N.; Eliav, R.; Adamovich, Y.; Hagai, T.; Adler, J.; Navon, A.; Shaul, Y. NADH Binds and Stabilizes the 26S Proteasomes Independent of ATP. *J Biol Chem* 2014, *289*, 11272–11281, doi:10.1074/jbc.m113.537175.
- 159. Cagnetta, A.; Cea, M.; Calimeri, T.; Acharya, C.; Fulciniti, M.; Tai, Y.-T.; Hideshima, T.; Chauhan, D.; Zhong, M.Y.; Patrone, F.; et al. Intracellular NAD\* Depletion Enhances Bortezomib-Induced Anti-Myeloma Activity. *Blood* 2013, *122*, 1243–1255, doi:10.1182/blood-2013-02-483511.
- 160. Jenner, P. Oxidative Stress in Parkinson's Disease. Ann Neurol 2003, 53, S26–S38, doi:10.1002/ana.10483.
- 161. Shringarpure, R.; Grune, T.; Sitte, N.; Davies\*, K.J.A. 4-Hydroxynonenal-Modified Amyloid-β Peptide Inhibits the Proteasome: Possible Importance in Alzheimer's Disease\*. *Cell Mol Life Sci Cmls* 2000, *57*, 1802–1809, doi:10.1007/pl00000660.
- 162. Lee, M.; Hyun, D.; Jenner, P.; Halliwell, B. Effect of Proteasome Inhibition on Cellular Oxidative Damage, Antioxidant Defences and Nitric Oxide Production. *J Neurochem* 2001, 78, 32–41, doi:10.1046/j.1471-4159.2001.00416.x.
- 163. Ling, Y.-H.; Liebes, L.; Zou, Y.; Perez-Soler, R. Reactive Oxygen Species Generation and Mitochondrial Dysfunction in the Apoptotic Response to Bortezomib, a Novel Proteasome Inhibitor, in Human H460 Non-Small Cell Lung Cancer Cells. *J Biol Chem* 2003, 278, 33714–33723, doi:10.1074/jbc.m302559200.
- 164. Mehta, N.J.; Marwah, P.K.; Njus, D. Are Proteinopathy and Oxidative Stress Two Sides of the Same Coin? *Cells* 2019, *8*, 59, doi:10.3390/ cells8010059.
- 165. Scherz-Shouval, R.; Shvets, E.; Fass, E.; Shorer, H.; Gil, L.; Elazar, Z. Reactive Oxygen Species Are Essential for Autophagy and Specifically Regulate the Activity of Atg4. *Embo J* 2007, *26*, 1749–1760, doi:10.1038/sj.emboj.7601623.
- 166. Bensaad, K.; Cheung, E.C.; Vousden, K.H. Modulation of Intracellular ROS Levels by TIGAR Controls Autophagy. *Embo J* 2009, 28, 3015–3026, doi:10.1038/emboj.2009.242.
- 167. Chen, Y.; Azad, M.B.; Gibson, S.B. Superoxide Is the Major Reactive Oxygen Species Regulating Autophagy. *Cell Death Differ* 2009, *16*, 1040–1052, doi:10.1038/cdd.2009.49.
- 168. Dodson, M.; Darley-Usmar, V.; Zhang, J. Cellular Metabolic and Autophagic Pathways: Traffic Control by Redox Signaling. *Free Radical Bio Med* 2013, 63, 207–221, doi:10.1016/j.freeradbiomed.2013.05.014.

# THE BIOCHEMICAL CHARACTERIZATION OF CDK4 AS A REDOX-SENSITIVE PROTEIN

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# INTRODUCTION

Eukaryotic cells divide when they are stimulated with proculminates in the expression of cyclin D and stimulation of liferative signals such as growth factors and hormones [1-3]. cell cycle entry from G0 to G1 [18-20]. ROS therefore both activates and inactivates CDK4 and CDK6 activity through Proliferative signals are opposed by stress signals, which can activate cell cycle checkpoints [4,5]. Communication between upstream signaling. Furthermore, our laboratory previously signaling pathways that regulate cell division, metabolic status described the disulfide-dependent association of CDK4 with and genome integrity, but also cell-cell contacts or cytoskeletal FOXO3 and FOXO4 under oxidizing conditions, suggesting integrity are crucial for the decision to enter the cell cycle [6]. that CDK4 contains (a) redox-sensitive cysteine(s). In the pres-Cell division is a major metabolic commitment, and especially ent study we explore whether the activity of the CDK4-cyclin D complex is also regulated by oxidation of cysteines. in metazoans comes with the risk of the acquisition of oncogenic mutations. Sustained proliferative signaling is indeed a universal hallmark for cancer cells [7]. One of the ways cells The kinase activity of most cyclin-dependent kinases is largely integrate these signals is through signal transduction mediatcontrolled by binding of the appropriate cyclins, the levels of ed by the reversible oxidation of specific cysteines, known as which fluctuate throughout the cell cycle. CDK4 and CDK6 redox signaling [8]. This was elegantly illustrated in a recent associate with D-type cyclins D1, D2 and D3, resulting in a study that shows that oscillatory H2O2-dependent protein protein complex that is required for cells to transition from thiol oxidation is essential for the coupling of cell division G1 into S-phase during cell proliferation. While levels of most cyclins fluctuate throughout the cell cycle, cyclin D levels and metabolism in yeast [9]. The correlation of the cellular oxidation state with cell cycle phase was also demonstrated in are regulated by the levels of mitogens and growth factors a study that uses genetically encoded fluorescent redox sensors [21–23]. Although redox changes are thought to control the [10]. Furthermore, cell fate decisions regarding proliferation cell cycle in several ways [8,24] and D-type cyclins have been and differentiation during embryonic development are driven described to be redox-regulated [18], limited evidence exists by hypoxic and oxidative environments, respectively [11]. Loss to date describing direct redox control of CDKs [25]. of redox control of the cell cycle can result in inappropriate re-entry into the cell cycle, resulting in developmental defects, cancer or neurodegenerative diseases [12].

Prolonged exposure to higher levels of reactive oxygen species (ROS) triggers a cell cycle arrest, for instance through the activation of the p53 tumor suppressor (reviewed in ref. [13]), replication fork stalling [14] and accumulation of p16<sup>INK4A</sup>, which inhibits the D-cyclin type CDKs CDK4 and CDK6[15]. But besides the growth arrest in response to high levels of oxidants, stimulation of growth factor receptors results in the production of H<sub>2</sub>O<sub>2</sub> (generated by NADPH oxidase (NOX) enzymes), which further enables proliferative growth factor receptor signaling through inhibition of protein tyrosine phosphatases. Indeed, exogenous H2O2 has long been recognized as a mimetic of for instance insulin, PDGF

# THE BIOCHEMICAL **CHARACTERIZATION OF CDK4 AS A REDOX-SENSITIVE PROTEIN**

# ABSTRACT

Cyclin-dependent kinases (CDKs), together with their corresponding regulatory cyclin control the timely progression through the cell cycle. CDK4, and its paralog CDK6, stimulate the transition of G1 to S-phase upon binding to the D-type cyclins. Reactive oxygen species (ROS) can both stimulate and inhibit cell cycle progression, and this is at least in part mediated through the reversible oxidation of cysteine residues in key regulatory proteins. In this chapter, we show that CDK4 and cyclin D form a temporary covalently linked complex under oxidizing conditions. This is mediated by the formation of a disulfide bond involving cysteine 135 in CDK4, which stabilizes the otherwise hydrostatic non-covalent interaction between these proteins. Moreover, disulfide formation leads to an increased kinase activity of the CDK4-cyclin D complex. We further characterize the disulfide-dependent CDK4/cyclin D complex with respect to differential binding partners and substrates. The identification

Here, we show that an oxidizing cellular environment triggers the formation of an intermolecular disulfide between CDK4 and any of the D-type cyclin isoforms D1, D2 and D3, that otherwise bind through non-covalent interactions. This disulfide involves cysteine 135 in CDK4, which is in close proximity to cysteine 7 in cyclin D. These results suggest that the stabilized interaction enhances the kinase activity of the complex under oxidizing conditions.

and EGF [16,17]. The combined action of the growth factor receptor tyrosine kinase and NOX-derived H<sub>2</sub>O<sub>2</sub> eventually



### Figure 1. CDK4 forms a disulfide-dependent complex with Cyclin D. (figure legend continues on next page)

(A) Parallel reducing and non-reducing SDS-PAGE and western blot analysis (WB) of Flag-CDK4. Cells were incubated with 200 µM of H<sub>2</sub>O<sub>2</sub> for 2 minutes where indicated. Exposure of 293T cells to H<sub>2</sub>O<sub>2</sub> induces a mass shift of a fraction of CDK4. (B) Parallel reducing and non-reducing SDS-PAGE and western blot analysis (WB) of Flag-CDK4 immunoprecipitates (IP). Flag-CDK4 and HA-tagged cyclin D1 were expressed in 293T cells and exposed to 200 µM of H<sub>2</sub>O, for 2 minutes. CDK4 and cyclin D form an intermolecular disulfide-dependent complex upon exposure to H<sub>2</sub>O<sub>2</sub>, and migrate as a single band under non-reducing conditions. (C) The intermolecular disulfide-dependent complex between CDK4 and cyclin D is lost when samples were incubated with 20 mM DTT for 10 minutes prior to washing. (D) The H<sub>2</sub>O<sub>2</sub>-induced, cysteine-dependent complex between CDK4 and cyclin D is induced within 30 seconds of H,O, treatment, and diminishes after 5 minutes of H,O, treatment.

# RESULTS

# **CDK4 Forms a Disulfide-Dependent Complex with** Cyclin D

CDK4 contains 4 cysteines at positions 78, 135, 202 and 215. The published crystal structures of CDK4 in complex with CDK4 was identified in multiple mass-spectrometry-based cyclin D1 reveals that C135 is situated at the cyclin D1 bindscreens for redox sensitive proteins (see ref [25] and chapters ing interface [26]. Two cysteines in cyclin D1 (C7/C8) are in close proximity of CDK4 C135 (Figure 2A and S1 in more 3 and 5). To study whether CDK4 is indeed prone to cysteine oxidation in the form of intermolecular disulfide formation, detail). Mutational analysis showed that the H2O2-induced we expressed Flag-CDK4 in HEK293T cells followed by interaction between CDK4 and cyclin D1 indeed depends on immunopurification and SDS-PAGE under parallel reduc-C135 (Figure 2B). Note that CDK4 also forms another disuling and non-reducing conditions. Exposure of these cells to fide-mediated complex mediated by cysteines C78 and C202, H<sub>2</sub>O<sub>2</sub> causes a fraction of CDK4 to shift to a higher molecular indicated by the bands detected with the anti-flag antibody weight (HMW) of 75-100 kDa, which indicates that indeed that run slightly lower than CDK4-cyclin D. It is possible cysteines in CDK4 become oxidized (Figure 1A). Moreover, this band contains S-S-dependent CDK4 homodimers me-CDK4 seems to form intermolecular disulfides since the obdiated by C78 and C202, as it involves two CDK4 cysteines. served large mass shift is reversible and absent in reduced sam-Together, the observation of a C135-dependent complex beples (middle panel). tween CDK4 and cyclin D1 seems to be in agreement with the positioning of cysteines as shown in the crystal structure of the CDK4-cyclin D1 complex.

To investigate whether CDK4 is able to form a disulfide-dependent complex with its regulatory binding partner cyclin D1 upon exposure to H<sub>2</sub>O<sub>2</sub>, HA-tagged cyclin D1 was co-ex-While CDK4 is widely reported to interact with cyclin D1, pressed with Flag-CDK4. Indeed, CDK4 and cyclin D form relatively little is known about its interaction with the other an intermolecular disulfide-dependent complex upon expocyclin D isoforms [28,29]. To find out whether the other sure to H<sub>2</sub>O<sub>2</sub>, and migrate as a single band under non-reduccyclin D isoforms are also capable of forming a disulfide-deing conditions (Figure 1B). This CDK4-cyclin D complex pendent complex with CDK4, Flag-CDK4 and HA-cyclin is resistant to washing with a buffer supplemented with 1M D1, D2 or D3 were co-expressed in HEK293T and stimulated NaCl, as can be expected for a covalent interactions such as with H<sub>2</sub>O<sub>2</sub>. Both cyclin D2 and -D3 form a H<sub>2</sub>O<sub>2</sub>- dependisulfide bridges. The disulfide-dependent complex between dent high-molecular weight complex with CDK4, similar to CDK4 and cyclin D is sensitive to reduction, as both proteins cyclin D1. However, the induction of the disulfide-dependent migrate at their own molecular weight when IP samples are interaction with CDK4 by H<sub>2</sub>O<sub>2</sub> is much less strong as comincubated with the reducing agent DTT (Figure 1C) before pared to cyclin D1 (Figure 2C, non-reducing IP). (Figure 2C, reducing IP). Of note, in these experiments we observe a washing. Furthermore, the complex between CDK4 and Cyclin D is induced rapidly (within 20s) upon exposure to considerable fraction of cyclin D binding non-covalently to H<sub>2</sub>O<sub>2</sub> (Figure 1D). The complex is transient as its abundance CDK4 before  $H_2O_2$  treatment, suggesting that a pre-existing decreases after 5 minutes, and after 15 minutes it is almost non-covalent interaction serves as the starting point for the non-detectable. covalent interaction between CDK4-cyclin D. The observation that  $H_2O_2$  also increases the amount of total cyclin D1 In summary, CDK4 is able to form a disulfide-dependent binding could be due to loss of non-covalently bound cyclin complex with cyclin D1 upon H<sub>2</sub>O<sub>2</sub> exposure, that is rapidly D1 in the washing steps of the immunoprecipitation protocol. and transiently formed under oxidizing conditions. The total amount of cyclin D2 and D3 pulled down by CDK4

# CDK4 Cysteine 135 is Required for the Interaction Between CDK4 and Cyclin D





### Figure 2. CDK4 Cysteine 135 is required for the interaction between CDK4 and Cyclin D.

(A) Crystal structure of CDK4 in complex with cyclin D1 (PDB ID: 2W96) visualized using UCSF Chimera. The four CDK cysteines 78, 135, 202 and 215 are indicated in yellow. (B) Cells expressing Flag-CDK4 cysteine mutants and cyclin D were subjected to H<sub>2</sub>O<sub>2</sub> for 2 minutes. Samples were used in a Flag-CDK4 immunoprecipitation and subjected to analysis under non-reducing and reducing conditions. The complex between CDK4 and cyclin D is dependent on C135. (C) Cells expressing Flag-CDK4 and HA-cyclin D1, D2 or D3 were subjected to H<sub>2</sub>O<sub>2</sub> for 2 minutes before Flag-CDK4 immunoprecipitation. Samples were analyzed under non-reducing and reducing conditions.

is however not much affected by  $H_2O_2$ . We speculate that the non-covalent interaction of CDK4 with cyclin D2 and D3 is more resistant to washing during IP, and that these two cyclin D isoforms form a disulfide-dependent complex with CDK4 to a lesser extent than cyclin D1. Of the cysteines of cyclin D in proximity to CDK4-C135, only the cysteine homologous

to C7 in Cyclin D1 (C5 in cyclin D2 and D3) is conserved in all three cyclin D isoforms, and is therefore likely to be involved in the disulfide-dependent interaction with CDK4. In summary, all cyclin D isoforms (D1, D2 and D3) are able to form a disulfide-dependent complex with CDK4, which is dependent on C135 in CDK4.



Figure 3. Characterization of CDK4 redox-dependent covalent complexes. (A) Flag-CDK4 was immunoprecipitated from cells co-expressing Flag-CDK4 and HA-cyclin D. Samples are separated using SDS-PAGE under non-reducing conditions in the first dimension, so disulfide-mediated complexes migrate at their combined MW. (B) The entire lane is excised and incubated in reducing sample buffer before separation by SDS-PAGE in the second dimension, where disulfide-mediated complex members migrate at their own MW. Proteins migrating at their own MW in both the first and the second dimensions are shown on a diagonal, whereas disulfide-mediated complexes migrate below the diagonal in the second dimension. Gels were either stained for total protein or immunoblotted and stained using anti-Flag(-CDK4) or anti-HA(-cyclin D) antibodies. M: monomeric protein (Flag-CDK4 anf HA-cyclin D). (C) Scatter plot of the mass spectrometry data from cells expressing Flag-CDK4, showing the log, fold change of proteins in H<sub>2</sub>O, treated cells versus control. Colored dots represent proteins with a *p*-value < 0.05 as calculated using inference of protein differential abundance by probabilistic dropout analysis (proDA). Horizontal dotted lines are positioned at log, fold change of 1 and -1 (i.e. a 2-fold change). For the identity of specific interactors see Table 1.



# Characterization of CDK4 Redox-Dependent Covalent Complexes

To investigate the possibility that CDK4 forms also other cysteine-dependent protein complexes we immunoprecipitated CDK4 and subjected it to diagonal SDS-PAGE and western blotting (see chapter 3, Figure 2A for a schematic overview of this method). A large number of disulfide-dependent complexes containing CDK4 is visible. Note that 1) CDK4 and cyclin D have a similar molecular weight (~34 kDa without affinity tags) and that 2) migratory properties of proteins on SDS-PAGE may be different than expected when samples are analyzed under non-reducing conditions due to SDS accessibility. Spots 1-3 (~60, ~75 and ~100 kDa, Figure 3B) are already present before H2O2 treatment and contain CDK4 but not cyclin D (or other proteins as judged by the absence of spots of similar intensities at the same vertical position in the simply blue stained gel). These spots therefore most likely stem from S-S-dependent CDK4 homodimers. The differential horizontal poistion could be due to oligomerization or alternative disulfide linkage, similar to what we observed for TIPRL (see chapter 3). The intensities of these spots does not increase with H<sub>2</sub>O<sub>2</sub>. and are independent of C135. We cannot fully exclude that spots 1-3 are caused by some background signal, corresponding with their low intenities in the first dimension and absence in previous experiments.

The S-S-dependent CDK4-cyclin D complex observed in Figures 1 and 2 is clearly visible and indicated as spot 4 on both western blots. It is also lightly visible under endogenous conditions (cyclin D western blot only, spot 4b), suggesting that a small amount of cyclin D already interacts without H<sub>2</sub>O<sub>2</sub> treatment. Indeed, spot 4 is absent in the experiment using the CDK4 C135S mutant, corroborating our previous observation. Spot 6 and 7 likely derive from disulfide formation between cyclin D and one of the redox-dependent CDK4 complexes that gave rise to spots 1-3. That would be in accordance with the idea that cyclin D binds CDK4 C135, and that this cysteine is not involved in CDK4 S-S-homodimerization.

The complex that falls apart in spot 5 is best visible in the cyclin D blot, but there could be some signal for CDK4 as well. Strikingly, the staining for cyclin D in this spot is much more prominent in the CDK4 C135S pulldown. There are several possible explanations for this observation. i) Perhaps the absence of CDK4 C135 leaves the cysteine in cyclin D available for the formation of a disulfide dependent complex with another binding partner. Since the experiment uses Flag-CDK4 C135S as a bait, this disulfide-containing complex of cyclin D and another protein still interacts with CDK4 non-covalently. ii) When CDK4 is unable to form a S-S-dependent CDK4-cyclin D complex, it will start forming non-native interactions. This is supported by our data in Figure 2B, where the band pattern in the CDK C135S mutant (non-reducing) is different from that in WT CDK. iii) Cyclin D is also capable of forming S-S-dependent homodimers, which in their turn bind non-covalently to CDK4. Because CDK4 and cyclin D have a similar molecular weight, this S-S-dependent cyclin D homodimer will end up around the same MW as would CDK4-cyclin D (spot 4). Although these findings need to be interpreted with caution, this data suggests CDK4 forms disulfides mainly with cyclin D through C135 upon exposure of cells to  $H_2O_2$ .

We next aimed to identify potential new interaction partners of the CDK4-cyclin D covalent complexes. We therefore performed a preliminary label-free MS/MS experiment to identify proteins that interact with CDK4 in a H<sub>2</sub>O<sub>2</sub>-dependent manner (Figure 3C and Table 1). Interestingly, we identify proteins that are known to be involved in redox signaling, such as the cytosolic peroxiredoxins 1 and 2 (PRDX1-2), GAPDH, the redox-sensitive glycolytic enzyme GAPDH and the thioltransferase enzyme GSTO1. Although these interactions need to be verified in more detail, these observations suggest that CDK4 can form several redox-dependent interactions.

**Functional Characterization of Redox-Dependent** on the disulfide-mediated complex between CDK4 and cyclin Complexes of CDK4 and cyclin D D as we also observe this effect in the C135S mutant. This is To answer the question whether the disulfide-mediated interfurther corroborated by the observation that when we incubate the samples with DTT to reduce the covalent interaction action affects the activity of the CDK4-cyclin D complex, a kinase assay was performed. Interestingly, CDK4 immunobetween CDK4 and cyclin D, the H<sub>2</sub>O<sub>2</sub>-induced increase in precipitated from H<sub>2</sub>O<sub>2</sub>-treated cells displays a higher activkinase activity is not affected (Figure 4B). Surprisingly, the ity in a subsequent in vitro kinase assay using recombinant kinase activity of CDK4 in complex with cyclin D3 is much GST-Rb fragment as a substrate (Figure 4A). However, the stronger as compared to cyclins D1 and D2, irrespective of the cellular redox state (supplementary Figure S4). Togethincrease in Rb1 phosphorylation at S807/811 is not dependent



Figure 4. Functional characterization of redox-dependent complexes of CDK4 and cyclin D. (A) In vitro kinase assay using immunoprecipitated Flag-CDK4 mutants from cells subjected to H<sub>2</sub>O<sub>2</sub> for 2 minutes. Immunoprecipitates were washed with kinase buffer followed by incubation with ATP and recombinant GST-Rb fragment as a substrate. Rb phosphorylation increases upon treatment with H,O,. (B) In vitro kinase assay using immunoprecipitated Flag-CDK4 from cells subjected to H<sub>2</sub>O<sub>2</sub> for 2 minutes. Where incubated, immunoprecipitates were incubated with 20 mM DTT for 10 minutes prior to washing. (C) Phosphoproteomics results for CDK6-knockout U2OS cells upon treatment with H<sub>2</sub>O<sub>2</sub> Colored dots represent proteins with p-values < 0.05. Colored dots in the green quadrant with -log, ratios >1 or < -1 are listed in Table 2. (D) Phosphoproteomics results for H<sub>2</sub>O<sub>2</sub>-treated CDK6-knockout U2OS cells upon treatment LEE011 Colored dots represent proteins with p-values < 0.05. Colored dots in the green quadrant with -log, ratios >1 or < -1 are listed in Table 2.

er, these results indicate that the kinase activity of the disulfide-bound CDK4-cyclin D complex is not redox regulated even though H<sub>2</sub>O<sub>2</sub> stimulates the covalent CDK4-cyclin D interaction.

It is possible that the formation of the covalent complex of oxidized CDK4 and cyclin D can determine substrate specificity. The observation that the kinase activity for Rb1 is not dependent on the disulfide-mediated interaction between CDK4 and cyclin D does not mean there there are no changes in kinase activity per se. One reason could be an altered substrate specificity of the complex, phosphorylating substrates other than Rb1. As a preliminary experiment, we performed phosphopeptide enrichment mass-spectrometry. CDK4 and closely related CDK6 are considered largely redundant. In addition, in contrast to CDK4, the closely related CDK6 does not contain a cysteine around position C135, suggesting that CDK6 is unable to form a disulfide-dependent complex with cyclin D. Therefore, we knocked out CDK6 and CDK4 in U2OS cell lines using CRISPR-Cas9 technology and stimulated H<sub>2</sub>O<sub>2</sub>-treated cells with the CDK4/6 inhibitor LEE011 (ribociclib). To accurately quantify relative levels of phosphorylated proteins we made use of Stable Isotope Labelling by Amino acids in Cell Culture (SILAC), followed by phosphopeptide enrichment. Firstly, multiple phosphorylation sites are detected that change in CDK6-knockout U2OS cells upon treatment with H<sub>2</sub>O<sub>2</sub> (Figure 4C and Table 2). Phosphorylation on sites that are specific for CDK4 should be inhibited by treatment with LEE011. Using these criteria, a H<sub>2</sub>O<sub>2</sub>-dependent and CDK4-specific phosphorylation site was detected in TNIK (a kinase involved in JNK and Wnt pathway activation), and multiple sites were detected in CAMK2G and OSBPL10 (a calcium/calmodulin-dependent kinase and a lipid receptor, respectively) from this preliminary experiment (Figure 4D and Table 2). It is possible that these substrates are indeed disulfide-dependent substrates of CDK4, since these sites do not change significantly in the CDK4 KO cells treated with H<sub>2</sub>O<sub>2</sub> (Table 3), and since CDK6 does not contain a cysteine around position C135. Future experiments will

be needed to confirm these preliminary results, and focus on establishing the effect of these phosphorylations.

# DISCUSSION

The activity of CDK family members is strictly dependent on association with their complementary cyclins, the abundance of which is regulated in a cell cycle-phase dependent manner, or by the levels of mitogens and growth factors. D-type cyclins associate with CDK4 and CDK6 to enable cell cycle progression from G1 to S-phase by phosphorylating members of the retinoblastoma (Rb) family proteins, thereby releasing their inhibitory effect on the E2F1 transcription factor [30,31].

Here, and based on earlier observations pointing in that direction [25], we aimed to assess whether CDK4 could be redox sensitive. We show that the complex between CDK4 and cyclin D can be covalently linked through the formation of a disulfide bond, which is induced by a more oxidative cellular environment (i.e. H<sub>2</sub>O<sub>2</sub> treatment). We provide evidence that this interaction is mediated by cysteine 135 of CDK4. All three cyclin D isoforms D1, D2 and D2 are able to form this interaction. Additionally, the data suggest that the kinase activity of the complex is increased under oxidizing conditions, although this seems to occur independently of disulfide formation between CDK4-cyclin D.

The interaction between CDK4 and cyclin D is well documented. Consistent with literature, we observe a variable fraction of cyclin D interacting with CDK4 even without exposure to H<sub>2</sub>O<sub>2</sub> (see e.g. Figure 1B, reducing IP). This disulfide-independent interaction could support the hypothesis that pre-existing complexes between CDK4-cyclin D can be crosslinked under oxidizing conditions through the formation of a disulfide bond. If this is indeed the case, low-affinity interactions can be locked in a high affinity complex through this mechanism, similar to what was shown for FOXO4 and TNPO1 [32]. The fraction of disulfide-independent bound cyclin D in the experiments is somewhat variable, possibly due to variation in the levels of overexpression which affects the itself can also be oxidized, and the increased kinase activity of CDK4 upon H<sub>2</sub>O<sub>2</sub> stimulation would seem to corroborate the findings on p16<sup>INK4A</sup>, since both processes stimulate CDK4 kinase activity and potentially cell cycle progression from G1 to S-phase. Because of the low stoichiometry of the CDK4-cyclin D complex it is still possible that the complex is inactivated by H<sub>2</sub>O<sub>2</sub>, but this effect is obscured by the inactivation of p16<sup>INK4A</sup> (and this activation of CDK4/6). We are currently in the process of assessing the effects of  $p16^{INK4A}$ and CDK4 oxidation on the cell cycle, and whether and how exactly the disulfide-bound CDK4-cyclin D complex influences Rb phosphorylation and S-phase entry.

stoichiometry of the complex. Furthermore, the IP protocol used to identify disulfide-dependent interactions includes a high-salt washing step that could lead to loss of non-covalent interactions. Future experiments should therefore be performed using a more stable cell expression system or CDK4 knockout cell lines for more comparable results. The diagonal SDS-PAGE experiment also provides evidence for the disulfide-dependent dimerization of CDK4 with cyclin D, as well as different S-S-dependent CDK4 homodimers. (Figure 3B).

The kinase activity of the disulfide-bound CDK4-cyclin D As most of the experiments were performed in the presence of complex is not directly affected by the disulfide bond between cyclin D, it is possible that we overlook any effects of CDK4 CDK4-cyclin D (Figure 4A, 4B and Supplementary Figure oxidation that are independent of cyclin D. As an example, mutational analysis of CDK4 reveals another disulfide-mediated S4), even though overall kinase activity is increased under oxidizing conditions. The reason for this is not entirely clear, complex dependent on two CDK4 cysteines C78 and C202, but it is possible that there is still plenty cyclin D remaining possibly containing S-S-dependent CDK4 homodimers. in the samples even after stringent washing with 1M NaCl, and that this remaining cyclin D pool can phosphorylate Rb1. In the proteomics experiment, we identify a number of The same washing conditions are also reason for the loss of H<sub>2</sub>O<sub>2</sub>-induced interaction partners for CDK4. Many of non-covalently bound cyclin D1 in conditions not treated these are known-redox-sensitive proteins such as peroxirewith H<sub>2</sub>O<sub>2</sub>. Possibly, kinase activity this is dependent on the doxins 1 and 2. Peroxiredoxins are dedicated H<sub>2</sub>O<sub>2</sub> scavenmolecular and cellular context. For example, the stoichiomgers, but, more importantly, they are also known to actively etry of CDK4 and cyclin D overexpression might influence participate in the oxidation of proteins through redox relays kinase activity of the complex. On top of that, the cellular [35,36]. Further experiments need to be done to test whethcontext including dephosphorylation events by phosphatases er peroxiredoxins are responsible for the oxidation of CDK4 such as PP1 [33] and cyclin E expression can affect kinase through a redox relay. In addition, we identify GSTO1 as an activity of the covalent CDK4-cyclin D complex, albeit not interaction partner of CDK4. GSTO1 catalyzes thioltransin short timescales like those used in this study. It has been ferase reactions using glutathione as a cofactor, which opens described that phosphorylation of CDK4 on T172 by the up the possibility that oxidized CDK4 is reduced by GSTO1. CDK-activating kinase CDK7 stimulates kinase activity [34]. It is important to keep in mind that the proteomics experi-A next step could be to test the CDK4 phosphorylation state ment was performed in with endogenoud cyclin D in order to of T172 upon oxidation and its subsequent kinase activity. enrich for potential new interaction partners, and that these cells (293T) have inactive Rb. However, it is possible that new interaction partners bind only as a trimeric complex - when We recently showed that the CDK4/6 inhibitor and tumor suppressor p16<sup>INK4A</sup> can also be oxidized, upon which it cyclin D is also present.

forms amyloid-like fibrils and it loses its ability to inhibit CDK4/6 (chapter 1 and [39]). The observation that CDK4

In order to assess whether the formation of the covalent complex of oxidized CDK4 and cyclin D can determine substrate specificity we set up preliminary phosphoproteomics experiments, which were perfomed in the presence of overexpressed cyclin D and in an Rb-proficient U2OS cell line. If the oxidation of CDK4-cyclin D indeed affects substrate specificity, these results offer a starting point for the identification of new substrates. In line with this, new functions of CDK4/6 besides their well-documented role in cell cycle progression through Rb phosphorylation are starting to emerge. For example, CDK6-cyclin D3 has been shown to act as a rate-limiting regulator of carbon flow into the pentose phosphate- and serine pathways [37].

CDK6 is related to CDK4 and their structures are highly similar. Although CDK6 contains two extra cysteines in an extended loop that is not present in CDK4, CDK6 does not contain a homologous cysteine at C135. Furthermore, there is no other cysteine present at the binding interface with cyclin D (data not shown). This raises the question if CDK6 is also subject to oxidation and disulfide-dependent dimerization with cyclin D. Interestingly, like CDK4, CDK6 is also able to form a disulfide-linked complex with cyclin D and also shows increased kinase activity upon stimulation with H<sub>2</sub>O<sub>2</sub> (supplementary Figure S2). In a preliminary experiment, the interaction between CDK6 and cyclin D seems dependent on C306 (data not shown). CDK6 does not have any cysteine



### Figure 5.

The region around CDK4 C135 could serve as a template for the design of a cysteine-directed covalent cyclin D binder to prevent complex formation of cyclin D with both CDK4 and CDK6 and inhibit their activity (left panel). If indeed the reactive cysteine in cyclin D1 is C7, the region around this cysteine could serve as a template for the design of a covalent, CDK4-specific inhibitor that targets C135 and does not also target CDK6.

around the cyclin D binding interface like CDK4 does (C135). regulated in cancers, and CDK4 inhibitors are currently being This would seem to suggest that the covalent interaction beexploited in the clinic (i.e. Palbociclib). These inhibitors are tween CDK6 and D-type cyclins is of a different nature than small molecule ATP-analogs that bind to the ATP-binding their canonical, non-covalent interaction, and different from pocket. Since all kinases bind ATP, ATP-analogs are prone the interaction between CDK4-cyclin D. Therefore, uncovto off-target binding which could result in a limited response ering the exact properties of the interaction CDK4/6 surface and /or adverse side effects [40]. There is a recent surge in with cyclin D is a vital issue for future research. While the the development of cysteine-directed, covalent drugs. The CDK4-cyclinD1 and CDK6-cyclin D3 complexes are the here described identification of a disulfide at the interface of most characterized (e.g. [38]), the data suggests that both CDK4 and Cyclin D could be a starting point for the design CDK4 and CDK6 can interact with cyclins D1, D2 and D3 novel CDK4/6 inhibitors that are not based on the ATP-bindin a disulfide-linked complex. Expression patterns of D-type ing pocket. The region around CDK4 C135 could serve as a cyclins vary between tissue types, and any differences in the template for the design of a cysteine-directed covalent cyclin D binder to prevent complex formation with both CDK4 and preference for a cyclin D isoform, as well as differences in their redox regulation would be interesting because this would CDK6 and inhibit their activity (Figure 5, left panel). Conversely, if we can confirm that the reactive cysteine in cyclin allow for a context-dependent response. D1 is indeed C7, the region around this cysteine in cyclin D1 This research shows that CDK4 is a redox-sensitive protein. could serve as a template for the design of a covalent, CDK4 The observation that CDK4 and cyclin D can interact covainhibitor that targets C135 (Figure 5, right panel).. This lently upon oxidizing conditions is especially interesting, since could be the first CDK4-specific inhibitor (i.e. that does not this potentially links the cellular redox state to the decision also target CDK6), since CDK6 does not contain a cysteine to commit to the cell cycle transition from G1 to S-phase. By on its interaction surface with cyclin D.

linking pre-existing CDK4-cyclin D complexes, low levels of H<sub>2</sub>O<sub>2</sub> can potentially contribute to Rb phosphorylation and MATERIALS AND METHODS cell cycle progression from G1 to S-phase. Taken together, the data suggest that more oxidizing conditions can potentially stimulate cell cycle entry though oxidation of CDK4 Cell Lines and Culturing and subsequent covalent complex formation between CDK4 HEK293T and U2OS cells were cultured in bicarbonate-buffand cyclin D. Hypothetically, this regulation could be part ered DMEM, supplemented with 10% FBS (Bodinco BDCof a larger mechanism of finetuning of cellular processes by 40506-C05), 2 mM L-glutamine (Lonza, BE17-605E) and H<sub>2</sub>O<sub>2</sub>, depending on the concentration and duration of oxi-100 U/mL penicillin-streptomycin (Lonza, DE17-602E) dants exposure, as well as the oxidation of context-dependent and kept at 37°C and under a 6% CO<sup>2</sup> atmosphere. Transand cell-specific target proteins. More specifically, low levels of fections were carried out using PEI (Sigma-Aldrich, P3640) could H<sub>2</sub>O<sub>2</sub> stimulate proliferation, amongst others thought or FugeneHD reagent (Promega, E2311) following the manthe oxidation and activation of CDK4 and inactivation of ufacturer's instructions. After two days, cells were harvested p16<sup>INK4A</sup>, whereas higher or prolonged levels of H<sub>2</sub>O<sub>2</sub> cause for further analysis. CRISPR knockout lines were created by plating 200k U2OS cells. After 24h, cells were transfected oxidative stress and cell cycle arrest. with pX458 (addgene plasmid ID 48138) containing a gRNA The redox regulation of CDK4 could also be of importance against CDK6. The top 15% GFP-expressing cells were sorted as a potential new drug target, regardless of the functional in 96-wells plates, and monoclonal knockout lines were veri-

effect of CDK4 oxidation. CDK4/6 activity is frequently upfied by western blotting and sequencing.

### **Plasmids and Reagents**

Full length human CDK4 and CDK6 were a kind gift from Sander van den Heuvel (Utrecht University), Addgene plasmid ID 1866 and 1874, respectively. Constructs with att recombination sites were were amplified from full-length CDK4 and CDK6 using the following primers: CDK4\_F\_5'-GGGGACAAGTTTGTACAAAAAG-CAGGCTTCGCTACCTCTCGATATGAGCCAG-3', CDK4 R 5'-GGGGACCACTTTGTACAAGAAAGCT-GGGTCTCACTCCGGATTACCTTCATCC-3', CD-K6\_F\_5'-GGGGACAAGTTTGTACAAAAAG-CAGGCTTCGAGAAGGACGGCCTGTGCCGCG-3', CDK6\_R\_5'-GGGGACCACTTTGTACAAGAAAGCT-GGGTCTTAAACGGCTGTATTCAGCTCC-3'. Using Gateway technology (Invitrogen) entry clones were generated. CDK4 cysteine mutants were created by site-directed mutagenesis PCR using the following primers:

C D K 4 \_ C 7 8 S \_ F \_ 5' - G C T G A T G G A C G T -CAGTGCCACATCCCGAACTGACDK4-3', CDK4\_C78S\_C78S\_R\_5'-GTCAGTTCGG-GATGTGGCACTGACGTCCATCACDK4-3', CDK4\_ C135S F 5'-TTTCCTTCATGCCAATAGCATC-G T T C A C C G A G A T C T G A A G C D K 4 - 3', CDK4\_C135S\_R\_5'-CTTCAGATCTCGGTGAAC-GATGCTATTGGCATGAAGGAAACDK4-3', CDK4 C202S F 5'-ACATGTGGAGTGTTGG-CAGTATCTTTGCAGAGATGTTTCGCDK4-3', CDK4\_C202S\_R\_5'-CGAAACATCTCTGCAAAGA-TACTGCCAACACTCCACATGTCDK4-3', CDK4 C215S\_F\_5'-TCGAAAGCCTCTCTTCAGT-GGAAACTCTGAAGCCGACCDK4-3', CDK4 C215S R 5'-GTCGGCTTCAGAGTTTCCACT-GAAGAGAGGCTTTCGA-3', and verified by sequencing. Gateway technology (Life Technologies) was used to create N-terminally tagged Flag-His and HA-expression vectors (backbones pCDNA3) from the resulting CDK4 cysteine mutant entry clones. HrA-tagged Cyclin-D1-3 constructs were purchased from Addgene (plasmid IDs 8948, 8950 and 10912, respectively). CDK6 sgRNA sequences are 5'-CCGC-

CACGCATTCGTACTGC-3' and 5'-CGCGCTTCAACG-CCACGAAA-3'. β-mercaptoethanol was used in a concentration of 100 µM. 30% H<sub>2</sub>O<sub>2</sub> (Sigma 31642) was freshly diluted to a stock of 10 or 100 mM in H<sub>2</sub>O for every experiment. Unless stated otherwise, H<sub>2</sub>O<sub>2</sub> treatments were 200µM for 2 minutes. LEE011 (ribociclib) was used at a concentration of 10µM for 30 minutes.

# Co-immunoprecipitations, in vitro Kinase Assay and Western Blotting

After treatment as indicated, cells were lysed using a buffer containing 50 mM Tris-HCl pH 7.5, 1% TX100, 1.5 mM MgCl2, 5 mM EDTA, 100 mM NaCl, NaF, Leupeptin and Aprotinin. 100 mM iodoacetamide was added to the lysis buffer to prevent post-lysis cysteine oxidation and to inactivate disulfide reducing enzymes. After centrifugation at 14000 rpm for 10 min, 5% of the supernatant was kept as input and the remaining supernatant was used for immunoprecipitation with anti-Flag-M2 affinity gel (Sigma A222). After a 2 h incubation whilst gently mixing, immunoprecipitates were washed 4 times with lysis buffer containing 1 M NaCl and samples were boiled for 5 min in sample buffer with or without the reducing agent  $\beta$ -mercaptoethanol. Where stated, samples were incubated with 20 mM DTT. Samples were separated on a 10% polyacrylamide gel and transferred to immobilon-FL membranes (using standard protocols) before staining and antibody detection. Samples for in vitro kinase assays were taken after high salt wash of the immunoprecipitates. Samples were incubated with 1 µg of recombinant GST-Rb1 (Sigma-Aldrich SRP0256) each, in a kinase buffer consisting of 200 µM ATP, 1 mM DTT, and 0.1 mM Oxaloacetate for 30 minutes at 30°C.

Antibodies that were used are Flag M2 (Sigma F3165), HA (12CA5, monoclonal from hybridoma cell lines and SC805), CDK4 (Transduction Laboratories C18720), CDK6 (Santa Cruz SC-177), cyclin D1 (Abcam ab134175) and phospho-Rb S807/811 (Cell Signaling Technology CS9308). Detection of fluorescent secondary antibodies was performed using the LI-COR Biosciences Odyssey Infrared Imaging System or the Amersham Typhoon NIR Plus Biomolecular Imager of UniProt was searched with both the peptide as well as the (GE Healthcare), detection of secondary HRP-antibodies was protein false discovery rate set to 1%. Downstream analysis performed on the FUJIFILM Luminescent Image Analyser was done using R version 4.0.2. LAS-3000.

A Summarized Experiment object was created using LFQ data **2D Diagonal Electrophoresis** from the MaxQuant proteinGroups file and corresponding protein information. Proteins were filtered for reverse hits Immunoprecipitates were separated in the first dimension on a 10% SDS-PAGE gel and total protein content was stained and standard contaminants. Next, we selected proteins that using SimplyBlue. Gel lanes were cut out and incubated with were identified with three or more unique peptides and were 2x Laemmli sample buffer containing  $\beta$ -mercaptoethanol for measured in at least one sample in 2 or more replicates. Data 30' at room temperature. In the second dimension, reduced was log<sub>2</sub>-transformed and normalized using quantile normalgel lanes were loaded on a second 10% SDS-PAGE gel at a right ization, which ensures overall intensity differences due to IP efficiency differences between samples are equalized while angle to the first dimension. Detection of proteins was done using SimplyBlue stain and using western blotting. maintaining identical statistical distributions. ProDA model fitting was performed using sample names as design input and Mass Spectrometry the number of proteins in the data as the number of subsa-For the identification of CDK4 interactors the lysate of mples. To test for differential protein abundance, the proDa 4x20cm dishes were used for each pulldown on 75 ml of Flagfit object was used for comparing wild-type against mutant M2 beads similar to the immunoprecipitation experiments TIPRL or H<sub>2</sub>O<sub>2</sub>-treated against control conditions.

described above. All immunoprecipitations were performed using three biological replicates. After washing, beads were resuspended with 8M urea in 1M ammonium bicarbonate (ABC), reduced and alkylated in 10 mM TCEP and 40 mM stagetips.

U2OS cells were grown in SILAC medium containing chloroacetamide (CAA) for 30 minutes at RT. After fourfold DMEM without arginine and lysine (PAA), supplemented dilution with 1M ABC, proteins were digested overnight onwith mM L-glutamine (Lonza, BE17-605E) and 100 U/mL bead with 250 ng Trypsin/LysC (Promega V5071) per sample penicillin-streptomycin (Lonza, DE17-602E), 10% dialized at 37°C. Samples were cleaned up with in-house-made C18 FBS (Gibco), 73µg/mL light/K0 (Sigma) or heavy/K8 (Sigma or Silantes) L-Lysine and 29.4µg/mL light/R0 (Sigma) or heavy/R0 (Sigma or Silantes) L-arginine. Labelling efficiency Mass spectrometry was performed as previously described was confirmed >95%. After transfection and treatments, cells [32]. Peptides were separated on a 30-cm pico-tip column were washed twice with cold PBS. Cells were lysed in a buffer (75 µm ID, New Objective) and were packed in-house with containing 8M Urea, 1M Ammonium Bicarbonate, 40mM 3 µm aquapur gold C-18 material (Dr. Maisch) using a 140-CAA, 10mM TCEP and phosphatase inhibitor cocktail 2 and 3 (both Sigma-Aldrich). Lysates were boiled to 95°C for min gradient (7-80% ACN 0.1% FA), delivered by an easynLC 1000 (LC120, Thermo Scientific), and electro-sprayed 5 minutes, cooled on ice for 15 minutes, and sonicated using directly into an Orbitrap Fusion Tribrid Mass Spectrometer a probe sonicator (Heilscher) for 30 seconds at 70% ampli-(Thermo Scientific). Raw files were analyzed with the Maxtude/0.5 cycle. Samples were heated to 95°C for 5 minutes Quant software version 1.5.2.8 with oxidation of methionine, and cooled on ice for 15 minutes again, then samples were alkylation with N-ethylmaleimide and carbamidomethylation diluted four times with a 2M Ammonium Bicarbonate soluset as variable modifications. The Human protein database tion. Heavy and light lysates were mixed 1:1 (as determined

# Stable Isotope Labelling by Amino acids in Cell Culture (SILAC) and Phosphopeptide Enrichment

using the Bradford Protein Assay, Bio-Rad). Samples were digested overnight at 37°C with Lys-C (Promega). Phosphopeptides were enriched using TiO2 as described in [41]. A second phosphopeptide enrichment was performed with TiO2 beads on C8 stagetips made in-house.

Mass spectrometry was performed as follows: peptides were separated on a 30 cm column (75  $\mu m$  ID fused silica capillary with emitter tip (New Objective)) packed with 3 µm aquapur gold C-18 material (dr. Maisch) using a 140-minute gradient (7% to 80% ACN 0.1% FA), delivered by an easy-nLC 1000 (Thermo). Peptides were electro-sprayed directly into a Thermo Scientific Orbitrap Fusion Tribrid Mass Spectrometer and analyzedin Top Speed data dependent mode with the resolution of the full scan set at 240000 and an intensity threshold of 5000 ions. Most intense ions were isolated by the quadrupole and fragmented with a HCD collision energy of 30%. The maximum injection time of the iontrap was set to 35 milliseconds.

Mass spectrometry data was processed using MaxQuant and further analyzed using Perseus 1.5.5.3 and and R. Sites were filtered for potential contaminants and reverse identification. SignA values were calculated, phosphosites with SignA values smaller than 0.05 are considered significant. Sites were filtered for localization precision value > 0.75.

TABLES

Table 1. MSMS data corresponding to Figure 3B: H<sub>2</sub>O<sub>2</sub>-dependent interactors of CDK4

uniprot ID	gene	protein	log <sub>2</sub> ratio	<i>p</i> -value
Q06830	PRDX1	Peroxiredoxin-1	6.6	<0.001
Q5VU66	TPM3	Tropomyosin alpha-3 chain	4.7	0.001
P32119	PRDX2	Peroxiredoxin-2	4.1	0.004
E7EVA0	MAP4	Microtubule-associated protein	3.7	0.011
Q9P258	RCC2	Protein RCC2	3.6	0.006
E9PFM2	RBBP7	Histone-binding protein RBBP7	3.6	0.006
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	2.9	< 0.001
E7ETK8	AARS	AlaninetRNA ligase, cytoplasmic	2.6	0.010
E9PHK9	TCOF1	Treacle protein	2.4	0.012
P78417	GSTO1	Glutathione S-transferase omega-1	1.8	0.006

Table 2. Posphorylation site affected by H2O2 - and LEE11 sites in CDK4 knockout sells

uniprot ID	gene	protein	site	log <sub>2</sub> ratio
sites for CL	0K4KO + H <sub>2</sub> O	versus CDK4KO		
Q53EU6	AGPAT9	Glycerol-3-phosphate acyltransferase 3	S68	3.3
P18031	PTPN1	Tyrosine-protein phosphatase non-receptor type 1	S50	3.3
Q13085	ACACA	Acetyl-CoA carboxylase 1	S80	2.6
P42345	MTOR	Serine/threonine-protein kinase mTOR	S1261	2.5
075592-2	MYCBP2	E3 ubiquitin-protein ligase MYCBP2	S3440	2.4
F6RU81	ELMSAN1	ELM2 and SANT domain-containing protein 1	T628	2.3
B3KSY4	hCG_1787779	9 Coronin	S245	2.3
F6RU81	ELMSAN1	ELM2 and SANT domain-containing protein 1	S636	2.2
<i>Q8WW12</i>	PCNP	PEST proteolytic signal-containing nuclear protein	S77	2.2
~ 013546-2	RIPK1	Receptor-interacting serine/threonine-protein kinase 1	S274	2.2
~ C9JXL3	SLC4A7	Sodium bicarbonate cotransporter 3	S255	2.1
09H8S9	MOB1B	MOB kinase activator 1B	T35	1.9
C9JXL3	SLC4A7	Sodium bicarbonate cotransporter 3	\$258	1.9
F5GXJ4	STIM2	Stromal interaction molecule 2	\$748	1.9
060716-5	CTNND1	Catenin delta-1	\$352	17
F8VR72	MAPKAPK5	MAP kinase-activated protein kinase 5	\$15	17
P30622_2	CLIP1	CAP-Gly domain-containing linker protein 1	\$143	1.6
C0K015	R APH1	Ras associated and pleckstrin homology domains containing protein 1	\$623	1.6
00V580	RBM7	RNA binding protein 7	\$136	1.0
001082	SPTRN1	Spectrin beta chain, non erythrocytic 1	T2187	1.0
001002 H0V4W2	TRRAP	Transformation/transcription domain associated protein	\$1700	1.0
R1AM\$2	38061	Sentin 6	T/18	1.5
C01167	50901 DMS2	Miamatah ranair andanyalaga DMS2	1410 \$405	1.5
D12270	TDD	Nucleannetain TDD	3493 T2127	1.5
F12270 F511470	CDV17	Curlin demodent binnen 17	12137	1.5
COLINIC	CDK17	Duct an existence in the ended of the second s	539	1.4
Q9UNIO OODVD4	DUSP12	Oranteel his disc sector solution and a sector 11	5353	1.4
Q9DAD4	DADN	Oxysteroi-binding protein-related protein 11	5189	1.4
B4DDG8	PAKN	Poly(A)-specific ribonuclease PARN	5496	1.4
C9J10/	PMS2	Mismatch repair endonuclease PMS2	5497	1.4
Q801V5	SGK223	Tyrosine-protein kinase SgK223	5694	1.4
090035	SRRM2	Serine/arginine repetitive matrix protein 2	\$2692	1.4
Q15208	S1K38	Serine/threonine-protein kinase 38	\$264	1.4
E/ENL/	TRAPPC12	Trafficking protein particle complex subunit 12	\$167	1.4
Q9UPN4-3	CEP131	Centrosomal protein of 131 kDa	S47	1.3
Q9H4G0-4	EPB41L1	Band 4.1-like protein 1	S467	1.3
Q9H307	PNN	Pinin	S66	1.3
F5H7/4	RIN3	Reticulon-3	\$204	1.3
Q6IN85-4	SMEK1	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	S498	1.3
Q6IN85-4	SMEK1	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	\$502	1.3
Q9UHR4	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	\$331	1.2
Q96B23-2	C18orf25	Uncharacterized protein C18orf25	S67	1.2
G8JL86	COBLL1	Cordon-bleu protein-like 1	\$371	1.2
075420	GIGYF1	PERQ amino acid-rich with GYF domain-containing protein 1	S862	1.2
Q15154-2	PCM1	Pericentriolar material 1 protein	S93	1.2
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	T2328	1.2
Q9H1K0	ZFYVE20	Rabenosyn-5	S226	1.2

Q9H1K0	ZFYVE20	Rabenosyn-5	S226	1.2
P49674	CSNK1E	Casein kinase I isoform epsilon	S354	1.1
E9PG60	IQSEC1	IQ motif and SEC7 domain-containing protein 1	S75	1.1
B7Z6Y0	MELK	Maternal embryonic leucine zipper kinase	S142	1.1
Q9BXB4	OSBPL11	Oxysterol-binding protein-related protein 11	S174	1.1
Q2KHR3-2	QSER1	Glutamine and serine-rich protein 1	S376	1.1
Q13573	SNW1	SNW domain-containing protein 1	S224	1.1
P53814-5	SMTN	Smoothelin	S523	1.0
P08559-3	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	S269	-2.3
Q6PCE3	PGM2L1	Glucose 1,6-bisphosphate synthase	S175	-1.8
075179-2	ANKRD17	Ankyrin repeat domain-containing protein 17	S1939	-1.3
Q8WUF5	PPP1R13L	RelA-associated inhibitor	S84	-1.3
Q8TER5-4	ARHGEF40	Rho guanine nucleotide exchange factor 40	T371	-1.2
Q8WUF5	PPP1R13L	RelA-associated inhibitor	S280	-1.2
Q8WUF5	PPP1R13L	RelA-associated inhibitor	S81	-1.2
C9K0X4	ABLIM1	Actin-binding LIM protein 1	S382	-1.1
C9J2I0	AGFG1	Arf-GAP domain and FG repeat-containing protein 1	T99	-1.1
P08559-3	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	S201	-1.1
P39023	RPL3	60S ribosomal protein L3	S13	-1.1
P42677	RPS27L	40S ribosomal protein S27	S78	-1.0
sites for CL	$K4KO + H_2O$	$_2$ versus CDK4KO + $H_2O_2$ + LEE011		
F5H6G1	RB1	Retinoblastoma-associated protein	S834	5.0
F5H564	EIF4G3	Eukaryotic translation initiation factor 4 gamma 3	S760	1.9
P50750-2	CDK9	Cyclin-dependent kinase 9	S464	1.7
H0YLX2	RFX7	DNA-binding protein RFX7	S321	1.4
015014	ZNF609	Zinc finger protein 609	S1055	1.2
F5H6Z0	CDK17	Cyclin-dependent kinase 17	S39	1.1

# Table 3. Phosphoproteomics data corresponding to Figures 3C-D: H<sub>2</sub>O<sub>2</sub> - and LEE11-affected sites in CDK6 knockout cells

uniprot ID	gene	protein	site	log <sub>2</sub> rati
tes for CI	<b>К6 КО Н,О,</b>	versus CDK6 KO		
18031	PTPN1	Tyrosine-protein phosphatase non-receptor type 1	S50	2.3
13085	ACACA	Acetyl-CoA carboxylase 1	S80	2.1
42345	MTOR	Serine/threonine-protein kinase mTOR	S1261	2.0
9Y580	RBM7	RNA-binding protein 7	S136	1.8
13546-2	RIPK1	Receptor-interacting serine/threonine-protein kinase 1	S274	1.8
6RU81	ELMSAN1	ELM2 and SANT domain-containing protein 1	T628	1.6
9BXB4	OSBPL11	Oxysterol-binding protein-related protein 11	S174	1.5
6RU81	ELMSAN1	ELM2 and SANT domain-containing protein 1	S636	1.4
7ER32	MKL1	MKL/myocardin-like protein 1	S312	1.4
)5VW31	NFIB	Nuclear factor 1	S12	1.4
7EWM1	NCOA2	Nuclear receptor coactivator 2	S771	1.3
'8VXY0	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	S95	1.2
C7EPK0	LIMCH1	LIM and calponin homology domains-containing protein 1	S334	1.2
)96RT1-6	ERBB2IP	Protein LAP2	S872	1.1
C9JXL3	SLC4A7	Sodium bicarbonate cotransporter 3	S258	1.1
°08559-3	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	S269	-2.4
<i><b><u>26PCE3</u></b></i>	PGM2L1	Glucose 1,6-bisphosphate synthase	S175	-1.5
219338	NCL	Nucleolin	T121	-1.4
208559-3	PDHA1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	S201	-1.4
28TEV9-2	SMCR8	Smith-Magenis syndrome chromosomal region candidate gene 8 protein	S498	-1.4
28TER5-4	ARHGEF40	Rho guanine nucleotide exchange factor 40	T371	-1.3
28WUF5	PPP1R13L	RelA-associated inhibitor	S84	-1.3
Q9UJU6	DBNL	Drebrin-like protein	S274	-1.2
C9J2I0	AGFG1	Arf-GAP domain and FG repeat-containing protein 1	S101	-1.1
sites for CL	) K6 KO + H,(	), versus CDK6 KO + H,O, + LEE011		
Q9UKE5-2	TNIK	TRAF2 and NCK-interacting protein kinase	S519	1.4
Q13555-6	CAMK2G	Calcium/calmodulin-dependent protein kinase type II subunit gamma	S321	1.3
Q96PK6	RBM14	RNA-binding protein 14	S520	1.3
Q13555-6	CAMK2G	Calcium/calmodulin-dependent protein kinase type II subunit gamma	S320	1.2
Q9BXB5	OSBPL10	Oxysterol-binding protein-related protein 10	S199	1.2
O9BXB5	OSBPL10	Oxysterol-binding protein-related protein 10	S201	1.1

# SUPPLEMENTARY FIGURES AND LEGENDS



Figure S1. Crystal structure of CDK4 in complex with cyclin D1. Crystal structure of CDK4 in complex with cyclin D1 (PDB ID: 2W96) visualized using UCSF Chimera, including an enlargement of part of the binding interface between CDK4 and cyclin D1. The four CDK4 cysteines 78, 135, 202 and 215 and cyclin D cysteines 7, 8, 38, 47, 68, 73, 106, 125, 189, 239, 243, and 247 are indicated in yellow. C285 of cyclin D is not present in the crystal structure, dashed lines are cysteines not clearly visible in this angle of representation.



### **Figure S2**. (figure legend continues on next page)

(A) Crystal structure of CDK6 in complex with a viral cyclin (PDB ID: 1JOW) visualized using UCSF Chimera. CDK6 cysteines 15, 83, 207 and 280 are indicated in yellow. C7 and C306 of CDK6 is not present in the crystal structure. (B) Parallel reducing and non-reducing SDS-PAGE and western blot analysis (WB) of Flag-CDK6 immunoprecipitates (IP) and a complementary in vitro kinase assay using recombinant GST-Rb as a substrate. Flag-CDK6 and cyclin D1 were expressed in 293T cells and exposed to 200 µM of H<sub>2</sub>O<sub>2</sub> for the indicated time. CDK6 and cyclin D form an intermolecular disulfide-dependent complex upon exposure to H<sub>2</sub>O<sub>2</sub>, and migrate as a single band under non-reducing conditions. The  $H_2O_2$ -induced complex between CDK6 and cyclin D is induced within 30 seconds of H,O, treatment, and decreases after 5 minutes of H,O, treatment. (C) Cells expressing Flag-CDK6 and HA-cyclin D1, D2 or D3 were subjected to H<sub>2</sub>O<sub>2</sub> for 2 minutes before Flag-CDK6 immunoprecipitation and *in vitro* kinase assay. Samples were analyzed under non-reducing and reducing conditions.



### Figure S3

Scatter plot of the mass spectrometry data from cells expressing Flag-CDK4 or Flag-CDK6, showing the  $\log_2$  fold change of proteins in  $H_2O_2$  treated cells versus untreated control for the first two conditions, or CDK4 versus CDK6 in the last 2 conditions. Colored dots represent proteins with a *p*-value < 0.05 as calculated using inference of protein differential abundance by probabilistic dropout analysis (proDA). Horizontal dotted lines are positioned at  $\log_2$  fold change of 1 and -1 (i.e. a 2-fold change).



### Figure S4

Parallel reducing and non-reducing SDS-PAGE and western blot analysis (WB) of Flag-CDK4 immunoprecipitates (IP) and a complementary *in vitro* kinase assay using recombinant GST-Rb as a substrate. 293T cells expressing Flag-CDK4 and HA-cyclin D1, D2 or D3 were and exposed to 200  $\mu$ M of H<sub>2</sub>O<sub>2</sub> 2 minutes. Kinase activity of CDK4 in complex with cyclin D3 is greatly enhanced compared to cyclins D1 and D2.

# REFERENCES

- Malumbres, M.; Barbacid, M. To Cycle or Not to Cycle: A Critical Decision in Cancer. Nat Rev Cancer 2001, 1, 222-231, doi:10.1038/35106065.
- Pardee, A.B. A Restriction Point for Control of Normal Animal Cell Pr liferation. *Proc National Acad Sci* 1974, *71*, 1286–1290, doi:10.1072 pnas.71.4.1286.
- Meloche, S.; Pouysségur, J. The ERK1/2 Mitogen-Activated Protein Kinase Pathway as a Master Regulator of the G1- to S-Phase Transition. Oncogene 2007, 26, 3227–3239, doi:10.1038/sj.onc.1210414.
- Yang, H.W.; Chung, M.; Kudo, T.; Meyer, T. Competing Memories of Mitogen and P53 Signalling Control Cell-Cycle Entry. *Nature* 2017, 549, 404–408, doi:10.1038/nature23880.
- Heldt, F.S.; Barr, A.R.; Cooper, S.; Bakal, C.; Novák, B. A Comprehe sive Model for the Proliferation–Quiescence Decision in Response Endogenous DNA Damage in Human Cells. *Proc National Acad S* 2018, *115*, 201715345, doi:10.1073/pnas.1715345115.
- Spiller, D.G.; Wood, C.D.; Rand, D.A.; White, M.R.H. Measurement of Single-Cell Dynamics. *Nature* 2010, 465, 736–745, doi:10.1038/ nature09232.
- 7. Hanahan, D.; Weinberg, R.A. Hallmarks of Cancer: The next Generation. *Cell* **2011**, *144*, 646 674, doi:10.1016/j.cell.2011.02.013.
- Burhans, W.C.; Heintz, N.H. The Cell Cycle Is a Redox Cycle: Linkir Phase-Specific Targets to Cell Fate. *Free Radical Bio Med* 2009, 4 1282 1293, doi:10.1016/j.freeradbiomed.2009.05.026.
- Amponsah, P.S.; Yahya, G.; Zimmermann, J.; Mai, M.; Mergel, S.; Müłhaus, T.; Storchova, Z.; Morgan, B. Peroxiredoxins Couple Metabolis and Cell Division in an Ultradian Cycle. *Nat Chem Biol* 2021, 1– doi:10.1038/s41589-020-00728-9.
- Huang, B.K.; Ali, S.; Stein, K.T.; Sikes, H.D. Interpreting Heterogeneir in Response of Cells Expressing a Fluorescent Hydrogen Peroxide Bio sensor. *Biophys J* 2015, 109, 2148–2158, doi:10.1016/j.bpj.2015.08.05
- Dennery, P.A. Oxidative Stress in Development: Nature or Nurture? *Free Radical Bio Med* 2010, 49, 1147–1151, doi:10.1016/j.freeradbiomed.2010.07.011.
- Sarsour, E.H.; Kumar, M.G.; Chaudhuri, L.; Kalen, A.L.; Goswar P.C. Redox Control of the Cell Cycle in Health and Disease. *Antion Redox Sign* 2009, *11*, 2985–3011, doi:10.1089/ars.2009.2513.
- Shi, T.; Dansen, T.B. Reactive Oxygen Species Induced P53 Activation: DNA Damage, Redox Signaling, or Both? *Antioxid Redox Sign* 2020, 33, 839–859, doi:10.1089/ars.2020.8074.
- Hornsveld, M.; Feringa, F.M.; Krenning, L.; Berg, J. van den; Smits, L.M.M.; Nguyen, N.B.T.; Rodríguez-Colman, M.J.; Dansen, T.B.; Medema, R.H.; Burgering, B.M.T. A FOXO-Dependent Replication Checkpoint Restricts Proliferation of Damaged Cells. *Cell Reports* 2021, 34, 108675, doi:10.1016/j.celrep.2020.108675.

 Vurusaner, B.; Poli, G.; Basaga, H. Tumor Suppressor Genes and ROS: Complex Networks of Interactions. *Free Radical Bio Med* 2012, *52*, 7–18, doi:10.1016/j.freeradbiomed.2011.09.035.

- Lennicke, C.; Cochemé, H.M. Redox Regulation of the Insulin Signalling Pathway. *Redox Biol* 2021, 42, 101964, doi:10.1016/j. redox.2021.101964.
- Goldkorn, T.; Balaban, N.; Matsukuma, K.; Chea, V.; Gould, R.; Last, J.; Chan, C.; Chavez, C. EGF-Receptor Phosphorylation and Signaling Are Targeted by H2O2 Redox Stress. *Am J Resp Cell Mol* **1998**, *19*, 786–798, doi:10.1165/ajrcmb.19.5.3249.
- Burch, P.M.; Heintz, N.H. Redox Regulation of Cell-Cycle Re-Entry: Cyclin D1 as a Primary Target for the Mitogenic Effects of Reactive Oxygen and Nitrogen Species. *Antioxid Redox Sign* 2005, *7*, 741–751, doi:10.1089/ars.2005.7.741.
- Lee, S.-R.; Kwon, K.-S.; Kim, S.-R.; Rhee, S.G. Reversible Inactivation of Protein-Tyrosine Phosphatase 1B in A431 Cells Stimulated with Epidermal Growth Factor\*. *J Biol Chem* **1998**, *273*, 15366–15372, doi:10.1074/jbc.273.25.15366.
- 20. Frijhoff, J.; Dagnell, M.; Godfrey, R.; Östman, A. Regulation of Protein Tyrosine Phosphatase Oxidation in Cell Adhesion and Migration. *Antioxid Redox Sign* **2014**, *20*, 1994–2010, doi:10.1089/ars.2013.5643.
- Matsushime, H.; Roussel, M.F.; Sherr, C.J. Novel Mammalian Cyclins (CYL Genes) Expressed during G1. *Cold Spring Harb Sym* 1991, 56, 69–74, doi:10.1101/sqb.1991.056.01.010.
- Matsushime, H.; Roussel, M.F.; Ashmun, R.A.; Sherr, C.J. Colony-Stimulating Factor 1 Regulates Novel Cyclins during the G1 Phase of the Cell Cycle. *Cell* **1991**, *65*, 701–713, doi:10.1016/0092-8674(91)90101-4.
- Matsushime, H.; Ewen, M.E.; Strom, D.K.; Kato, J.-Y.; Hanks, S.K.; Roussel, M.F.; Sherr, C.J. Identification and Properties of an Atypical Catalytic Subunit (P34PSK-J3/Cdk4) for Mammalian D Type G1 Cyclins. *Cell* **1992**, *71*, 323–334, doi:10.1016/0092-8674(92)90360-0.
- 24. Latimer, H.R.; Veal, and E.A. Peroxiredoxins in Regulation of MAPK Signalling Pathways; Sensors and Barriers to Signal Transduction. *Mol Cells* **2016**, *39*, 40 45, doi:10.14348/molcells.2016.2327.
- 25. Putker, M.; Vos, H.R.; Dorenmalen, K. van; Ruiter, H. de; Duran, A.G.; Snel, B.; Burgering, B.M.T.; Vermeulen, M.; Dansen, T.B. Evolutionary Acquisition of Cysteines Determines FOXO Paralog-Specific Redox Signaling. *Antioxid Redox Sign* **2015**, *22*, 15 28, doi:10.1089/ ars.2014.6056.
- 26. Day, P.J.; Cleasby, A.; Tickle, I.J.; O'Reilly, M.; Coyle, J.E.; Holding, F.P.; McMenamin, R.L.; Yon, J.; Chopra, R.; Lengauer, C.; et al. Crystal Structure of Human CDK4 in Complex with a D-Type Cyclin. *Proc National Acad Sci* **2009**, *106*, 4166 4170, doi:10.1073/ pnas.0809645106.
- Tchakarska, G.; Sola, B. The Double Dealing of Cyclin D1. *Cell Cycle* 2019, *19*, 1–16, doi:10.1080/15384101.2019.1706903.

- 28. Mullany, L.K.; White, P.; Hanse, E.A.; Nelsen, C.J.; Goggin, M.M.; Mullany, J.E.; Anttila, C.K.; Greenbaum, L.E.; Kaestner, K.H.; Albrecht, J.H. Distinct Proliferative and Transcriptional Effects of the D-Type Cyclins in Vivo. *Cell Cycle* **2008**, *7*, 2215–2224, doi:10.4161/ cc.7.14.6274.
- 29. Ely, S.; Liberto, M.D.; Niesvizky, R.; Baughn, L.B.; Cho, H.J.; Hatada, E.N.; Knowles, D.M.; Lane, J.; Chen-Kiang, S. Mutually Exclusive Cyclin-Dependent Kinase 4/Cyclin D1 and Cyclin-Dependent Kinase 6/ Cyclin D2 Pairing Inactivates Retinoblastoma Protein and Promotes Cell Cycle Dysregulation in Multiple Myeloma. *Cancer Res* 2005, 65, 11345–11353, doi:10.1158/0008-5472.can-05-2159.
- 30. Kato, J.; Matsushime, H.; Hiebert, S.W.; Ewen, M.E.; Sherr, C.J. Direct Binding of Cyclin D to the Retinoblastoma Gene Product (PRb) and PRb Phosphorylation by the Cyclin D-Dependent Kinase CDK4. *Gene* Dev 1993, 7, 331–342, doi:10.1101/gad.7.3.331.
- 31. Lundberg, A.S.; Weinberg, R.A. Functional Inactivation of the Retinoblastoma Protein Requires Sequential Modification by at Least Two Distinct Cyclin-Cdk Complexes. *Mol Cell Biol* **1998**, *18*, 753–761, doi:10.1128/mcb.18.2.753.
- 32. Putker, M.; Madl, T.; Vos, H.R.; Ruiter, H. de; Visscher, M.; Berg, M.C.W. van den; Kaplan, M.; Korswagen, H.C.; Boelens, R.; Vermeulen, M.; et al. Redox-Dependent Control of FOXO/DAF-16 by Transportin-1. *Mol Cell* **2013**, *49*, 730 742, doi:10.1016/j. molcel.2012.12.014.
- 33. Nelson, D.A.; Krucher, N.A.; Ludlow, J.W. High Molecular Weight Protein Phosphatase Type 1 Dephosphorylates the Retinoblastoma Protein\*. *J Biol Chem* **1997**, *272*, 4528–4535, doi:10.1074/jbc.272.7.4528.
- 34. Kato, J.Y.; Matsuoka, M.; Strom, D.K.; Sherr, C.J. Regulation of Cyclin D-Dependent Kinase 4 (Cdk4) by Cdk4-Activating Kinase. *Mol Cell Biol* **1994**, *14*, 2713–2721, doi:10.1128/mcb.14.4.2713.
- Stöcker, S.; Maurer, M.; Ruppert, T.; Dick, T.P. A Role for 2-Cys Peroxiredoxins in Facilitating Cytosolic Protein Thiol Oxidation. *Nat Chem Biol* 2017, 14, doi:10.1038/nchembio.2536.
- 36. Dam, L. van; Pagès-Gallego, M.; Polderman, P.E.; Es, R.M. van; Burgering, B.M.T.; Vos, H.R.; Dansen, T.B. The Human 2-Cys Peroxiredoxins Form Widespread, Cysteine-Dependent- and Isoform-Specific Protein-Protein Interactions. *Antioxidants* 2021, *10*, 627, doi:10.3390/antiox10040627.
- 37. Wang, H.; Nicolay, B.N.; Chick, J.M.; Gao, X.; Geng, Y.; Ren, H.; Gao, H.; Yang, G.; Williams, J.A.; Suski, J.M.; et al. The Metabolic Function of Cyclin D3–CDK6 Kinase in Cancer Cell Survival. *Nature* 2017, 546, 426 430, doi:10.1038/nature22797.
- 38. Anders, L.; Ke, N.; Hydbring, P.; Choi, Y.J.; Widlund, H.R.; Chick, J.M.; Zhai, H.; Vidal, M.; Gygi, S.P.; Braun, P.; et al. A Systematic Screen for CDK4/6 Substrates Links FOXM1 Phosphorylation to Senescence Suppression in Cancer Cells. *Cancer Cell* **2011**, *20*, 620 634, doi:10.1016/j.ccr.2011.10.001.

- Göbl, C.; Morris, V.K.; Dam, L. van; Visscher, M.; Polderman, P.E.; Hartlmüller, C.; Ruiter, H. de; Hora, M.; Liesinger, L.; Birner-Gruenberger, R.; et al. Cysteine Oxidation Triggers Amyloid Fibril Formation of the Tumor Suppressor P16INK4A. *Redox Biol* 2019, 101316, doi:10.1016/j.redox.2019.101316.
- Álvarez-Fernández, M.; Malumbres, M. Mechanisms of Sensitivity and Resistance to CDK4/6 Inhibition. *Cancer Cell* 2020, *37*, 514–529, doi:10.1016/j.ccell.2020.03.010.
- Urbaniak, M.D.; Martin, D.M.A.; Ferguson, M.A.J. Global Quantitative SILAC Phosphoproteomics Reveals Differential Phosphorylation Is Widespread between the Procyclic and Bloodstream Form Lifecycle Stages of Trypanosoma Brucei. *J Proteome Res* 2013, *12*, 2233–2244, doi:10.1021/pr400086y.

# 51 BIOCHEMICAL CHARACTERIZATION OF CDK4

GENERAL DISCUSSION




# GENERAL DISCUSSION

### **REACTIVITY AND** SPECIFICITY IN REDOX **SIGNALING**

As discussed extensively in this thesis, the reversible oxidation of proteins downstream of  $H_2O_2$  is considered a major cell signaling mechanism. There are numerous examples of signaling pathways that proceed through the reversible oxidation of cysteine residues, of which we described several in chapters 3, 4 and 6. It has been difficult to explain how  $H_2O_2$ as a second messenger achieves the reactivity (i.e. how it reacts with low abundant targets) and specificity (i.e. reacting with specific thiols on specific proteins) required for proper signal transduction (see also Figure 5 in chapter 1).

Firstly, most protein thiols in general have been found to have a low reactivity with H<sub>2</sub>O<sub>2</sub> [8,9]. On top of that, the two cytosolic PRDXs (PRDX1 and PRDX2) are expected to scavenge more than 99% of cytosolic  $H_2O_2$  [10]. Together with the abundance and reactivity of GPXs and other peroxidases, most  $H_2O_2$  is converted or cleared at rates that are hard to beat [11-13]. This means that cysteine thiols in H<sub>2</sub>O<sub>2</sub> effector proteins are generally outcompeted by peroxiredoxins for the reaction with  $H_2O_2$ .

Thirdly, H<sub>2</sub>O<sub>2</sub> is undoubtedly an inherently unspecific oxidant because it lacks complexity, and it is poorly understood how H<sub>2</sub>O<sub>2</sub> causes the oxidation of specific redox-sensitive proteins in particular pathways in the context of virtually limitless potential targets in a cell. Any redox-regulated signal transduction protein should be able to react selectively despite the competition of extremely reactive enzymes like peroxiredoxins. Only this will ensure the signal specificity required for the proper response to a certain stimulus [13].

There are several proposed explanations for this problem, which are not mutually exclusive [5]. These models are elaborately discussed in the first chapter of this thesis (General Introduction). For some proteins it has been shown that the poor reactivity-based disadvantage can be overcome by

a 'redox relay' in which peroxiredoxins (or other peroxidases) initially react with  $H_2O_2$  and then oxidize a target [14–19]. In chapter 2, we explored this peroxiredoxin-based relay on a proteome-wide scale, and investigated whether it provides the required reactivity and specificity for cysteine-oxidation based redox signaling. As mentioned, mammalian cells express five 2-cys peroxiredoxin isoforms, each with their own localization, oxidation kinetics and structural differences around their catalytic sites. Widespread peroxiredoxin-based redox relay could therefore not only explain the reactivity but could also grant selectivity in H<sub>2</sub>O<sub>2</sub>-dependent redox signaling.

We show that the different 2-cys peroxiredoxin isoforms indeed participate in the formation of such mixed disulfide intermediates, and that they each have their own subset of targets.

Oxidized peroxiredoxins could in principle relay oxidizing equivalents to other thiols via two molecular mechanisms: C<sub>p</sub>-SOH and C<sub>p</sub>-S-S-C<sub>p</sub>-mediated (Figure 1, left). Our results suggest that there are large differences between peroxiredoxin isoforms in terms of their preferred relay mechanisms, allowing for a layer of specificity. The percentage of C<sub>p</sub>-S-S-C<sub>n</sub>-mediated binders ranges from 21% to 16% for PRDX2 and PRDX3, 44% and 58% for PRDX1 and PRDX4, and, as much as 73% of PRDX5, respectively. The preference for either mechanism might come from different oxidation kinetics between peroxiredoxin isoforms. For example, the rate constant for disulfide formation is 13 s<sup>-1</sup> for PRDX1 and only 0.6 s<sup>-1</sup> for PRDX2, resulting in a longer lifetime of the PRDX2 sulfenic acid. Different sensitivities to overoxidation also underlie persistence of the C<sub>p</sub>-SOH [20]. A longer C<sub>p</sub>-SOH lifetime allows peroxiredoxins to react with a different set of protein thiols involving the C<sub>p</sub>-SOH mechanism, whereas a longer lifetime of the disulfide would promote interaction with via the  $C_p$ -S-S- $C_p$ -mediated mechanism. It is likely one of the underlying causes for the differences in the preferred mechanism between isoforms, as reflected in the percentage of  $C_p$ -S-S- $C_p$ -mediated interactors.



**Figure 1.** Possible outcomes of the intermolecular disulfide formation between a peroxiredoxin and a target protein. **i**) The disulfide is resolved via a disulfide exchange reaction with another nearby cysteine from the target protein (complex), forming an intra- or intermolecular disulfide bond in the target protein and leaving peroxiredoxin in a reduced state. **ii**) The intermolecular disulfide between the peroxiredoxin and its target protein is the final product, representing a novel post-translational modification (PTM) on cysteine which we call 'S-peroxiredoxinylation' (S-PRDXylation). The disulfide can still take part in a disulfide exchange reaction with the peroxiredoxin resolving cysteine ( $C_R$ ), thereby reducing the target and forming the canonical disulfide  $C_p$ -S-S-C<sub>R</sub>. **iii**) The recycling of the PRDXylated target protein could require the TRX system.

Peroxiredoxins are predicted to switch from mostly reduced to mostly oxidized within a very narrow range of  $H_2O_2$  concentrations [20]. Since each peroxiredoxin isoform has a unique combination of rate constants for each step in the peroxiredoxin catalytic cycle (sulfenic acid formation, sulfenic acid condensation and disulfide reduction), it is possible that peroxiredoxin isoforms switch from mostly reduced to mostly oxidized at distinct peroxide concentrations. The accumulation of  $C_p$ -SOH and  $C_p$ -S-S- $C_R$  at distinct concentrations of  $H_2O_2$  per peroxiredoxin isoform may differentially modulate  $H_2O_2$ -mediated redox signaling.

Another layer of specificity of PRDX1-5 interactors might result from amino acids surrounding the cysteine in a target protein. As  $C_p$ -SOH and  $C_p$ -S-S- $C_R$  are structurally distinct, the local environment of an interacting cysteine could determine whether an interaction is favorable. Likewise, the local amino acid composition around the peroxiredoxin catalytic center might influence the affinity for targets. In **chapter 2**, we explore possible differences in the local amino acid composition of peroxiredoxin targets separated by their interaction mechanism and by the peroxiredoxin isoform they interact with. Our mass-spectrometry data also suggest that different peroxiredoxin isoforms interact with each other in a cysteine-dependent manner. The nature of these interactions in terms of their cysteine-dependency and macromolecular composition is not entirely clear. It is possible that peroxiredoxins form multimeric complexes involving two different monomeric isoforms forming form heterodimeric complexes, or perhaps a homodimer interacting with another monomeric isoform. Since peroxiredoxins interact with a diverse set of proteins, including many redox relay target proteins, thioredoxin (TRX) and glutathione S-transferase pi ( $\pi$ GST, for PRDX6, an isoform that is structurally similar to PRDX1-5) it is possible that a heterodimeric peroxiredoxin complex has yet another subset of target proteins [21,22]. Although further work needs to be carried out to elucidate the nature of these interactions, this could further expand the repertoire of peroxiredoxin-based redox signaling.

So far, the end-product of peroxiredoxin-dependent cysteine oxidation is unknown. There are multiple possible outcomes following the intermolecular disulfide formation between a peroxiredoxin and a target protein (**Figure 1**). These include:



#### Figure 2. (figure legend continues on next page)

**A)** The interaction between PRDX2 and its binding partner histone acetyltransferase 1 (HAT1). PRDX2 knockout 293T cells were transfected with Flag-PRDX2 and cysteines mutants. Oxidizing conditions induce a mass shift of a fraction of PRDX2. Parallel reducing and non-reducing SDS-PAGE and western blot analysis (WB) of Flag-PRDX2 immunoprecipitations (IP). Cells were incubated with 25 μM of H<sub>2</sub>O<sub>2</sub> for 2 minutes where indicated. Under non-reducing conditions, HAT1 shows a H<sub>2</sub>O<sub>2</sub> induced mass-



shift. This mass-shift is less pronounced in conditions with PRDX2 cysteine mutants, and is lost when samples are analyzed under reducing conditions. B) interaction between PRDX2 and its binding partner TIPRL. PRDX2 knockout cells were transfected with Flag-PRDX2 and cysteines mutants as in A). Oxidizing conditions induce a mass shift of a fraction of PRDX2. Parallel reducing and non-reducing SDS-PAGE and western blot analysis (WB) of Flag-PRDX2 immunoprecipitations (IP). Cells were incubated with 25  $\mu$ M of H<sub>2</sub>O<sub>2</sub> for 2 minutes where indicated. Under non-reducing conditions, PRDX2 is able to form several disulfide-dependent heterodimers with TIPRL upon stimulation with H<sub>2</sub>O<sub>2</sub>, as indicated by a mass-shift. This mass-shift is less not there in conditions with PRDX2 cysteine mutants, and is lost when samples are analyzed under reducing conditions. C) TIPRL and PRDX2 oxidation kinetics. PRDX2 knockout cells were transfected with HA-PRDX2 and cysteines mutants, and Flag-TIPRL. Cells were incubated with different concentrations of H<sub>2</sub>O<sub>2</sub> for 2 minutes as indicated, before harvesting and analysis of samples under reducing and non-reducing conditions. There is no clear difference in the extent of TIPRL disulfide formation in the presence or absence of PRDX2.

- i) The disulfide is resolved via a disulfide exchange reaction with another nearby cysteine in the target protein (complex), forming an intra- or intermolecular disulfide bond in the target protein and releasing peroxiredoxin in a reduced state. This has been shown for the relay between PRDX2 and STAT3 [16].
- ii) The intermolecular disulfide between the peroxiredoxin and its target protein is the final product, representing a novel post-translational modification (PTM) on cysteine which we refer to as 'S-peroxiredoxinylation' (S-PRDXylation). Like other PTMs, S-PRDXylation could alter the target protein's conformation, protein function, activity, etc. Alternatively, PRDXylation might protect proteins from undesired (thiol) oxidation. Besides a role as a post-translational modification impacting the function of specific proteins, widespread PRDXylation could in principle also serve as a redox buffer. Importantly, the mixed disulfide between peroxiredoxin and the PRDXylated target protein can still take part in a disulfide exchange reaction with the peroxired oxin resolving cysteine  $(C_p)$ , thereby reducing and releasing the target and forming the canonical disulfide  $C_p$ -S-S- $C_p$ .
- iii) The recycling of the PRDXylated target protein could require the TRX system. If this is the case, the use of TRX-based disulfide exchange interactions as a readout for protein thiol oxidation as used in ref. [17] can not distinguish between PRDXylated proteins and disulfide bonds in proteins as described under i).

Of note, our mass spectrometry-based screen does not distinguish between these different types of end-products described above. The possible outcomes of the peroxiredoxin-based redox relay described above are not mutually exclusive and may act in parallel. In an attempt to characterize a few peroxiredoxin interactors, we investigated the interaction between PRDX2 and its binding partner histone acetyltransferase 1 (HAT1). In PRDX2-deficient cells, restoring PRDX2 levels with wild-type PRDX2 induces HAT1 oxidation in the form of disulfides, as described in i) (Figure 2A, non-reducing input). Similar behavior was observed for mutant PRDX2- $C_p S$ , albeit to a lesser extent, but addback of PRDX2- $C_{pp} S$ barely induces HAT1 disulfide formation. This suggests that PRDX2 facilitates HAT1 disulfide formation, and that the relay intermediate between PRDX2 and HAT1 is resolved via a disulfide exchange reaction with another nearby cysteine, resulting in the formation of intermolecular HAT1 disulfide bonds, according to the scenario described above at i).

We found that PRDX2 is able to form several disulfide-dependent heterodimers with TIPRL upon stimulation with H<sub>2</sub>O<sub>2</sub> (Figure 2B). However, we did not observe differences in the extent of TIPRL disulfide formation in the presence or absence of active peroxiredoxins. This suggests that the interaction between TIPRL and PRDX2 does not result in additional disulfide bonds in TIPRL, and that TIPRL is PRDXylated by PRDX2 as described in iii). Interestingly, even though the oxidation of TIPRL is not catalyzed by a PRDX2-dependent relay, TIPRL forms disulfide-dependent dimers with similar kinetics as peroxiredoxins (Figure 2C). Despite the strong redox-regulated interaction between PRDX2 and TIPRL, it is of course possible that TIPRL oxidation is catalyzed by other peroxiredoxin isoforms.

An important implication of a redox relay is that it allows oxiredoxin catalytic cysteines (chapter 2). The specific set redox signaling to gradually change into oxidative damage of binders per peroxiredoxin isoform led us to hypothesize with increasing H<sub>2</sub>O<sub>2</sub> levels. As described in section B), that some of these could function as adaptor proteins that the floodgate model suggests that both redox signaling and facilitate the peroxiredoxin-based redox relay. Adaptor prorandom oxidative damage do not occur until H<sub>2</sub>O<sub>2</sub> levels teins have been shown to be involved in peroxidase-dependent are high enough to cause overoxidation of peroxiredoxredox relays. For example, the PRDX2-STAT3 redox relay has recently been shown to depend on association with the ins. In other words, redox signaling and random oxidative damage would occur approximately simultaneously, after membrane-associated scaffold protein ANXA2 [27]. Likethe hyperoxidation of peroxiredoxins. This is in contrast to wise, Orp1-dependent Yap1 oxidation is dependent on the peroxiredoxin-based redox relays, which can only take place presence of the adapter protein Ybp1, shielding oxidized Orp1 when peroxiredoxins are catalytically active and not hyperfrom reduction [28,29]. Scaffold proteins may recruit target oxidized. H<sub>2</sub>O<sub>2</sub>-dependent signaling would thus occur at proteins and bring them in close proximity to peroxiredoxins, before peroxiredoxins react with H<sub>2</sub>O<sub>2</sub> to form C<sub>p</sub>-SOH and concentrations below those required for overoxidation of peroxiredoxins. At higher [H<sub>2</sub>O<sub>2</sub>], peroxiredoxin overoxida- $C_{p}$ -S-S- $C_{R}$  (Figure 3E). Alternatively, redox relay targets and tion would thus inactivate redox signaling and change H<sub>2</sub>O<sub>2</sub> peroxiredoxins may form scaffold dependent complexes prior to peroxiredoxin oxidation, facilitating efficient transfer of oxfrom a signaling to a damaging agent. Peroxiredoxin-based redox relays thus allow for a concentration-dependent H<sub>2</sub>O<sub>2</sub> idizing equivalents directly upon oxidation. A scaffold protein effect in which redox signaling precedes oxidative damage. would not only increase the chances that a peroxiredoxin finds a target, but could also provide another means of achieving Interestingly, it has been shown that oxidized glutaredoxins specificity, coming from the interaction of specific peroxire-(GRX) can also be reduced by target proteins such as the doxin isoforms (and their targets) with specific adaptors for rxYFP-Grx1p and Grx1-roGFP2 fusion protein-based redox the relay of oxidation to subsets of target proteins.

probes as well as peroxiredoxins [23-25]. This could be described as a GRX-based redox relay, analogous with a PRDXbased redox relay.

It should also be noted that all typical post-translational modifications (PTMs) are controlled by enzymes that catalyze the TIPRL addition of the PTM, but also by enzymes that catalyze the in-Redox-dependent inactivation of protein tyrosine phosphaverse reaction; the removal of the PTM. For example, protein tases is known to facilitate growth factor signaling upon the phosphorylation is catalyzed by kinases whereas phosphatases activation of growth factor receptors, allowing for sustained catalyze dephosphorylation reactions. It seems obvious that phosphorylation-mediated signaling [30,31]. In chapter 3, also thiol oxidation is controlled bidirectionally in order to we identified the protein phosphatase 2A (PP2A)-regulatory protein TIPRL (TOR signaling pathway regulator-like; function in signaling [5,26]. Assuming that is also the case for peroxiredoxin-based redox relays, there should be enzymes TOR: Target of rapamycin) as a redox-sensor. A slightly more that actively remove oxidative modifications from peroxireoxidizing cellular redox state rapidly causes the oxidation of doxin target proteins. cysteines C14 and C87, upon which TIPRL forms three differentially linked homodimers with a disulfide between We find a fair number of proteins in our screen that interact C14-C14, C87-C87 or C14-C87. Our preliminary experi-

with specific peroxiredoxin isoforms independent of the perments suggest that the redox-dependent homodimerization

## **REDOX CONTROL OF CELLULAR SIGNALING**



Scaffold proteins may recruit target proteins and bring them in close proximity to peroxiredoxins, before peroxiredoxins react with  $H_2O_2$  to form  $C_n$ -SOH and  $C_n$ -S-S- $C_n$ . Alternatively, redox relay targets and peroxiredoxins may form scaffold dependent complexes prior to peroxiredoxin oxidation, facilitating efficient transfer of oxidizing equivalents directly upon oxidation.

of TIPRL might play a role in its regulation of PP2A-C and downstream PP2A targets mTORC1 and PKB.

Although the reversible oxidation of the catalytic cysteine of protein tyrosine phosphatases has emerged as a mechanism of activity regulation, the Ser/Thr phosphatase PP2A does not contain a catalytic cysteine. Nevertheless, PP2A is redox regulated in several manners. For example, the cysteines 266 and 269 of PP2A, comprising a potentially redox -active CXXC-motif, have been shown to be sensitive to oxidation, resulting in the inhibition of PP2A catalytic activity [32,33]. Furthermore, H<sub>2</sub>O<sub>2</sub> has been shown to inhibit PP2A catalytic activity by increased levels of oxidized glutathione (GSSG), suggesting that PP2A can be glutathionylated [34]. In contradiction with these studies, it was reported that PP2A is activated rather than inactivated in response to H<sub>2</sub>O<sub>2</sub>, leading to the dephosphorylation of the Rb, p130 and p107 pocket proteins [35]. Finally, hypoxia is also thought to influence PP2A activity, although depending on the context, this may lead to either activation or inactivation of phosphatase activity [36-38]. In all cases, however, the exact nature of the modifications and the mechanism underlying PP2A (in)activation requires further research.

We described in chapter 3 that TIPRL is required for resistance to prolonged exposure to oxidants. However, the ability of TIPRL to resolve redox stress is not dependent on its oxidation and subsequent dimerization. It was suggested that

TIPRL can function as a scaffold protein mediating the interaction of PP2A with MKK7, thereby inhibiting TRAIL-induced apoptosis [39]. Investigating the role of TIPRL in redox stress resistance in the light of MKK7 regulation could be a direction for future work.

Our results suggest that oxidized TIPRL is more potent at inhibiting PP2A catalytic function even though we were unable to find a direct role downstream of the oxidation of TIPRL. Moreover, TIPRL-bound PP2A was described to lack A- and B- subunits in vitro [40], which suggests a mechanism for reduced phosphatase activity. The selective (dis)assembly of the PP2A holoenzyme could allow for target-specific redox regulation of PP2A phosphatase activity. Furthermore, rather than affecting PP2A-C catalytic activity in general, oxidation of TIPRL may affect pathways downstream of PP2A in different ways. This is in line with the literature discussed above (reviewed in ref. [41]), which suggests a context-dependent effect of a more oxidizing cellular environment on PP2A activity. This potentially allows fine-tuning of PP2A-mediated activity by separating dephosphorylation events regulated by the redox state from those that are not. Notwithstanding the requirement for further studies, we hypothesize that the redox sensitivity of TIPRL may facilitate and fine-tune the redox regulation of PP2A.

cells. Interestingly, the p21-CDK4-cyclin D complexes are functionally active in senescent cells, yet Rb is in a hypophosphorylated state, suggesting that kinase activity is directed at a substrate other than Rb in the context of senescence [47,48]. In other words, the reactivation of CDK4 in senescent cells could affect different CDK4 substrates than Rb and affect CDK4 signaling in a different manner. On the other hand, CDK4 is expressed more broadly than p16<sup>INK4A</sup>, suggesting that the redox regulation of CDK4-cyclin D is more ubiquitous than that of p16<sup>INK4A</sup>. Of course, in our experiments for both the oxidation of p16<sup>INK4A</sup> and the oxidation of CDK4-cyclin D, not all of the total p16<sup>INK4A</sup>/CDK4-cyclin D protein pool is oxidized, leaving a fraction for 'canonical' regulation. This could also be a possible explanation for why p16<sup>INK4A</sup> is still functional as a cell-cycle inhibitor after treating cells with oxidants (see Figure S1, chapter 4). Although we did find evidence that CDK4/6 is reactivated upon oxidation of p16<sup>INK4A</sup>, and that this partially relieves E2F1 repression, we did not find evidence of perturbation of the S-phase checkpoint in additional cell-cycle analysis experiments using flow cytometry and video time-lapse microscopy (data not shown). The reactivation of CDK4/6 that we observed might therefore not be strong enough for full re-entry of the cell cycle under the tested conditions, but we cannot exclude that this might occur in other situations. Additionally, treatment with oxidizing agents also inhibits the cell cycle through several other pathways, possibly obscuring cell cycle re-entry downstream of p16<sup>INK4A</sup> oxidation. For example, oxidizing conditions activate p53 through the p38-MAPK pathway, thereby triggering a p53-dependent cell cycle arrest and cell death [49].

Redox Control of the G1-S Cell Cycle Transition The transition of the G1 to S phase of the cell cycle is under control of the closely related CDK4 and CDK6, both of which depend on the D-type cyclins for activity and can be inactivated by p16<sup>INK4A</sup>. In chapter 4, we described how mild oxidizing conditions can cause the oxidation of the only cysteine in the p16<sup>INK4A</sup> tumor suppressor, resulting in its disulfide-dependent homodimerization. This triggers a dramatic structural rearrangement, resulting in the formation of amyloid-like aggregates (termed 'oxaggregation') and its inactivation as a CDK4/6 inhibitor. In chapter 6, we described how cysteine C135 of cyclin-dependent kinase 4 (CDK4) is subject to oxidation, leading to the formation of a covalently linked complex with its classical interaction partner cyclin D, as well as increased kinase activity of the complex. It is possible that both processes complement each other, i.e. the oxidation-dependent inactivation of p16<sup>INK4A</sup> as well as -activation of CDK4-cyclin D potentially result in the phosphorylation of Rb, thereby releasing the E2F1 transcription factor and thus stimulating cells to progress from G1 to S. Whether, how and in which situations these two mechanisms complement each other, is still unclear. P16<sup>INK4A</sup> is an important cell cycle regulator and tumor suppressor and its expression in healthy cycling cells is normally low. Accumulation of  $p16^{{\scriptscriptstyle\rm INK4A}}$  is a marker for senescence and aging that is induced upon several types of cellular stress, ensuring a

cell cycle arrest under those conditions, thus preventing cell cycle progression under unfavorable circumstances and/or of In this sense, a comparison can be drawn with the regulation damaged cells. As a result, loss of p16<sup>INK4A</sup> function, or loss of signaling by protein phosphorylation. The direct effects of downstream Rb, are one of the most frequent markers of of phosphatase activity depend on the phosphorylation state oncogenic transformation [42]. Although the CDK4-cyclin within the cell. In other words, a phosphatase can dephos-D complex is associated with proliferation, CDK4-cyclin D in phorylate its targets only if they are available, which depends complex with p21<sup>CIP1</sup> also accumulates in senescent cells [43on the kinases that are active within a system, This can result 46]. Since senescent cells also exhibit elevated p16<sup>INK4A</sup> levels, in different effects of increased phosphatase activity between it is thus possible that the redox regulation of the  $p16^{INK4A}$  and cell types. For example, the SHP2 tyrosine phosphatase is the CDK4-cyclin D pathways might converge in senescent shown to act as a tumor suppressor in hepatocytes, whereas



Figure 4. Disulfides can serve as molecular staples that direct and crosslink pre-existing protein complexes.

it is thought to promote tumorigenesis in monocytes [50,51], and this may stem from a differential phosphorylated crucial target in these cells. Likewise, cell type, redox status, p16-expression, ROS type, cell cycle phase, and much more will likely dictate the effect of p16<sup>INK4A</sup> oxaggregation.

We can only speculate if and why cells require CDK4/6 (re) activation and cell cycle progression in oxidizing conditions (in cells expressing  $p16^{INK4A}$ ). The observation that  $p16^{INK4A}$  is highly prone to oxidation even under physiological levels of  $H_2O_2$  may suggest that  $p16^{INK4A}$  oxaggregation plays a role under mild oxidative conditions. This would be in good agreement with a large body of literature on how low levels of ROS can dramatically increase the rate of proliferation, even though this is not in the context of high  $p16^{INK4A}$  levels (reviewed in refs [1,52]). Exposing cells to prolonged or high levels of  $H_2O_2$  caused by perturbations of the redox balance triggers the activation of cell cycle checkpoints and cell cycle arrest, thus leading to the opposite effect.

Together, it is possible that the oxidation of cell cycle regulators ensures the fine-tuning of the redox control of the cell

cycle. One might imagine that, as a prerequisite for proliferation, ROS stimulate cell cycle entry though the activation of CDK4-cyclin D and inactivation of p16<sup>INK4A</sup>. As the cell cycle progresses, it is important that ROS do not exceed concentrations that might cause random damage and oxidative distress. When they do exceed the physiological levels, cell cycle checkpoints are activated and the cell cycle is halted. Complementary redox-regulated mechanisms that might play a role in fine-tuning the redox control of the cell cycle are the ROS-dependent activation of the p53 tumor suppressor, activation of the G1/S checkpoint and the ROS-induced arrest in S phase via PP2A-dependent pRB dephosphorylation [53]. The adequate calibration of the cell cycle machinery in light of the redox state is crucial for an appropriate response to changes in ROS levels. For example, it is possible that cells require low levels of ROS to enter the cell cycle and stimulate proliferation, but at the same time require the reducing power to prevent proliferation. This would ensure a 'break' on the cell cycle if the reducing capacity of the cell is inadequate. This could prevent potentially hazardous levels of ROS can jeopardize the proper progression of the cell cycle, leading to for instance oncogenic mutations or a permanent cell cycle arrest. This is a more common concept in biology. For example, the Myc transcription factor activates proliferation as well as apoptosis, only stimulates proliferation if specific signals block the apoptotic pathway [54]. In this line of reasoning, it can be assumed that the oxidation-mediated inactivation of p16<sup>INK4A</sup> and -activation of CDK4-cyclin D could be part of a larger mechanism that adjusts the cell cycle so that it exclusively proceeds under favorable redox conditions.

can be assumed that the oxidation-mediated inactivation of High levels of ROS can lead to random damage to proteins, p16<sup>INK4A</sup> and -activation of CDK4-cyclin D could be part of including protein unfolding and aggregation, processes that a larger mechanism that adjusts the cell cycle so that it excluhave been associated with aging. As discussed, low levels of H<sub>2</sub>O<sub>2</sub> act as an essential second messenger and are associated with healthy cell physiology [57]. In chapter 5, we discussed Interestingly, tumor cells are characterized by increased levels how these seemingly opposite effects of  $H_2O_2$  as a signaling of ROS [55], meaning that both p16<sup>INK4A</sup> and CDK4-cyclin molecule and H<sub>2</sub>O<sub>2</sub> as a driver of age-related protein aggrega-D are more often in the oxidized state, thereby promoting tion can be united in one hypothesis [57,58]. In an attempt to regain homeostasis, age-related damage might trigger stress proliferation of cancer cells. Whether the redox regulation of p16<sup>INK4A</sup> and/or CDK4-cyclin D indeed contribute to cancer response pathways that partially depend on redox signaling, progression remains to be addressed. As discussed in chapter and thus are accompanied by the production of  $H_2O_2$  as a sig-1, the single cysteine in p16<sup>INK4A</sup> is likely acquired recently in naling molecule. Gradually, more damage accumulates, again terms of evolution, and was substituted thereafter multiple accompanied by a further increase in  $H_2O_2$  levels to boost the times in several branches of mammalian evolution. This supstress response pathways. As a result, H<sub>2</sub>O<sub>2</sub> levels accumulate ports the hypothesis that there is evolutionary pressure against and lead to ROS-associated damage. This creates a vicious the redox dependent inactivation of p16<sup>INK4A</sup>. cycle, in which ROS-dependent damage triggers redox-dependent stress-response pathways which in turn lead to more The non-covalent interaction between CDK4 and cyclin D ROS production. We discuss many examples of the interplay is well established. It may well serve as the starting point for between redox signaling and protein stability.

the covalent interaction between CDK4-cyclin D, in which the preassembled complex is poised for oxidation and covalent A question that emerges from this overview is whether alinteraction through disulfide bond formation. There is an tered redox signaling is a cause or consequence of protein increasing number of examples that suggest that a pre-existaggregation, and whether the vicious cycle described above applies also here. It is clear that there is a complex relationing protein complex can become covalentltly linked in this manner, thereby stabilizing an otherwise weak interaction or ship between ROS, redox signaling and proteostasis. Whereas three-dimensional conformation. This context, the disulfide protein oxidation can trigger aggregation, increases in H<sub>2</sub>O<sub>2</sub> bond is functioning as a 'molecular staple' (Figure 4). For production upon the gradual accumulation of aggregates example, disulfides are thought to crosslink the pre-existmight be a stress response by itself. A small change in redox ing complex between the FOXO4 transcription factor and state or aggregation can in this way rapidly lead to a feed-forthe nuclear import factor Transportin 1 (TNPO1), which ward loop, making redox-regulated protein aggregation an is required for nuclear import and activation of FOXO4 by irreversible process. increased oxidizing conditions [56]. To what extent this is a In **chapter 4**, we described how p16<sup>INK4A</sup> can form fibrils general mechanism in redox-regulated pathways is unclear and is an issue that should be addressed in further research. under physiological conditions, triggered by oxidation of the Moreover, the potential role for scaffold proteins in facilitatsingle cysteine residue and subsequent S-S-dependent homodimerization. We present evidence that p16<sup>INK4A</sup> can form ing these interactions should be examined.

### CROSSTALK BETWEEN REDOX SIGNALING AND PROTEIN HOMEOSTASIS

aggregates that have the typical features of amyloid fibrils, including the binding of diagnostic dyes, presence of a cross-β sheet structure, and typical dimensions found in EM. To our knowledge, this is the first report of the critical dependence on a reversible disulfide cross-linked dimer as a subunit for fibril formation, which highlights the role of the cellular redox state as an important regulator of fibril formation.

From a structural point of view, it is interesting to identify the starting point for the redox-induced conformational changes of p16<sup>INK4A</sup>, i.e. is sulfenylation of C72 sufficient for p16<sup>INK4A</sup> aggregation, or is disulfide formation required to induce β-amyloid formation? The starting point for conformational changes could provide insights for other proteins that possibly follow this mechanism, for example the availability of a secondary cysteine to allow for disulfide formation can be a determining factor in case disulfide formation is required. A major difficulty in answering this question is that it is nearly impossible to separate -S-S- from -SOH in an experimental setting, since disulfide formation is always preceded by sulfenylation. In an attempt to answer this question nonetheless, we collaborated with Agnieszka Bronowska (Newcastle University) who performed in silico simulations of how different C72 oxidation states affect p16<sup>INK4A</sup> conformational stability using all-atom and steered molecular dynamics (MD) simulations and constant force pulling simulations and metadynamics. Both non-oxidized (p16<sup>INK4A</sup>-SH) p16<sup>INK4A</sup> as well as glutathionylated p16<sup>INK4A</sup> (p16<sup>INK4A</sup>-SSG) maintain their secondary structure when challenged with mechanical forces (data not shown). In accordance, the NMR structure of p16<sup>INK4A</sup>-SSG showed no signs of aggregation (Figure 2A in chapter 4), GSHylation indeed prevented amyloid formation. However, when sulfenylated p16<sup>INK4A</sup> (p16<sup>INK4A</sup>-SOH) or p16<sup>INK4A</sup>-hydrazine (an adduct of diamide before disulfide formation) was used in the simulations, fewer residues maintained their secondary structure compared to p16<sup>INK4A</sup>-SH or -SSG, and more residues adopted a  $\beta$ -sheet structure. Furthermore, residues 67-115 within the normally α-helical core structure of p16<sup>INK4A</sup> are the first to change their conformation following the sulfenylation of p16<sup>INK4A</sup>, as suggested also by the algorithms used for prediction of aggregation prone regions (Figure S9A in chapter 4). The alpha-helix in this region contains two adjacent valine residues V95, V96, which are considered thermodynamically less favorable in alpha-helices due to steric hindrance [59]. Indeed, V96 seems especially important in this conformational change, since its in silico mutation into alanine (V96A) maintains a high number of structured residues. Whether this residue is indeed important in p16<sup>INK4A</sup> oxaggregation, and whether mutant p16<sup>INK4A</sup>-V96A is indeed resistant to oxaggregation needs to be examined in an experimental setup. But it is striking to note that, like also observed for the single cysteine at position 72, several vertebrate species including mammals have changes in V95, V96 or both, that are more favorable in helices. Although speculative, these adaptations could be a means to omit redox-dependent aggregation of p16<sup>INK4A</sup>.

It is possible that the oxaggregation of p16<sup>INK4A</sup> is initiated through a peroxiredoxin-catalyzed redox relay leading to p16<sup>INK4A</sup> C72 oxidation. We have made a start to investigate the effect of peroxiredoxins on the aggregation of p16<sup>INK4A</sup>, and we tested whether tethering of PRDX1 to p16<sup>INK4A</sup> affects its oxidation-induced aggregation. HEK293T cells expressing Flag-tagged PRDX1 WT and catalytic dead mutant  $C_{pp}$  S tethered to p16<sup>INK4A</sup> were exposed to oxidants and processed for a filter trap assay for the detection of protein aggregates in cell extracts (see also the scheme in Figure 5A in chapter 4). The tethering of p16<sup>INK4A</sup> to PRDX1 together with exposure to  $H_2O_2$  drastically increases the trapping of p16<sup>INK4A</sup> on the filter membrane, indicative of protein aggregation (Figure 5A). This seems dependent on the oxidation by  $H_2O_2$  as well as the catalytic activity of PRDX1, as mutation of the PRDX1 catalytic cysteines diminishes filter trapping. This is in contrast with the reported chaperone function of peroxiredoxins (discussed below), and this preliminary experiment suggests that PRDX1 promotes p16<sup>INK4A</sup> aggregation in a H<sub>2</sub>O<sub>2</sub>- and cysteine-dependent manner. P16<sup>INK4A</sup> aggregation is dependent on oxidation and dimerization (chapter 4). Therefore, although we do not clearly observe dimer formation of p16<sup>INK4A</sup> when tethered to PRDX1, this experiment also



Figure 5. The effect of peroxiredoxins on the aggregation of p16<sup>INK4A</sup>. A) Tethering p16<sup>INK4A</sup> to PRDX1 and exposure to H<sub>2</sub>O<sub>2</sub> increases the trapping of p16<sup>INK4A</sup> on the filter trap membrane. Flag-p16<sup>INK4A</sup>, YFP-p16<sup>INK4A</sup> and Flag-PRDX1 tethered to p16<sup>INK4A</sup> were expressed in 293T cells knockout for PRDX1 and PRDX2, and treated with 250 µM diamide or 100 µM H,O, Samples were analyzed under parallel reducing and non-reducing conditions and subjected to a filter trap assay. Due to low expression of Flag-p16 constructs, Flag-p16 dimerization is not detectable and Flag-p16 is only detected on the filter trap membrane. Equal amounts of protein were used as input for the filter trap assay. B) Co-expression of HA-PRDX1 and HA-PRDX2 with Flag-p16 and exposure to H<sub>2</sub>O<sub>2</sub> increases the trapping of p16<sup>INK4A</sup> on the filter trap membrane. C The recycling of the PRDXylated target protein could require the TRX system. Co-expression of Flag-TIPRL with HA-PRDX1 or HA-PRDX2 also promote the aggregation of TIPRL.

suggests that PRDX1 promotes p16<sup>INK4A</sup> oxidation. Of note, peroxiredoxins, which could obscure mutant-specific effects. the cysteine mutant of PRDX1 tethered to p16 results in a Technically, it remains to be verified whether the peroxiredoxin-dependent aggregation of p16<sup>INK4A</sup> is indeed also dependent smear on the SDS-PAGE (non-reducing input), but there is no increase in filter trapping in these conditions. This could on C72 in p16<sup>INK4A</sup>, but the combined observations seem to be an indication for unfolding and random intermolecular point in that direction disulfide formation of this protein.

There are several quality control networks in place to main-P16<sup>INK4A</sup> aggregation is also affected by PRDX2 in a cystetain a healthy proteome. These include the clearance of (misine-dependent manner, and also occurs when peroxiredoxfolded) proteins by the ubiquitin-proteasome system (UPS) in is co-expressed rather than tethered to p16<sup>INK4A</sup> (Figure and autophagy, and chaperone-mediated protein (re)folding. 5B). This observation is supported by the identification of Redox signaling can also regulate proteostasis through the p16<sup>INK4A</sup> as a cysteine-dependent interactor for PRDX2 in chaperone function of peroxiredoxins. Depending on their our screen in chapter 2 [21]. Interestingly, co-expression of redox status as well as post-translational modifications, 2-cys p16<sup>INK4A</sup> with the resolving cysteine mutant of peroxiredoxperoxiredoxins are known to oligomerize into a decameric or in PRDX2 C<sub>p</sub>S, is also capable of promoting aggregation of dodecameric doughnut-like structure [60,61]. For example, p16<sup>INK4A</sup>, suggesting that the interaction might proceed via PRDX2 was shown to exist in an equilibrium of dimers and the C<sub>p</sub>-SOH mediated mechanism as described in chapter decamers in solution, in which the oxidation of PRDX2 by 2. Note that these experiments are performed in wild-type H<sub>2</sub>O<sub>2</sub> and subsequent disulfide formation promotes disso-HEK293T cells which also express endogenous, wildtype ciation into dimers, whereas overoxidation of PRDX2 in a



Figure 6. Peroxiredoxins exist in an equilibrium of dimers and decamers in solution. Decamers have chaperone-like activity. The oxidation of PRDX2 by H<sub>2</sub>O<sub>2</sub> and subsequent disulfide formation promotes dissociation into dimers, whereas overoxidation of PRDX2 promotes the formation of the decameric form

more oxidizing environment promotes the formation of the decameric form (Figure 6) [62,63]. Since a lack in reductive power can likely stabilize existing disulfides but not cause overoxidation of peroxiredoxins (own data, not shown and refs. [64,65]), it is likely that a lack of reductive power results in dissociation into dimers, whereas a more oxidizing environment can cause overoxidation of peroxiredoxins and lead to decameric chaperones. This chaperone structure of 2-cys peroxiredoxins has been shown to inhibit protein aggregation, thus providing a redox-dependent protective mechanism that maintains proteostasis under oxidative stress conditions [66].

The coordinated action of small HSPs is thought to disaggregate amyloid fibrils (chapter 5) [58]. Considering the redox-dependent chaperone function of peroxiredoxins, it is possible that dodecameric peroxiredoxins resolve the aggregation and amyloid formation of p16<sup>INK4A</sup> in concert with small HSPs. Hypothetically, this could even be linked to the cell cycle, in which low  $[H_2O_2]$  causes p16<sup>INK4A</sup> oxaggregation and possibly reactivation of the cell cycle, whereas high  $[H_2O_2]$  promote disaggregation and reactivation of p16<sup>INK4A</sup> through the chaperone function of peroxiredoxins, thereby blocking the cell cycle. Alternatively, it is possible that p16<sup>IN</sup> <sup>K4A</sup> is actively oxidized via a redox relay by peroxiredoxins,

thereby promoting the oxidation and subsequent β-amyloid formation. Of note, these two hypotheses are not mutually exclusive, as these mechanisms might be activated under distinct redox conditions. Since peroxiredoxins are more often in an overoxidized state in a more oxidizing environment (but not with a lack of reductive capacity), this in turn stimulates the toroid formation and chaperone function of peroxiredoxins [62,63]. It is possible that the chaperone function is only activated upon high levels of H<sub>2</sub>O<sub>2</sub> in an attempt to relieve proteotoxic stress. If this is the case, it is possible that oxaggregation is regulated over a range of oxidation states. This could hypothetically even link cell cycle progression to H<sub>2</sub>O<sub>2</sub>-concentrations: low levels of H<sub>2</sub>O<sub>2</sub> could cause peroxiredoxin-mediated oxaggregation and inactivation of p16<sup>INK4A</sup> and allow cell cycle progression from G1 to S-phase, whereas at higher H<sub>2</sub>O<sub>2</sub> levels the peroxiredoxin chaperone function could resolve the  $p16^{{\scriptscriptstyle\rm INK4A}}$  aggregates, thereby inducing a cell cycle arrest.

It is unknown whether peroxiredoxin-dependent protein aggregation is a more general feature of peroxiredoxins and involves the aggregation of other proteins besides p16<sup>INK4A</sup>. We therefore examined the effect of PRDX1 and PRDX2 expression on TIPRL, a protein for which there is no evidence that it tends to aggregate. TIPRL aggregation is also promoted by the presence teins. A first step could be to investigate in silico whether agof PRDX1 and PRDX2 in a manner similar to p16<sup>INK4A</sup>, algregation-prone proteins are depleted or enriched in exposed though this does not seem to depend on PRDX catalytic activcysteines, or to investigate the insoluble protein fraction upon ity (Figure 5C). This preliminary experiment was performed an oxidant stimulus using mass spectrometry. in HEK293T cells that are knockout for PRDX1 and PRDX2 (DKO), suggesting that TIPRL is not able to aggregate without CONCLUDING REMARKS the presence of PRDX1/2. Furthermore, TIPRL aggregation is likely fully dependent on TIPRL cysteines. Interestingly, these findings seem to be in contrast with our earlier findings In this thesis we have presented several signaling pathways in Figure 2, in which we showed that TIPRL homodimerizathat proceed through the reversible oxidation of cysteine residues on the proteins p16<sup>INK4A</sup>, TIPRL, CDK4/CDK6 and tion is not dependent on peroxiredoxins. Why aggregation does seem dependent on the presence of peroxiredoxins is not cyclin D and PRDX1-5. It is clear that the redox regulation clear from these experiments. A possible explanation for this of these proteins contributes to essential cellular functions dependency on peroxiredoxins may be that only the PRDXylatsuch as cell cycle arrest, phosphatase signaling, G1-to-S traned form of TIPRL aggregates. These findings raise the followsition and protein stability. For all these proteins mentioned ing questions for future research: How widespread is protein above, it is obvious that context matters a great deal. There are oxaggregation?, Which proteins does it affect?, What type of many possible outcomes of H<sub>2</sub>O<sub>2</sub>-induced cysteine oxidation aggregates are formed? Is a peroxiredoxin-dependent redox-rein many different pathways, which suggests a level of specificlay always involved? ity and fine-tuning of the response to changes in the cellular redox environment. The outcome of H<sub>2</sub>O<sub>2</sub>-dependent sig-A remarkable, but casual observation is that in our laboranaling may depend on, for example, the strength and source

tory for a wide selection of proteins, the cysteine mutant constructs seem more difficult to express at high levels than their wild-type counterparts. This is at least the case for most proteins discussed in this thesis - TIPRL, p16<sup>INK4A</sup>, CDK4 and CDK6, and PRDX1-5 as well as other examples from our lab such as p53. There are several possible explanations for this observation. It is possible that proteins can prevent permanent damage as a result of a highly oxidizing environment through the formation of disulfide bonds (for instance through PRDXylation) and thereby prevent their degradation. A prerequisite for this would be that these disulfide bonds are reversible in order to restore normal protein conformation and functionality. Further experimental studies are required to substantiate or reject this hypothesis, or to investigate whether it applies to a subset of redox-sensitive pro-



#### Figure 7. The tiers of PRDX-mediated specificity in H<sub>2</sub>O<sub>2</sub>-signaling.

Divided in the aspects determined by peroxiredoxins themselves and those determined by target proteins. Independent of peroxiredoxin properties, the localized production of H2O. as well as the floodgate mechanism might contribute to H2O2-signaling specificity.

of H<sub>2</sub>O<sub>2</sub> generation, its duration, the subcellular location as well as cell state, tissue type, the presence of cofactors, etc. Finetuning the response to redox conditions is of importance since it would ensure cellular integrity. For example, a proper cellular judgement of whether ROS levels are either adequate or too high for cells to enter the cell cycle would contribute to the maintenance of genomic integrity. Although the architecture of many redox-regulated protein networks has been mapped, their dynamic function and integration of different networks often remains unclear. It will be challenging to understand the integration of different redox-regulated networks with respect to their sensitivity to oxidation and the hierarchy in forwarding of signals to execute cell fate decisions.

One approach to tackling such challenges might be to make use of localized, inducible production of H<sub>2</sub>O<sub>2</sub> rather than an extracellular bolus of  $H_2O_2$ . This can be achieved by targeting the genetically encoded H<sub>2</sub>O<sub>2</sub> generating enzyme D-amino acid oxidase (DAAO) to specific sites [67].

H<sub>2</sub>O<sub>2</sub> is unequivocally a small molecule without much handles to discriminate what thiols it reacts with, which means that molecular features that can explain sensitivity and selectivity for reacting with H2O2 must be present in its targets in order to achieve specific signal propagation. An enigma in  $H_2O_2$ -mediated signaling is how redox regulated proteins are oxidized specifically when their intrinsic reactivity with H<sub>2</sub>O<sub>2</sub> is low. Above, we discussed different manners in which this reactivity and specificity could be achieved (summarized in Figure 7). Most likely, all mechanisms mentioned play a role to some extent, since examples can be found for all. Additionally, the differential localization of the peroxiredoxin isoforms might contribute to increased scavenging of H<sub>2</sub>O<sub>2</sub> in specific compartments to prevent a local H<sub>2</sub>O<sub>2</sub> build-up, or alternatively it might ensure a redox-relay to local isoform-specific targets - or both. It is unclear what determines the more dominant mechanism in the case of two seemingly competing ones (such as direct oxidation and peroxiredoxin-based redox relays). Nevertheless, it is clear that peroxiredoxin-based redox regulation is important in cytosolic protein oxidation. Simultaneous deletion of cytosolic PRDX1 and PRDX2 results in a decrease - rather than an increase - of overall cytosolic protein thiol oxidation, which is in agreement with thiol oxidation being predominantly catalyzed by peroxiredoxins [17].

From a pathological viewpoint, the precise role of H<sub>2</sub>O<sub>2</sub>-mediated thiol oxidation is mostly unknown. Are increased levels of oxidants promoting or protecting against tumorigenesis? Does protein oxidation stimulate or prevent the build-up of toxic protein aggregates? The answer to these questions is beginning to look ambiguous, with examples emerging supporting both sides. For example, the deregulation of peroxiredoxins has been associated with several pathologies [68,69], but it is unclear whether these are due to the pro-oxidative or anti-oxidative function of peroxiredoxins. Nonetheless it would be useful in the future to be able to generate targeted interventions to specific thiol oxidations, more so because of the advantages that come with covalent targeting of substrates.

# REFERENCES

- 26. Netto, L.E.S.; Oliveira, M.A. de; Tairum-Jr, C.; Neto, J.F. da S. Conferring Specificity in Redox Pathways by Enzymatic Thiol/Disulfide Exchange Reactions. *Free Radical Res* 2015, *50*, 1 99, doi:10.3109/10 715762.2015.1120864.
- Talwar, D.; Messens, J.; Dick, T.P. A Role for Annexin A2 in Scaffolding the Peroxiredoxin 2–STAT3 Redox Relay Complex. *Nat Commun* 2020, *11*, 4512, doi:10.1038/s41467-020-18324-9.
- Bersweiler, A.; D'Autréaux, B.; Mazon, H.; Kriznik, A.; Belli, G.; Delaunay-Moisan, A.; Toledano, M.B.; Rahuel-Clermont, S. A Scaffold Protein That Chaperones a Cysteine-Sulfenic Acid in H2O2 Signaling. *Nat Chem Biol* **2017**, *13*, 909 915, doi:10.1038/nchembio.2412.
- 29. Veal, E.A.; Ross, S.J.; Malakasi, P.; Peacock, E.; Morgan, B.A. Ybp1 Is Required for the Hydrogen Peroxide-Induced Oxidation of the Yap1 Transcription Factor. *J Biol Chem* 2003, *278*, 30896–30904, doi:10.1074/jbc.m303542200.
- 30. Frijhoff, J.; Dagnell, M.; Godfrey, R.; Östman, A. Regulation of Protein Tyrosine Phosphatase Oxidation in Cell Adhesion and Migration. *Antioxid Redox Sign* **2014**, *20*, 1994–2010, doi:10.1089/ars.2013.5643.
- 31. Czech, M.P.; Lawrence, J.C.; Lynn, W.S. Evidence for the Involvement of Sulfhydryl Oxidation in the Regulation of Fat Cell Hexose Transport by Insulin. *Proc National Acad Sci* 1974, 71, 4173–4177, doi:10.1073/ pnas.71.10.4173.
- Sommer, D.; Coleman, S.; Swanson, S.A.; Stemmer, P.M. Differential Susceptibilities of Serine/Threonine Phosphatases to Oxidative and Nitrosative Stress. *Arch Biochem Biophys* 2002, 404, 271–278, doi:10.1016/ s0003-9861(02)00242-4.
- 33. Foley, T.D.; Petro, L.A.; Stredny, C.M.; Coppa, T.M. Oxidative Inhibition of Protein Phosphatase 2A Activity: Role of Catalytic Subunit Disulfides. *Neurochem Res* 2007, 32, 1957–1964, doi:10.1007/s11064-007-9394-x.
- 34. Rao, R.K.; Clayton, L.W. Regulation of Protein Phosphatase 2A by Hydrogen Peroxide and Glutathionylation. *Biochem Bioph Res Co* 2002, 293, 610 616, doi:10.1016/s0006-291x(02)00268-1.
- 35. Cicchillitti, L.; Fasanaro, P.; Biglioli, P.; Capogrossi, M.C.; Martelli, F. Oxidative Stress Induces Protein Phosphatase 2A-Dependent Dephosphorylation of the Pocket Proteins PRb, P107, and P130\*. *J Biol Chem* 2003, 278, 19509–19517, doi:10.1074/jbc.m300511200.
- 36. Conza, G.D.; Cafarello, S.T.; Loroch, S.; Mennerich, D.; Deschoemaeker, S.; Matteo, M.D.; Ehling, M.; Gevaert, K.; Prenen, H.; Zahedi, R.P.; et al. The MTOR and PP2A Pathways Regulate PHD2 Phosphorylation to Fine-Tune HIF1α Levels and Colorectal Cancer Cell Survival under Hypoxia. *Cell Reports* **2017**, *18*, 1699–1712, doi:10.1016/j. celrep.2017.01.051.
- Heikkinen, P.T.; Nummela, M.; Leivonen, S.-K.; Westermarck, J.; Hill, C.S.; Kähäri, V.-M.; Jaakkola, P.M. Hypoxia-Activated Smad3-Specific Dephosphorylation by PP2A2. *J Biol Chem* 2010, *285*, 3740–3749, doi:10.1074/jbc.m109.042978.

- 8. Raghuraman, G.; Rai, V.; Peng, Y.; Prabhakar, N.R.; Kumar, G.K. Pattern-Specific Sustained Activation of Tyrosine Hydroxylase by Intermittent Hypoxia: Role of Reactive Oxygen Species-Dependent Downregulation of Protein Phosphatase 2A and Upregulation of Protein Kinases. *Antioxid Redox Sign* 2009, 11, 1777–1789, doi:10.1089/ ars.2008.2368.
- 39. Song, I.S.; Jun, S.Y.; Na, H.J.; Kim, H.T.; Jung, S.Y.; Ha, G.H.; Park, Y.H.; Long, L.Z.; Yu, D.Y.; Kim, J.M.; et al. Inhibition of MKK7–JNK by the TOR Signaling Pathway Regulator-Like Protein Contributes to Resistance of HCC Cells to TRAIL-Induced Apoptosis. *Gastroenterol*ogy **2012**, *143*, 1341 1351, doi:10.1053/j.gastro.2012.07.103.
- 40. Nakashima, A.; Tanimura-Ito, K.; Oshiro, N.; Eguchi, S.; Miyamoto, T.; Momonami, A.; Kamada, S.; Yonezawa, K.; Kikkawa, U. A Positive Role of Mammalian Tip41-like Protein, TIPRL, in the Amino-Acid Dependent MTORC1-Signaling Pathway through Interaction with PP2A. *Febs Lett* **2013**, *587*, 2924 2929, doi:10.1016/j. febslet.2013.07.027.
- Raman, D.; Pervaiz, S. Redox Inhibition of Protein Phosphatase PP2A: Potential Implications in Oncogenesis and Its Progression. *Redox Biol* 2019, 27, 101105, doi:10.1016/j.redox.2019.101105.
- 42. Forbes, S.A.; Beare, D.; Boutselakis, H.; Bamford, S.; Bindal, N.; Tate, J.; Cole, C.G.; Ward, S.; Dawson, E.; Ponting, L.; et al. COSMIC: Somatic Cancer Genetics at High-Resolution. *Nucleic Acids Res* 2017, 45, D777–D783, doi:10.1093/nat/gkw1121.
- Atadja, P.; Wong, H.; Veillete, C.; Riabowol, K. Overexpression of Cyclin D1 Blocks Proliferation of Normal Diploid Fibroblasts. *Exp Cell Res* 1995, 217, 205–216, doi:10.1006/excr.1995.1080.
- 44. Stein, G.H.; Drullinger, L.F.; Soulard, A.; Dulić, V. Differential Roles for Cyclin-Dependent Kinase Inhibitors P21 and P16 in the Mechanisms of Senescence and Differentiation in Human Fibroblasts. *Mol Cell Biol* **1999**, *19*, 2109–2117, doi:10.1128/mcb.19.3.2109.
- Leontieva, O.V.; Lenzo, F.; Demidenko, Z.N.; Blagosklonny, M.V. Hyper-Mitogenic Drive Coexists with Mitotic Incompetence in Senescent Cells. *Cell Cycle* **2012**, *11*, 4642–4649, doi:10.4161/cc.22937.
- 46. Ye, C.; Zhang, X.; Wan, J.; Chang, L.; Hu, W.; Bing, Z.; Zhang, S.; Li, J.; He, J.; Wang, J.; et al. Radiation-Induced Cellular Senescence Results from a Slippage of Long-Term G2 Arrested Cells into G1 Phase. *Cell Cycle* **2013**, *12*, 1424–1432, doi:10.4161/cc.24528.
- 47. Brookes, S.; Gagrica, S.; Sanij, E.; Rowe, J.; Gregory, F.J.; Hara, E.; Peters, G. Evidence for a CDK4-Dependent Checkpoint in a Conditional Model of Cellular Senescence. *Cell Cycle* 2015, *14*, 1164–1173, doi:10.1080/15384101.2015.1010866.
- 48. Duff, M.L.; Gouju, J.; Jonchère, B.; Guillon, J.; Toutain, B.; Boissard, A.; Henry, C.; Guette, C.; Lelièvre, E.; Coqueret, O. Regulation of Senescence Escape by the Cdk4–EZH2–AP2M1 Pathway in Response to Chemotherapy. *Cell Death Dis* **2018**, *9*, 199, doi:10.1038/s41419-017-0209-y.

- 49. Shi, T.; Soest, D.M.K. van; Polderman, P.E.; Burgering, B.M.T.; Dansen T.B. DNA Damage and Oxidant Stress Activate P53 through Differ ential Upstream Signaling Pathways. *Free Radical Bio Med* 2021, *172* 298–311, doi:10.1016/j.freeradbiomed.2021.06.013.
- 50. Bard-Chapeau, E.A.; Li, S.; Ding, J.; Zhang, S.S.; Zhu, H.H.; Princen F.; Fang, D.D.; Han, T.; Bailly-Maitre, B.; Poli, V.; et al. Ptpn11/Shp Acts as a Tumor Suppressor in Hepatocellular Carcinogenesis. *Cance Cell* **2011**, *19*, 629–639, doi:10.1016/j.ccr.2011.03.023.
- Loh, M.L.; Vattikuti, S.; Schubbert, S.; Reynolds, M.G.; Carlson, E. Lieuw, K.H.; Cheng, J.W.; Lee, C.M.; Stokoe, D.; Bonifas, J.M.; e al. Mutations in PTPN11 Implicate the SHP-2 Phosphatase in Leu kemogenesis. *Blood* 2004, *103*, 2325–2331, doi:10.1182/blood-2003 09-3287.
- Chiu, J.; Dawes, I.W. Redox Control of Cell Proliferation. *Trends Cell Biol* 2012, *22*, 592 601, doi:10.1016/j.tcb.2012.08.002.
- 53. Ranjan, P.; Heintz, N.H. S-Phase Arrest by Reactive Nitrogen Species J Bypassed by Okadaic Acid, an Inhibitor of Protein Phosphatases PP1 PP2A Available online: https://www-sciencedirect-com.proxy.librar\_ uu.nl/science/article/pii/S0891584905005307?casa\_token=w8tF1l01 hdkAAAAA:C2jHD9ch-41ThQAcmdU8iyMzlWFOBTO5UT9Lvc 1MWs5082jA08KYeC1x\_BE7e\_cacShYKdUwVZk (accessed on 1 May 2021).
- Harrington, E.A.; Bennett, M.R.; Fanidi, A.; Evan, G.I. C-Myc-induced Apoptosis in Fibroblasts Is Inhibited by Specific Cytokines. *Embo*. 1994, 13, 3286–3295, doi:10.1002/j.1460-2075.1994.tb06630.x.
- Cairns, R.A.; Harris, I.S.; Mak, T.W. Regulation of Cancer Cell Metabolism. *Nat Rev Cancer* 2011, *11*, 85–95, doi:10.1038/nrc2981.
- 56. Putker, M.; Madl, T.; Vos, H.R.; Ruiter, H. de; Visscher, M.; Berg M.C.W. van den; Kaplan, M.; Korswagen, H.C.; Boelens, R.; Ver meulen, M.; et al. Redox-Dependent Control of FOXO/DAF-10 by Transportin-1. *Mol Cell* **2013**, *49*, 730 742, doi:10.1016/j molcel.2012.12.014.
- 57. Hekimi, S.; Lapointe, J.; Wen, Y. Taking a "Good" Look at Free Radical in the Aging Process. *Trends Cell Biol* **2011**, *21*, 569–576, doi:10.1016/ tcb.2011.06.008.
- Dam, L. van; Dansen, T.B. Cross-Talk between Redox Signallin and Protein Aggregation. *Biochem Soc Trans* 2020, doi:https://doi org/10.1042/BST20190054.
- 59. Lyu, P.C.; Liff, M.I.; Marky, L.A.; Kallenbach, N.R. Side Chain Contr butions to the Stability of Alpha-Helical Structure in Peptides. *Scien* **1990**, *250*, 669–673, doi:10.1126/science.2237416.
- 60. Parsonage, D.; Youngblood, D.S.; Sarma, G.N.; Wood, Z.A.; Karplus and P.A.; Poole, L.B. *Analysis of the Link between Enzymatic Activit and Oligomeric State in AbpC, a Bacterial Peroxiredoxin†,‡*; Biochem istry; American Chemical Society, 2005; Vol. 44; ISBN 44-31-10583.

- Wood, Z.A.; Poole, L.B.; Hantgan, R.R.; Karplus, P.A. Dimers to Doughnuts: Redox-Sensitive Oligomerization of 2-Cysteine Per oxiredoxins †,‡. *Biochemistry-us* 2002, *41*, 5493 5504, doi:10.1021, bi012173m.
  - 62. Schröder, E.; Littlechil\*, J.A.; Lebedev, A.A.; Errington, N.; Vagin, A.A.; Isupov, M.N. Crystal Structure of Decameric 2-Cys Peroxiredoxin from Human Erythrocytes at 1.7Å Resolution. *Structure* 2000, *8*, 605–615, doi:10.1016/s0969-2126(00)00147-7.
  - 63. Pastor-Flores, D.; Talwar, D.; Pedre, B.; Dick, T.P. Real-Time Monitoring of Peroxiredoxin Oligomerization Dynamics in Living Cells. *Proc National Acad Sci* **2020**, *117*, 16313–16323, doi:10.1073/pnas.1915275117.
  - 64. Fernandez-Caggiano, M.; Schröder, E.; Cho, H.-J.; Burgoyne, J.; Barallobre-Barreiro, J.; Mayr, M.; Eaton, P. Oxidant-Induced Interprotein Disulfide Formation in Cardiac Protein DJ-1 Occurs via an Interaction with Peroxiredoxin 2. *J Biol Chem* 2016, 291, 10399 10410, doi:10.1074/jbc.m115.699850.
  - 65. Matte, A.; Low, P.S.; Turrini, F.; Bertoldi, M.; Campanella, M.E.; Spano, D.; Pantaleo, A.; Siciliano, A.; Franceschi, L.D. Peroxiredoxin-2 Expression Is Increased in β-Thalassemic Mouse Red Cells but Is Displaced from the Membrane as a Marker of Oxidative Stress. *Free Radical Bio Med* 2010, *49*, 457–466, doi:10.1016/j.freeradbiomed.2010.05.003.
  - 66. Jang, H.H.; Lee, K.O.; Chi, Y.H.; Jung, B.G.; Park, S.K.; Park, J.H.; Lee, J.R.; Lee, S.S.; Moon, J.C.; Yun, J.W.; et al. Two Enzymes in One Two Yeast Peroxiredoxins Display Oxidative Stress-Dependent Switching from a Peroxidase to a Molecular Chaperone Function. *Cell* 2004, *117*, 625–635, doi:10.1016/j.cell.2004.05.002.
  - 67. Saravi, S.S.S.; Eroglu, E.; Waldeck-Weiermair, M.; Sorrentino, A.; Steinhorn, B.; Belousov, V.; Michel, T. Differential Endothelial Signaling Responses Elicited by Chemogenetic H2O2 Synthesis. *Redox Biol* 2020, 36, 101605, doi:10.1016/j.redox.2020.101605.
  - Perkins, A.; Poole, L.B.; Karplus, P.A. Tuning of Peroxiredoxin Catalysis for Various Physiological Roles. *Biochemistry-us* 2014, *53*, 7693 7705, doi:10.1021/bi5013222.
  - 69. Park, M.H.; Jo, M.; Kim, Y.R.; Lee, C.-K.; Hong, J.T. Roles of Peroxiredoxins in Cancer, Neurodegenerative Diseases and Inflammatory Diseases. *Pharmacol Therapeut* **2016**, *163*, 1–23, doi:10.1016/j. pharmthera.2016.03.018.

NEDERLANDSE SAMENVATTING REFERENTIES CURRICULUM VITAE PUBLICATIONS ACKNOWLEDGEMENTS





### NEDERLANDSE SAMENVATTING

Het menselijk lichaam bestaat uit een geschatte 38 biljoen cellen, met een enorme diversiteit aan morfologieën en functies [1]. Ondanks deze diversiteit en complexiteit zijn alle cellen opgebouwd uit dezelfde bouwstenen. Cellen worden omringd door een celmembraan, gevuld met onder andere water, suikers, eiwitten en eiwitfabrieken (ribosomen), erfelijk materiaal in de vorm van DNA, energiecentrales (mitochondriën) en nog veel meer. Eiwitten zijn de functionele bouwstenen van de cellen in ons lichaam. In onze cellen zijn veel verschillende taken te vervullen, en daarom zijn er veel verschillende eiwitten, ieder met een eigen functie. Ons lichaam kent 21 aminozuren waar alle eiwitten uit zijn opgebouwd. De lengte van eiwitten kan variëren van enkele tot duizenden aminozuren. Dit betekent dat je met slechts tien aminozuren al verschillende ketens kunt maken, en met een gemiddeld formaat eiwit van 300 aminozuren.

Het totale aantal verschillende eiwitten (het proteoom) is niet precies bekend, maar schattingen variëren van minimaal 20.000, tot maar liefst zo veel als 400.000.

Cellen maken eiwitten op basis van een genetische code die is opgeslagen in het DNA. Ieder eiwit heeft een eigen DNA code (een gen). Alle lichaamscellen hebben in principe een complete set van het DNA tot hun beschikking, en kunnen dus theoretische alle eiwitten maken. Het produceren van eiwitten wordt geregeld door 'genregulatie'; hiermee worden bepaalde genen aan- of uit uitgezet. Om ervoor te zorgen dat een cel zijn specifieke functie kan uitvoeren, moeten alleen die genen aan staan die de cel nodig heeft. Een bètacel in de alvleesklier moet bijvoorbeeld eiwitten produceren die belangrijk zijn voor de glucosehuishouding (insuline), maar heeft geen eiwitten nodig die specifiek zijn voor bijvoorbeeld levercellen. Van een actief gen wordt de DNA-code eerst gekopieerd tot mRNA, een proces dat transcriptie heet. De mRNA-code wordt vervolgens afgelezen in eiwitfabrieken, die er een eiwit van maken. Dit proces heet translatie. De functie van een

eiwit wordt bepaald door de structuur van het eiwit. Eiwitten worden gemaakt als een lange streng van aminozuren, en worden daarna gevouwen in driedimensionale structuren.

Bovenop de functionele diversiteit van cellen zijn deze cellen onderworpen aan constante veranderingen in de interne en externe omgeving. Omdat cellen en organismen alleen levensvatbaar zijn binnen relatief beperkte condities, proberen cellen en organismen continu om hun toestand stabiel te houden ondanks de veranderingen in hun omgeving. Dit concept staat bekend als 'homeostase'. Cellen handhaven bijvoorbeeld een constante temperatuur, zuurgraad en hoeveelheid voedingsstoffen. Zodra er veranderingen in het evenwicht plaatsvinden, neemt de cel deze signalen waar met behulp van sensoren en reageert erop door eiwitten aan of uit te zetten die de balans kunnen herstellen. Door de grote diversiteit aan eiwitten en cellen is het aantal mogelijke combinaties aan reacties bijna oneindig. De reeks aan signalen die wordt doorgegeven om intern en tussen verschillende cellen te communiceren heet 'signaaltransductie'. Als cellen niet goed in staat zijn homeostase te waarborgen, kan dit leiden tot in een verstoring van cellulaire processen en kan het bijdragen aan het ontstaan van ziekten zoals kanker, neurodegeneratieve aandoeningen en diabetes [2].

Één manier waarop cellen reageren op veranderingen in hun omgeving is door het aan- of uitzetten van genen die coderen voor eiwitten die helpen de balans te herstellen. Een andere manier is door kleine wijzigingen aan te brengen op al bestaande eiwitten, die daardoor actief of minder actief worden of een iets andere functie krijgen, en zo signaaltransductie in gang zetten. Dit noem je post-translationele modificaties (PTMs).

De reversibele oxidatie van het aminozuur cysteïne door reactieve vormen van zuurstof (reactive oxygen species, ROS) is een voorbeeld van een PTM. Het ROS-molecuul dat hiervoor verantwoordelijk is, is waterstofperoxide (H2O2). H2O2 kan het aminozuur cysteïne oxideren via een redoxreactie (reductie-oxidatie), wat zorgt voor een 'oxidatieve modificatie' (zie

leiden tot oxidatie van specifieke, laag abundante eiwitten is ook Figuur 4 in hoofdstuk 1). Deze manier van signalen doorgeven in cellen wordt redox-signaaltransductie genoemd. niet goed duidelijk (zie ook Figuur 5 in hoofdstuk 1).

Een oxidatieve modificatie van een eiwit veroorzaakt een wijzi-Er zijn verschillende hypotheses die (deels) kunnen verklaren ging in de structuur van dat eiwit, die op zijn beurt een effect hoe H<sub>2</sub>O<sub>2</sub> de benodigde reactiviteit en specificiteit kan behakan hebben op het functioneren van dat eiwit. Op die manier len. Eén van die hypotheses komt van de observatie dat peroxikunnen redox-gereguleerde structuurveranderingen in een redoxin eiwitten, die normaal als antioxidant H<sub>2</sub>O<sub>2</sub> weghalen, eiwit functioneren als schakelaar. óók als peroxidases kunnen werken [6-11]. Hierbij reageert H<sub>2</sub>O<sub>2</sub> eerst met de extreem reactieve cysteïne van peroxire-Redox-signaaltransductie is een fundamentele vorm van doxin, waarna de geoxideerde peroxiredoxin een disulfide signaaltransductie, cruciaal voor cellen om homeostase te intermediair vormt met een minder reactief cysteïne in een handhaven en dus voor al het leven op aarde. Het doel van doeleiwit (zie ook Figuur 6D in hoofdstuk 1). Geoxideerde het onderzoek beschreven in dit proefschrift is om de moleperoxiredoxins kunnen zo de oxidatie van andere eiwitten faculaire mechanismen te begrijpen die ten grondslag liggen ciliteren via disulfide uitwisselingsreacties. Dit mechanisme aan redox-signaaltransductie, en welk effect veranderingen wordt een 'peroxiredoxin-afhankelijke redox relay' genoemd. in de redox status van een cel hebben op signaaltransductie. Onderzoekers hebben laten zien dat deze peroxiredoxin-afhankelijke redox relay ook op grotere schaal voorkomt [10,11]. Dit proefschrift behandelt drie belangrijke thema's, opgedeeld Dit kan verklaren hoe zoveel intrinsiek niet-reactieve eiwitten in zeven hoofdstukken. Ten eerste onderzoeken we hoe de toch geoxideerd worden als respons op H2O2-afhankelijke sigoxidatie van cysteïnes door H<sub>2</sub>O<sub>2</sub> efficiënt en specifiek kan naaltransductie, ondanks de aanwezigheid van een abundant gebeuren. Ten tweede kijken we naar wat oxidatie door H<sub>2</sub>O<sub>2</sub> en reactief antioxidantsysteem.

doet op de functie van bepaalde eiwitten in de cel. We bekijken ook wat deze functieveranderingen voor effect hebben op het gedrag van cellen. Ten derde onderzoeken we welk effect redoxregulatie heeft op het ontvouwen van eiwitten en eiwitaggregatie.

Een belangrijk vraagstuk over hoe H<sub>2</sub>O<sub>2</sub> werkt als signaaltransductiemolecuul is hoe het kan dat H2O2 specifieke cysteïnes kan oxideren in signaaltransductieroutes, in de context van een vrijwel ongelimiteerd aantal potentiele doelwitten in een cel. H<sub>2</sub>O<sub>2</sub> reageert alleen met de juiste cysteïnes in de juiste eiwitten om een bepaald signaal door te geven, terwijl er ook heel veel andere eiwitten met cysteïnes in de cel aanwezig zijn. Cellen zijn uitgerust met een sterk systeem van antioxidanten; abundante eiwitten (zoals peroxiredoxins) waarvan verwacht wordt dat ze >99% van alle cellulaire  $H_2O_2$  weghalen [3]. Ten tweede hebben de meeste cysteïnes in eiwitten een lage reactiviteit met H<sub>2</sub>O<sub>2</sub> [4,5]. Hoe het mogelijk is dat H<sub>2</sub>O<sub>2</sub> tóch kan

Hoewel dit model de *reactiviteit* van H<sub>2</sub>O<sub>2</sub> verklaart, is het nog onduidelijk hoe de oxidatie van specifieke eiwitten kan worden bereikt in  $H_2O_2$ -afhankelijke signaaltransductie. Dit is nodig omdat cellen een specifieke respons nodig hebben om te reageren op een verandering in hun cellulaire omgeving door middel van relevante biologische signalen. De zogenaamde 2-cys peroxiredoxins hebben vijf verschillende isovormen in zoogdieren, ieder met een eigen subcellulaire lokalisatie, oxidatiekinetiek en structurele verschillen rond hun katalytische centrum. Onze hypothese is daarom dat de verschillende peroxiredoxin-eiwitten ook kunnen zorgen voor de benodigde selectiviteit in redox-signaaltransductie.

In hoofdstuk 2 onderzoeken we peroxiredoxin- af hankelijke redox relay op een proteoom-brede schaal. We gebruiken een grootschalige systematische analyse m.b.v. massa-spectrometrie om cysteïne-afhankelijke bindingspartners te identificeren van de vijf 2-cys peroxiredoxin isovormen. We laten zien dat alle isovormen van peroxiredoxins cysteïne-afhankelijke heterodimeren kunnen vormen met talloze andere eiwitten, en dat iedere isovorm een voorkeur heeft voor een andere subset van deze disulfide-afhankelijke bindingspartners. We bestuderen welke isovorm-specifieke eigenschappen ten grondslag kunnen liggen aan deze observaties en we laten zien dat peroxiredoxin-afhankelijke redox relays via twee verschillende moleculaire mechanismen kunnen verlopen. Dit is een sterke aanwijzing dat peroxiredoxins een rol kunnen spelen in het faciliteren van niet alleen reactiviteit maar ook selectiviteit in de signaaltransductie van  $H_2O_2$ , om zo een specifiek signaal te genereren.

Hoofstukken 3, 4 en 6 gaan verder in op cysteïne-afhankelijke redox regulatie van verschillende signaaltransductieeiwitten. In hoofdstuk 3 bestuderen we het eiwit TIPRL, een eiwit waar niet veel over bekend is. TIPRL is betrokken bij de regulatie van PP2A, dat verantwoordelijk is voor het verwijderen van fosfaatgroepen van eiwitten. Fosforylering van eiwitten (ook een PTM) is een belangrijke vorm van signaaltransductie in een cel, waarbij fosfaatgroepen op eiwitten worden geplaatst. Het is belangrijk dat de fosfaatgroepen op het juiste moment worden verwijderd. We laten zien dat TIPRLcysteïnes erg gevoelig zijn voor de oxidatie door H2O2. Na de oxidatie van TIPRL kunnen twee TIPRL-eiwitten elkaar binden via een zwavelbrug, en zo een homodimeer vormen. TIPRL vormt drie verschillende zwavelbrug-afhankelijke homodimeren via cysteïnes C14 en C87 (C14-C14, C87-C87 en C14-C87). Onze resultaten suggereren ook dat TIPRL normaal gesproken PP2A inhibeert en zo het verwijderen van fosfaatgroepen vertraagt, en dat de oxidatie en dimerisatie van TIPRL ervoor zorgen dat deze inhibitie van PP2A nóg efficiënter verloopt. Toekomstig onderzoek is nodig om uit te wijzen welk effect dit precies heeft op de cel.

**Hoofstuk 4** beschrijft de oxidatie en daaropvolgende zwavelbrug-afhankelijke dimerisatie van het tumorsuppressoreiwit  $p16^{INK4A}$ . Dit zorgt ervoor dat het eiwit een drastische structurele verandering ondergaat en  $\beta$ -amyloïde fibrillen vormt, eiwitaggregaten die kenmerkend zijn voor amyloïdoses zoal Parkinson en Alzheimer. P16<sup>INK4A</sup> zorgt er normaal voor dat een cel stopt met delen door de eiwitten CDK4 en CDK6 te remmen. De amyloïdevorming van p16<sup>INK4A</sup> zorgt ervoor dat CDK4 en CDK6 niet meer geremd worden. We gebruiken de term 'oxaggregatie' voor de kritieke afhankelijkheid van een zwavelbrug-afhankelijke dimeer als subeenheid voor fibrilvorming. Deze observaties brengen de cellulaire redox status in verband met de regulatie van de celcyclus via de formatie van  $\beta$ -amyloïde fibrillen.

In hoge concentraties reageren ROS niet alleen met cysteïnes, maar ook met andere willekeurige moleculen. Dit kan eiwitschade veroorzaken, zoals eiwitontvouwing en -aggregatie. Opstapeling van kapotte eiwitten speelt een rol bij veroudering en ouderdomsziekten zoals de ziekte van Alzheimer. Daarentegen functioneert  $H_2O_2$  zoals genoemd als een belangrijk signaaltransductiemolecuul dat belangrijk is voor het gezond functioneren van cellen. In **hoofdstuk 5** bediscussieren we hoe deze schijnbaar tegenovergestelde effecten van  $H_2O_2$  - als signaalmolecuul, en als drijfveer van eiwitaggregatie tijdens veroudering – verenigd kunnen worden in één hypothese. We geven een overzicht van de literatuur over de complexe relatie tussen redox-signaaltransductie en eiwitaggregatie.

In **hoofdstuk 6** beschrijven we een voorbeeld van hoe de cellulaire redox status samenhangt met de voortgang van de celcyclus [12]. Een van de belangrijkste kenmerken van kanker is de ontsporing van celdeling. We laten zien dat de celdelingsregulatoreiwitten CDK4 en cycline D tijdelijk een covalent gebonden eiwitcomplex vormen onder invloed van ROS. Dit covalente eiwitcomplex wordt veroorzaakt door de oxidatie van cysteïne C135 in CDK4 en de vorming van een zwavelbrug tussen CDK4 en cycline D. Deze interactie stabiliseert op die manier een normaal gesproken hydrostatische, niet-covalente interactie, vergelijkbaar met een moleculair nietje (de zwavelbrug) in twee vellen papier (de eiwitten). We laten zien dat de zwavelbrug-afhankelijke binding de activiteit van het CDK4-cycline D complex verhoogt, en zo potentieel de celdeling kan versnellen. Dit onderzoek geeft aan dat de redoxgevoelige cysteïne C135 in het CDK4-cycline D complex een goed aanknopingspunt zou kunnen zijn voor nieuwe medicijnen tegen kanker.

Ten slotte vatten we het werk in dit proefschrift samen in hoofdstuk 7. We bespreken de vernieuwende concepten en mogelijke implicaties van dit werk.

# REFERENTIES

- Sender, R.; Fuchs, S.; Milo, R. Revised Estimates for the Number of Human and Bacteria Cells in the Body. *Plos Biol* 2016, *14*, e1002533, doi:10.1371/journal.pbio.1002533.
- Galluzzi, L.; Yamazaki, T.; Kroemer, G. Linking Cellular Stress Responses to Systemic Homeostasis. *Nat Rev Mol Cell Bio* 2018, *19*, 731–745, doi:10.1038/s41580-018-0068-0.
- Winterbourn, C.C. Biological Production, Detection, and Fate of Hydrogen Peroxide. *Antioxid Redox Sign* 2017, 29, ars.2017.7425, doi:10.1089/ ars.2017.7425.
- Winterbourn, C.C. The Biological Chemistry of Hydrogen Peroxide. *Methods Enzymol* 2013, *528*, 3–25, doi:10.1016/b978-0-12-405881-1.00001-x.
- Marinho, H.S.; Real, C.; Cyrne, L.; Soares, H.; Antunes, F. Hydrogen Peroxide Sensing, Signaling and Regulation of Transcription Factors. *Redox Biol* 2014, 2, 535 562, doi:10.1016/j.redox.2014.02.006.
- Delaunay, A.; Pflieger, D.; Barrault, M.-B.; Vinh, J.; Toledano, M.B. A Thiol Peroxidase Is an H2O2 Receptor and Redox-Transducer in Gene Activation. *Cell* 2002, *111*, 471–481, doi:10.1016/s0092-8674(02)01048-6.
- 7. Veal, E.A.; Findlay, V.J.; Day, A.M.; Bozonet, S.M.; Evans, J.M.; Quinn, J.; Morgan, B.A. A 2-Cys Peroxiredoxin Regulates Peroxide-Induced Oxidation and Activation of a Stress-Activated MAP Kinase. *Mol Cell* 2004, *15*, 129 139, doi:10.1016/j.molcel.2004.06.021.
- Sobotta, M.C.; Liou, W.; cker, S.S. ouml; Talwar, D.; Oehler, M.; Ruppert, T.; Scharf, A.N.D.; Dick, T.P. Peroxiredoxin-2 and STAT3 Form a Redox Relay for H2O2 Signaling. *Nat Chem Biol* 2014, *11*, 1 8, doi:10.1038/nchembio.1695.
- Barata, A.G.; Dick, T.P. A Role for Peroxiredoxins in H2O2- and ME-KK-Dependent Activation of the P38 Signaling Pathway. *Redox Biol* 2020, *28*, 101340, doi:10.1016/j.redox.2019.101340.
- Stöcker, S.; Maurer, M.; Ruppert, T.; Dick, T.P. A Role for 2-Cys Peroxiredoxins in Facilitating Cytosolic Protein Thiol Oxidation. *Nat Chem Biol* 2018, *14*, 148–155, doi:10.1038/nchembio.2536.
- Brandstaedter, C.; Delahunty, C.; Schipper, S.; Rahlfs, S.; Yates, J.R.; Becker, K. The Interactome of 2-Cys Peroxiredoxins in Plasmodium Falciparum. *Sci Rep-uk* 2019, *9*, 13542, doi:10.1038/s41598-019-49841-3.
- Burhans, W.C.; Heintz, N.H. The Cell Cycle Is a Redox Cycle: Linking Phase-Specific Targets to Cell Fate. *Free Radical Bio Med* 2009, 47, 1282 1293, doi:10.1016/j.freeradbiomed.2009.05.026.
- Erdős, G.; Mészáros, B.; Reichmann, D.; Dosztányi, Z. Large-Scale Analysis of Redox-Sensitive Conditionally Disordered Protein Regions Reveals Their Widespread Nature and Key Roles in High-Level Eukaryotic Processes. *Proteomics* 2019, *19*, 1800070, doi:10.1002/ pmic.201800070.

# CURRICULUM VITAE



Loes van Dam was born on the 23<sup>rd</sup> of March 1989 in Rotterdam, the Netherlands. She attended College Den Hulster in Venlo, the Netherlands where she passed her VWO and International Baccalaureate exams in 2007. After a gap year of working and traveling, she moved to Utrecht to start a Bachelor's in Biomedical Sciences at the University Utrecht, the Netherlands in 2008. After receiving her Bachelor Diploma in 2011, she continued her education in the Master's Programme Cancer, Genomics and Developmental Biology at the Graduate School of Life Sciences at Utrecht University. During this time, Loes completed several internships. During her first internship she studied TOR signaling pathway regulator-like (TIPRL) as a cysteine-dependent redox-sensor in the lab of Dr. Tobias Dansen (University Medical Center, Utrecht) and under the supervision of Dr. Marrit Putker. She wrote her thesis on the reciprocal regulation between metabolism and the cell cycle machinery under the supervision of Dr. Joanna Kaplon in the lab of Prof.

Dr. Daniel Peeper (Netherlands Cancer Insitute, the Netherlands). During her last internship she studied the role of ASS1 in the chemoresistance of malignant pleural mesothelioma in the lab of Prof. Dr Courtney Broaddus (University of California, San Fancisco, USA) under the supervision of Dr. Dario Barbone. She received her Master's degree cum laude in 2014. In 2015, she started her PhD in the group of dr. Tobias Dansen in the Department of Molecular Cancer Research (MCR) at the University Medical Center, Utrecht, the results of which are described in this thesis.

Loes will continue her scientific career as a postdoctoral researcher to explore the gastronomic and textural properties of filamentous fungi under the supervision of Dr. Leonie Johanna Jahn and Prof. Morten Otto Alexander Sommer at the Novo Nordisk Foundation Center for Biosustainability at the Technical University of Denmark (DTU).

# PUBLICATIONS

#### (Most recent on top)

L. van Dam, M. Pagès-Gallego, P.E. Polderman, R.M. van Es, B.M.T. Burgering, H.R. Vos, T.B. Dansen The Human 2-Cys Peroxiredoxins Form Widespread, Cysteine-Dependent- and Isoform-Specific Protein-Protein Interactions.

Antioxidants 2021, 10, 627, doi:10.3390/antiox10040627.

L. van Dam, T.B. Dansen

Cross-Talk between Redox Signalling and Protein Aggregation. Biochem Soc Trans 2020, doi:10.1042/BST20190054.

C. Göbl\*, V.K. Morris\*, L. van Dam\*, M. Visscher, P.E. Polderman, C. Hartlmüller, H. de Ruiter, M. Hora, L. Liesinger, R. Birner-Gruenberger, H.R. Vos, B. Reif, T. Madl, T.B. Dansen Cysteine Oxidation Triggers Amyloid Fibril Formation of the Tumor Suppressor P16<sup>INK4A</sup> Redox Biol 2019, 101316, doi:10.1016/j.redox.2019.101316.

J. Kaplon\*, L. van Dam\*, D. Peeper

Two-Way Communication between the Metabolic and Cell Cycle Machineries: The Molecular Basis. Cell Cycle 2015, 14, 2022-2032, doi:10.1080/15384101.2015.1044172.

\*equal contributions

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APPENDICES

#### COLOFON

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