Melanin-dependent modification of phagolysosomal processing of conidia of the human pathogenic fungus *Aspergillus fumigatus* in macrophages

Dissertation

zur Erlangung des akademischen Grades

„doctor rerum naturalium“ (Dr. rer. nat.)

vorgelegt dem Rat der Biologisch-Pharmazeutischen Fakultät

der Friedrich-Schiller-Universität Jena

von Diplom Biologin Hella Schmidt

geboren den 19. September 1986 in Burgstädt

Jena, Februar 2017

Diese Arbeit wurde am Leibniz-Institut für Naturstoff-Forschung und Infektionsbiologie e.V., Hans-Knöll-Institut, Jena, in der Abteilung Molekulare und Angewandte Mikrobiologie – Lehrstuhl für Mikrobiologie und Molekularbiologie, Friedrich-Schiller-Universität, Jena unter Leitung von Prof. Dr. Axel A. Brakhage angefertigt

1. Gutachter: Prof. Dr. Axel A. Brakhage, Friedrich-Schiller-Universität, Jena
2. Gutachter: Prof. Dr. Markus Gräler, Universitätsklinikum Jena
3. Gutachter: PD Dr. Norbert Reiling, Forschungszentrum Borstel

Datum der öffentlichen Verteidigung: 22. Juni 2017

Table of Content

CD with supplementary tables S2-S6

Summary

The human pathogenic fungus *Aspergillus fumigatus* represents one of the major threats to human health. This ubiquitous saprophyte has evolved versatile strategies to avoid attacks by the immune system and establish an infection in the immunocompromised host. Infection is initiated after inhalation of the airborne asexual spores (conidia) that settle in the lung alveoli and start to germinate. The formation of hyphae allows for penetration of the lung epithelia and dissemination of the infection. In the lung, conidia encounter resident alveolar macrophages that recognize, phagocytose, and eliminate the conidia by forming a fungicidal phagolysosome. However, pigmentation with 1,8-dihydroxynaphthalene (DHN)-melanin protects the conidia from degradation inside the phagolysosome by blocking the acidification of the lumen.

This project aimed to describe the interference of *A. fumigatus* conidia with the host phagolysosomal maturation to provide insights into the DHN-melanin-dependent fungal immune evasion mechanisms. A new protocol to purify conidia-containing phagolysosomes was developed, allowing for enrichment of the phagolysosomal fraction. The dual proteome of host and pathogen in the purified phagolysosomal fraction was determined by LC-MS/MS. Abundance of identified proteins was quantified with a label-free method and the wild-type conidia-containing phagolysosomal proteome was compared against the proteome of pigmentless *pksP* mutant conidia-containing phagolysosomes. Differentially abundant proteins were compiled in a host regulatory module that reflects regulated processes in the phagolysosome.

The combination of high resolution imaging techniques, microbiological and molecular biological experiments, proteomics and bioinformatics enabled the handling of a complex data set and the generation of the following model about *A. fumigatus'* immune evasion strategy: The encounter of alveolar macrophages and *A. fumigatus* conidia results in a differential activation of macrophages depending on the cell wall structure of the conidia, in particular on the presence of DHN-melanin. DHN-melanin producing wild-type conidia initiate phagocytosis and formation of a phagosome, which tightly enwraps the pathogen, most likely *via* direct physical contact between the fungal surface and phagosomal membrane. The direct contact in the phagosome modulates the phagolysosomal maturation such that the progression to a fungicidal compartment is inhibited. Several mechanisms were detected that are responsible for the modified maturation: the disturbance of lipid raft formation blocks assembly of the vacuolar proton pump vATPase that drives phagolysosomal acidification. Second, impairment of fusion events by targeting host small GTPases hinders the delivery of lysosomal peptidases and hydrolytic enzymes. Third, the reduction of degradative properties of the phagolysosome due to the block of acidification and fusion with the lytic vesicles, together with a decreased delivery of components of the antigen presentation machinery, results in impaired antigen processing and presentation properties of the macrophage. Fourth, the interference with MAPK and mTOR signaling pathways modulates the regulation of pro-inflammatory immune responses, induction of autophagy and apoptosis and finally influences the metabolic profile of the macrophages.

This study provides a comprehensive insight into the interaction of *A. fumigatus* with alveolar macrophages and provides a conceptual frame for future mechanistic studies to validate the current immune evasion model.

Zusammenfassung

Der humanpathogene Pilz *Aspergillus fumigatus* stellt eine große Bedrohung für die Gesundheit des Menschen dar. Dieser ubiquitäre Saprophyt hat eine Vielzahl an Strategien entwickelt, dem menschlichen Immunsystem zu entgehen und eine Infektion im immunsupprimierten Patienten auszulösen. Eine Infektion kann durch das Einatmen der über die Luft verbreiteten, asexuellen Sporen (Konidien) initialisiert werden, die sich in den Lungalveoli niederlassen und dort auskeimen. Die Bildung von Hyphen ermöglicht ein Durchwachsen des Lungenepithels und eine Dissemination der Infektion. Im Lungengewebe treffen die Konidien auf die ansässigen Alveolarmakrophagen, die Konidien erkennen, phagozytieren und im Normalfall im Phagolysosomen durch dessen fungizide Eigenschaften abbauen. Die Pigmentierung mit 1,8-Dihydroxynaphthol (DHN)-Melanin schützt die Konidien vor einem Verdau im Phagolysosomen, indem die Ansäuerung des Lumen blockiert wird.

Ziel dieses Projektes war es zu beschreiben, wie *A. fumigatus* Konidien die phagolysosomale Reifung in der Wirtszelle beeinträchtigen und Einblick in die DHN-Melanin-abhängige Immunevasionsstrategie zu gewähren. Dazu wurde zunächst ein Protokoll entwickelt, das die Anreicherung der phagolysosomalen Fraktion ermöglichte. LC-MS/MS-Analyse detektierte das duale Proteom von Wirt und Pathogen in den aufgereinigten Phagolysosomen. Mit Hilfe einer markierungsfreien Methode wurden die Proteine quantifiziert und das Wildtyp-Konidien-beinhaltende phagolysosomale Proteom mit dem Proteom von Phagolysosomen verglichen, die Konidien der *pksP* Mutante phagozytierten. Die differentiell vorkommenden Wirtsproteine wurden bioinformatisch zu einem regulatorischen Modul zusammengefasst, welches regulierte Prozesse im Phgaolysosom wiedergibt.

Die Kombination von hochauflösenden Bildgebungsverfahren, mikrobiellen- und molekularbiologischen Experimenten, Proteomik und Bioinformatik ermöglichte die Handhabung eines komplexen Datenbestandes und die Erstellung des folgenden Modells der Immunevasionsstrategie von *A. fumigatus.* Das Aufeinandertreffen von Alveolarmakrophagen und *A. fumigatus* Konidien resultiert in einer Aktivierung der Makrophagen, die von der konidialen Zellwand abhängt, im Besonderen vom Vorkommen des DHN-Melanins. Die DHN-Melanin produzierenden Wildtyp-Konidien initiieren die Phagozytose und Bildung eines Phagosomens, welches das Pathogen eng umschließt. Dabei entsteht wahrscheinlich ein direkter, physischer Kontakt zwischen pilzlicher Zellwand und phagolysosomaler Membran. Dieser direkte Kontakt im Phagosom, moduliert den phagolysosomalen Reifungsprozess so, dass er deutlich von dem des *pksP* Mutantenkonidien-beinhaltenden Phagolysosomen abweicht, welches zur Bildung eines fungiziden Organells prozessiert. Verschiedene Mechanismen wurden gefunden, die für diese Modulierung verantwortlich sind: An erster Stelle steht die Störung der Bildung von „Lipid Rafts“, die eine Assemblierung der

vakuolaren Protonenpumpe, der vATPase, verhindert. Durch ausbleibende vATPase-Aktivität bleibt die Ansäuerung des Phagolysosoms aus. Zweitens sind GTPasen betroffen, was zur Folge hat, dass Fusionen mit weiteren endozytischen Vesikeln behindert werden und damit auch die Anlieferung von lysosomalen Peptidasen und hydrolytischen Enzymen. Drittens werden durch die Blockierung der Ansäuerung und der Fusion mit lytischen Vesikeln die Zersetzungseigenschaften des Phagolysosoms reduziert. Zusätzlich dazu ist der Zugang von Komponenten der Antigenpräsentationsmaschinerie vermindert, was die Antigenpozessierungs- und –präsentationseigenschaften des Makrophagen beeinträchtigt. Viertens führt die Interferenz mit MAPK und mTOR Signalwegen zu einer Modulation von pro-inflammatorischen Immunreaktionen, sowie von Autophagie- und Apoptoseinduktion und beeinflusst zuletzt den Energiemetabolismus des Makrophagen.

Diese Studie bietet tiefgehende Einsichten in die Interaktion von *A. fumigatus* mit alveolaren Makrophagen und liefert ein wissenschaftliches Konzept für zukünftige mechanistische Studien, die das aktuelle Immunevasions-Modell evaluieren können.

1. Introduction

1.1. The pathogen *Aspergillus fumigatus*

1.1.1. Saprophytic *versus* pathogenic lifestyle

Aspergillus fumigatus is a saprophytic mold belonging to the phylum of Ascomycota. It is ubiquitously distributed and preferentially resides in habitats with a rich nutritional and aerated environment, such as compost heaps. In soil, the fungus grows in a 'vegetative' stage *via* formation of hyphae and has an important role in the recycling of carbon and nitrogen (Haines, 1995). *A. fumigatus* is a thermotolerant species. Although it prefers growth at ambient temperatures, the organism can tolerate temperatures up to 56 °C, the spores even survive temperatures up to 70 °C (Bhabhra and Askew, 2005).

A. fumigatus reproduces *via* asexual spores (conidia). A sexual reproduction has been reported, but is a rare occurrence (O'Gorman *et al.*, 2009). Conidia are generated on a conidiophore and are equipped with a layer of hydrophobic proteins (hydrophobins) forming the rodlet fascicles and a dark pigment (1,8-dihydroxynaphthalene (DHN) – melanin) for protection against environmental stressors, such as UV light, oxidants and reactive oxygen species (ROS), but also from attacks by the immune system (Eisenman and Casadevall, 2012) (Figure 1). Due to their small size of only 2-3 µm and their hydrophobicity, they are easily airborne. When an *A. fumigatus* culture is exposed to airflow, the pigmented conidia are released in a dark cloud that resembles fume – the origin of the species' name.

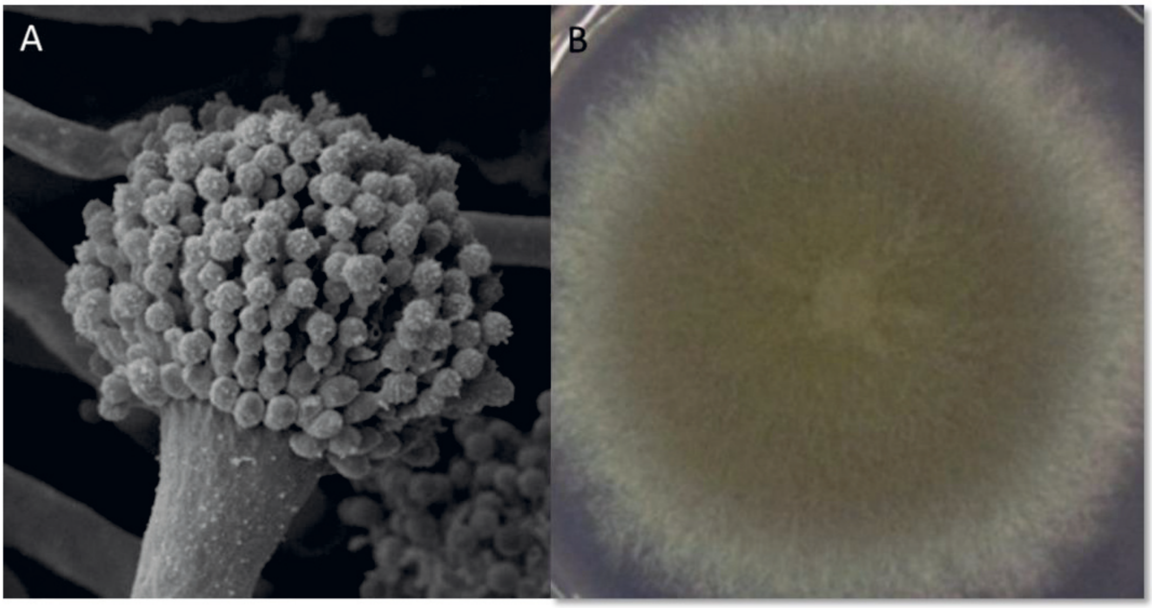

Figure 1: A. *fumigatus* conidiophore and culture. (A) 1500 x magnification of a conidiophore. Imaging J. Schmaler-Ripcke; EMZ Uni-Jena. (B) Culture plate with *A. fumigatus.* Taken from (Heinekamp *et al.*, 2012)

The cell wall of *A. fumigatus* is composed of a rigid mesh of polysaccharides, mainly β-1,3-glucans, chitins, galactomannans and α-1,3-glucans. Many glycosylphosphatidylinositol (GPI) - anchored proteins are integrated in the cell wall. They function in cell wall and DHN-melanin biosynthesis, adhesion to host cells and protection from environmental stresses (Bernard and Latge, 2001). Conidia possess additional outer layers of hydrophobin and DHN-melanin that are shed upon swelling and germination (Diamond, 1993) (Figure 2).

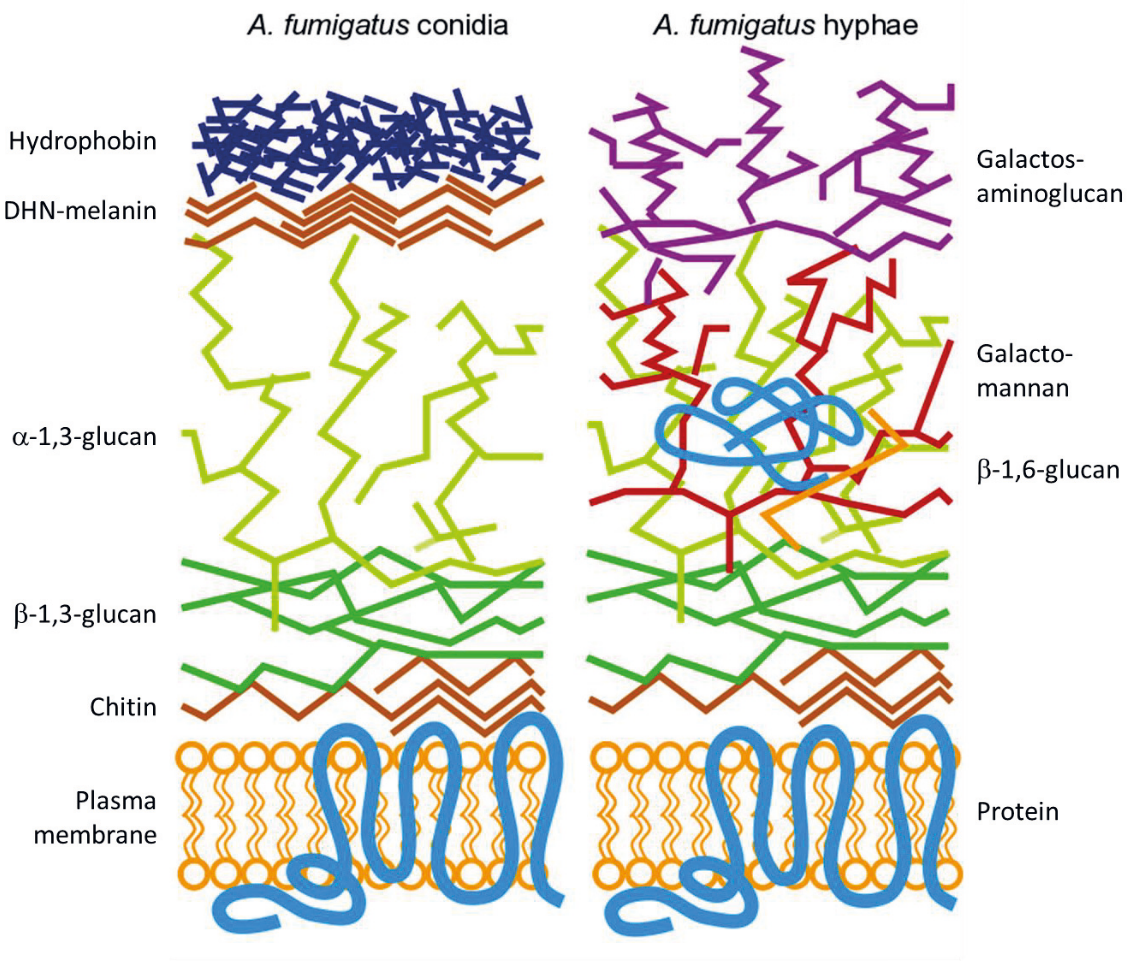

Figure 2: Schematic cell wall structure of A. *fumigatus* conidia and hyphae. Modified from (Erwig and Gow, 2016).

1.1.2. Virulence determinants

Several virulence determinants have been identified in *A. fumigatus* that allow for transformation to a pathogenic lifestyle. The expression of adhesins on the conidial surface, production of pigments and toxic molecules (Bignell *et al.*, 2016), secretion of proteases to degrade the extracellular matrix of the host tissue (Latge, 1999) and detoxifying mechanisms, such as enzymes and efflux pumps (Ferreira *et al.*, 2005) are some factors, which were investigated and confirmed for their contribution to *A. fumigatus* virulence . Additionally, the small size and hydrophobicity of conidia enables an efficient dispersal and access into even the lung alveoli. Furthermore, conidia can tolerate stresses that are imposed by the environment, such as high and low temperatures, dehydration and oxygen limitation (Kozakiewicz and Smith, 1994). To grow inside host tissue, *A. fumigatus* is able to activate specific nutrient sensing and acquisition systems as well as adjust biosynthetic and metabolic pathways to the resources available (Kwon-Chung and Sugui, 2013, Dagenais and Keller, 2009)

1.1.3. Pathogenesis

A. fumigatus conidia enter the human host *via* the airways. Due to their small size, they are able to penetrate deep into the lung tissue and settle in the lung alveoli. Each individual inhales about 200 conidia every day (Dagenais and Keller, 2009) and the immunocompetent host clears the infection without any apparent symptoms. In the case of an immunocompromised host, the lack of competent immune cells enables the invading conidia to establish an infection through outgrowth of hyphae in the lung tissue. These hyphae then penetrate the blood vessels and disseminate the infection throughout the entire body, leading to a systemic infection and, in many cases, to the death of the patient. The mortality rate for invasive aspergillosis (IA) ranges from 40-90 %, depending on the host's immune status, the site of infection, and the therapeutic treatment (Lin *et al.*, 2001).

Besides invasive aspergillosis, *A. fumigatus* is the cause of further diseases of clinical relevance. Patients with impaired lung functions, *i.e.* cystic fibrosis (CF) and asthma patients, can develop a hypersensitivity reaction towards *A. fumigatus* conidia known as allergic bronchopulmonary aspergillosis (ABPA) (Stevens *et al.*, 2003). A non-invasive fungal ball, called an aspergilloma, can also form in preexisting lung cavities as are present in tuberculosis patients (Moodley *et al.*, 2014).

In the recent years, an increase in the incidences of *Aspergillus* infections has been reported, correlating with the increasing number of patients receiving immunosuppressive treatments after solid-organ or hematopoietic stem cell transplantations (Pérez-Sáez *et al.*, 2014, Singh and Husain, 2013). Further high risk groups for infection are individuals suffering from leukemia or genetic immunodeficiencies, such as chronic granulomatous disease (CGD) or human immunodeficiency virus (HIV) infection (Kousha *et al.*, 2011). Thus, *A. fumigatus* infections are associated with high morbidity and mortality and represent a significant threat to human health.

1.2. Interaction of *A. fumigatus* with the innate immune system and immune evasion

1.2.1. Anatomical barriers, lung epithelia and complement system

The mucosal epithelium of the airway plays an important role in the defense against invading *A. fumigatus,* because the majority of inhaled conidia is already removed from the lung by ciliary action within hours (Latge, 1999). Lung surfactants A and D in the mucosal fluid enhance agglutination, phagocytosis and killing of conidia (Madan *et al.*, 1997).

Conidia that reach deeper parts of the respiratory track bind to epithelial cells, are phagocytosed and can be killed inside an acidic phagolysosome (Paris *et al.*, 1997). For A546 it was shown that still a percentage of engulfed conidia is able to survive and germinate (Wasylnka and Moore, 2003). Activation of epithelial cells after contact with fungal conidia results in the production of pro-inflammatory cytokines (Tomee *et al.*, 1997). However, secreted mycotoxins such as gliotoxin inhibit ciliary activity and fungal proteases are able to cause damage and detachment of epithelial cells (Amitani *et al.*, 1995). The activated or disintegrated epithelia in turn, displays increased adhesion properties and thus, promotes the establishment of infection foci (Bromley and Donaldson, 1996).

The complement system reviewed in (Janeway *et al.*, 2001, Zipfel and Skerka, 2009) as the humoral component of the innate immune system is indispensable for defense against *A. fumigatus*. Depending on the morphotype, activation *via* all three pathways has been reported. While resting conidia mainly and slowly activate the alternative pathway, hyphae activate all three complement pathways (Kozel *et al.*, 1989, Sturtevant and Latge, 1992b). The common outcome of complement activation is the generation of C3 convertase, which generates C3b that binds to the surface of conidia and hyphae. The quantity of C3b deposition correlates with pathogenicity (Henwick *et al.*, 1993). C3b-mediated opsonization of the pathogen promotes phagocytosis, release of damaging compounds, oxidative burst and intracellular killing by innate immune cells (Sturtevant and Latge, 1992a). The anaphylatoxin C5a, which is generated further downstream of the complement cascade, initiates a strong pro-inflammatory response, which is crucial for fungal defense as shown by the susceptibility of C5-deficient mice towards aspergillosis (Svirshchevskaya *et al.*, 2009, Hector *et al.*, 1990). The generation of the pore-forming complex C9 in contrast, is blocked by the thick cell wall and only plays a minor role in immune response (Kozel *et al.*, 1989).

Strategies of *A. fumigatus* to evade attack by the complement system comprise hiding in brain abscesses (Rambach *et al.*, 2008), masking of binding structures for C3 decomposition on the cell wall by pigmentation (Behnsen *et al.*, 2008), acquisition of host-derived complement inhibitors (factor H (FH), FH-like and FH-related protein, C4bp) (Vogl *et al.*, 2008), production of complement inhibitors (Washburn *et al.*, 1990) and proteolysis of complement components by fungal proteases (Behnsen *et al.*, 2010, Rambach *et al.*, 2010) (Figure 3). Finally, the soluble pattern recognition receptor pentraxin 3 (Ptx3) also decorates conidia to promote complement activation *via* the classical and alternative pathway (Garlanda *et al.*, 2002).

1.2.2. Interaction with alveolar macrophages

Studies on the interactions between *A. fumigatus* and phagocytes vary greatly depending on the experimental conditions and the cellular model. Thus, results always have to be regarded with care and need to be verified by additional models or *in vivo* experiments.

Resident alveolar macrophages belong to the first line of immune defense (Dagenais and Keller, 2009). They are activated by the engagement of conserved fungal surface structures to surface exposed or intracellular pathogen recognition receptors (PRRs). Activated macrophages engulf the conidium in a phagosome that subsequently acquires biocidal properties and completely degrades the pathogen. Swelling of conidia and activity of vacuolar ATPase (vATPase) are required for efficient intracellular killing (Philippe *et al.*, 2003).

Besides initiation of particle ingestion, macrophages also produce pro-inflammatory cytokines, such as Tumor necrosis factor α (TNF-α), Interleukin (IL)-12, Interferon (IFN)-γ, IL-18, IL-6, IL-1β, Macrophage inflammatory protein (MIP)-1, MIP-1α, MIP-2, Granulocyte-colony stimulating factor (G-CSF), and Granulocyte-monocyte (GM)-CSF and present antigens to activate further cells of the innate and adaptive immune response (Balloy *et al.*, 2005, Steele *et al.*, 2005, Gersuk *et al.*, 2006, Heinekamp *et al.*, 2015) .

Although macrophages belong to the first line of defense and are able to phagocytose invading conidia, their killing rate is rather slow (Schaffner *et al.*, 1983). In addition, they are unable to neutralize hyphae and germination and outgrowth of the fungus from macrophages has been observed (Wasylnka and Moore, 2003, Slesiona *et al.*, 2012). The major role of macrophages in *A. fumigatus* infection consists of the phagocytosis of conidia, establishment of a potent inflammatory response that is to say, the release of cytokines, recruitment of neutrophilic granulocytes and activation of the adaptive immunity (Figure 3).

1.2.3. Interaction of *A. fumigatus* with neutrophilic granulocytes

Neutrophils are the most abundant immune cells. They are short-lived and migrate through the blood stream (Summers *et al.*, 2010). Upon activation, they represent the key effector cells in the defense against *A. fumigatus*, in particular for the extracellular killing of hyphae (Bonnett *et al.*, 2006). Accordingly, individuals suffering from neutropenia are at high risk for IA (Baddley, 2011). In a mouse model, neutropenic animals infected with *A. fumigatus* have high mortality rates and severe lesions in the lungs. Macrophage-depleted animals, in contrast, show a 100 % survival rate (Mircescu *et al.*, 2009).

Neutrophils possess a similar set of PRRs as macrophages to recognize the different morphotypes of *A. fumigatus*. They efficiently kill hyphae *via* oxidative and non-oxidative mechanisms and produce chemokines and cytokines to further promote the inflammation (Scapini *et al.*, 2000). NADPH oxidase (NOX) and myeloperoxidase (MPO) perform the oxidative defense by generating hydrogen peroxide, hydroxyl anions and hypochlorous acid. Neutrophilic granules are released in response to hyphae and conidia and contain enzymes, such as lysozyme, cathepsins, elastase, proteinase and antimicrobial peptides of the non-oxidative defense (Feldmesser, 2006, Park and Mehrad, 2009, Segal, 2005). Lactoferrin depletes the environment from available iron (Zarember *et al.*, 2007) and defensins exert further fungistatic effects (Silva *et al.*, 2014, Levitz *et al.*, 1986). Besides the extracellular degranulation, neutrophils are professional phagocytes and able to kill ingested conidia by activation of the oxidative burst and release of granules into the phagosome (Segal, 2005).

Further antifungal strategies of neutrophils include the formation of aggregates around conidia to confine the infection, prevent germination (Bonnett *et al.*, 2006) and the production of neutrophil extracellular traps (NETs) (Brinkmann *et al.*, 2004). Those structures are composed of chromatin decorated with histones and antimicrobial peptides. NETosis represents a special case of cell death, where fungal parts are trapped within the released DNA mash. It has been observed *in vitro* and *in vivo* during interaction of *A. fumigatus* with neutrophils (Bruns *et al.*, 2010, Hasenberg *et al.*, 2011). NETs are not able to kill entrapped fungi, but they restrict the propagation of conidia and hyphae, thus executing a fungistatic function in immune defense (Figure 3).

Altogether, neutrophils deploy a broad range of fungistatic and fungicidal armory, rendering them indispensable for defense against *A. fumigatus* infection.

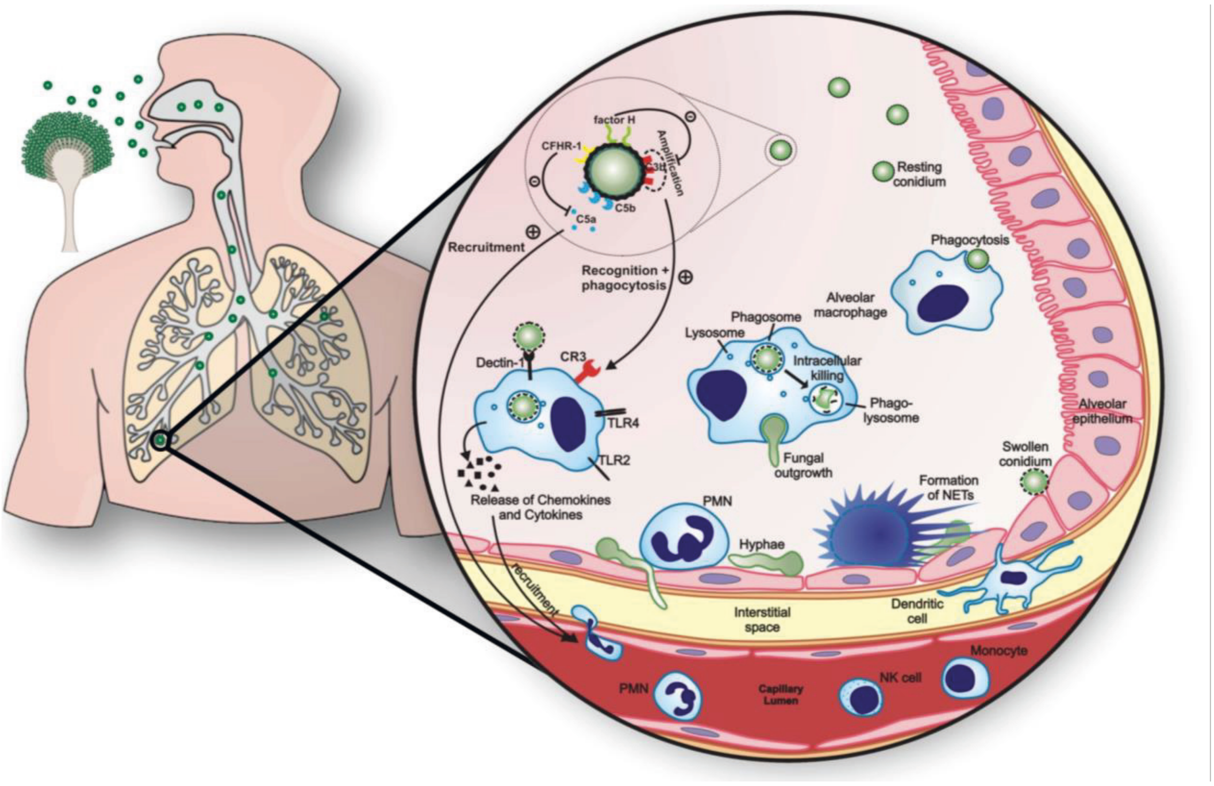

Figure 3: Interactions of *A. fumigatus* conidia with the human innate immunity. Taken from (Brakhage *et al.*, 2010). CR – Complement receptor, TLR – Toll-like receptor, PMN – Polymorphonuclear neutrophils, NK cell – Natural killer cells, NETs – Neutrophil extracellular traps

1.3. Phagocytosis by macrophages and intracellular processing

Engagement and downstream signaling of several PRRs orchestrate the recognition of a pathogen by phagocytes. Phagocytic receptors of macrophages are the dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin (DC-SIGN), the C-type lectin Dectin-1, Fcγ receptor (FcγR) and complement receptor C3R, which are expressed on the cell surface. DC-SIGN was first described on dendritic cells (DCs) and binds fungal galactomannans (Serrano-Gomez *et al.*, 2004), Dectin-1 recognizes β-1,3-glucans (Steele *et al.*, 2005), FcγR and C3R mediate the sensing of C3b or pentraxin-opsonized conidia (Gresnigt *et al.*, 2012). Toll-like receptors (TLR) 2, TLR4 and TLR6 help to fine tune the immune reaction to the morphotypes (Chai *et al.*, 2011, Meier *et al.*, 2003, Rubino *et al.*, 2012) and induce the production of pro-inflammatory cytokines. In addition, a contribution of intracellular TLR9 in binding fungal DNA and mediating the inflammatory response was reported (Ramaprakash *et al.*, 2009).

Dectin-1 is a membrane-spanning receptor that possesses an immunoreceptor tyrosine-activating motif (ITAM) (Brown *et al.*, 2003). The binding of carbohydrates initiates signaling *via* Syk and Src kinases and results in the activation of NFκB to activate expression of effector genes. Dectin-1-mediated signaling has also been implicated in discrimination between different fungal stages (Steele *et al.*, 2005), controlling phagolysosomal maturation (Mansour *et al.*, 2013), generation of ROS (Ma *et al.*, 2014), autophagy induction (Ma and Underhill, 2013) and antigen presentation *via* major histocompatibility complex (MHC) class II (Ma *et al.*, 2012).

After recognition of conidia, a phagocytic cup forms *via* rearrangement of the actin cytoskeleton and activity of myosin motor proteins (Goodridge *et al.*, 2012). The plasma membrane-derived cup closes around the conidium and generates the nascent phagosome. To acquire fungicidal activity, nascent phagosomes start fusing extensively with lysosomes and vesicles of the endosomal compartment that deliver hydrolytic enzymes. Small Rab GTPases govern the fusion process. Rab5 is a marker of the early phagolysosome and mediates homotypic fusion with early endosomes. A conversion to Rab7-positive phagolysosomes represents a late stage of maturation, where homotypic fusions with late endocytic vesicles take place (Flannagan *et al.*, 2009, Desjardins *et al.*, 1994, Desjardins *et al.*, 1997). vATPase subunits are assembled to the active enzyme complex (Sun-Wada *et al.*, 2009). The activity of the proton pump lowers the luminal pH, which in turn enables the activity of acidic lysosomal enzymes (Forgac, 2007).

Pathogen pigmentation is an important virulence determinant. It not only protects microorganisms from environmental stressors, such as UV irradiation, oxidants and temperature extremes, but also renders conidia inert from recognition and elimination by the immune system (Liu and Nizet, 2009). Examples include staphyloxanthin from *Staphylococcus aureus* (Clauditz *et al.*, 2006, Liu *et al.*, 2005), pyocyanin from *Pseudomonas* spp. (Lau *et al.*, 2004) and melanins from *Cryptococcus neoformans* (Wang *et al.*, 1995) and further *Aspergillus* spp (Heinekamp *et al.*, 2012, Pal *et al.*, 2014). Wild-type *A. fumigatus* conidia produce DHN-melanin in a multistep biosynthetic pathway. The corresponding genes, *pksP, ayg1, arp2, arp1, abr1 and abr2* are organized in a biosynthetic gene cluster (Heinekamp *et al.*, 2012). The polyketide synthase PksP initiates melanin biosynthesis by condensing malonyl-CoA and acetyl-CoA into heptaketide naphthopyrone (YWA1). A sequence of shortening, reduction, dehydration and oxidative polymerization reactions catalyzed by the other enzymes of the multistep biosynthesis results in the formation of polymeric DHN melanin. The exact structure of DHN-melanin, its biosynthesis and degradation has not been entirely resolved. The biosynthesis most likely starts in the cytosol, where precursors are compartmentalized into endosomes. Endosomes are trafficked to the cell surface, where they exocytose their content, resulting in the deposition of DHN-melanin at the conidial cell wall (Upadhyay *et al.*, 2016). A blockage of DHN-melanin biosynthesis by deletion of the *pksP* gene results in a mutant strain with attenuated virulence in a mouse model and higher susceptibility to ROS (Jahn *et al.*, 2000, Jahn *et al.*, 1997, Langfelder *et al.*, 1998).

DHN-melanin of *A. fumigatus* conidia was interpreted to interfere either directly or indirectly with the host endocytic pathways (Heinekamp *et al.*, 2012). Experiments were conducted with melanized wild-type conidia and compared to the non-pigmented *pksP* mutant conidia to determine their phagocytosis and intracellular fate. Wild-type conidia are able to survive, germinate and to cause severe damage to the macrophage compared to the *pksP* mutant conidia (Slesiona *et al.*, 2012) (Figure 4). Analysis of melanin ghosts, conidia devoid of any cellular structure except for the melanin shell, demonstrated that melanin alone is responsible for phagolysosomal maturation arrest (Youngchim *et al.*, 2004, Thywissen *et al.*, 2011).

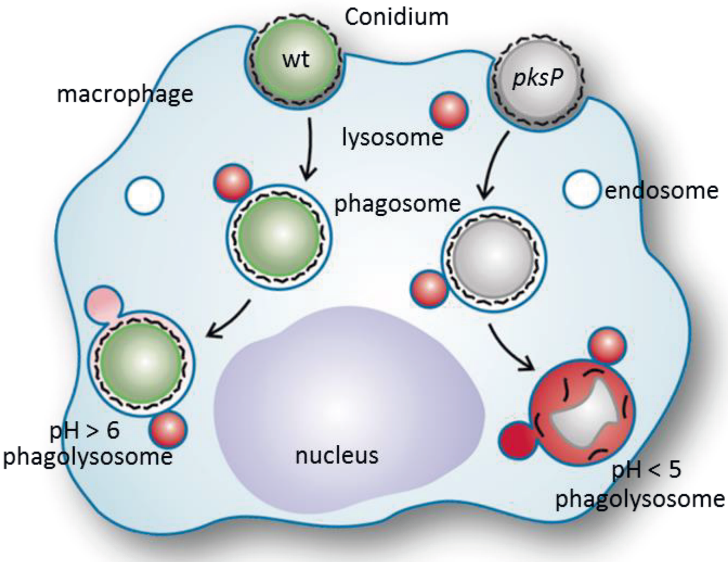

Figure 4: Intracellular fate of melanized (wt) and non-pigmented *pksP*-mutant conidia. Taken from (Heinekamp *et al.*, 2012)

The modification of phagolysosomal maturation has been reported for several intracellular pathogens, such as *Mycobacterium tuberculosis, Salmonella, Legionella* and *Coxiella* spp (Thi *et al.*, 2012). They target intracellular signaling pathways to arrest or delay the phagolysosomal maturation. *Mycobacterium* and *Salmonella* interact with phosphoinositol-3-kinase to block GTPase Rab conversion which, consequently, prevents the acquisition of Rab7 and Rab9 and inhibits interactions of the phagosome with endosomes and lysosomes (Koul *et al.*, 2004, Meresse *et al.*, 1999).

A. fumigatus conidia-containing phagosomes fuse with vesicles of the endocytic compartment, but do not acidify, due to a lack of assembled vATPase (Thywissen *et al.*, 2011). Thus, conidia-containing phagolysosomes fail to establish the fungicidal environment required to degrade the pathogen.

2. Aim of the study and motivation

This study focusses on the analysis the processes occurring in phagolysosomes containing conidia of *A. fumigatus,* which are influenced by the pigmentation of conidia with DHN-melanin. Therefore, all experiments were carried out with conidia of the wild-type strain and compared to conidia of the non-pigmented *pksP* mutant strain.

Because DHN-melanin is on the outmost layer of conidia and the phagolysosomal membrane tightly encloses conidia, it is conceivable that the conidial melanin binds to the phagolysosomal membrane.

Here, high resolution imaging techniques, such as confocal laser scanning (CLSM) and transmission electron microscopy (TEM) were applied to obtain a detailed picture about characteristics of conidia-containing phagolysosomes and the localization of certain phagolysosomal components to evaluate their involvement in the differential maturation process.

Further experiments concerned whether the phagolysosomal protein composition was affected after ingestion of DHN-melanized conidia and a dual proteomic analysis of phagolysosomes containing wild-type or *pksP* mutant conidia was performed.

The proteomic analysis required the establishment of a robust protocol to purify conidia-containing phagolysosomes, extract proteins and process the sample for LC-MS/MS detection. For analysis of the complex proteomic data and comparison between the wild-type and *pksP* mutant conidia-containing phagolysosomal proteome, proteome databases were used to identify proteins, a label-free quantification was performed and bioinformatics methods were employed to generate a regulatory module representing the differentially abundant proteins as well as to predict a host-pathogen interaction network.

Studying the mechanisms of *A. fumigatus* interaction with the host inside the phagolysosomes by means of imaging, proteomics and bioinformatics provides the basis for further mechanistic studies that will clarify the immune evasion process and finally help to find new targets for more specific treatment of invasive aspergillosis.

3. Material and Methods

3.1. Materials and chemicals

3.1.1. Antibodies and fluorescent probes

Primary antibodies		
EEA1	Cell Signaling Technologies	#3288
Lamp1	Santa Cruz	sc-19992
MAPK	Cell Signaling Technologies	#9102
mTOR	Cell Signaling Technologies	#2983
Ndufb9	Abcam	ab200198
Rab5	Cell Signaling Technologies	#3547
Vamp8	Cell Signaling Technologies	#13060
vATPase V_1B_2	Abcam	ab73404
Secondary antibodies		
Goat anti-rabbit IgG-HRP	Santa Cruz	sc-2031
Rabbit anti-goat IgG-HRP	ThermoFisher Scientific	#31402
Goat anti-rabbit-DyLight 633	ThermoFisher Scientific	#35562
Fluorescent probes		
Calcofluor White (CFW) (Fluorescence Brightener 26)	Sigma Aldrich	#F3543
fluorescein isothiocyanate (FITC)	Sigma-Aldrich	#F7250
DiD Vybrant	ThermoFisher Scientific	#V22887
Cholera Toxin Beta (CTB)-Alexa647	LifeTechnologies	#C34778
Filipin III	Sigma-Aldrich	#F4746

3.1.2. Chemicals

Tween80	AppliChem
Sucrose	Carl Roth
Imidazole	Merck Millipore
Protease inhibitor	cOmplete, Roche
Sodium dodecylsulfate (SDS)	SERVA
Triethylammonium bicarbonate (TEAB)	Fluka
Glycerol	Carl Roth
Tris(2-carboxyethyl)phosphine (TCEP)	Sigma-Aldrich
Iodoacetamide	Sigma-Aldrich
Formic acid	Carl Roth
Acetonitrile	VWR
Trifluoric acid (TFA)	Carl Roth
Formaldehyde	Carl Roth
Glyceraldehyde	Sigma-Aldrich
Triton X-100	VWR
Bovine serum albumin (BSA)	Sigma-Aldrich
Goat serum	Santa Cruz
Cacodylate buffer	Sigma-Aldrich

3.1.3. Enzymes

Benzonase nuclease	Merck Millipore
DNase	Epicenter
Trypsin	SERVA

3.2. Strains, cell culture and media

3.2.1. Media

3.2.1.1. Dulbecco's Modified Eagle Medium (DMEM)

To make DMEM full medium 10 % (v/v) FBS (GE Healthcare), 1 % (v/v) ultraglutamine (Biozyme) and 27.5 µg/mL gentamycin were added to DMEM (Biozyme). The full medium was stored at 4 °C. Prior to usage for cell culture, the medium was warmed up to 37 °C in a water bath.

3.2.1.2. *Aspergillus* minimal medium (Hill and Kafer, 2001)

70 mM $NaNO_3$, 7 mM KCl and 12 mM KH_2PO_4 were dissolved in double distilled water and adjusted to pH 6.5 with NaOH. After autoclaving the medium, 4 mM $MnSO_4$ x 7 H_2O, 1 x Huntner's trace elements and 1 % (w/v) glucose were added. To prepare culture plates, the medium was autoclaved with 15 g/L European agar (Omnilab).

3.2.2.3. 1000x Huntner's Trace Elements (Hill and Kafer, 2001)

5 g/L $FeSO_4$ x 7 H_2O and 50 g/L Na_2EDTA were dissolved in distilled water and the pH was adjusted to 5.5 with KOH pellets to make solution (1). For solution (2) 22 g/L $ZnSO_4$ x 7 H_2O, 11 g/L H_3BO_3, 5 g/L $MnCl_2$, x 4 H_2O, 1.6 g/L $CoCl_2$ x 6 H_2O, 1.6 g/L $CuSO_4$ x 7 H_2O and 1.1 g/L $(NH_4)_6$ Mo_7O_{24} x 4 H_2O were dissolved in that order. Solutions (1) and (2) were combined and the pH was adjusted to 6.6 with decreasing concentrations of KOH. The solution was stored at 4 °C and sterile filtered before use.

3.2.2. Strains and cell culture

RAW 264.7 macrophages (ATCC TIB-71) were cultured to a confluent layer in Dulbecco's modified eagle (DMEM) full medium at 37 °C and 5 % (v/v) CO_2.

A. fumigatus wild-type strain ATCC 46645 and the *pksP* mutant (described in (Jahn *et al.*, 1997, Langfelder *et al.*, 1998)) were cultured on *Aspergillus* minimal medium (AMM) agar plates (Weidner *et al.*, 1998) and conidia harvest 5 days after incubation at 37 °C in 0,9 % (w/v) NaCl, 0,01 % (v/v) Tween80.

3.3. Proteomic methods

3.3.1. Magnetic labeling of conidia

Conidia were incubated with EZ link sulfo-NHS-LC biotin (LifeTechnologies) in 50 mM Na_2CO_3 for 2 h at 4 °C, washed and streptavidin-coupled magnetic beads (Miltenyi) were added in labeling buffer (PBS containing 2 mM EDTA) for 15 min, 4 °C.

3.3.2. Purification of phagolysosomes

RAW 264.7 macrophage cells were cultivated overnight in 4-well plates to a cell density of 4 x 10^6 cells per well and infected at a multiplicity of infection (MOI) = 5 with magnetically labeled *A.*

fumigatus conidia. Co-incubation was stopped after 2 h, cells were washed with PBS, scratched off and collected in homogenization buffer (3 mM imidazole, 250 mM sucrose with protease inhibitors) with benzonase nuclease. Cell lysis was achieved by pressing the cell suspension 60 times through a needle (27G) and monitored by light microscopy. DNase was added and the lysate was incubated for 5 min at 37 °C.

For the sampling of the whole cell proteome, proteins of the lysate were precipitated and processed as described below.

To purify the phagolysosomal fraction the lysate was loaded onto LS columns (Miltenyi, Germany) on the QuadroMACS separator (Miltenyi, Germany). Phagolysosomes with magnetically labeled conidia were retained on the stand and the proteins were eluted directly from the column with elution buffer at 98 °C (2 % (w/v) SDS, 100 mM TEAB, 10 % (v/v) glycerol, 1 mM TCEP).

3.3.3. Processing of proteins

The volume of the eluted protein solution was reduced to 100 µL and proteins were precipitated with methanol and chloroform as described by Wessel *et al.* (Wessel and Flugge, 1984). Each 100 µg of the precipitated proteins were resuspended in 100 mM TEAB buffer, disulfide bonds were reduced with 200 mM TCEP, alkylated with 375 mM iodoacetamide and digested with 4 µg trypsin overnight at 37 °C. Reaction was stopped with formic acid and the sample was resuspended in acetonitrile, TFA for LC-MS/MS analysis.

3.3.4. Tandem mass tag (TMT) labeling for label-based quantification

For a label-based quantification, the TMT sixplex Label Reagents (Thermo Scientific) were added to the reduced and alkylated digest according to the manufacturer's protocol. The labeled samples were simultaneously measured in LC-MS/MS. Samples were labeled as following: pksP 1 - 126, pksP 2 - 127, pksP 3 -128, wt 1 - 129, wt 2 - 130 und wt 3 - 131 (Figure 5).

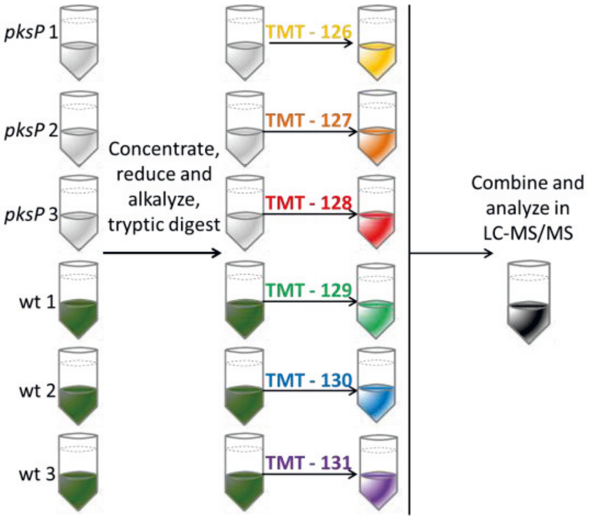

Figure 5: TMT labeling of biological replicates of phagolysosomal proteins. Protein samples of the purified phagolysosomes containing conidia of the two different strains with each three biological replicates were processed separately for TMT labeling. Every sample received an individual isobaric tag as indicated. The labeled samples were combined and analyzed simultaneously in LC-MS/MS. Figure according to manufacturer's homepage (https://www.thermofisher.com)

3.3.5. LC-MS/MS of protein samples

Different methods were applied to measure the label-free and label-based samples of purified conidia-containing phagolysosomes or the label-free sample of whole cell lysate. The sub-proteome of the conidia-containing phagolysosomes was measured with an analytical method designated as method M#1 and the whole cell proteome was measured with method M#2. To measure the TMT-labeled proteome of conidia-containing phagolysosomes method M#3 was applied. Details of liquid chromatography (LC) and mass spectrometry (MS) are described in the supplementary information (Supplement I.). LC-MS/MS analysis was carried out on an Ultimate 3000 RSLC nano system coupled to a QExactive Plus mass spectrometer (both Thermo Fisher Scientific) in the proteomics group by Dr. Thomas Krüger.

3.3.6. Protein database search and quantification

Thermo raw files were processed by the Proteome Discoverer (PD) software v1.4 (M#1, M#3) and v2.1 (M#2) (Thermo). In brief, tandem mass spectra were searched against monthly updated databases of *Mus musculus* (*M. musculus*; UniProt) and *A. fumigatus* (*Aspergillus* Genome Database, AspGD) using the algorithms of Mascot v2.4.1 (Matrix Science, UK), Sequest HT and MS Amanda. Two missed cleavages were allowed for tryptic peptides. The precursor mass tolerance was set to 10 ppm and the fragment mass tolerance was set to 0.02 Da. Dynamic modification was oxidation of Met. Static modification was based on the carbamidomethylation of Cys by iodoacetamide. Percolator node and a reverse decoy database were used for (qvalue) validation of the peptide spectral matches (PSMs) using a maximum Delta CN of 0.05 and a strict target false discovery (FDR) rate of < 1%. At least 2 peptides per protein were required for positive protein hits. Label-free quantification was performed by two different methods: 1.) The Precursor Ions Area - Top3 method compares the 3 most abundant peptides of each protein by using the peak area of the respective precursor ion. The mass tolerance was set to 2 ppm and the signal-to-noise ratio should be > 3. For the 2.) OpenMS method a max. retention time difference of 0.33 min, a max. m/z difference of 10 ppm, a q-value threshold of 0.01 and a protein level false discovery rate of <0.05 was used. The abundance values were normalized based on the total peptide amount. Only unique peptides were considered for quantification. The significance threshold for differential protein regulation was set to factor ≥ 2.0 or log2 fold change ≥ 1 (log2 ≥ 1, up-regulation, enriched in *pksP* mutant and log2 ≤ -1 down-regulation, enriched in wild-type conidia-containing phagolysosomes) for the label-free experiments (M#1 and M#2). The Integration tolerance for the TMT quantitation was 5 ppm using the most confident centroid. TMT ratios were normalized based on quan value isotopic corrections and the protein median. For quantification (126+127+128)/(129+130+131), 126/129, 127/130, 128/131 ratios were compared. For evaluation of the significance levels, a differential regulation factor of ≥1.5 (up- or down-regulation) was applied. At least 2 peptides per protein were required for positive protein hits.

Calculated ratios based on ≥4 reporter ions (average) were considered as high confident data. An average variability ≤30% was considered as high confident data. Medium confidence data was defined in the range of 30-50%. Only those proteins have been considered whose single reporter ion ratios (for all replicate comparisons and all LC-MS/MS replicates) showed a consistent tendency of up- or down-regulation.

3.4. Bioinformatics

3.4.1. Comparison of the proteome datasets

First, the protein datasets of purified conidia-containing phagolysosomes from label-free and label-based quantification were compared and second, the protein datasets of label-free LC-MS/MS measurement of the purified conidia-containing phagolysosomes and whole cells were compared against each other by using the free Venny 2.1.0 software (Oliveros, 2007 - 2015). Considered were the overlap of the total detected proteins and of the proteins identified as differentially abundant.

3.4.2. Identification of the regulator module from LC-MS/MS data

Dr. Sebastian Vlaic of the Department of Systems Biology and Bioinformatics headed by Prof. Reinhard Guthke kindly performed the analysis of the normalized proteome data. After pre-processing of the LC-MS data a total of 2431 proteins were identified for *M. musculus* while 65 proteins were identified in the data set of *A. fumigatus*. Based on an absolute log2 fold-change cutoff threshold of 1, 636 *M. musculus* and 22 *A. fumigatus* proteins were selected as differentially abundant. Identification of the murine regulatory module was performed similar to an approach of Barrenas *et al* (Barrenas *et al.*, 2012). In brief, differentially abundant proteins were mapped onto the murine protein-protein interaction network obtained from the STRING database. Identification of the regulatory module was then performed by the extraction of network regions that were significantly enriched with differentially abundant proteins. A more detailed description is added to the supplement (Supplement II).

3.4.3. Analysis of gene ontology (GO) term enrichment

The regulatory module was then analyzed regarding their biological function using the GOstats package for R (Falcon and Gentleman, 2007). Mapping of different protein identifiers was performed using the org.Mm.eg.db annotation package for R (Carlson) as well as the Ensembl biomart resource (Kinsella *et al.*, 2011) using the biomaRt package for R (Durinck *et al.*, 2009). Considered were the GO areas ‘biological process’ (BP), ‘molecular function’ (MF) and ‘cellular compartment’ (CC) as well as the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway terms (Kanehisa *et al.*, 2017). The corresponding *p*-value determines the validity of the enrichment.

3.5. Imaging methods

3.5.1. Calcofluor white (CFW) staining of conidia

$1x10^8$ conidia were stained with 0.1 mg/mL CFW in 0.9 % (w/v) NaCl, 0.01 % (v/v) Tween80 for 25 min at room temperature and immediately used for infection of cells.

3.5.2. Fluorescein isothiocyanate (FITC) staining of conidia

$2x10^8$ conidia were stained with 0.1 mg/mL FITC in 5 mL 100 mM Na_2CO_3 for 30 min at 37 °C and washed twice with PBS, 0.01 % (v/v) Tween80 before infection of cells

3.5.3. Immunofluorescence

Cells were infected at an MOI = 2 with conidia and incubated at 37° C and 5 % (v/v) CO_2. After co-incubation cells were fixed with 3.7 % (v/v) formaldehyde for 10 min at room temperature. For immunofluorescence cells were treated with 0.25 % (v/v) Triton X-100, blocked with 3 % (w/v) BSA and 3 % (v/v) goat serum and then incubated overnight at 4 °C with the primary antibody. Secondary antibody was added for 1 hour at room temperature.

Alternatively, cells were fixed by placing 10 min into – 20 °C with ice-cold methanol and 3 min into – 20 °C with ice-cold acetone.

For permeabilization with saponin, a 5 % (w/v) solution was prepared and added in a 1:10 dilution to blocking buffer and to the incubation buffers for primary and secondary antibodies.

3.5.4. Staining of lipid membrane with DiD

For a membrane staining, cells were pre-incubated with 3 μL/mL DiD in culture medium for 20 min, 37 °C, 5 % (v/v) CO_2. Imaging was done immediately after co-infection with conidia without fixing of cells.

3.5.5. Staining of monosialotetrahexosylganglioside (GM1) with Cholera Toxin B (CTB)

To visualize GM1 ganglioside, cells were incubated with 1 μg/mL CTB-Alexa 647 for 1 h prior to infection and fixed with 3.7 % (v/v) formaldehyde.

3.5.6. Staining of cholesterol with filipin III

Cholesterol staining was done after co-infection of conidia and macrophages. Cells were fixed and quenched with 1.5 mg/mL glycine and incubated with 50 μg/mL filipin III for 1 h at room temperature.

3.5.7. Confocal laser scanning microscopy

All images were acquired on a Zeiss LSM 780 confocal microscope with a Zeiss Plan appochromat 63x/1.4 oil objective. Three technical and two biological replicates were analyzed for each strain. Six images were taken per technical replicate, making 36 images in total per strain.

Cholesterol samples were imaged with a Zeiss LSM 710 confocal microscope with a Zeiss Plan appochromat 63x/1.4 oil objective using the UV laser with wavelength of 351 and 364 for excitation. In two independent experiments 11 images were taken per strain.

3.5.8. Image analysis

The total number of ingested conidia per image was determined. The conidia-containing phagolysosomes with a specific fluorescence from the target molecule, as indicated by a circular fluorescence signal around the conidium, were considered as positive for the desired marker. By determining the number of phagolysosomes positive for the marker and the total number of ingested conidia the ratio of target-positive phagolysosomes was calculated.

Alternatively, the colocalization tool of the Zen black software was used to determine the colocalization coefficient of conidial and target-specific fluorescence.

3.5.9. Electron microscopy

RAW 264.7 macrophage cells were cultured overnight to a confluent layer in 75 cm^2 culture flask and infected with an MOI = 2 of wild-type or *pksP* mutant conidia. Flasks were placed for 30 min at 4 °C to allow conidia to settle and synchronize phagocytosis. Infected cell culture was incubated for 30 min or 2 h at 37 °C in a CO_2 incubator. The interaction was stopped and samples fixed with 2.5 % (v/v) glutaraldehyde in cacodylate buffer for 30 min at room temperature. Sampled were washed twice with cacodylate buffer for 15 min. Cells were detached with a cell scraper and the suspension collected in 2 mL Eppendorf cups. The sample was spun down for 5 min at 1000 x g and resuspended in 500 µL cacodylate buffer. Cells were post-fixed with 1% (w/v) osmium tetroxide in cacodylate buffer (100 mM, pH 7.4) for 2 h. Cells were again washed twice for 15 min with cacodylate buffer and samples were dehydrated in an ascending ethanol series and stained with 2% (w/v) uranyl acetate in 50% (v/v) ethanol. The samples were embedded in Araldite resin (PANO GmbH, Wetzlar, Germany) according to the manufacturer's instruction. Ultrathin sections of 70 nm thickness were cut using an ultra-microtome Ultracut E (Reichert-Jung, Wien, Austria). The sections were mounted on Formvar-carbon coated 100 mesh grids (Quantifoil Micro Tools GmbH, Großlöbichau, Germany). The ultrathin sections were stained with lead citrate for 10 min (Venable and Coggeshall, 1965) and examined in a Zeiss CEM 902 A electron microscope (Carl Zeiss AG, Oberkochen, Germany) using a 1k FastScann CCD camera (camera and software TVIPS GmbH, Munich, Germany). Contrasting, dehydration, embedding and thin sectioning as well as imaging was carried out by the Electron Microscopy Center (Elektronenmikroskopisches Zentrum, EMZ, Universität Jena) headed by Dr. Martin Westermann.

Samples for freeze-fracturing and microscopy were also prepared at the EMZ after macrophages and wild-type conidia were incubated for 3 hours, washed with PBS and fixed for 15 min at room temperature with 3.7 % (v/v) formaldehyde in cacodylate buffer.

3.6. Biochemical methods

3.6.1. Determination of protein concentration

2 µL of protein solution of a concentration range of 0.25 mg/mL to 5 mg/mL were spotted onto detection cards and measured against the reference buffer with the Direct Detect Infrared Spectrometer (Merck Millipore).

3.6.2. Cellular compartmentation

Macrophage cells were cultured over-night in a 4-well plate and infected with wild-type or *pksP* mutant conidia at an MOI = 5. After 2 h of co-incubation, the different cell fractions were compartmentalized with the cellular compartmentation kit (QIAGEN, Germany). Target proteins in both fractions were detected *via* western blotting, using glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and cytochrome c oxidase subunit 4 (COX4) as loading standard for the cytosolic and the membrane fraction, respectively.

3.6.3. Western blotting

For each purification experiment a sample was loaded on a 4-12 % Bis-Tris Protein Gel (NuPAGE, ThermoFisher Scientific, Germany). The proteins were separated electrophoretically and blotted onto a low fluorescent PVDF membrane (Amersham, GE Healthcare Life Science, Germany). The Smart Protein Layer Kit (DyeAGNOSTICS, Germany) was used for visualization of the total protein amount and as a protein standard to quantify the amounts of loaded target protein. The membrane was incubated with the primary specific antibody and the secondary HRP-coupled antibody to detect the target protein *via* luminescence (Towbin *et al.*, 1979).

4. Results

4.1. Electron microscopic studies of conidia-containing phagolysosomes

Previous studies identified DHN-melanin of the conidial cell wall as an important virulence determinant that influences the intracellular fate of the conidium. A reduction of ROS production, interference with the host apoptotic pathway, inhibition of phagolysosomal maturation and increased host cell damage was attributed to melanization (Jahn *et al.*, 2000, Jahn *et al.*, 1997, Volling *et al.*, 2011). Accordingly, it seemed likely that there is a direct or indirect interaction of the fungal surface and the phagolysosomal membrane. To study the phagolysosome as the immediate contact site in more detail, samples of macrophages containing ingested wild-type or *pksP* mutant conidia were prepared for electron microscopy. 30 min post infection, both wild-type and *pksP* conidia reside in a phagolysosome with a luminous vacuole of approximately 1.5 times the conidial surface area on average (Figure 6A). 3 h post infection, the phagolysosomal shape remains almost unchanged around the *pksP* conidia, but has diminished in size and the membrane is wrapped closely around the wild-type conidium (Figure 7B-D).

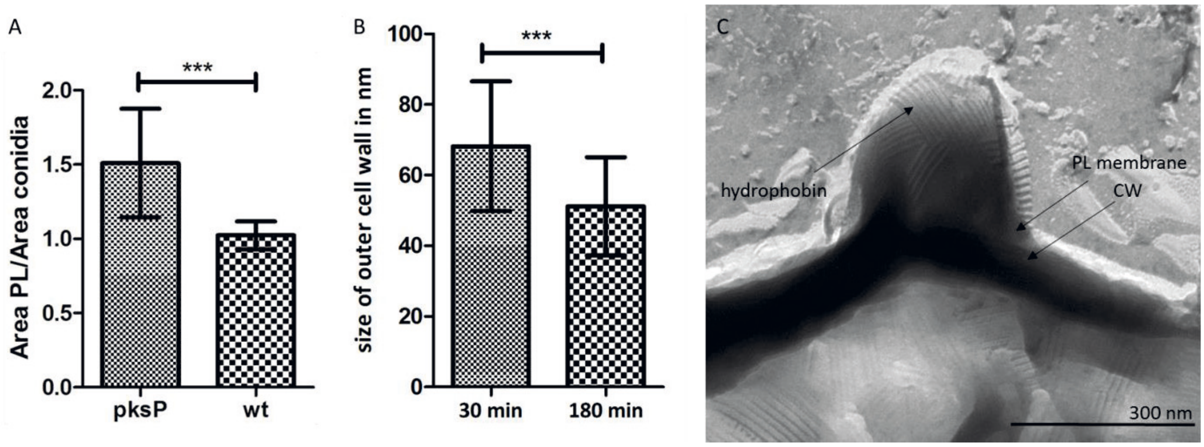

Figure 6: Size of phagolysosomes and degradation of fungal cell wall. (A) Ratio of phagolysosomal (PL) to conidial area 2 h after infection of macrophages with wild-type or *pksP* mutant conidia. Columns represent the mean values of 14 analyzed images with standard deviations; *** $p < 0.0001$. (B) Thickness of the wild-type conidial cell wall 30 min and 3 h past infection. Columns represent the mean values of 20 analyzed images with standard deviations; *** $p < 0.0001$. (C) Electron micrograph of a freeze-fractured sample showing the constriction of conidial surface hydrophobin layer into a fissioning vesicle.

The thick, highly contrasted layer around wild-type conidia visible in the electron micrographs presumably represents the DHN-melanin and hydrophobin coat. There are little protuberances from this layer suggesting the disintegration and degradation of the outer conidial surface. Where phagolysosomal membrane and conidial surface are in close proximity, the formation of vesicles that constrict and engulf particles of the melanin-hydrophobin layer is visible (Figure 7D). A close up of a freeze-fracturing micrograph shows how a particle of hydrophobin is packed in a proturbing vesicle (Figure 6C). Intriguingly, the thickness of the outer layer decreases by 25 % from the early (30 min post-infection) to the late time point (3 h post-infection) of internalization, from almost 70 to 50 nm on average, pointing to a subsequent digestive process (Figure 6B).

Except for the budding vesicles, there are few endocytic vesicles in proximity of the wild-type conidia-containing phagolysosomes, indicating a decreased fusion rate of the organelle. This observation is in line with the decreased size of wild-type conidia-containing phagolysosomes. By subsequent fusion events, membranes as well as enzymatic components are delivered that result in the growth of the organelle (Desjardins, 1995, Haas, 2007). In contrast, *pksP* mutant conidia-containing phagolysosomes are surrounded by a number of vesicles or multivesicular bodies (MVB), dynamically fusing and fissioning with or from the compartment (Figure 7B).

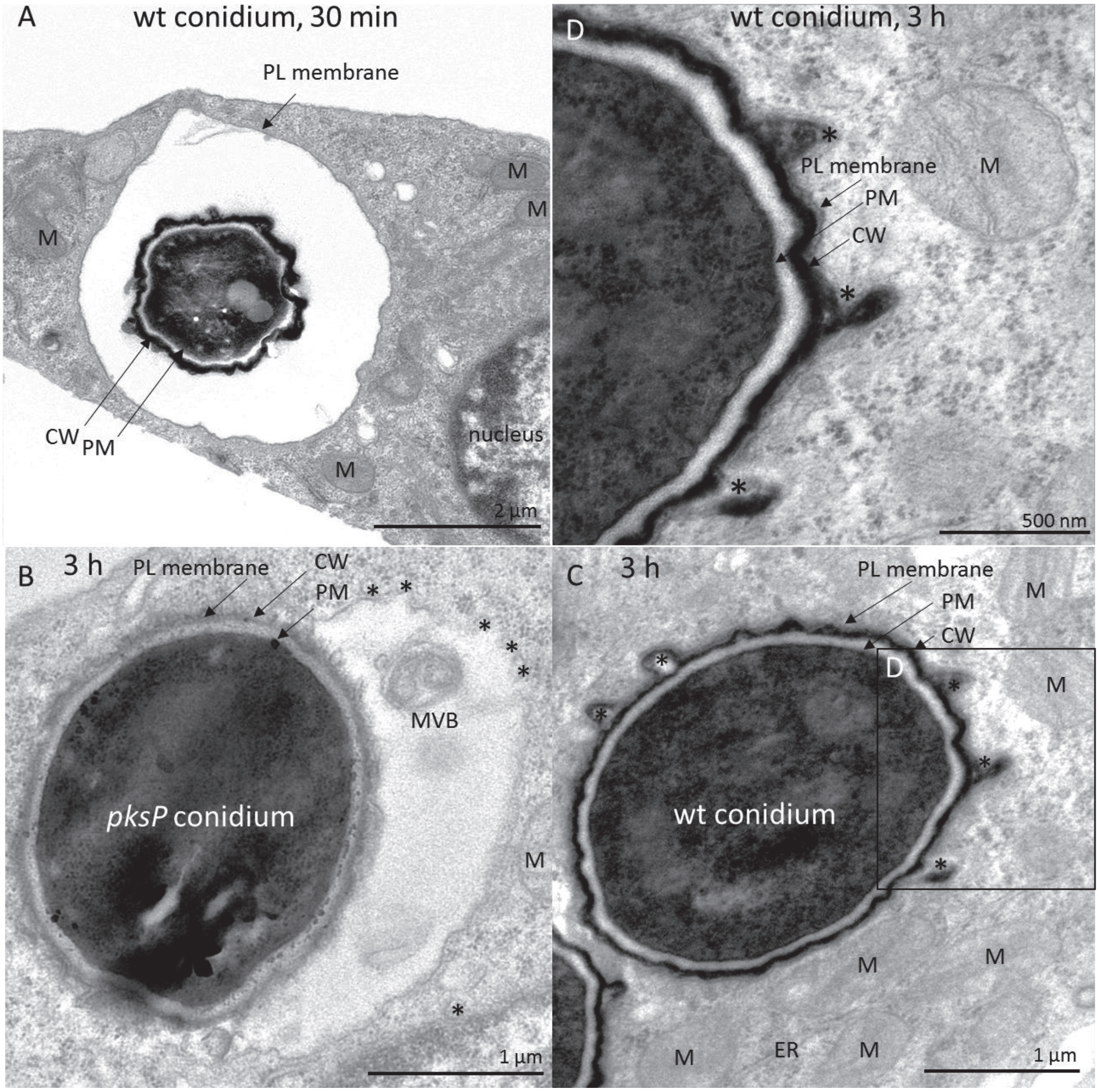

Figure 7: Electron micrographs of conidia-containing phagolysosomes. (A) 30 min after infection of macrophages, the wild-type conidium is enclosed in a luminous phagosome. The hydrophobin-melanin coat of the outer conidial cell wall (CW) is visible as a thick, highly contrasted layer. (B) 3 h after infection the *pksP* mutant conidia-containing phagolysosomes still possesses a large lumen of ~ 1.5 times the conidial area. Multivesicular Bodies (MVB) and several vesicles (*) surround the organelle. The conidial cell wall is visible as a blurry line around the plasma membrane (PM). (C) 3 h after infection the phagolysosomal membrane (PL membrane) tightly enwraps the wild-type conidium. The conidial cell wall is still visible as discrete line, but is decreased in thickness. (D) Section of (C): Vesicles containing parts of the cell wall are budding from the phagolysosomes. PL membrane – phagolysosomal membrane, CW – fungal cell wall, melanin and hydrophobin layer of the wt conidia, PM – fungal plasma membrane, M – mitochondria, * – vesicles

4.2. Establishment of a protocol to purify conidia-containing phagolysosomes

Wild-type and *pksP* mutant conidia-containing phagolysosomes are distinct in size, their interactivity with the endosomal compartment as demonstrated by electron microscopy and in their functions, that is to say, acidification, ROS generation and degradation properties. Thus, *A. fumigatus* conidia possess a DHN-melanin-dependent ability to modify the phagolysosomal maturation process.

Intracellular pathogens have developed different mechanisms to interfere with the phagolysosomal maturation (reviewed in (Brumell and Scidmore, 2007)) but little is known about the immune evasion mechanism of *A. fumigatus.* A modulation of phagolysosomal maturation is supposedly reflected in the protein composition of conidia-containing phagolysosomes, as they are the site of immediate interaction between host and pathogen. To isolate conidia-containing phagolysosomes a protocol is adapted from the Steinhäuser *et al.* (Steinhauser *et al.*, 2013) publication about the purification of *Mycobacteria*-containing phagolysosomes to *A. fumigatus* conidia. The established workflow is illustrated in Figure 8**.** In detail, the adaptations consider the magnetic labeling of conidia, cell lysis, magnetic separation and protein extraction.

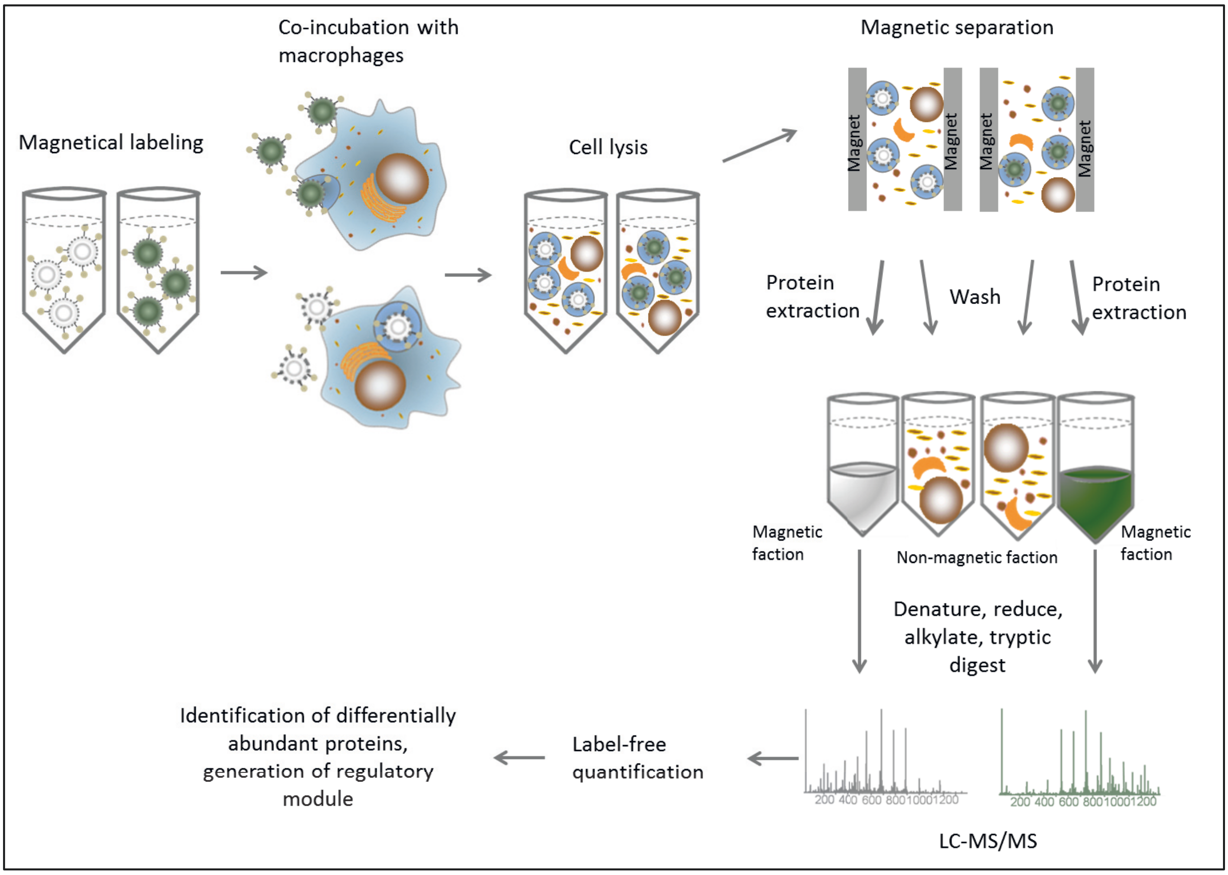

Figure 8: Workflow to purify conidia-containing phagolysosomes. Wild-type and *pksP* mutant conidia are labeled with magnetic beads and incubated with macrophages for 2 h. The cell lysate is loaded onto a magnetic column to separate the magnetic fraction from the cell debris. The protein is extracted on-column, precipitated and concentrated. To measure samples in LC-MS/MS, disulfide bonds are reduced, protein alkylated and digested with trypsin. After label-free quantification, differentially regulated proteins are identified and compiled to the regulatory module.

4.2.1. Magnetic labeling of *A. fumigatus* conidia

The attachment of an N-hydroxysulfosuccinimide (NHS)-biotin linker to amide residues on the conidial surface *via* ester bonds and ligation of streptavidin-tagged magnetic beads to the biotin linker achieves the magnetic labeling of conidia. Due to the different surface properties of wild-type and *pksP* mutant conidia the concentration of linker has to be adjusted to both strains for equal labeling. The efficiency of biotinylation is monitored microscopically after addition of a streptavidin-coupled Alexa635 fluorophore to the conidia suspension (data not shown). Nonspecific effects of the label on intracellular processing of the conidia are excluded by comparing the ratio of acidified phagolysosomes of labeled and unlabeled wild-type and *pksP* mutant conidia. 16.8 % and 20.8 % of labeled and unlabeled wild-type conidia-containing phagolysosomes and 68.4 % and 77.1 % of labeled and unlabeled *pksP* mutant conidia-containing phagolysosomes acidify, respectively, with no statistical significant difference. Thus, the labeling has no significant effect on the acidification of the phagolysosome (Figure S1).

4.2.2. Cell lysis

A time point of two hours post infection of RAW264.7 macrophages with conidia is chosen to investigate differences in the proteome of wild-type and *pksP* conidia-containing phagolysosomes. This time point represents a late stage of phagolysosomal maturation (Desjardins *et al.*, 1994), where acidification and dynamic fusion with endosomal vesicles was reported to take place (Thywissen *et al.*, 2011). To achieve a thorough lysis of the cell membrane, yet ensure the integrity of the phagolysosomal membrane, the cells are sheared by pressing through a needle. Phagolysosomal membrane integrity is confirmed after staining of the sample with the fluorescent, lipophilic dye DiD. Also, cells are pre-incubated with fluorescent dextran microbeads (3000 MW dextran beads). The small size of the beads leads to an engulfment *via* pinocytosis. The beads are transported in lysosomes along the endocytosis pathway and delivered to phagolysosomes by fusion of the compartments. Only intact phagolysosomes retain the beads. After the shearing procedure, more than 90 % of cells are lysed and phagolysosomes remained intact, which is determined by the continuous dextran and DiD fluorescence around the conidia (Figure 9).

Figure 9: Membrane integrity of conidia-containing phagolysosomes after cell lysis. 3000 MW dextran beads are added to the cells and incubated overnight. Macrophages are infected with CFW-labeled conidia and lysed 2 h post-infection by shearing of the cell suspension. The lysate is stained with DiD and samples are monitored by LSM. A circular fluorescence of dextran (green) and DiD (red) around the conidia (blue, CFW) indicates a phagolysosome with a continuous and intact membrane (arrows). Scale bar represents 10 µm.

4.2.3. Protein extraction

The entire lysate is loaded onto a magnetic column and washed extensively to flush out contaminating cell debris. Following addition of the lysis buffer to the columns, proteins are obtained by on-column extraction, concentrated *via* methanol/chloroform precipitation and processed for LC-MS/MS measurement. The extraction protocol yields on average 2 mg of protein.

4.3. Protein identification and quantification

4.3.1. Comparison of quantification methods

The LC-MS/MS analysis of the prepared samples results in a complex dual proteome dataset comprising host and *A. fumigatus* proteins from phagolysosomes of macrophages infected with wild-type and *pksP* mutant conidia. 95 % of all proteins are present in both the wild-type and the *pksP* mutant conidia-containing phagolysosomes, suggesting that differences in the phagolysosomal composition are of a rather quantitative then qualitative nature (Table S2 and S3). To handle and compare the data, two quantification methods are applied and compared.

First, a label-free quantification Is carried out by using the ‘Top Three’ method, which considers the ‘area under the curve’ values of the peptide spectrum. A total of 2431 murine phagolysosomal proteins and 65 *A. fumigatus* proteins are identified (Tables S2 and S3). The ratio of protein levels in *pksP* mutant *versus* wild-type conidia-containing phagolysosomes represents the relative differences in protein abundance. Based on a log2-fold-change cut-off threshold, 1, 637 murine and 22 fungal proteins are identified as being differentially regulated. Of the 637 regulated proteins of the phagolysosome, 472 are overrepresented in the *pksP* phagolysosome and 165 in the wild-type phagolysosome. On the fungal side, 8 proteins are identified as specific for *pksP* conidia and 14 proteins as specific for the wild-type conidia.

Second, a label-based TMT method is performed. The two samples with three replicates each are labeled with a sixplex isobaric tag and measured simultaneously. Identical peptides peak at the same retention time. The quantification is based on the fragmentation pattern of the reporter ions from the isobaric tags (Rauniyar and Yates, 2014). This approach identifies a total of 2373 murine and 47 fungal proteins. Here, an absolute log2 fold-change cut-off threshold of 0.5 selects 26 murine candidates and 1 fungal candidate specifically enriched in phagolysosomes. 15 of 26 regulated proteins are enriched in the *pksP* mutant and 11 enriched in wild-type conidia-containing phagolysosomes. The single differentially regulated fungal protein is more abundant in wild-type phagolysosomes (Tables S4 and S5).

42 % (1413 proteins) of the total proteins are detected with both methods, 1018 proteins (30 %) are found exclusively in the label-free method and 960 proteins (28 %) only in the label-based analysis.

Although the number of total identified proteins is almost identical and the overlap between the dataset high, there are big differences in the identified differentially abundant proteins. Whereas 637 host proteins fulfill the criteria for a differential regulation in the label-free method, only 26 do so with the label-based approach. A group of six proteins are classified as regulated in both experiments and of those, 4 candidates show the same direction of regulation (Figure 10).

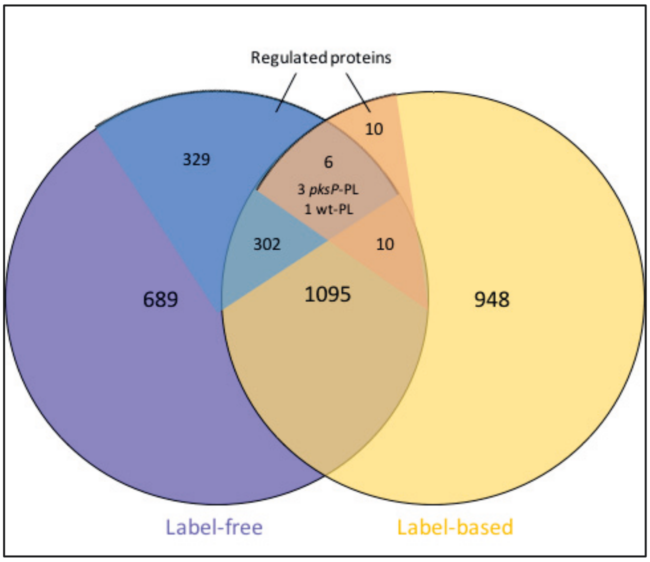

Figure 10: Comparison of host phagolysosomal proteome detected with label-free and label-based quantification. Protein samples from the phagolysosomal purification are measured and quantified with a label-free and a label-based method. Venn diagram shows the overlap of total detected and differentially regulated proteins. 6 regulated proteins are identified by both methods, 3 of those are enriched in *pksP* mutant and 1 in wild-type conidia-containing phagolysosomes.

With regard to the fungal proteins, 53 % (38 proteins) of identified proteins are detected by both approaches. The label-free analysis measures additional 27 proteins (37 %), the label-based approach another seven (10 %). 22 proteins differentially regulated proteins are found by the label-free experiment and only one protein by the label-based method. However, this single regulated candidate is detected by both approaches and shows the same direction of enrichment (Figure S2).

The comparison of quantification methods demonstrates that the label-free approach is more sensitive for detecting differentially regulated proteins. Generally, the median and mean values of peptide spectrum matches (PSMs), as an indicator for the quality of the detection, are two-fold higher. The TMT-label-based approach, on the other side, shows lower deviations and was previously described as the more accurate method (Megger *et al.*, 2014). For the following analysis of the differential phagolysosomal proteome, the label-free dataset is utilized (Table S2).

4.3.2. Identification of proteins representing the phagolysosomal fraction

Experiments are performed to assess the quality of the LC-MS/MS data from the purified sample and to confirm that the dataset is representative of the phagolysosome. Therefore, the dataset is compared with that of the whole cell proteome of macrophages infected with wild-type or *pksP* mutant conidia. A total number of 1986 proteins is detected in the whole cell sample (Table S6). 53 % of total phagolysosomal proteins and 39 % of the proteins determined as regulated on phagolysosomal level are also detected in the whole cell proteome. Consequently, 47 % of total phagolysosomal proteins and 61 % of differentially abundant proteins are found only in the purified sample (Figure 11A-B). Thus, the purification of the phagolysosomal fraction enables the identification of a set of regulated proteins that are distinct from regulated candidates at whole cell level.

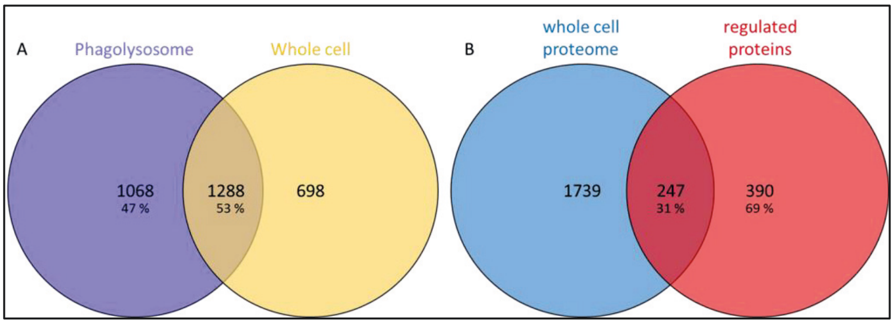

Figure 11: Comparison of proteome data between whole cell and phagolysosomal sample. (A) Proteins detected in the phagolysosomal fraction and in the whole cell sample overlap by 53 %. (B) Proteins identified as differentially abundant are by 31 % covered in the whole cell proteome.

At the whole cell level, 1028 proteins fulfill the criteria for differential abundance. 158 proteins are more enriched in macrophages challenged with *pksP* mutant conidia and 870 proteins are up-regulated in macrophages infected with wild-type conidia. However, the subsets of regulated proteins from whole cell and phagolysosomal sample largely differ from each other. 29 % of differentially abundant proteins in the phagolysosomal fraction are also regulated at the whole cell level. Of those overlapping proteins, only 35 % have the same direction of regulation (Figure 12). Thus, a very distinct set of proteins is regulated at the whole cell level and the direction of regulation is opposite in many cases compared to the results from the phagolysosomal fraction.

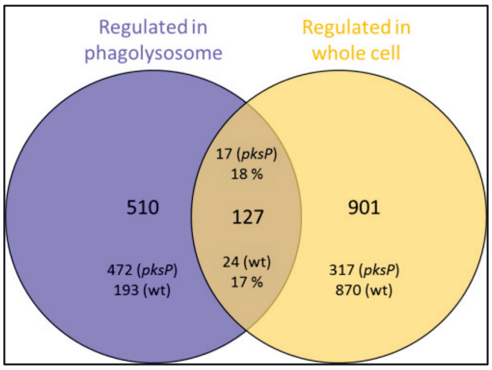

Figure 12: Comparison of identified differentially regulated proteins in the purified phagolysosome or in the whole cell. The Venn diagram shows the overlap of proteins identified as differentially abundant at whole cell or phagolysosomal level of macrophages challenged with conidia. Of the 127 overlapping candidates, 17 are found to be enriched in *pksP* mutant and 24 in wild-type conidia-containing phagolysosomes.

Furthermore, the representation of the gene ontology (GO) annotations ‘lysosome’ (count = 69, *p*-value = 5.3×10^{-6}) and ‘lysosomal membrane’ (count = 63, *p*-value = 3.2×10^{-10}) shows a major enrichment in the phagolysosomal purification compared to the whole cell proteome (count = 41, *p*-value 0.06 and count = 40, *p*-value = 1.8×10^{-4}). The opposite is true for the GO term ‘cytosol’ (count = 362, *p*-value = 8.5×10^{-21} *versus* count = 359, *p*-value = 4.2×10^{-41}). According to GO term enrichment, the dataset represents a concentration of phagolysosomal proteins compared to the whole cell dataset.

4.3.3. The top ten most abundant proteins in conidia-containing phagolysosomes

Among the ten most abundant proteins of phagolysosomes containing the *pksP* conidia are the lipid raft protein stomatin, lysosomal peptidases cathepsins D and Z, subunits of the V_1 cytosolic and V_0 transmembrane domain of the vATPase complex, the lysosomal-associated membrane protein 1 (Lamp1), a splicing factor and a protein of the 60S ribosomal subunit (Table 1). In the wild-type conidia-containing phagolysosome there are proteins involved in RNA processing and transport, such as an RNA-dependent helicase, a THO complex subunit, cleavage stimulation factor and regulation of nuclear pre-mRNA domain-containing protein. Additionally, a protein of the Arp2/3 complex (Arp2) and dedicator of cytokinesis (Dock2), responsible for actin polymerization and cytoskeletal rearrangements, a paralog of autophagy-related gene (ATG) 16L2 autophagy regulator, an endoplasmic reticulum (ER) membrane protein, a subunit of chromosome-condensing protein and a nuclear receptor with co-activation or co-repressing functions is highly abundant in the wild-type conidia sample (Table 2).

The functions represented by the most abundant proteins in the *pksP* mutant and wild-type conidia-containing phagolysosome indicate that, depending on the engulfed conidium strain, distinct pathways are active in the macrophage.

Table 1: Top ten of abundant proteins on *pksP* mutant conidia-containing phagolysosomes.

Accession	Gene symbol	Description	Σ Coverage	Σ# Peptides	Σ# PSMs	Fold-change *pksP*/wt
P54116	Stom	Erythrocyte band 7 integral membrane protein	47.89	13	916	3.558
P18242	Ctsd	Cathepsin D	36.10	13	887	2.590
Q921H8	Acaa1a	3-ketoacyl-CoA thiolase A, peroxisomal	67.22	22	844	2.367
Q9WUU7	Ctsz	Cathepsin Z	30.07	8	547	2.023
P50516	Atp6v1a	V-type proton ATPase catalytic subunit A	32.25	19	536	2.291
Q9JHF5	Tcirg1	V-type proton ATPase subunit a	25.90	18	506	3.403
Q3TWW8	Srsf6	Serine/arginine-rich splicing factor 6	30.68	14	458	2.062
P11438	Lamp1	Lysosome-associated membrane glycoprotein 1	13.30	5	439	3.836
P41105	Rpl28	60S ribosomal protein L28	50.36	10	404	2.226
P51863	Atp6v0d1	V-type proton ATPase subunit d 1	22.22	9	383	2.573

Table 2: Top ten of abundant proteins on wild-type conidia-containing phagolysosomes.

Accession	Gene symbol	Description	Σ Coverage	Σ# Peptides	Σ# PSMs	Fold-change *pksP*/wt
Q8K363	Ddx18	ATP-dependent RNA helicase DDX18	26.06	17	532	0.479
P61161	Actr2	Actin-related protein 2	19.04	9	267	0.429
B1AZI6	Thoc2	THO complex subunit 2	8.91	15	264	0.339
Q99LI7	Cstf3	Cleavage stimulation factor subunit 3	15.76	11	204	0.450
O70378	Emc8	ER membrane protein complex subunit 8	21.74	5	194	0.406
Q3UKJ7	Smu1	WD40 repeat-containing protein SMU1	17.54	8	185	0.359
Q6NXI6	Rprd2	Regulation of nuclear pre-mRNA domain-containing protein 2	11.50	13	159	0.283
Q8CG47	Smc4	Structural maintenance of chromosomes protein 4	14.39	20	145	0.419
Q8C3J5	Dock2	Dedicator of cytokinesis protein 2	7.60	13	144	0.193
Q91W39	Ncoa5	Nuclear receptor coactivator 5	17.27	11	140	0.451

4.3.4. *A. fumigatus* differentially regulated proteins

The dual proteome analysis of the purified phagolysosome fraction enables quantification of the *A. fumigatus* protein profile in response to the host immune defense mechanism in order to identify potential fungal effectors interacting with the host endocytic pathway. It can be assumed that the protein extraction protocol does not lead to lysis of the conidium and the detected proteins are either surface-associated or released by *A. fumigatus.* Nevertheless, it must be considered that *pksP* conidia are exposed to an acidic environment and are prone to the degradative machinery of the phagolysosome, while wild-type conidia reside in a more neutral organelle. Consequently, enriched in the *pksP* conidia-containing phagolysosome are a number of stress response proteins: A GTPase with a function in response to drug and macroautophagy, an RNA helicase induced upon contact with the airway epithelia, aldehyde dehydrogenases, one of them reported to be up-regulated by exposure to neutrophils and a transaldolase with a role in oxidative stress response (Table 3).

The wild-type conidia proteome contains a different set of stress response elements, such as proteins connected to drug response, unfolded protein response in mitochondria, a catalase and glyceraldehyde-3-phosphate dehydrogenase (GAPDH), but also components involved in nucleosome assembly, transcription, mRNA processing and ribosome activity. Furthermore, a serine/threonine phosphatase and a 14-3-3 protein, both involved in signaling, as well as a high abundant conidial protein with unknown function are overrepresented in the wild-type conidia-containing phagolysosome (Table 4).

Table 3: List of differentially abundant *pksP* mutant conidia proteins in the phagolysosome.

Accession	Description	ΣCoverage	Σ# Peptides	Σ# PSMs	Fold-change *pksP*/wt
Afu4g08040	Ortholog(s) have GTP binding activity, role in endocytosis	10.09	2	95	2.591
Afu1g12070	Ortholog(s) have glycine dehydrogenase (decarboxylating) activity, role in glycine catabolic process, one-carbon metabolic process, protein lipoylation and mitochondrion localization	31.43	4	81	33.56
Afu1g11730	Ortholog(s) have GTPase activity, role in ER to Golgi vesicle-mediated transport, Golgi to plasma membrane transport, cellular response to drug, macroautophagy and Golgi apparatus, glyoxysome localization	17.49	2	50	2.191
Afu2g13530	Putative translation elongation factor EF-2 subunit; protein abundant in conidia; protein induced by heat shock	11.68	10	46	2.003
Afu2g10750	Putative RNA helicase; transcript induced by exposure to human airway epithelial cells	5.46	3	45	6.956

Accession	Description	ΣCoverage	Σ# Peptides	Σ# PSMs	Fold-change *pksP*/wt
Afu6g11430	Putative aldehyde dehydrogenase; hypoxia repressed protein; transcript up-regulated in conidia exposed to neutrophils; immunoreactive protein	2.86	2	44	2.170
Afu2g00720	Putative aldehyde dehydrogenase (NAD^+)	3.05	2	21	2.255
Afu5g09230	Putative transaldolase; abundant protein in conidia and mycelia; protein induced by hydrogen peroxide and hypoxia, pentose phosphate shunt	5.56	2	2	4.536

Table 4: List of differentially abundant wild-type conidia proteins in the phagolysosome.

Accession	Description	ΣCoverage	Σ# Peptides	Σ# PSMs	Fold-change *pksP*/wt
Afu3g05360	H2A1, has domain(s) with predicted DNA-binding, protein heterodimerization activity, role in nucleosome assembly and nucleosome, nucleus localization	8.68	4	89	0.414
Afu2g11510	Ortholog(s) have role in cellular response to drug, rRNA processing, ribosomal large subunit biogenesis, ribosomal subunit export from nucleus and nucleolus, pre-ribosome, large subunit precursor, spindle localization	3.85	2	62	0.250
Afu2g09090	Ortholog(s) have role in mitochondrion inheritance, negative regulation of proteolysis, protein folding, replicative cell aging and mitochondrial inner membrane, plasma membrane localization, mitochondrial unfolded protein response	6.43	2	35	0.358
Afu5g02410	Putative DEAD/DEAH box helicase; predicted gene pair with AFUA_3G08160 (eukaryotic translation initiation factor eIF4A; ATP-dependent RNA helicase, *tifA*)	5.54	4	31	0.177
Afu6g03890	CatA, spore-specific catalase; abundant protein in conidia; calcium down-regulated; predicted secretory signal sequence	12.80	8	30	0.482
Afu2g13780	Ortholog(s) have role in mRNA *cis* splicing, *via* spliceosome and U2 snRNP localization	2.42	3	23	0.345
Afu5g01970	GpdA, glyceraldehyde-3-phosphate dehydrogenase; predicted gene pair with AFUA_5G01030; protein induced by hydrogen peroxide; reacts with rabbit immunosera exposed to *A. fumigatus* conidia: induced by L-tyrosine, glycolysis	11.83	4	16	0.271
Afu1g11710	Ribosomal protein L1	5.99	2	12	0.148
Afu1g04950	Ortholog(s) have protein serine/threonine phosphatase activity, synthesis of glycogen, cell wall, role in membrane fusion	5.88	2	10	0.091
Afu1g13670	CcpA, protein of unknown function; abundant in conidia	10.21	2	6	0.148
Afu1g14680	Ortholog(s) have DNA binding activity and cytosol, nucleus localization	1.49	3	5	0.471

Accession	Description	ΣCoverage	Σ# Peptides	Σ# PSMs	Fold-change *pksP*/wt
Afu1g13900	Ortholog(s) have DNA-directed RNA polymerase activity, role in mRNA export from nucleus, nucleolus organization, protein localization to nucleolar rDNA repeats and DNA-directed RNA polymerase I complex, cytosol localization	0.89	2	4	0.473
Afu6g06750	14-3-3 family protein; predicted gene pair with AFUA_2G03290 (*artA*), role in exocytosis and vesicle transport	9.56	3	4	0.295
Afu1g06280	Ortholog(s) have endoplasmic reticulum localization	3.29	2	2	0.395

4.4. The regulatory module

To get a better insight into regulated phagolysosomal processes after phagocytosis of either wild-type or *pksP* mutant conidia, the identified differentially abundant proteins are compiled into a regulatory module (Figure 13). The host regulatory module is composed of 302 phagolysosomal proteins (knots in the module) connected by 3448 reported interactions (edges). 178 of the 302 proteins were measured by LC-MS/MS and again 109 of those proteins were identified as differentially abundant. 79 proteins were enriched in the *pksP* mutant and 30 on the wild-type conidia-containing phagolysosome.

The regulatory module displays regions with proteins of higher proximity. These regions with a high level of connectivity of proteins are termed 'submodules'. The degree of connectivity is in accordance with functional or structural similarities. Hence, the submodules represent regulated biological processes or structures in the phagolysosomal proteome. Although not all proteins of the regulatory module were identified by LC-MS/MS one can assume the regulation of also the non-detected proteins due to their close affiliation to the PPI network.

14 submodules comprise 5 or more proteins and are included for analysis of annotated and enriched GO terms as well as KEGG pathway terms. Table 5 lists terms that are enriched in the regulatory module. Most prominent are vATPase activity and electron transport chain as well as transport processes in the endosomal compartment. Submodules considered for validation experiments and detailed discussion represent the functions 'Electron transport chain', 'Iron homeostasis', 'Stress response', 'vATPase-dependent acidification', 'Endocytosis', 'Vesicle transport', 'Carboxylic acid metabolism', 'Generation of ROS *via* NADPH oxidase', 'Immune response' and 'Signaling'. In detail, those submodules comprise proteins involved in generation of precursors and energy, regulation of autophagy and apoptosis, soluble N-ethylmaleimide-sensitive-factor attachment receptor (SNARE)-mediated membrane trafficking and Rab GTPase-regulated vesicle fusion, mitogen-activated protein kinase (MAPK) signaling pathway, regulation of signal transduction and cellular metabolism as well as components of enzyme complexes vATPase, NADH dehydrogenase and lipid rafts (Table S1). The mentioned submodules are highlighted in Figure 13.

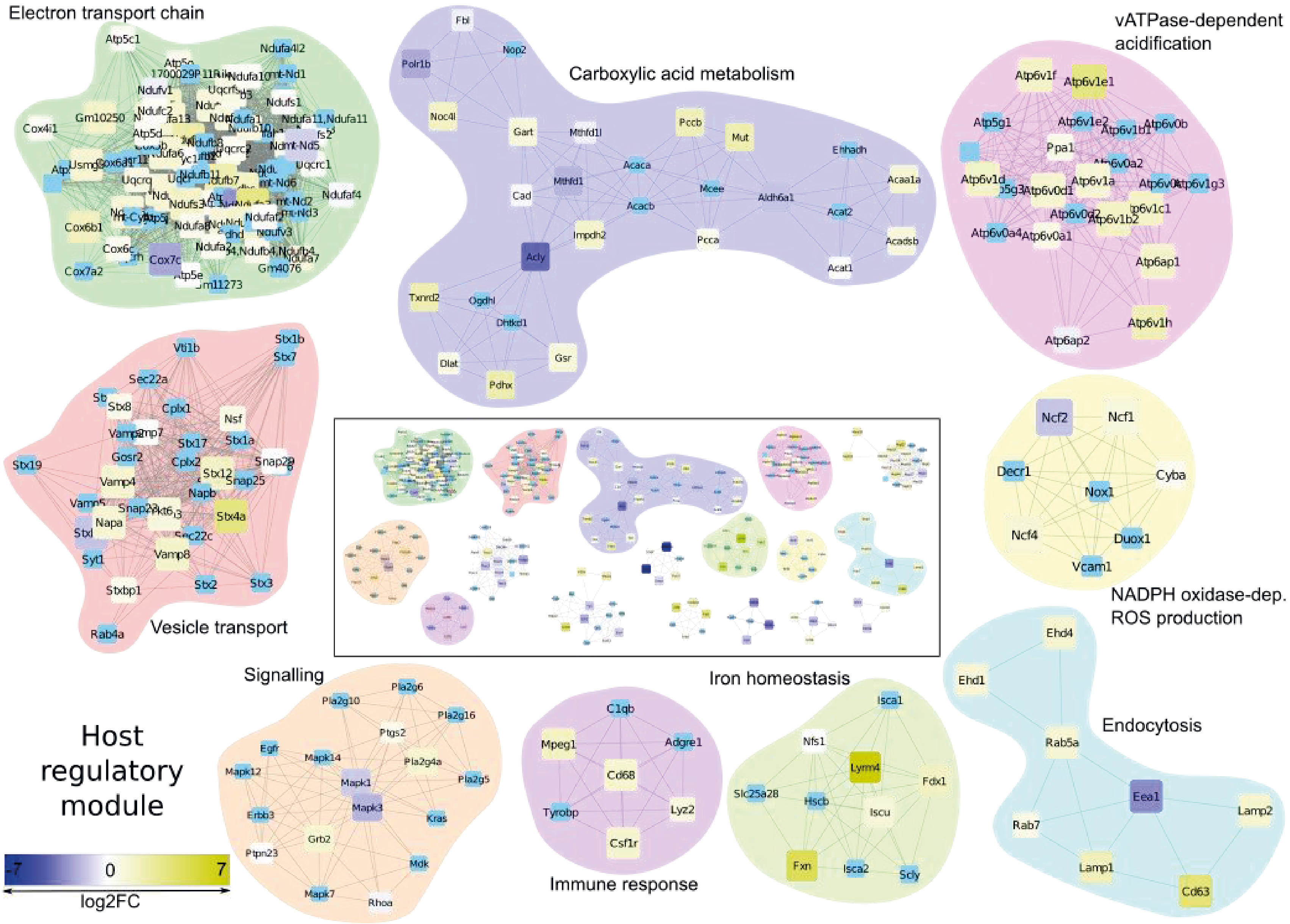
Electron transport chain
Atp5c1
Ndufa4l2
1700029P11Rik
Ndufa10
mt-Nd1
Ndufv1
Uqcrfs1
Ndufs1
Cox4i1
Gm10250
Ndufc2
Ndufa11,Ndufa11
Atp5d
Ndufb8
Uqcrc2
mt-Nd5
Uqcrc1
Usmg5
Cox6a1
Uqcrq
Ndufb11
mt-Nd6
Ndufaf4
Ndufs3
mt-Nd2
mt-Nd3
mt-Cytb
Ndufa8
Ndufaf2
Ndufv3
Cox6b1
Cox6c
Ndufa2
Ndufb4
Ndufa7
Cox7c
Gm4076
Cox7a2
Atp5e
Gm11273
Carboxylic acid metabolism
Fbl
Nop2
Polr1b
Noc4l
Gart
Mthfd1l
Pccb
Mut
Ehhadh
Acaca
Acaa1a
Cad
Mthfd1
Mcee
Aldh6a1
Acat2
Acacb
Impdh2
Pcca
Acadsb
Acly
Acat1
Txnrd2
Ogdhl
Dhtkd1
Dlat
Gsr
Pdhx
vATPase-dependent acidification
Atp6v1f
Atp6v1e1
Atp5g1
Atp6v1e2
Atp6v1b1
Atp6v0b
Ppa1
Atp6v0a2
Atp6v1d
Atp6v0d1
Atp6v1a
Atp6v1g3
Atp6v0d2
Atp6v1c1
Atp6v1b2
Atp6v0a4
Atp6v0a1
Atp6ap1
Atp6v1h
Atp6ap2
Vesicle transport
Vti1b
Stx1b
Stx7
Sec22a
Stx8
Cplx1
Nsf
Stx17
Stx1a
Stx19
Gosr2
Cplx2
Snap29
Vamp4
Stx12
Snap25
Napb
Vamp5
Snap23
Stx4a
Napa
Sec22c
Syt1
Vamp8
Stxbp1
Stx2
Stx3
Rab4a
NADPH oxidase-dep. ROS production
Ncf2
Ncf1
Decr1
Cyba
Nox1
Ncf4
Duox1
Vcam1
Endocytosis
Ehd4
Ehd1
Rab5a
Eea1
Lamp2
Rab7
Lamp1
Cd63
Signalling
Pla2g6
Pla2g10
Pla2g16
Ptgs2
Egfr
Mapk14
Pla2g4a
Mapk12
Mapk1
Pla2g5
Mapk3
Erbb3
Kras
Grb2
Ptpn23
Mdk
Mapk7
Rhoa
Immune response
C1qb
Mpeg1
Adgre1
Cd68
Tyrobp
Lyz2
Csf1r
Iron homeostasis
Isca1
Nfs1
Lyrm4
Fdx1
Slc25a28
Hscb
Iscu
Fxn
Isca2
Scly
Host regulatory module
-7
0
7
log2FC

Table 5: List of most enriched GO and KEGG pathway terms in the regulatory module

Biological Process			Molecular Function		
GO BP ID	**Term**	***p*-value**	**GO MF ID**	**Term**	***p*-value**
GO:0006810	transport	2.04E-35	GO:0015078	hydrogen ion transmembrane transporter activity	9.00E-44
GO:0015992	proton transport	1.08E-33	GO:0003954	NADH dehydrogenase activity	1.02E-40
GO:0051234	establishment of localization	1.30E-33	GO:0008137	NADH dehydrogenase (ubiquinone) activity	4.29E-39
GO:0006818	hydrogen transport	1.83E-33	GO:0050136	NADH dehydrogenase (quinone) activity	4.29E-39
GO:0006906	vesicle fusion	7.51E-33	GO:0005484	SNAP receptor activity	4.81E-37
GO:1902600	hydrogen ion transmembrane transport	1.16E-32	GO:0000149	SNARE binding	9.08E-35
GO:0055114	oxidation-reduction process	5.30E-32	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	5.52E-34
GO:0090174	organelle membrane fusion	6.72E-31	GO:0016651	oxidoreductase activity, acting on NAD(P)H	6.48E-34
GO:0048284	organelle fusion	2.30E-28	GO:0016491	oxidoreductase activity	4.23E-25
GO:0044801	single-organism membrane fusion	1.00E-27	GO:0036442	hydrogen-exporting ATPase activity	5.95E-24

Cellular Compartment			KEGG Pathway		
GO CC ID	**Term**	***p*-value**	**KEGG ID**	**Term**	***p*-value**
GO:0070469	respiratory chain	1.21E-78	190	oxidative phosphorylation	1.51E-119
GO:0098800	inner mitochondrial membrane protein complex	1.56E-71	1100	metabolic pathways	2.14E-37
GO:0005739	mitochondrion	1.77E-70	4130	SNARE interactions in vesicular transport	7.91E-28
GO:0098803	respiratory chain complex	8.28E-67	4145	phagosome	1.36E-15
GO:0005746	mitochondrial respiratory chain	2.31E-65	640	propanoate metabolism	4.91E-08
GO:1990204	oxidoreductase complex	1.62E-63	280	valine, leucine and isoleucine degradation	6.37E-06
GO:0098798	mitochondrial protein complex	5.11E-63	4142	lysosome	1.67E-05
GO:0044455	mitochondrial membrane part	2.40E-60	630	glyoxylate and dicarboxylate metabolism	2.16E-05
GO:0098796	membrane protein complex	3.27E-59	4912	GnRH signaling pathway	9.84E-05
GO:0044429	mitochondrial part	1.23E-58	4370	VEGF signaling pathway	2.15E-04

Figure 13: Host regulatory module. 302 phagolysosomal proteins are compiled to the regulatory module and connected *via* 3448 edges representing ascribed interactions. 178 proteins are part of the detected phagolysosomal proteome, 109 proteins are classified as differentially abundant. The scale from blue to yellow indicates the log-fold change of regulated proteins. Light blue boxes represent detected, but not regulated proteins and white boxes are predicted proteins. Size of the boxes encodes the differential abundances. Large boxes are differentially regulated small boxes are not. 17 submodules represent proteins with a close functional or structural similarity. 9 of the most interesting submodules are highlighted and enlarged.

Several proteins phagolysosomes with an annotation to apoptosis or regulation of apoptosis are identified with a higher abundance in the *pksP* mutant conidia-containing. Volling *et al.* described a phosphatidylinositol-3 kinase (PI3K)/ serine/threonine kinase Akt-mediated inhibition of apoptosis in macrophages that had engulfed *A. fumigatus* wild-type conidia (Volling *et al.*, 2011). Of this pathway, a B cell CLL/Lymphoma 2 (Bcl-2) like protein with anti-apoptotic functions is detected as enriched in wild-type conidia-containing phagolysosomes. The pro-apoptotic Bcl-2 antagonist/killer 1 (Bak1) in contrast is more abundant in *pksP* mutant conidia-containing phagolysosomes. Table 6 lists further candidates that are measured by LC-MS/MS and reported to have a role in the apoptotic process.

Table 6: Apoptosis regulators. Proteins with known functions in the process or regulation of apoptosis are identified with a GO term enrichment analysis in the group of differentially abundant proteins. The *pksP*/wt ratio shows the direction of regulation. > 2 enriched in *pksP* mutant conidia-containing phagolysosomes; < 0.5 enriched in wt conidia-containing phagolysosomes

Pro-apoptotic			**Anti-apoptotic**		
Protein	**Description**	**Fold-change *pksP*/wt**	**Protein**	**Description**	**Fold-change *pksP*/wt**
Aifm2	Apoptosis-inducing factor 2	2.18	Ralb	Ras-related protein Ral-B	4.24
Praf2	PRA family protein 2	4.96	IL9	Interleukin-9	2.31
Bak1	Bcl2-antagonist/killer 1	4.68	Pex11b	Peroxisomal membrane protein	2.74
HtrA2	HtrA serine peptidase 2	2.19	Spp1	Osteopontin	2.04
Slk	STE20-like kinase	10.40	Arl6ip1	ADP-ribosylation factor-like 6 interacting protein	3.20
Fam162a	Family with sequence similarity 162 member A	2.03	Emc4	ER membrane protein complex subunit 4	2.80
Hip1	Huntingtin interacting protein 1	2.83	C5ar1	Complement component 5a receptor 1	3.48
Stk4	Serine/threonine kinase 4	17.73	Gsn	Gelosin	2.89
ArhGEF7	Rho Guanine Nucleotide Exchange Factor 7	2.00	Pak2	p21.activated kinase	2.19
			Sqstm1	Sequestosome	2.45
			Mif	Macrophage migration inhibition factor	3.72
			Ywhaq	14-3-3 protein theta	2.15
			Bcl2l13	Bcl-2-like protein 13	0.3
Role in apoptotic processes					
Rad21	RAD21 cohesin complex component				2.27
Dnase2	Deoxyribonuclease 2a				2.25
Ghitm	Growth hormone inducible transmembrane protein				2.95

4.5. Reduced assembly of vATPase on wild-type conidia-containing phagolysosomes

To validate the proteomic data, additional experiments are performed. ‘vATPase-driven phagolysosomal acidification’ is highly represented in the host regulatory module. As previously published, vATPase-dependent acidification of the phagolysosome is inhibited by DHN-melanin containing wild-type conidia (Thywissen *et al.*, 2011). vATPase activity is regulated by the assembly and disassembly of the vATPase V_1 and V_0 complex (Lafourcade *et al.*, 2008). To confirm the strong hint that *A. fumigatus* blocks assembly of the complex, the localization of vATPase V_1 subunit is assessed after infection of macrophages with wild-type or *pksP* mutant conidia. Cells are lysed after two hours of co-incubation and membrane *versus* cytosolic fraction analyzed for the abundance of V_1 vATPase domain by western blotting. In macrophages incubated with wild-type conidia a larger proportion of V_1B vATPase subunit localizes to the cytosol (64 %), whereas macrophages that have phagocytosed *pksP* mutant conidia have a smaller proportion of cytosolic V_1 subunit (50 %) (Figure 14A-B). This suggests that wild-type conidia inhibit the assembly of a functional vATPase complex or cause the disassembly of vATPase.

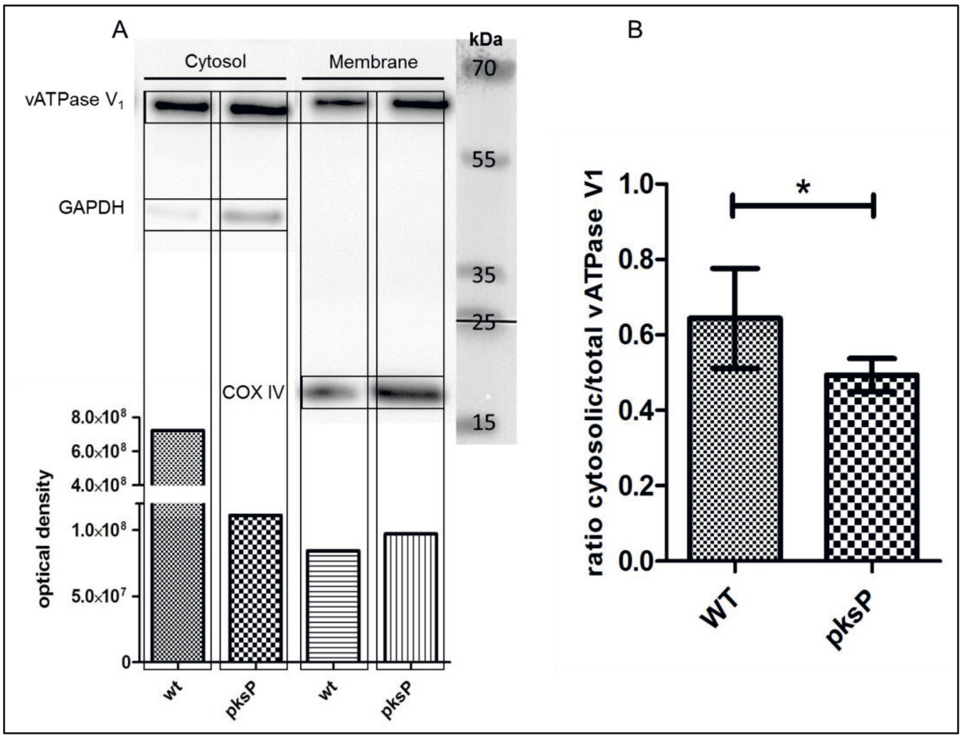

Figure 14 Wild-type conidia-containing phagolysosomes have a higher ratio of disassembled vATPase. After 2 h of incubation of macrophages with wild-type or *pksP* mutant conidia, the cell lysates are fractionated into cytosolic and membrane part. For each fraction an immunoblot detection for the cytosolic vATPase subunit V_1B_2 is performed. (A) Western blotting of V_1 in cytosolic and membrane fraction with intensity plots. (B) Amount of cytosolic V_1B_2 to the total amount (cytosolic and membrane-associated) amount of V_1. Columns represent mean values of three replicates with SD, * $p < 0.05$

4.6. Reduced formation of lipid rafts on wild-type conidia-containing phagolysosomes

vATPase assembly as well as recruitment of actin and subunits of heteromeric G-proteins were reported to correlate with the generation of lipid rafts on the phagolysosomal membrane (Dermine *et al.*, 2001). Further studies describe a contribution of lipid rafts to the functional organization of the phagolysosomal membrane during maturation (Garin *et al.*, 2001, Goyette *et al.*, 2012). Previous work of our lab already established a link between *A. fumigatus* intracellular survival strategy and the disturbance of lipid raft formation (Thywissen, 2012). The proteome data indicates a differential assembly of vATPase complex in phagolysosomes containing *pksP* mutant or wild-type conidia and suggests that lipid raft formation on wild-type conidia-containing phagolysosomal membranes is disrupted. To confirm the involvement of membrane rafts in the conidia-phagolysosome interaction, macrophages are stained for lipid raft markers after co-incubation with *A. fumigatus* wild-type and *pksP* mutant conidia. The typical raft components ganglioside GM1 and cholesterol are imaged with CTB (Blank *et al.*, 2007) and filipin III (Mukherjee *et al.*, 1998), respectively. Furthermore, the lipophilicity of the membrane is visualized with the lipophilic dye DiD (Figure 15A and D). 26 % and 67 % of wild-type and *pksP* conidia-containing phagolysosomes, respectively, are positive for DiD staining. 56 % and 52 % of the wild-type conidia-containing phagolysosomes show a clear GM1 and filipin signal, respectively, opposed to 88 % and 75 % of the *pksP* conidia-containing phagolysosomes (Figure 15B-C and E-F). Altogether, the fluorescence staining experiments show that wild-type conidia-containing phagolysosomes are less lipophilic and less frequently positive for lipid raft markers.

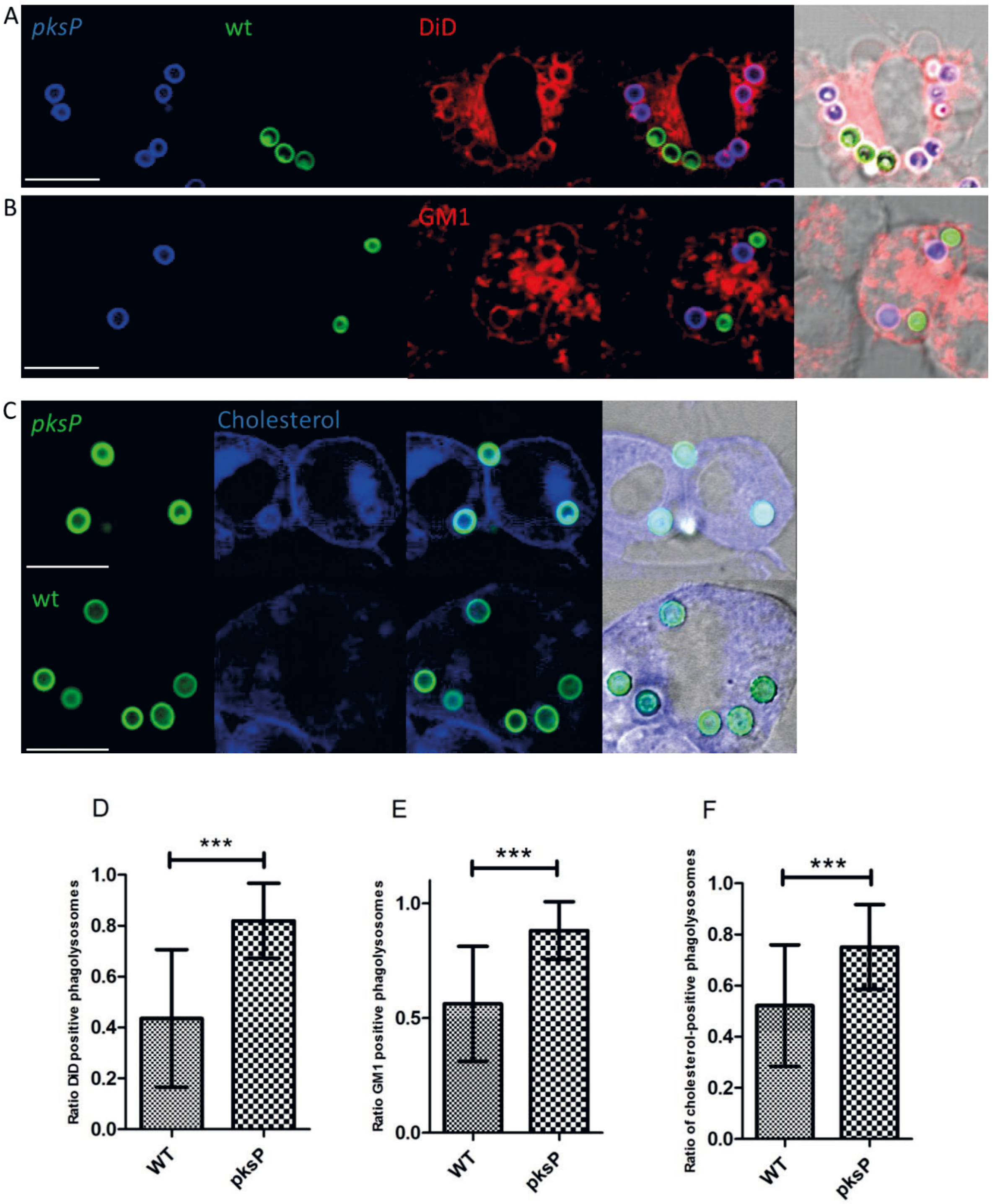

Figure 15: Membrane lipid staining of conidia-containing phagolysosomes. Images are representative of macrophages that are incubated with wild-type or *pksP* mutant conidia for 2 h and analyzed microscopically for localization of membrane lipid-specific dyes in the conidia-containing phagolysosome. (A and B) *pksP* mutant conidia (blue) are labeled with CFW and wild-type conidia (green) with FITC. (A) Lipid membranes (red) are stained with DiD, lipophilic dye or (B) GM1, lipid raft specific ganglioside (red), is stained with a CTB-Alexa647 conjugate. (C) Conidia of wild-type and *pksP* mutant are labeled with FITC (green) and cholesterol (blue) is stained with filipin III. Arrows indicate phagolysosomes with a positive fluorescence signal. Scale bars represent 10 μm (D-F). Diagrams show the ratio of phagolysosomes positive for lipid membrane dye DiD, lipid raft markers GM1 and cholesterol. Columns represent mean values with SD, *** $p < 0.0001$ (D and E) *** $p < 0.001$ (F).

4.7. Differentially abundant proteins

4.7.1. Evaluation of differentially abundant proteins by western blot

A selected set of proteins are tested for their abundance in wild-type or *pksP*-mutant conidia-containing phagolysosome by means of immunoblotting. Thus, a sample of the purified phagolysosomal protein extract is separated by SDS-PAGE, blotted and visualized with specific antibodies. Spots are normalized to the total protein load using the Smart Protein Layer kit.

The differential abundance of cathepsin Z, Lamp1, MAPK p44 and p42 (levels of total protein irrespective of phosphorylation status) and NADH dehydrogenase 1 beta subcomplex 9 (Ndufb9) is assessed by western blotting. Cathepsin Z, Lamp1 and Ndufb9 are more abundant in the *pksP* conidia-containing phagolysosome as indicated by the LC-MS/MS detection. However, opposed to the LC-MS data, MAPK p44 and p42 show an enrichment in the *pksP* sample (Figure 16).

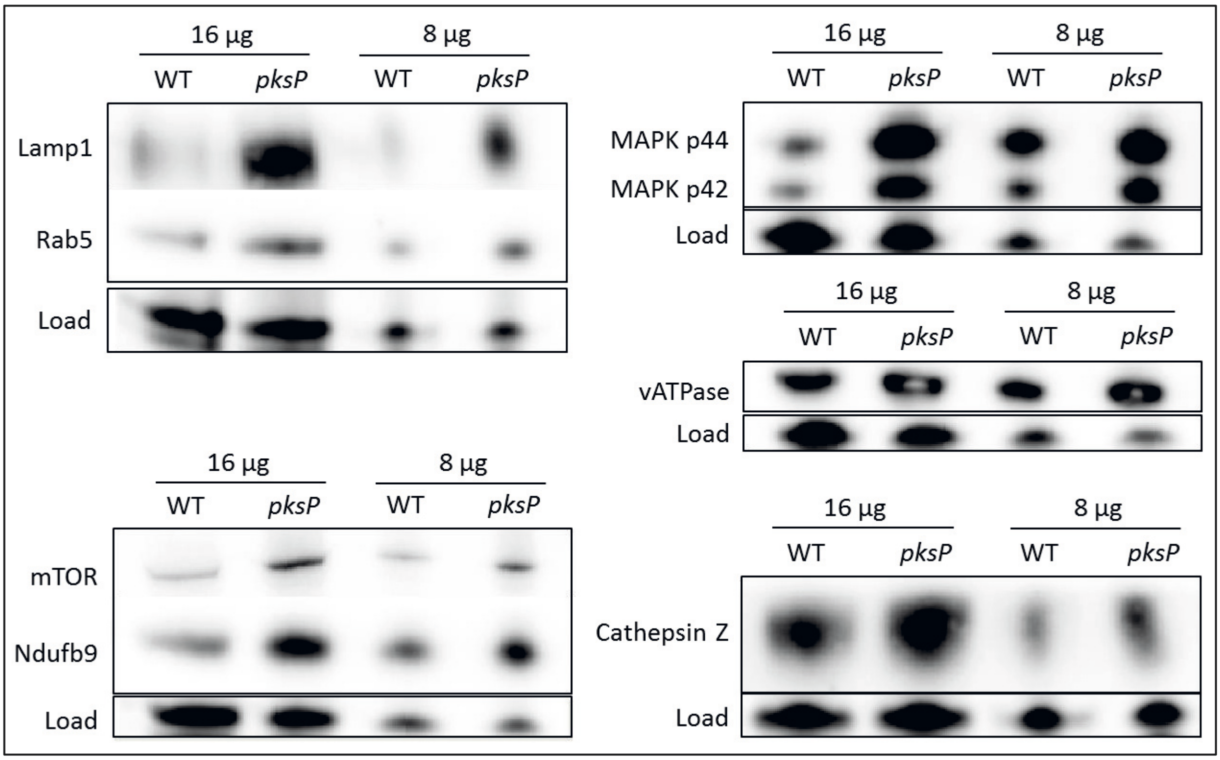

Figure 16: Western blots of regulated phagolysosomal proteins. 16 or 8 µg of protein extract from purified wild-type or *pksP* mutant conidia-containing phagolysosomes are loaded onto a gel and separated by SDS-PAGE. The indicated candidate proteins from the proteome data are immunoblotted and the optical density of the spots normalized to an internal loading control supplied from the Smart Protein Layer kit for a comparison.

4.7.2. Immunofluorescence data supports a differential recruitment of vesicle-associated membrane protein 8 (Vamp8) to wild-type *versus pksP* conidia-containing phagolysosomes

The recruitment of Vamp8 to conidia-containing phagolysosomes is assessed by immunofluorescence. Vamp8 localizes more often to *pksP* conidia-containing phagolysosomes (Figure 17).

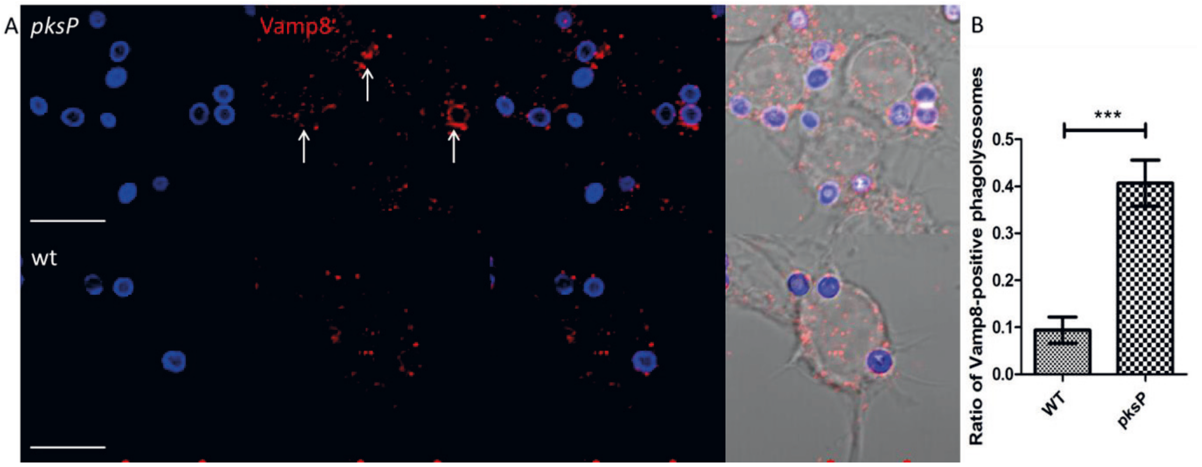

Figure 17: Vamp8 recruitment to conidia-containing phagolysosomes. (A) Images are representative of Vamp8 immunofluorescence staining of macrophages 2 h after infection with wild-type or *pksP* mutant conidia at MOI = 2. Arrows indicate Vamp8-positive phagolysosomes. Scale bars refer to 10 µm. (B) Columns represent the mean values of the proportion of Vamp8-positive phagolysosomes with SD. *** $p < 0.0001$

4.7.3. Regulation of molecular target of rapamycin (mTOR) signaling pathway

Studies showed that mTOR induces a metabolic reprogramming as well as autophagy in response to starvation (Jung *et al.*, 2010, Covarrubias *et al.*, 2015). Thus, the involvement of mTOR signaling in the differential progression of wild-type and *pksP* conidia-containing macrophage phagolysosomes is tested. LC-MS/MS analysis does not detect mTOR, but some of its regulators, such as late endosomal/lysosomal adaptor, MAPK and mTOR activator (Lamtor 1 and 2) are enriched in *pksP* mutant conidia-containing phagolysosomes.

Western blot analysis detects a higher abundance of mTOR in *pksP* conidia-containing phagolysosomes (Figure 16) and further supports the hypothesis that mTOR signaling is involved in the programming of macrophage activity depending on the presence of melanization of conidia.

5. Discussion

The ability to adapt to various environments is a survival benefit of the ubiquitous saprophyte *Aspergillus fumigatus* (Dagenais and Keller, 2009). Versatile mechanisms for stress tolerance and resistance are a prerequisite to enable growth and germination, even under adverse conditions. Among others, the equipment of conidia with layers of hydrophobic proteins and DHN-melanin is an insurance for *A. fumigatus* conidia to survive in hostile environments and germinate when the conditions turn in favor of fungal growth (Heinekamp *et al.*, 2012). The layers render conidia immunologically inert and permit their survival inside the phagolysosome of lung alveolar macrophages. The macrophages, thus, provide a protective niche for conidia from further host immune reactions, especially from neutrophilic granulocytes that are potent killers of conidia and hyphae.

In this study, the employment of imaging techniques, a protocol to purify conidia-containing phagolysosomes and proteomics in combination with bioinformatics provide a potent toolkit for the generation of hypotheses of the interaction of conidia with macrophages.

Previous studies showed that pigmentation of conidia with DHN-melanin interferes with a range of innate immune cell functions. It slows down recognition and phagocytosis, induces lower ROS production, prevents host cell apoptosis and inhibits the phagolysosomal acidification (Jahn *et al.*, 1997, Langfelder *et al.*, 1998, Volling *et al.*, 2011).

5.1. Insights from electron microscopy

Electron microscopy images show a tight wrapping of the phagolysosomal membrane around the wild-type conidium suggesting a direct physical contact. Furthermore, the number of vesicles of the endocytic compartment and fusion partners in the environment of the wild-type conidia-containing phagolysosome is reduced, although it was reported that wild-type conidia-containing phagolysosomes still fuse with lysosomal vesicles (Thywissen *et al.*, 2011). This finding was deduced by measuring the delivery of fluorescent dextran beads to the conidia-containing phagolysosome. Jahn *et al.* monitored the co-localization of conidia with Lamp1 and cathepsin D and found a reduced recruitment of those phagolysosomal markers to wild-type conidia-containing phagolysosomes (Jahn *et al.*, 2002). Taking the previous studies and electron microscopy findings into account, one can hypothesize that the delivery of typical markers to promote the maturation and fungicidal activity of wild-type conidia-containing phagolysosomes is blocked, while fusions still take place to a reduced extend.

Besides allowing the observations of these fusion characteristics, the electron micrographs show that the wild-type cell wall is subsequently disintegrated and packed into vesicles that are budding off the phagolysosomes already at 30 min after incubation. The fission events are accompanied by a reduction in cell wall thickness by 25 % within 2.5 hours. The degradation mechanism of fungal DHN-melanin remains unknown and is the subject of ongoing research. Most certainly, potent oxidative enzymes, such as P450 monoxygenases are required to accomplish the hydroxylation of the insoluble polymer.

5.2. Purification of conidia-containing phagolysosomes

The phagolysosome represents the site of immediate contact between conidium and host. The maturation process is regulated by the recruitment of an array of proteins that orchestrate the fungal killing (Desjardins, 1995, Haas, 2007). To uncover how *A. fumigatus* inhibits the intracellular degradation, the phagolysosomal proteome is studied and compared to the proteome of *pksP* mutant conidia-containing phagolysosomes that possess a fungicidal capacity.

Several protocols currently exist for the purification of cargo-containing phagolysosomes. Latex beads-containing phagolysosomes have sedimentation characteristics that allow for a separation of phagolysosomes from the cell debris by ultra-centrifugation on a sucrose gradient (Desjardins *et al.*, 1994). Hoffmann *et al.* (Hoffmann *et al.*, 2012) took advantage of the *Legionella* effector protein SidC that selectively anchors to the phagolysosomal membrane in order to purify *Legionella*-containing vacuoles (LCVs). SidC was targeted with an affinity-purified antibody and a secondary antibody coupled to magnetic beads for magnetic separation and enrichment of LCVs. Steinhäuser *et al.* (Steinhauser *et al.*, 2013) used magnetic labeling of *Mycobacterium tuberculosis* to pull out bacteria-containing phagolysosomes from the whole cell lysate. However, existing protocols are not applicable to purify *A. fumigatus* conidia-containing phagolysosomes. First, conidia-containing phagolysosomes display different sedimentation properties and secondly, according to current knowledge, they do not express a specific marker comparable to SidC on LCVs. Lastly, magnetic labeling of wild-type conidia is far less efficient than labeling of *pksP* mutant conidia, because reactive groups of the wild-type conidial cell wall are apparently shielded by the rodlet and melanin layer.

To accomplish the challenging endeavor of purifying *A. fumigatus* conidia-containing phagolysosomes the protocol by Steinhäuser *et al.* (Steinhauser *et al.*, 2013) is adapted. This includes the magnetic labeling of conidia by attaching streptavidin-tagged magnetic beads to the biotinylated conidial surface. The concentration of the linker is optimized to enable an even labeling of wild-type and *pksP* mutant conidia. The magnetic labeling has no effect on macrophage functions, such as phagocytosis and phagolysosomal acidification. Furthermore, the cell lysis is optimized to achieve a thorough lysis of the plasma membrane, but at the same time maintain phagolysosomal integrity. Then, conditions for an efficient separation of magnetic from non-magnetic fraction are tested and a process established to extract and concentrate phagolysosomal proteins.

Last, a label-free quantification is compared to a label-based quantification method, considering the total number of identified proteins and the sensitivity to detect differential abundant proteins. Label-based quantification typically delivers the more accurate results (Megger *et al.*, 2014), but is less sensitive and identifies few regulated proteins. Thus, further discussions are based on the dataset generated with the label-free quantification. Strict thresholds and criteria are applied to overcome measurement variances and to identify regulated proteins.

5.3. Quality control of the phagolysosomal proteome

LC-MS/MS identified the dual phagolysosomal proteome of murine host and fungal pathogen. The dataset was first controlled for its quality. The GO terms ‘lysosome’ and ‘lysosomal membrane’ are more highly enriched in the dataset of purified phagolysosomes compared to the whole cell proteome dataset. This analysis confirms that the protocol indeed allowed for concentration of the phagolysosomal fraction. However, the terms ‘mitochondrion’ and ‘ribosome’ are also higher enriched in the purified phagolysosome dataset, indicating that those compartments are not efficiently separated from the phagolysosome or play a specific role in the phagolysosomal maturation. *E.g.* it is possible that *de novo* synthesis of proteins contributes to the processing of phagosomes to phagolysosomes.

On one hand, it is likely that cellular organelles are trapped in the sticky actin mesh that surrounds the phagolysosome and thus, appear in the proteome dataset (Gilberti and Knecht, 2015). On the other hand, West *et al.* reported a specific function of mitochondria in the defense of intracellular pathogens. In this model, mitochondria are recruited to the phagolysosomes, where electrons that are transported along the respiratory chain complexes escape and contribute to the generation of ROS (West *et al.*, 2011). Also, extra-ribosomal functions of ribosomal proteins were investigated. They have been implicated in regulating RNA synthesis and ribosome biogenesis, nuclear stress response, regulation of apoptosis and cell cycle progression. However, there are no reports yet concerning direct anti-microbial functions of ribosomal proteins (Warner and McIntosh, 2009, Lu *et al.*, 2015).

The comparison between whole cell proteome and phagolysosomal proteome demonstrates that the datasets resemble each other to approximately 50 %. More importantly, the direction of regulation of proteins that are identified as differentially abundant proteins is partly opposite in whole cell and the purified fraction. Thus, at whole cell level, different proteins and processes are regulated and a purification of phagolysosomes is required to clearly identify phagolysosomal processes.

Several groups have already investigated the phagolysosomal protein composition in different experimental set-ups. The explicit phagolysosomal protein composition depends on many factors, such as (i) the use of cell line or primary cells (Guo *et al.*, 2015, Dill *et al.*, 2015), (ii) the engulfed particle *e.g.* latex beads, pathogenic bacteria (Lee *et al.*, 2010) or molecules that are exposed to the macrophages, such as pathogen-associated molecular patterns (PAMPs), opsonins or apoptotic cell markers (Dill *et al.*, 2015, Shui *et al.*, 2011). (iii) The activation status of the macrophage with additional cytokines, such as interferon gamma (IFNy) (Trost *et al.*, 2009) has to be considered as well as (iv) the fraction of the phagolysosome *e.g.* total membrane (Shui *et al.*, 2008) or parts of the membrane, such as detergent-resistant membrane (DRM) *versus* detergent-soluble membrane (DSM) parts (Goyette *et al.*, 2012). Finally, (v) the age of the phagolysosome (Goyette *et al.*, 2012, Rogers and Foster, 2007) needs to be taken into account.

The proteomes which were measured by the aforementioned studies, share many similarities to the proteome of *A. fumigatus pksP* mutant conidia-containing phagolysosomes. These similarities mainly refer to the presence of vATPase subunits, vesicle fusion and trafficking mediators, lysosomal markers and lytic enzymes as well as components of the immune response and antigen processing machinery. The highest overlap of phagolysosomal proteins detected in this work exists with studies carried out on the RAW264.7 cell line, the model system also applied here. Interestingly, the wild-type conidia-containing phagolysosomes display only few of the typical proteins and processes that are detected in other studies. Thus, wild-type *A. fumigatus* conidia do not seem to elicit a comparable activation as reported for macrophages that were challenged with latex beads, bacterial intracellular pathogens, such as *Mycobacteria* or mycobacterial PAMPs, opsonins, apoptotic cell markers or INFγ-stimulated macrophages.

5.4. Highly regulated proteins

To realize a comparison between protein abundances in the complex sets of wild-type and *pksP* mutant conidia-containing phagolysosomal proteome a data processing workflow is established that encompasses label-free quantification and normalization. Strict thresholds and selection criteria are applied to handle the biological variations and identify differentially abundant proteins.

Approximately 30 % of the total number of identified proteins fulfill the criteria and are classified as protein enriched in either wild-type or *pksP* mutant conidia-containing phagolysosomes depending on the log2-fold change.

Most abundant in *pksP* conidia-containing phagolysosomes are proteins annotated to the lysosomal compartment with functions in phagolysosomal acidification. The listed proteins suggest the presence of a fully matured phagolysosome with the capacity to kill intracellular pathogens. The abundance of stomatin, an established lipid raft marker that shares homologous domains with flotillin and prohibitin lipid rafts markers (Goyette *et al.*, 2012), indicates an involvement of lipid rafts in the phagolysosomal maturation process (Garin *et al.*, 2001).

In contrast, the wild-type conidia-containing phagolysosome does not show an enrichment of classical lysosomal markers or proteins indicative for phagolysosomal maturation. Thus, it is likely that the wild-type conidia-containing phagolysosome remains at an immature stage.

After highlighting murine proteins the following section focusses on fungal proteins found in the phagolysosomes. A range of typically intracellular fungal proteins is detected in the phagolysosome. The extracellular presence can be explained by a damage of the cell wall as a consequence of the acidic attack in the phagolysosome, mainly affecting *pksP* mutant conidia. But also wild-type conidia are prone to intracellular degradation, as shown by electron microscopy where parts of the outer cell wall are constricted in budding vesicles. It is conceivable that those proteins are actively released as a consequence of exposure to the immune system or physical stresses, such as oxidants that are generated in the phagolysosome. The *pksP* mutant conidia proteome in phagolysosomes contains many proteins connected to stress response. Among others, an aldehyde dehydrogenase and a transaldolase of the pentose phosphate pathway (PPP) are found that might represent an anti-oxidative response. The metabolism of glucose-6-phosphate *via* the PPP generates NADPH to reduce antioxidants, such as glutathione (Berg *et al.*, 2002, Sato *et al.*, 2009). Also, GTPases, which are usually intracellular proteins and mediators of endosomal trafficking, are present in the *pksP* mutant conidia phagolysosome, suggesting a damage of the conidium. The wild-type conidial proteome contains a spore-specific catalase with anti-oxidative function and the protein CcpA, which is highly exposed on conidia. Both have been related to virulence of *A. fumigatus* (Paehtz, 2015, Paris *et al.*, 2003b). However, in the context of a Bachelor thesis project in our department (Saskia Schmidt, 2016), a deletion mutant of *ccpA* was tested in phagocytosis, phagolysosomal acidification and killing assays with RAW264.7 macrophages. In none of these assays a significant difference to the behavior of wild-type conidia was observed (unpublished data).

Besides, the finding of a 14-3-3-protein indicates the presence of secreted vesicles. 14-3-3 proteins mediate all kinds of cellular processes, such as exocytosis and vesicle transport in *A. fumigatus* and are induced upon hypoxic stress (Teutschbein *et al.*, 2010, Kniemeyer *et al.*, 2011, Kraus *et al.*, 2002). Thus, this protein might contribute to immune evasion and survival of the conidium.

5.5. The regulatory module

A regulatory module is compiled that displays a protein-protein interaction network, which is significantly enriched with differentially regulated proteins. Within the regulatory module are proteins with a higher degree of interactions, representing a functional group here called a 'submodule' (Szklarczyk *et al.*, 2015). 17 submodules are defined in the host regulatory module. The enriched and annotated gene ontologies within each submodule allow for a discussion of processes that are modified in the wild-type conidia-containing phagolysosome in comparison to the *pksP* mutant conidia-containing phagolysosome. A selection of infection-related processes is discussed in the following and illustrated in Figure 18.

5.5.1. Generation of energy and precursors

Components of the oxidative phosphorylation (OXPHOS) system, which are typically localized to mitochondria, are enriched in the *pksP* conidia-containing phagolysosomal sample. The occurrence of non-phagolysosomal components might represent a specific function of those proteins in phagolysosomal maturation or can be due to the experimental conditions. In their proteomic study of phagolysosomes, Goyette *et al.* (Goyette *et al.*, 2012) reported the occurrence of proteins typically present in non-phagolysosomal cell compartments, such as the nucleus, ribosome or mitochondrion. Their frequency was especially high in cells with high autophagocytic activity. This can be explained by the dynamic interaction and exchange between these two organelles (Sanjuan *et al.*, 2007, Shui *et al.*, 2008).

After activation, macrophages undergo a metabolic reprogramming depending on the engulfed particle and extracellular stimuli, such as cytokines (Rodriguez-Prados *et al.*, 2010). All four complexes of the electron transport chain are enriched in the *pksP* mutant conidia-containing phagolysosomes, pointing to the fact that energy is generated *via* oxidative phosphorylation in those macrophages. The lack of the OXPHOS components in the wild-type conidia sample indicates that these cells obtain energy from alternative processes. Furthermore, an activation of carboxylic acid metabolizing pathways, such as propanoate metabolism, degradation of valine, leucine and isoleucine as well as fatty acid metabolism is prominent after phagocytosis of *pksP* mutant conidia, but seemingly reduced upon contact with wild-type conidia indicating the higher metabolic activity and hence, activation of macrophages challenged with *pksP* mutant conidia (Figure 18).

Wild-type conidia-containing phagolysosomes are enriched in ATP citrate lyase (Acly), which suggests the induction of fatty acid, lipid and cholesterol synthesis from metabolites generated during glycolysis. It has also been implicated in linking metabolism to immune response and histone acetylation (Wellen *et al.*, 2009, Infantino *et al.*, 2013). The data provides a hint that glycolysis might be the prominent energy generating pathway in macrophages stimulated with wild-type conidia. However, further experiments are required to test this hypothesis. Thus, engulfment of the *pksP* conidia results in activation of the OXPHOS pathway in macrophages to generate energy, whereas no apparent induction of a certain energy-generating metabolic pathway is observed in cells challenged with wild-type conidia.

5.5.2. Iron homeostasis

Iron availability is crucial for *A. fumigatus* germination, sexual and asexual propagation, antioxidative defense and growth (Haas, 2012). All eukaryotes depend on iron as activator and coordinator of oxygen for redox chemistry to maintain redox homeostasis in the cell (Kaplan and Kaplan, 2009). Enzymes involved in the biosynthesis of iron-sulfur clusters are highly abundant in *pksP* conidia-containing phagolysosomes but absent in wild-type conidia-containing phagolysosomes. This indicates the interference of *A. fumigatus* wild-type conidia with yet another host defense mechanism, the storage of iron in iron-sulfur clusters of proteins, where it is inaccessible for the pathogen.

5.5.3. vATPase-dependent acidification

Acidification of the phagolysosome is prerequisite for the degradation of phagocytosed material and is driven by the vATPase, the vacuolar ATP-dependent proton pump. Activity of the enzyme complex is regulated *via* assembly and disassembly of the membrane bound V_0 and cytosolic V_1 domain (Lafourcade *et al.*, 2008). A previous study of our laboratory showed that vATPase activity is the major driving force for the acidification of *A. fumigatus* conidia-containing phagolysosomes (Thywissen *et al.*, 2011). The proteomic data obtained here confirms a reduced abundance of V_1 subunits in the wild-type conidia-containing phagolysosome. In western blot experiments, the cytosolic V_1 subunit is more readily detected in the cytosolic fraction than in the membrane-associated fraction. This finding suggests that wild-type conidia not only reduce the recruitment of vATPase components to the phagolysosome, also they either inhibit the complex assembly to a functional proton pump or promote complex disassembly (Figure 18).

5.5.4. Lysosome-endosomal trafficking

Proteins of the SNARE, SNAP and syntaxin family, which mediate intracellular trafficking, docking and fusion processes, are mainly down-regulated in macrophages infected with wild-type conidia. Furthermore, the small GTPase Rab5 and its effector early endosomal antigen 1 (EEA1) show a differential regulation. Together these proteins mediate homotypic fusion of the early phagosome with early endosomes and are regarded as markers for an early stage of phagolysosomal maturation. The conversion of Rab5 to Rab7 on a phagosome promotes the progression from an early to a late maturation step. EEA1 is removed during this procession (Rink *et al.*, 2005). Rab5 has a low abundance in wild-type conidia-containing phagolysosomes compared to the *pksP* mutant conidia-containing phagolysosome that is confirmed by western blotting. Likewise, Eps15 homology (EH)-domain-containing proteins, which co-localize with Rab5 and control endocytic fusions, are less abundant in wild-type conidia-containing phagolysosomes, indicating that those phagolysosomes are less well equipped with fusion-mediators (Figure 18). Surprisingly, EEA1 has a high abundance in wild-type conidia-containing phagolysosomes, suggesting an arrest of the maturation process at an early stage and a Rab5-independent recruitment. Interference with endosomal trafficking and fusions by targeting small Rab GTPases has been reported for many intracellular pathogens, such as *Candida albicans* (Okai *et al.*, 2015), *C. glabrata* (Seider *et al.*, 2011), *Mycobacterium tuberculosis* (Via *et al.*, 1997), *Coxiella burnetii* (Ghigo *et al.*, 2002), *Helicobacter pylori* (Molinari *et al.*, 1997), *Salmonella enterica* (Smith *et al.*, 2007), *Chlamydia* species (Cortes *et al.*, 2007) and others (also reviewed in (Brumell and Scidmore, 2007)).

5.5.5. Intracellular signaling, induction of autophagy and apoptosis

mTOR signaling plays a major role in inducing metabolic reprogramming and autophagy under starvation conditions. Because the energy and precursor generating metabolic pathways are found to be differentially regulated, it seemed likely that the mTOR signaling axis is affected after ingestion of wild-type conidia. The proteomic data indicates a reduction in components of the Akt-mTOR signaling pathway in the wild-type conidia-containing phagolysosomes. The affected proteins are the mTOR regulators Lamtor1 and 2, RragC, a Ras-related GTP-binding protein that localizes to the mTOR complex, Slc38a7, required for mTOR transport to lysosomes and downstream mTOR effectors, such as cyclin D1 and eukaryotic initiation factor Eif4f. Western blotting confirms the differential abundance of mTOR, although LC-MS/MS does not detect the protein. This might be due to experimental conditions, such as the detection limit, ionization pattern or extraction procedure. However, the enrichment of mTOR signaling components on *pksP* conidia-containing phagolysosomes strongly indicates the involvement of mTOR in phagolysosomal maturation (Figure 18).

The contribution of autophagy to the degradation of pathogens and recycling of nutrients has been proposed by Kyrmizi *et al.* (Kyrmizi *et al.*, 2013). mTOR is inactivated downstream of insulin or insulin-like growth factor receptor or TLR signaling under nutrient starvation conditions (Kim, 2009). The inactivation of mTOR leads to the biogenesis of lysosomes, constriction of vacuoles from the phagolysosomes, as well as the induction of autophagy to redistribute degraded phagolysosomal cargo to the endosomal compartment (Puertollano, 2014, Krajcovic *et al.*, 2013, Jung *et al.*, 2010). On top of that, mTOR has been implicated in governing the metabolic reprogramming of activated macrophages to meet the high energy demands of the stimulated cells (Byles *et al.*, 2013) and in the generation of an innate immunological memory (Cheng *et al.*, 2014).

Another prominent signaling axis, the mitogen-activated protein kinase (MAPK) pathway, is differentially regulated in macrophages after ingestion of wild-type conidia (Figure 18). The MAP kinases or extracellular signal-regulated kinases (ERKs) mediate signaling downstream of TLR, Fc receptors and other phagocytic receptors (Lim *et al.*, 2014), initiate the formation of an autophagosome (Matsuzawa *et al.*, 2012) and the production of pro-inflammatory cytokines (Dubourdeau *et al.*, 2006). Chai *et al.* showed that pigmentation of conidia with DHN-melanin leads to a significantly reduced production of pro-inflammatory cytokines TNFα, IL-6, but also of the immunomodulatory cytokine IL-10 and that this induction was downstream of Dectin-1, TLR4 and mannose receptor signaling (Chai *et al.*, 2010). Here, the MAPK pathway is classified as down-regulated in wild-type conidia-containing phagolysosomes. The western blot control experiment demonstrate the opposite direction of regulation. The discrepancy between proteomic and western blot results emphasizes that proteomic studies deliver an initial characterization and that validation by further experimental techniques is required in any case. With the help of proteomics, a regulation of the MAKP pathway is tracked. The correct direction of regulation is validated by subsequent immunoblotting.

Both mTOR/Akt and MAPK signaling pathways result in the induction of autophagy (Jung *et al.*, 2010, Zhou *et al.*, 2015). By targeting the autophagy-activating pathways, the ingested wild-type conidia interfere with the generation of an autophagosome. In line with this hypothesis, Vamp8 and Vti1b, components of the autophagosomal SNARE complex, are reduced in wild-type conidia-containing phagolysosomes (Diao *et al.*, 2015). Also, Snap29 and Rubicon (Run domain Beclin-1-interacting and cysteine-rich domain-containing protein) (Zhong *et al.*, 2009) show a down-regulation in wild-type conidia-containing phagolysosomes, indicating a role of autophagy in the clearance of *A. fumigatus* conidia. Interestingly, Rubicon has recently been identified as the central switch from autophagy to Microtubule-Associated Protein 1 Light Chain 3 (LC3)-associated phagocytosis (LAP), an Atg5-dependent autophagy mechanism, where the LC3BI protein binds a phosphatidylethanolamine (PE) to form the active LC3BII protein that binds to phagolysosomes (Boyle and Randow, 2015, Martinez *et al.*, 2015). Chamilos *et al.* (Akoumianaki *et al.*, 2016, Chamilos *et al.*, 2016) demonstrated that DHN-melanin of *A. fumigatus* conidia blocks LAP activation in macrophages.

Previous studies in our lab described the inhibition of apoptosis in macrophages after engulfment of pigmented wild-type *A. fumigatus* conidia. This inhibition was due to sustained signaling *via* PI3K/Akt (Volling *et al.*, 2011). Through this axis, the activity of pro-apoptotic proteins, such as Bax and Bak1 (Tsuruta *et al.*, 2002, Datta *et al.*, 1997) is inhibited and anti-apoptotic Bcl-2 family members promote the cell survival and growth (Volling *et al.*, 2011, Pugazhenthi *et al.*, 2000). The inhibition of apoptosis is a strategy shared by several other intracellular pathogens, such as *C. albicans* (Ibata-Ombetta *et al.*, 2003) and *Leishmania* (Ruhland *et al.*, 2007), to stay inside the macrophage for a prolonged time and hide from immune responses (Volling *et al.*, 2007, Volling *et al.*, 2011). Several proteins with pro- as well as anti-apoptotic functions are identified in the conidia-containing phagolysosomes. Interestingly, the pro-apoptotic regulator Bak1 has increased abundance in *pksP* mutant conidia-containing phagolysosomes and the anti-apoptotic Bcl2-like protein 13 is enriched in wild-type conidia-containing phagolysosomes, supporting the findings of previous studies. However, the list of further apoptosis regulators identified in *pksP* mutant-conidia-containing phagolysosomes contains proteins with pro- and anti-apoptotic functions. Their exact activity in the context of the interaction between *A. fumigatus* conidia and macrophages will require further experimental assessment. Nevertheless, the data indicates that wild-type conidia interfere with the regulation of apoptosis.

5.5.6. Immune response and phagolysosomal degradative capacity

Cathepsins, the lysosomal peptidases and enzymes that degrade polysaccharides and glycolipids are enriched in the proteome of *pksP* mutant conidia-containing phagolysosomes, indicating that the degradative capacity of wild-type conidia-containing phagolysosomes is reduced (Figure 18). In line with this finding is the reduction of the antigen processing and presentation machinery of those phagolysosomes. Phagolysosomes containing the wild-type conidia display lower levels of the macrophage activation marker CD68 or macrophage colony-stimulating factor 1 (CSFR1).

Production of reactive oxygen species (ROS) is an important defense mechanism against *A. fumigatus* infection. Different studies have shown a necessary requirement of ROS for efficient fungal clearance (Philippe *et al.*, 2003, Grimm *et al.*, 2013) or at least an immunomodulatory role of ROS in the context of an *A. fumigatus* infection (Cornish *et al.*, 2008). ROS are generated by the NADPH oxidase (NOX). The NOX complex consists of 5 subunits: the membrane-integral NOX2 and $p22^{phox}$ and the cytosolic $p40^{phox}$, $p47^{phox}$ and $p67^{phox}$ subunits. The exchange of GDP to GTP on the small GTPase Rac activates the assembly and activity of the NOX enzyme (Bedard and Krause, 2007). The data suggests a reduced induction of ROS production after ingestion of wild-type conidia, because one of the five NOX subunits, $p47^{phox}$ (Ncf1) is less abundant in wild-type conidia-containing phagolysosomes (Figure 18). Also, up-stream elements of the Rac GTP-binding protein family that regulates the NOX assembly, such as guanine nucleotide exchange factors (GEFs) ArhGEFs and Rac GTPase activating protein (RacGAP1), have low levels in the wild-type sample. In accordance, Langfelder *et al.* (Langfelder *et al.*, 1998) showed a ten-fold increase in ROS production of polymorphonuclear neutrophils (PMNs) that were challenged with *A. fumigatus pksP* mutant conidia compared to wild-type conidia. Besides its fungicidal activity, ROS has also been implicated in the induction of the autophagy machinery and apoptosis (Huang *et al.*, 2009, Carmody and Cotter, 2001, Jacobson, 1996, Chandra *et al.*, 2000).

5.5.7. Lipid membrane organization

A current hypothesis supposes that lipid rafts, dynamically formed membrane microdomains characterized by a high cholesterol content, sphingolipids as well as protein markers flotillin, prohibitin and stomatin, are a necessary platform for assembly of protein complexes with cellular functions, such as intracellular signaling. Lafourcade *et al.* (Lafourcade *et al.*, 2008) observed that vATPase membrane-bound subunits preferentially distribute to detergent-resistant membrane (DRM) fractions that are indicative of lipid rafts. The GO term ‘Membrane Raft’ is enriched in the regulatory module. Furthermore, fluorescence staining of membrane lipids shows that wild-type conidia-containing phagolysosomes are depleted in the lipid raft components GM1 ganglioside and cholesterol. The metabolism of carboxylic acids as precursor for the biosynthesis of membrane lipids are more abundant in the *pksP* conidia-containing phagolysosomes, suggesting that engulfment of wild-type conidia interferes with the biosynthesis of lipids and the formation of lipid rafts. The depletion of lipid rafts, in turn, inhibits recruitment and assembly of vATPase complex and the vATPase-dependent phagolysosomal acidification (Figure 18).

5.6. Two levels of interactions between fungal conidia and host

According to the observations presented here, two levels of interaction between *A. fumigatus* conidia and host are conceivable. The first is of chemical nature and depends on the chemical properties of DHN-melanin. The findings from electron microscopy indicates a direct, physical contact of conidium and host membrane in the phagolysosome. Considering the hydrophobicity of the hydrophobin layer (Paris *et al.*, 2003a), one can speculate the occurrence of hydrophobic interactions between conidium and membrane lipids that might disturb the accumulation of lipid components required for lipid rafts. Due to the negative charge of DHN-melanin (Nosanchuk and Casadevall, 2003), ionic interactions with lipids of the phagolysosomal membrane that potentially disrupt the organization of membrane domains, such as lipid rafts are possible. Additionally, DHN-melanin possesses the capacity to trap free electrons and quench radicals from ROS (Jacobson, 2000, Commoner *et al.*, 1954). ROS have not only been implicated in antifungal defense, they are also mediators of apoptotic signaling (Jacobson, 1996, Chandra *et al.*, 2000, Carmody and Cotter, 2001). Volling *et al.* hypothesized that quenching of ROS by conidial DHN-melanin inhibits apoptosis induction (Volling *et al.*, 2011). Also, protective effects against anti-fungal drugs and lytic enzymes have been reported in the case of pigmentation with L-3,4-dihydroxyphenylalanine (L-DOPA)-melanin of *Crypotococcus neoformans* (Wang and Casadevall, 1994, Doering *et al.*, 1999). Thus, it is imaginable that DHN-melanin of wild-type *A. fumigatus* conidia counteracts the generation of radicals and degradative activity of lytic enzymes in the phagolysosome.

The second is of biochemical nature considering protein-protein interactions. Several fungal proteins are detected in the phagolysosome that might potentially bind proteins on the host side. In particular, CcpA (Paehtz, 2015), connected to virulence and the 14-3-3 family protein (Teutschbein *et al.*, 2010, Vodisch *et al.*, 2011), involved in signaling, are both more abundant in wild-type conidia-containing phagolysosomes and are interesting candidates to study interactions with host proteins. A bioinformatics approach to predict protein interactions *e.g.* as described by Remmele *et al.* (Remmele *et al.*, 2015*)* will be helpful to identify further candidates involved in this host-pathogen interaction.

5.7. Limitations

All experiments are carried out *in vitro* with RAW264.7 cells, an Abelson murine leukemia virus-induced tumor cell line, which is well-established system for studying macrophage cell biology. However, they still exhibit significant biological differences to the *in vivo* environment (Berghaus *et al.*, 2010). As RAW 264.7 cells are a cancerous cell line, it is likely that phagocytic activity, kinetics of phagolysosomal maturation, antigen presentation capacity and the metabolic profile have already undergone a reprogramming. Gou *et al.* (Guo *et al.*, 2015) showed in a comparison of the phagolysosomal proteome of RAW264.7 cells and bone marrow derived macrophages (BMDMs) challenged with beads that there are significant differences in the protein composition concerning the expression of receptors and activation status. Also, they reported a faster phagocytosis and phagolysosomal maturation in BMDMs, which is in line with observations from this project. As RAW264.7 cells are of leukemic origin, they are highly proliferating cells and in agreement with that, the processes ‘mRNA processing, ‘RNA splicing’ and ‘translation’ were mostly enriched in conidia-containing phagolysosomes. Hence, a careful use of data acquired from experiments with RAW264.7 cell line is recommended and should possibly be validated in other cell lines or primary cells of murine as well as human origin.

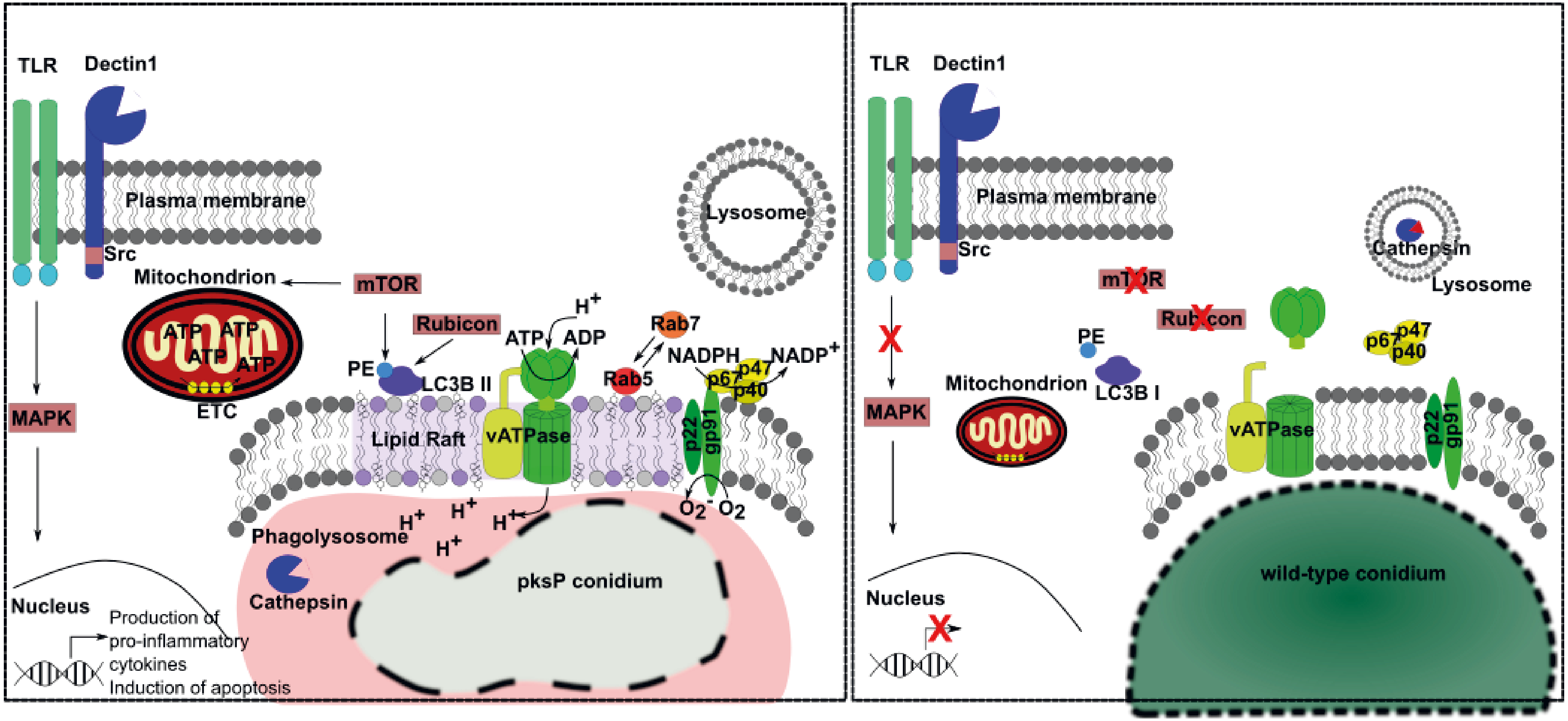

Figure 18: Model of the intracellular processing of *A. fumigatus* conidia. *Left:* Conidia of the *pksP* mutant strain are processed in a maturing phagosome. The formation of lipid rafts enables the recruitment and assembly of vATPase components to drive the acidification of the phagolysosome. Rab GTPases mediate the fusion with lysosomes that deliver hydrolytic enzymes *i.e.* cathepsins. They are activated by decreasing luminal pH of the phagolysosome. NADPH oxidase contributes to the elimination of conidia *via* production of ROS. MAPK signaling initiates a pro-inflammatory response and possibly apoptosis while mTOR signaling additionally induces autophagy. LC3BI binds phosphatidylethanolamine (PE) to form the active LC3BII that attaches to the phagolysosome during initiation of LAP. The activity of the mitochondrial electron transport chain generates energy for the immune response. *Right:* Wild-type conidia are tightly enclosed by the phagolysosomal membrane that is devoid of maturation markers. Enzyme complexes vATPase and NADPH oxidase are disassembled and inactive and intracellular signaling pathways to promote inflammation or autophagy induction are not apparent. The phagolysosome has a reduced ability to fuse with further lysosomes. Thus, it contains a neutral pH and components of the degradation machinery are neither delivered nor activated. This generates a niche for *A. fumigatus* to survive inside the macrophage, where it is protected from further immune responses at the same time.

Supplement

I. LC-MS/MS strategy for protein measurement

Before LC-MS/MS of all samples from all experiments were carried out, peptides were enriched and desalted based on a pre-concentration set-up using a nano trap column (Acclaim Pep Map 100, 2 cm x 75 µm, 3 µm) at a flow rate of 5 µL/min. After 4 min, a valve switch was performed to elute the pre-concentrated peptides onto the analytical column. For separation of peptides, Acclaim Pep Map RSLC nano columns with 15 cm (M#1), 50 cm (M#2) or 25 cm (M#3) length was used as stationary phase (Thermo Fisher Scientific). The binary mobile phase consisting of A) 0.1% (v/v) formic acid in H_2O and B) 0.1% (v/v) formic acid in 90/10 CAN/H_2O was applied for either 135 min (M#1), 360 min (M#2) or 210 min (M#3) gradient elution using the following gradients.

M#1: 0-5 min at 4% B, 10 min at 6.5% B, 15 min at 7.5% B, 20 min at 8% B, 25 min at 8.6% B, 30 min at 9.2% B, 35 min at 9.9% B, 40 min at 10.6% B, 45 min at 11.3% B, 50 min at 12.2% B, 55 min at 13.4% B, 60 min at 14.9% B, 65 min at 17% B, 70 min at 19.1% B, 75 min at 22.4% B, 80 min at 26% B, 88 min at 32% B, 94 min at 40% B, 100 min at 52% B, 103 min at 68% B, 106-114 min at 96% B, 115-135 min at 4% B.

M#2: 0-4 min at 4% B, 90 min at 9% B, 130 min at 12.5% B, 180 min at 17% B, 200 min at 20% B, 220 min at 24% B, 250 min at 35% B, 260 min at 44% B, 265 min at 50% B, 270 min at 55% B, 275 min at 70% B, 280-290 min at 96% B, 291-360 min at 4% B.

M#3: 0 – 15 min at 0% B, 45 min at 9% B, 90 min at 15% B, 110 min at 19% B, 120 min at 23% B, 140 min at 35% B, 145 min at 40% B, 152 min at 50% B, 155 min at 55% B, 160 min at 70% B, 164 min at 96% B, 174 min at 96% B, 175 min at 4% B, 176 – 210 min at 0% B.

The Nanospray Flex Ion Source (Thermo Fisher Scientific) provided with a stainless steel emitter was used to generate positively charged ions at 2.2 kV spray voltage. The hybrid quadrupole/orbitrap mass analyser was operated in Full MS / dd MS^2 (TopN) mode. Precursor ions were measured in full scan mode within a mass range of either m/z 300-1600 (M#1 or M#3) or m/z 300-1500 (M#2) at a resolution of 70k/140k FWHM (M#1/M#2 and M#3) using a maximum injection time of 120 ms and an AGC (automatic gain control) target of 10^6. For data-dependent acquisition, up to 10 most abundant precursor ions per scan cycle with an assigned charge state of z = 2-6 were selected in the quadrupole for further fragmentation using an isolation width of m/z 2.0. Fragment ions were generated in the HCD cell at a normalized collision energy of 30 V using nitrogen gas. Dynamic exclusion of precursor ions was set to 35 s (M#1), 40 s (M#2) or 30 s (M#3). Fragment ions were monitored at a resolution of 17.5k (FWHM) using a maximum injection time of 120 ms and an AGC target of $2x10^5$. The fixed first mass was set to m/z 120. The LC-MS/MS instrument was operated by means of the Thermo/Dionex Chromeleon Xpress v6.80 SR13 build 3818 software and the Thermo Qexactive Plus Tune / Xcalibur v3.0.63 2.3 build 1765 graphical interface software.

II. Identification of the regulatory modules

ModuleDiscoverer was used for the identification of murine and fungal regulatory modules. In brief, the algorithm employs a heuristic approach for the identification of the community structure (groups of densely connected proteins) underlying the protein-protein interaction (PPI) network. In this study, a protein community was defined as maximal clique, *i.e.*, a group of proteins, (i) where each protein is connected by an edge and (ii) no protein exists in the PPI network that enlarges the clique. The identified maximal cliques were then tested for their significant enrichment with differentially expressed proteins derived from the high-throughput LC-MS/MS experiments. For this enrichment test a permutation based *p*-value calculation was employed. All significantly enriched maximal cliques were filtered based on a user-defined *p*-value cutoff. Finally, any of the significantly enriched maximal cliques that overlap in at least one protein were unified into a new, extended sub-graph. Thus, the union of all significantly enriched maximal cliques forms the regulatory module that represents the molecular alterations underlying the respective phenotype.

For the murine regulatory module, the PPI network provided by the STRING-database (version 10) (Szklarczyk *et al.*, 2015) was downloaded. Relations between proteins with a score above 0.7 were filtered retaining a high-confidence PPI network composed of 15,787 proteins connected by 459,809 edges. Processing of the high-confidence PPI network using ModuleDiscoverer with 2,000,002 iterations resulted in a total of 82,413 unique maximal cliques. All of the identified 82413 protein communities were tested for their enrichment with any of the 636 differentially expressed proteins. *P*-values for each clique were obtained by permutation-based *p*-value calculation (Ge *et al.*, 2003) based on 10,000 protein sets containing 636 proteins randomly sampled from all 2431 proteins identified in the LC-MS/MS analysis (the statistical background). UniProt-IDs of the differentially expressed proteins, the sets of random proteins and the statistical background were translated into EnsemblProtein-IDs using the org.Mm.eg.database (Carlson) package and Ensembl BioMart (version 86) (Aken *et al.*, 2016). Based on this data 15,614 maximal cliques were identified with (i) at least one differentially expressed protein and (ii) at least half of the proteins present in the statistical background. Based on a *p*-value cutoff of 0.01 241 maximal cliques significantly enriched for differentially expressed proteins were identified. These 241 significantly enriched cliques were then merged based on their overlapping proteins. Stability of the regulatory module was tested using 100 bootstrap-samples (model-free re-sampling with replacement) of the clique database. Pairwise comparison of the sampled regulatory modules showed that the average similarity in terms of the graph edit distance for nodes and edges separately was above 95%.

III. Effect of magnetic labeling

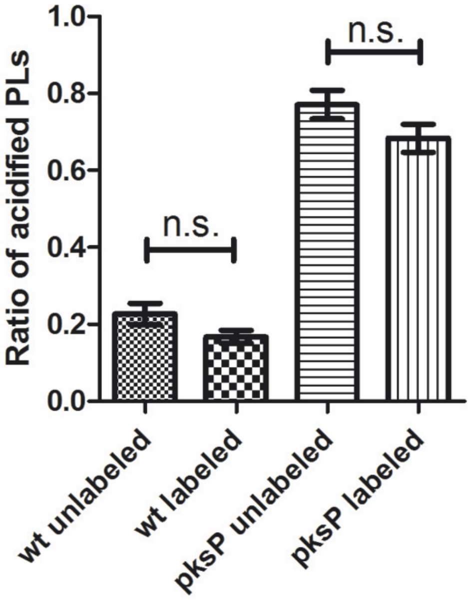

Figure S1 Magnetic labeling of conidia has no effect on acidification of phagolysosomes (PLs). Ratio of acidified phagolysosomes 2 h post-infection of macrophages with magnetically labeled and unlabeled conidia of the wild-type and the *pksP* mutant. Columns represent mean values with SD. N.s. $p > 0.05$

IV. Comparison of fungal proteins in the phagolysosome identified by label-free and label-based quantification

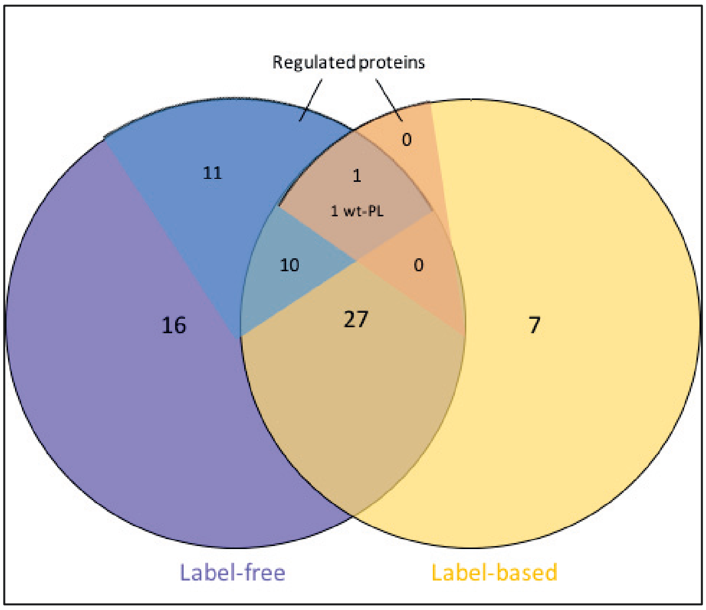

Figure S2 Comparison of fungal proteins in the phagolysosome detected with label-free or label-based quantification. Protein samples from the phagolysosomal purification were identified and quantified with a label-free and a label-based method. Venn diagram shows the overlap of total detected and the differentially regulated proteins. 1 protein was identified by both methods as differentially abundant in wild-type conidia-containing phagolysosomes.

V. Proteins of the host regulatory module

Table S1: **List of host regulatory module proteins.** [1] log2-fold change of protein quantities in *pksP* mutant *versus* wild-type conidia-containing phagolysosomes. Log2 *pksP*/wt > 2, enriched in *pksP* mutant and < 0.5 on wild-type conidia-containing phagolysosomes; '-' not detected in LC-MS/MS [2]Most enriched GO or KEGG pathway terms of the module BP – biological process, CC – cellular compartment, MF – molecular function.

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
		Submodule 1: Electron Transport Chain		
P56391	Cox6b1	cytochrome c oxidase, subunit Vib polypeptide 1	1.82	oxidation-reduction process (BP)
A2RSV8	Cox4i1	cytochrome c oxidase subunit IV isoform 1	0.33	electron transport chain (BP)
Q9CXV1	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	-	respiratory electron transport chain (BP)
Q7JCZ3	mt-Cytb	mitochondrially encoded cytochrome b	-	
P99028	Uqcrh	ubiquinol-cytochrome c reductase hinge protein	-	NADH dehydrogenase activity (MF)
Q9CQ68	1700029P11Rik	RIKEN cDNA 1700029P11 gene	-	oxidoreductase activity (MF)
Q5NCJ9	Uqcr10	ubiquinol-cytochrome c reductase, complex III subunit X	-	electron carrier activity (MF)
Q9CR68	Uqcrfs1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0.83	
Q9DB77	Uqcrc2	ubiquinol cytochrome c reductase core protein 2	0.35	mitochondrial membrane (CC)
Q9CZ13	Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	0.23	
Q9D0M3	Cyc1	cytochrome c-1	0.08	oxidative phosphorylation (KEGG)
Q9CQB4	Uqcrb	ubiquinol-cytochrome c reductase binding protein	-	
P48771	Cox7a2	cytochrome c oxidase subunit VIIa 2	-	
Q9CPX8	Uqcr11	ubiquinol-cytochrome c reductase, complex III subunit XI	-	
Q3UD06	Atp5c1	ATP synthase, H^+ transporting, mitochondrial F1 complex, gamma polypeptide 1	0.27	
Q9CZB0	Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	1.73	
G3X9L6	Gm10250	predicted pseudogene 10250	1.51	
Q9D881	Gm11273	predicted gene 11273	-	
P12787	Cox5a	cytochrome c oxidase subunit Va	1.47	
Q78IK2	Usmg5	upregulated during skeletal muscle growth 5	1.33	
Q9CPQ8	Atp5l	ATP synthase, H^+ transporting, mitochondrial F0 complex, subunit G	-0.24	
Q99LY9	Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	1.12	
Q9DB20	Atp5o	ATP synthase, H^+ transporting, mitochondrial F1 complex, O subunit	0.61	
J3QNM7	Gm5426	predicted pseudogene 5426	-	
P56135	Atp5j2	ATP synthase, H^+ transporting, mitochondrial F0 complex, subunit F2	-	
P17665	Cox7c	cytochrome c oxidase subunit VIIc	-2.09	
F7C106	Cox5b	cytochrome c oxidase subunit Vb	-	
Q9CQ69	Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	0.83	
Q06185	Atp5k	ATP synthase, H^+ transporting, mitochondrial F1F0 complex, subunit E	0.21	
Q9DCW5	Cox6a1	cytochrome c oxidase subunit *via* polypeptide 1	-	

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
Q9DCX2	Atp5h	ATP synthase, H^+ transporting, mitochondrial F0 complex, subunit D	-	
P97450	Atp5j	ATP synthase, H^+ transporting, mitochondrial F0 complex, subunit F	-	
Q545F5	Atp5e	ATP synthase, H^+ transporting, mitochondrial F1 complex, epsilon subunit	-0.03	
Q9CPQ1	Cox6c	cytochrome c oxidase subunit Vic	0.49	
Q4FK74	Atp5d	ATP synthase, H^+ transporting, mitochondrial F1 complex, delta subunit	0.29	
J3QPT4	Gm4076	predicted gene 4076	-	
A0A0R4J275	Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	0.85	
Q59J78	Ndufaf2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	0.04	
Q9D6J6	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	1.10	
Q9CQH3	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	1.39	
Q9CPU2	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	-	
O09111	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	-	
Q9ERS2	Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	1.34	
A2AP31	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	-	
A0A0R3P9C8	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	1.12	
Q7JCY4	mt-Nd6	mitochondrially encoded NADH dehydrogenase 6	-	
Q9MD82	mt-Nd5	mitochondrially encoded NADH dehydrogenase 5	-1.07	
Q7GIP5	mt-Nd3	mitochondrially encoded NADH dehydrogenase 3	-	
Q9MD59	mt-Nd2	mitochondrially encoded NADH dehydrogenase 2	-	
Q4JFN6	mt-Nd1	mitochondrially encoded NADH dehydrogenase 1	-	
Q9CQ91	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	3.53	
Q5M9P5	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0.61	
Q9JKL4	Ndufaf3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3	0.19	
Q9DCJ5	Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	0.56	
Q3U422	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3	-	
Q9DCS9	Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	0.81	
Q91YT0	Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	-0.33	
Q4FZG9	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	-	
Q9Z1P6	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	0.99	
Q9CQY9	Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	-	
Q9CR61	Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	2.26	
Q569N0	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-	
Q9CQ54	Ndufc2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	0.30	
A0A0N4SVQ1	Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	0.94	
Q9D1H6	Ndufaf4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	-0.15	
A0A0R4J081	Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	-2.56	
Q99LC3	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	0.22	
Q9CQZ6	Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	0.40	
Q91VD9	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	0.16	

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
Q9D6J5	Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	-	
Q9CPP6	Ndufa5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	1.17	
Q9CQC7	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4,NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4,NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	0.50	
Q9CQZ5	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	1.21	
Q9CQJ8	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	2.43	
E9QPX3	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	1.16	
P52503	Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	1.12	
Q9DC70	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0.36	
Q545K0	Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	-	
Q9CQ75	Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	0.46	
Q91WD5	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	-0.03	
Q9DCT2	Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	1.54	
G5E814	Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11,NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	-	
Submodule 2: RNA transport				
Q3UYV9	Ncbp1	nuclear cap binding protein subunit 1	0.49	RNA transport (BP)
K9J7E2	Gm4301	predicted gene 4301	-	RNA localization (BP)
E9Q5E2	BC005561	cDNA sequence BC005561	-	nuclear export (BP)
Q8BG81	Poldip3	polymerase (DNA-directed), delta interacting protein 3	-2.09	
E9Q4V5	Gm4308	predicted gene 4308	-	RNA binding (MF)
Q8VDW0	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-0.28	
Q3TIV5	Zc3h15	zinc finger CCCH-type containing 15	-	transcription export complex (CC)
E9Q6R7	Utrn	utrophin	-	THO complex (CC)
G3X9I4	Alyref2	Aly/REF export factor 2	-	
Q9Z1N5	Ddx39b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	-0.41	spliceosome (KEGG)
Q7TMY4	Thoc7	THO complex 7	2.00	mRNA surveillance pathway (KEGG)
A0A0R4J0J6	Thoc5	THO complex 5	-1.10	
B1AZI6	Thoc2	THO complex 2	-1.56	
Q5U4D9	Thoc6	THO complex 6	-1.03	
Q8VE80	Thoc3	THO complex 3	-1.27	
O08583	Alyref	Aly/REF export factor	0.06	
Q8R3N6	Thoc1	THO complex 1	0.14	
Submodule 3: Iron homeostasis				
Q8R0Z5	Slc25a28	solute carrier family 25, member 28	-	iron-sulfur cluster assembly (BP)
Q9D924	Isca1	iron-sulfur cluster assembly 1	-	iron ion homeostasis (BP)
Q3TV21	Fxn	frataxin	4.83	

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
A0A0R4J069	Scly	selenocysteine lyase	-	iron ion binding (MF)
A0A0R4J0T0	Hscb	HscB iron-sulfur cluster co-chaperone	-	
Q8K215	Lyrm4	LYR motif containing 4	7.39	mitochondrion (CC)
Q545P3	Fdx1	ferredoxin 1	1.76	
Q9Z1J3	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	0.04	sulfur relay system (KEGG)
Q9D7P6	Iscu	iron-sulfur cluster assembly enzyme	1.13	thiamine metabolism (KEGG)
Q9DCB8	Isca2	iron-sulfur cluster assembly 2	-	
Submodule 4: Translation				
Q60737	Csnk2a1	casein kinase 2, alpha 1 polypeptide	2.57	basal transcription machinery binding (MF)
Q08943	Ssrp1	structure specific recognition protein 1	0.45	
Q5XJE5	Leo1	Leo1, Paf1/RNA polymerase II complex component	-	transcription elongation factor complex (CC)
A2AQ19	Rtf1	RTF1, Paf1/RNA polymerase II complex component	-	
Q62018	Ctr9	CTR9 homolog, Paf1/RNA polymerase II complex component	4.57	ribosome biogenesis in eukaryotes (KEGG)
Q8K2T8	Paf1	Paf1, RNA polymerase II complex component	3.92	
Submodule 5: Stress response				
Q9Z2D6	Mecp2	methyl CpG binding protein 2	2.39	negative regulation of transcription from RNA polymerase II promoter (BP)
Q3ULN2	Gtf2b	general transcription factor IIB	2.17	
Q790L7	Ccnd1	cyclin D1	4.56	regulatory region DNA binding (MF)
F8WID3	Myc	myelocytomatosis oncogene	-	
A0A0R4J008	Hdac2	histone deacetylase 2	0.28	histone methyltransferase complex (CC)
P23798	Pcgf2	polycomb group ring finger 2	-	
Q02395	Mtf2	metal response element binding transcription factor 2	-	cell cycle (KEGG)
Q9CXG9	Phf19	PHD finger protein 19	-	
Q9DBY5	Cbx6	chromobox 6	-	
A0A0R4J1C0	Ezh1	enhancer of zeste 1 polycomb repressive complex 2 subunit	-	
Q921E6	Eed	embryonic ectoderm development	-1.19	
Q61188	Ezh2	enhancer of zeste 2 polycomb repressive complex 2 subunit	-1.94	
Q9Z1B8	Phf1	PHD finger protein 1	-	
Q00899	Yy1	YY1 transcription factor	-1.29	
Q80U70	Suz12	suppressor of zeste 12 homolog (Drosophila)	-0.27	
Submodule 6: vATPase-dependent acidification				
Q9CR84	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	-	energy coupled proton transmembrane transport, against electrochemical gradient (BP)
P15920	Atp6v0a2	ATPase, H^+ transporting, lysosomal V0 subunit A2	-	ATP hydrolysis coupled proton transport (BP)
Q920R6	Atp6v0a4	ATPase, H^+ transporting, lysosomal V0 subunit A4	-	
Q3U861	Atp6v1d	ATPase, H^+ transporting, lysosomal V1 subunit D	1.56	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances (MF)

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
Q14BC2	Atp5g3	ATP synthase, H^+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	-	transmembrane transporter activity (MF)
Q9D1K2	Atp6v1f	ATPase, H^+ transporting, lysosomal V1 subunit F	1.61	
Q8BVE3	Atp6v1h	ATPase, H^+ transporting, lysosomal V1 subunit H	2.09	proton-transporting V-type ATPase complex (CC)
Q1XID4	Atp6ap2	ATPase, H^+ transporting, lysosomal accessory protein 2	-0.31	proton-transporting two-sector ATPase complex (CC)
Q9Z1G4	Atp6v0a1	ATPase, H^+ transporting, lysosomal V0 subunit A1	0.72	
P50516	Atp6v1a	ATPase, H^+ transporting, lysosomal V1 subunit A	1.20	phagosome (KEGG)
Q9D593	Atp6v1e2	ATPase, H^+ transporting, lysosomal V1 subunit E2	-	oxidative phosphorylation (KEGG)
Q3U889	Atp6v0b	ATPase, H^+ transporting, lysosomal V0 subunit B	-	lysosome (KEGG)
Q80SY3	Atp6v0d2	ATPase, H^+ transporting, lysosomal V0 subunit D2	-	
Q8BMC1	Atp6v1g3	ATPase, H^+ transporting, lysosomal V1 subunit G3	-	
A3KML5	Atp6v0c	ATPase, H^+ transporting, lysosomal V0 subunit C	-	
Q9Z1G3	Atp6v1c1	ATPase, H^+ transporting, lysosomal V1 subunit C1	1.63	
Q4FK49	Ppa1	pyrophosphatase (inorganic) 1	0.63	
P50518	Atp6v1e1	ATPase, H^+ transporting, lysosomal V1 subunit E1	3.59	
Q3TWN7	Atp6ap1	ATPase, H^+ transporting, lysosomal accessory protein 1	1.51	
P51863	Atp6v0d1	ATPase, H^+ transporting, lysosomal V0 subunit D1	1.36	
P62814	Atp6v1b2	ATPase, H^+ transporting, lysosomal V1 subunit B2	1.75	
Q91YH6	Atp6v1b1	ATPase, H^+ transporting, lysosomal V1 subunit B1	-	
Submodule 7: Endocytosis				
P17047	Lamp2	lysosomal-associated membrane protein 2	1.35	endocytosis (BP)
Q549D0	Cd63	CD63 antigen	3.94	
Q3TM70	Ehd4	EH-domain containing 4	1.37	GTP binding (MF)
Q80ZZ0	Ehd1	EH-domain containing 1	1.14	
Q4FJQ0	Rab7	RAB7, member RAS oncogene family	0.71	endosome (CC)
Q8BL66	Eea1	early endosome antigen 1	-2.74	
Q3TA96	Lamp1	lysosomal-associated membrane protein 1	1.94	endocytosis (KEGG)
Q9CQD1	Rab5a	RAB5A, member RAS oncogene family	1.28	phagosome (KEGG)
Submodule 8: Vesicle transport				
O35166	Gosr2	golgi SNAP receptor complex member 2	-	vesicle-mediated transport (BP)
Q791P0	Vamp5	vesicle-associated membrane protein 5	-	membrane fusion (BP)
Q80W45	Stx2	syntaxin 2	-	membrane organization (BP)
P56371	Rab4a	RAB4A, member RAS oncogene family	-	
Q8BH40	Stx7	syntaxin 7	-	SNARE binding (MF)
P61264	Stx1b	syntaxin 1B	-	SNAP receptor activity (MF)
O08599	Stxbp1	syntaxin binding protein 1	0.50	syntaxin binding (MF)
H6RXZ1	Syt1	synaptotagmin I	-	
Q8R1Q0	Stx19	syntaxin 19	-	SNARE complex (CC)
Q8BXT9	Sec22c	SEC22 homolog C, vesicle trafficking protein	-	endomembrane system (CC)

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
B2RSR2	Sec22a	SEC22 homolog A, vesicle trafficking protein	-	cytoplasmic vesicle (CC)
O88983	Stx8	syntaxin 8	0.62	
Q9CQW1	Ykt6	YKT6 v-SNARE homolog (S. cerevisiae)	0.98	SNARE interactions in vesicular transport (KEGG)
Q9D3L3	Snap23	synaptosomal-associated protein 23	-	
P46460	Nsf	N-ethylmaleimide sensitive fusion protein	0.75	
Q91XH6	Vti1b	vesicle transport through interaction with t-SNAREs 1B	-	
Q3U5V8	Stx11	syntaxin 11	-	
Q9D0I4	Stx17	syntaxin 17	-	
P63040	Cplx1	complexin 1	-	
P70452	Stx4a	syntaxin 4A (placental)	3.64	
Q9ER00	Stx12	syntaxin 12	1.69	
P84086	Cplx2	complexin 2	-	
Q497P1	Stx1a	syntaxin 1A (brain)	-	
Q548T0	Stxbp2	syntaxin binding protein 2	-1.39	
Q8K1E0	Stx5a	syntaxin 5A	-	
Q64704	Stx3	syntaxin 3	-	
A0A0R4J0R1	Vamp8	vesicle-associated membrane protein 8	1.49	
P70280	Vamp7	vesicle-associated membrane protein 7	0.08	
Q8BSN6	Vamp4	vesicle-associated membrane protein 4	1.33	
P63024	Vamp3	vesicle-associated membrane protein 3	1.06	
P28663	Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	-	
P60879	Snap25	synaptosomal-associated protein 25	-	
Q9JKK1	Stx6	syntaxin 6	-	
Q9ERB0	Snap29	synaptosomal-associated protein 29	0.04	
Q8CHR4	Vamp2	vesicle-associated membrane protein 2	-	
Q9DB05	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	1.25	
		Submodule 9: Carboxylic acid metabolism		
Q3UAT9	Impdh2	inosine 5’-phosphate dehydrogenase 2	1.49	organic acid metabolic process (BP)
Q3V3R1	Mthfd1l	methylenetetrahydrofolate dehydrogenase ($NADP^+$ dependent) 1-like	-0.34	carboxylic acid metabolic process (BP)
Q922D8	Mthfd1	methylenetetrahydrofolate dehydrogenase ($NADP^+$ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	-1.76	
B2RQC6	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	-0.19	catalytic activity (MF)
Q921H8	Acaa1a	acetyl-Coenzyme A acyltransferase 1A	1.24	ligase activity (MF)
Q8QZT1	Acat1	acetyl-Coenzyme A acetyltransferase 1	-0.06	
Q9DBM2	Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	-	peroxisome (CC)
Q9DBL1	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	1.05	microbody (CC)
Q8CAY6	Acat2	acetyl-Coenzyme A acetyltransferase 2	-	nucleolus (CC)
P70700	Polr1b	polymerase (RNA) I polypeptide B	-2.00	
E9QN31	Nop2	NOP2 nucleolar protein	-	valine, leucine and isoleucine degradation (KEGG)

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
Q8BHY2	Noc4l	NOC4 like	1.71	propanoate metabolism (KEGG)
P35550	Fbl	fibrillarin	-0.33	glyoxylate and dicarboxylate metabolism (KEGG)
Q64737	Gart	phosphoribosylglycinamide formyltransferase	1.04	
A0A0M3HEQ0	Txnrd2	thioredoxin reductase 2	2.30	
A2ATU0	Dhtkd1	dehydrogenase E1 and transketolase domain containing 1	-	
P16332	Mut	methylmalonyl-Coenzyme A mutase	2.23	
Q9EQ20	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	-1.40	
Q9D1I5	Mcee	methylmalonyl CoA epimerase	-	
Q3UGC8	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	0.58	
Q99MN9	Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	1.97	
E9Q4Z2	Acacb	acetyl-Coenzyme A carboxylase beta	-	
Q5SWU9	Acaca	acetyl-Coenzyme A carboxylase alpha	-	
Q3V117	Acly	ATP citrate lyase	-3.56	
Q8BMF4	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	0.71	
P47791	Gsr	glutathione reductase	1.07	
E9Q7L0	Ogdhl	oxoglutarate dehydrogenase-like	-	
Q8BKZ9	Pdhx	pyruvate dehydrogenase complex, component X	2.29	
Submodule 10: Ribosome				
Q9DCI9	Mrpl32	mitochondrial ribosomal protein L32	-	translation (BP)
Q9CZ83	Mrpl55	mitochondrial ribosomal protein L55	2.63	peptide biosynthetic process (BP)
Q9CY16	Mrps28	mitochondrial ribosomal protein S28	2.56	
Q9D1P0	Mrpl13	mitochondrial ribosomal protein L13	0.35	structural constituent of ribosome (MF)
Q99N93	Mrpl16	mitochondrial ribosomal protein L16	0.72	
Q9D8P4	Mrpl17	mitochondrial ribosomal protein L17	-0.49	ribosome (CC)
Q9CPR5	Mrpl15	mitochondrial ribosomal protein L15	1.66	ribonucleoprotein complex (CC)
Q99N91	Mrpl34	mitochondrial ribosomal protein L34	-	
Q9DB15	Mrpl12	mitochondrial ribosomal protein L12	1.04	
Q99N95	Mrpl3	mitochondrial ribosomal protein L3	0.95	
Q9D338	Mrpl19	mitochondrial ribosomal protein L19	-0.18	
Q9CQF0	Mrpl11	mitochondrial ribosomal protein L11	1.14	
Q99N92	Mrpl27	mitochondrial ribosomal protein L27	3.85	
Q3UKS6	Mrpl40	mitochondrial ribosomal protein L40	2.33	
Q99N90	Mrpl36	mitochondrial ribosomal protein L36	-	
Q8BU88	Mrpl22	mitochondrial ribosomal protein L22	1.00	
Q9CQ06	Mrpl24	mitochondrial ribosomal protein L24	0.60	
Q9DCU6	Mrpl4	mitochondrial ribosomal protein L4	-	
Q9D773	Mrpl2	mitochondrial ribosomal protein L2	-1.20	

Submodule 11: RNA processing

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
P62309	Gm8186	predicted gene 8186	-6.27	mRNA splicing, *via* spliceosome (BP)
P62305	Snrpe	small nuclear ribonucleoprotein E	-1.00	nucleic acid binding (MF)
P62309	Snrpg	small nuclear ribonucleoprotein polypeptide G	-6.27	small nuclear ribonucleoprotein complex (CC)
P62876	Polr2l	polymerase (RNA) II (DNA directed) polypeptide L	1.68	spliceosome (KEGG)
Q497K3	Snrpf	small nuclear ribonucleoprotein polypeptide F	0.54	RNA polymerase (KEGG)
Q3UI46	Nedd8	neural precursor cell expressed, developmentally down-regulated gene 8	-	
Submodule 12: NADPH oxidase-dependent ROS production				
Q8CIZ9	Nox1	NADPH oxidase 1	-	reactive oxygen species metabolic process (BP)
Q3UPN1	Vcam1	vascular cell adhesion molecule 1	-	superoxide-generating NADPH oxidase activity (MF)
Q09014	Ncf1	neutrophil cytosolic factor 1	1.01	NADPH oxidase complex (CC)
A2AQ92	Duox1	dual oxidase 1	-	phagosome (KEGG)
P97369	Ncf4	neutrophil cytosolic factor 4	1.15	
Q4FJK0	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	-	
O70145	Ncf2	neutrophil cytosolic factor 2	-1.37	
B3VQI8	Cyba	cytochrome b-245, alpha polypeptide	0.41	
Submodule 13: Immune response				
E9QN37	Mpeg1	macrophage expressed gene 1	1.73	immune response (BP)
A0A0R4J1C8	Cd68	CD68 antigen	1.37	response to stimulus (BP)
A0A077S2U6	Lyz2	lysozyme 2	0.95	signaling receptor activity (MF)
P14106	C1qb	complement component 1, q subcomponent, beta polypeptide	-	cell surface (CC)
Q3U419	Tyrobp	TYRO protein tyrosine kinase binding protein	-	
Q0P635	Csf1r	colony stimulating factor 1 receptor	1.38	complement and coagulation cascades (KEGG)
Q3U9R0	Adgre1	adhesion G protein-coupled receptor E1	-	cytokine-cytokine receptor interaction (KEGG)
Submodule 14: Signaling				
Q9QXX3	Pla2g10	phospholipase A2, group X	-	intracellular signal transduction (BP)
Q01279	Egfr	epidermal growth factor receptor	-	regulation of intracellular signal transduction (BP)
P12025	Mdk	midkine	-	
Q4VAE6	Rhoa	ras homolog family member A	-0.25	phospholipase A2 activity (MF)
P97819	Pla2g6	phospholipase A2, group VI	-	receptor signaling protein serine/threonine kinase activity (MF)
Q6GTW1	Pla2g5	phospholipase A2, group V	-	MAP kinase activity (MF)
Q8R3U1	Pla2g16	phospholipase A2, group XVI	-	
Q3UMQ1	Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-dependent)	1.37	membrane raft (CC)
Q05769	Ptgs2	prostaglandin-endoperoxide synthase 2	0.52	caveola (CC)
Q5J7N1	Kras	Kirsten rat sarcoma viral oncogene homolog	-	microtubule cytoskeleton (CC)
Q9WVS8	Mapk7	mitogen-activated protein kinase 7	-	
O08911	Mapk12	mitogen-activated protein kinase 12	-	chemokine signaling pathway (KEGG)
Q61526	Erbb3	erb-b2 receptor tyrosine kinase 3	-	glycerophospholipid metabolism (KEGG)

Uniprot Accession	Gene	Description	log2FC[1]	GO terms[2]
Q63844	Mapk3	mitogen-activated protein kinase 3	-1.78	toll-like receptor signaling pathway (KEGG)
Q6PB44	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	-0.04	
P63085	Mapk1	mitogen-activated protein kinase 1	-1.19	
Q3U5I5	Grb2	growth factor receptor bound protein 2	1.35	
Q5U421	Mapk14	mitogen-activated protein kinase 14	-	
		Submodule: 15 Microtubule Movement		
Q9QWT9	Kifc1	kinesin family member C1	-1.30	mitotic sister chromatid segregation (BP)
Q8BH30	Kpna6	karyopherin (importin) alpha 6	1.02	motor activity (MF)
E9PUA5	Kifc5b	kinesin family member C5B	-1.30	kinesin complex (CC)
		Submodule 16: tRNA metabolism		
E9QB02	Mars	methionine-tRNA synthetase	-1.69	translational initiation (BP)
Q642K5	Gm9843	predicted gene 9843	-	translation factor activity, RNA binding
Q8JZQ9	Eif3b	eukaryotic translation initiation factor 3, subunit B	1.20	eukaryotic translation initiation factor 3 complex (CC)
Q3UHY8	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	-0.33	RNA transport (KEGG)
Q8R1B4	Eif3c	eukaryotic translation initiation factor 3, subunit C	1.06	aminoacyl-tRNA biosynthesis (KEGG)
		Submodule 17: DNA replication		
Q6ZQJ5	Dna2	DNA replication helicase/nuclease 2	-	DNA-dependent DNA replication (BP)
E9QPB3	Wdhd1	WD repeat and HMG-box DNA binding protein 1	-2.90	double-strand break repair (BP)
Q3U4X8	Lig1	ligase I, DNA, ATP-dependent	-1.63	DNA binding (MF)
Q3URU4	Mre11a	MRE11A homolog A, double strand break repair nuclease	-3.46	condensed chromosome (CC)
Q08297	Rad51	RAD51 recombinase	-	homologous recombination (KEGG)

References

AKEN, B. L., AYLING, S., BARRELL, D., CLARKE, L., CURWEN, V., FAIRLEY, S., FERNANDEZ BANET, J., BILLIS, K., GARCIA GIRON, C., HOURLIER, T., HOWE, K., KAHARI, A., KOKOCINSKI, F., MARTIN, F. J., MURPHY, D. N., NAG, R., RUFFIER, M., SCHUSTER, M., TANG, Y. A., VOGEL, J. H., WHITE, S., ZADISSA, A., FLICEK, P. & SEARLE, S. M. 2016. The Ensembl gene annotation system. *Database,* 2016.

AKOUMIANAKI, T., KYRMIZI, I., VALSECCHI, I., GRESNIGT, M. S., SAMONIS, G., DRAKOS, E., BOUMPAS, D., MUSZKIETA, L., PREVOST, M. C., KONTOYIANNIS, D. P., CHAVAKIS, T., NETEA, M. G., VAN DE VEERDONK, F. L., BRAKHAGE, A. A., EL-BENNA, J., BEAUVAIS, A., LATGE, J. P. & CHAMILOS, G. 2016. *Aspergillus* cell wall melanin blocks LC3-associated phagocytosis to promote pathogenicity. *Cell Host Microbe,* 19**,** 79-90.

AMITANI, R., TAYLOR, G., ELEZIS, E. N., LLEWELLYN-JONES, C., MITCHELL, J., KUZE, F., COLE, P. J. & WILSON, R. 1995. Purification and characterization of factors produced by *Aspergillus fumigatus* which affect human ciliated respiratory epithelium. *Infect Immun,* 63**,** 3266-71.

BADDLEY, J. W. 2011. Clinical risk factors for invasive aspergillosis. *Med Mycol,* 49 Suppl 1**,** S7-S12.

BALLOY, V., HUERRE, M., LATGE, J. P. & CHIGNARD, M. 2005. Differences in patterns of infection and inflammation for corticosteroid treatment and chemotherapy in experimental invasive pulmonary aspergillosis. *Infect Immun,* 73**,** 494-503.

BARRENAS, F., CHAVALI, S., ALVES, A. C., COIN, L., JARVELIN, M. R., JORNSTEN, R., LANGSTON, M. A., RAMASAMY, A., ROGERS, G., WANG, H. & BENSON, M. 2012. Highly interconnected genes in disease-specific networks are enriched for disease-associated polymorphisms. *Genome Biol,* 13**,** R46.

BEDARD, K. & KRAUSE, K. H. 2007. The NOX family of ROS-generating NADPH oxidases: physiology and pathophysiology. *Physiol Rev,* 87**,** 245-313.

BEHNSEN, J., HARTMANN, A., SCHMALER, J., GEHRKE, A., BRAKHAGE, A. A. & ZIPFEL, P. F. 2008. The opportunistic human pathogenic fungus *Aspergillus fumigatus* evades the host complement system. *Infect Immun,* 76**,** 820-7.

BEHNSEN, J., LESSING, F., SCHINDLER, S., WARTENBERG, D., JACOBSEN, I. D., THOEN, M., ZIPFEL, P. F. & BRAKHAGE, A. A. 2010. Secreted *Aspergillus fumigatus* protease Alp1 degrades human complement proteins C3, C4, and C5. *Infect Immun,* 78**,** 3585-94.

BERG, J. M., TYMOCZKO, J. L. & STRYER, L. 2002. Chapter 20.3: The Pentose Phosphate Pathway Generates NADPH and Synthesizes Five-Carbon Sugars. *In:* BERG, J. M., TYMOCZKO, J. L. & STRYER, L. (eds.) *Biochemistry.* 5th Edition ed. New York: W. H. Freeman.

BERGHAUS, L. J., MOORE, J. N., HURLEY, D. J., VANDENPLAS, M. L., FORTES, B. P., WOLFERT, M. A. & BOONS, G. J. 2010. Innate immune responses of primary murine macrophage-lineage cells and RAW 264.7 cells to ligands of Toll-like receptors 2, 3, and 4. *Comp Immunol Microbiol Infect Dis,* 33**,** 443-54.

BERNARD, M. & LATGE, J. P. 2001. *Aspergillus fumigatus* cell wall: composition and biosynthesis. *Med Mycol,* 39 Suppl 1**,** 9-17.

BHABHRA, R. & ASKEW, D. S. 2005. Thermotolerance and virulence of *Aspergillus fumigatus*: role of the fungal nucleolus. *Med Mycol,* 43 Suppl 1**,** S87-93.

BIGNELL, E., CAIRNS, T. C., THROCKMORTON, K., NIERMAN, W. C. & KELLER, N. P. 2016. Secondary metabolite arsenal of an opportunistic pathogenic fungus. *Phil Trans R Soc B,* 371**,** 20160023.

BLANK, N., SCHILLER, M., KRIENKE, S., WABNITZ, G., HO, A. D. & LORENZ, H. M. 2007. Cholera toxin binds to lipid rafts but has a limited specificity for ganglioside GM1. *Immunol Cell Biol,* 85**,** 378-82.

BONNETT, C. R., CORNISH, E. J., HARMSEN, A. G. & BURRITT, J. B. 2006. Early neutrophil recruitment and aggregation in the murine lung inhibit germination of *Aspergillus fumigatus* conidia. *Infect Immun,* 74**,** 6528-39.

BOYLE, K. B. & RANDOW, F. 2015. Rubicon swaps autophagy for LAP. *Nat Cell Biol,* 17**,** 843-5.

BRAKHAGE, A. A., BRUNS, S., THYWISSEN, A., ZIPFEL, P. F. & BEHNSEN, J. 2010. Interaction of phagocytes with filamentous fungi. *Curr Opin Microbiol,* 13**,** 409-15.

BRINKMANN, V., REICHARD, U., GOOSMANN, C., FAULER, B., UHLEMANN, Y., WEISS, D. S., WEINRAUCH, Y. & ZYCHLINSKY, A. 2004. Neutrophil extracellular traps kill bacteria. *Science,* 303**,** 1532-5.

BROMLEY, I. M. & DONALDSON, K. 1996. Binding of *Aspergillus fumigatus* spores to lung epithelial cells and basement membrane proteins: relevance to the asthmatic lung. *Thorax,* 51**,** 1203-9.

BROWN, G. D., HERRE, J., WILLIAMS, D. L., WILLMENT, J. A., MARSHALL, A. S. & GORDON, S. 2003. Dectin-1 mediates the biological effects of β-glucans. *J Exp Med,* 197**,** 1119-24.

BRUMELL, J. H. & SCIDMORE, M. A. 2007. Manipulation of Rab GTPase function by intracellular bacterial pathogens. *Microbiol Mol Biol Rev,* 71**,** 636-52.

BRUNS, S., KNIEMEYER, O., HASENBERG, M., AIMANIANDA, V., NIETZSCHE, S., THYWISSEN, A., JERON, A., LATGE, J. P., BRAKHAGE, A. A. & GUNZER, M. 2010. Production of extracellular traps against *Aspergillus fumigatus in vitro* and in infected lung tissue is dependent on invading neutrophils and influenced by hydrophobin RodA. *PLoS Pathog,* 6**,** e1000873.

BYLES, V., COVARRUBIAS, A. J., BEN-SAHRA, I., LAMMING, D. W., SABATINI, D. M., MANNING, B. D. & HORNG, T. 2013. The TSC-mTOR pathway regulates macrophage polarization. *Nat Commun,* 4**,** 2834.

CARLSON, M. org.Mm.eg.db: Genome wide annotation for Mouse. R package version 3.2.3. https://bioconductor.org/.

CARMODY, R. J. & COTTER, T. G. 2001. Signalling apoptosis: a radical approach. *Redox Rep,* 6**,** 77-90.

CHAI, L. Y., NETEA, M. G., SUGUI, J., VONK, A. G., VAN DE SANDE, W. W., WARRIS, A., KWON-CHUNG, K. J. & KULLBERG, B. J. 2010. *Aspergillus fumigatus* conidial melanin modulates host cytokine response. *Immunobiology,* 215**,** 915-20.

CHAI, L. Y., VONK, A. G., KULLBERG, B. J., VERWEIJ, P. E., VERSCHUEREN, I., VAN DER MEER, J. W., JOOSTEN, L. A., LATGE, J. P. & NETEA, M. G. 2011. *Aspergillus fumigatus* cell wall components differentially modulate host TLR2 and TLR4 responses. *Microbes Infect,* 13**,** 151-9.

CHAMILOS, G., AKOUMIANAKI, T., KYRMIZI, I., BRAKHAGE, A. A., BEAUVAIS, A. & LATGE, J. P. 2016. Melanin targets LC3-associated phagocytosis (LAP): a novel pathogenetic mechanism in fungal disease. *Autophagy,* 12**,** 888-9.

CHANDRA, J., SAMALI, A. & ORRENIUS, S. 2000. Triggering and modulation of apoptosis by oxidative stress. *Free Radic Biol Med,* 29**,** 323-33.

CHENG, S. C., QUINTIN, J., CRAMER, R. A., SHEPARDSON, K. M., SAEED, S., KUMAR, V., GIAMARELLOS-BOURBOULIS, E. J., MARTENS, J. H., RAO, N. A., AGHAJANIREFAH, A., MANJERI, G. R., LI, Y., IFRIM, D. C., ARTS, R. J., VAN DER VEER, B. M., DEEN, P. M., LOGIE, C., O'NEILL, L. A., WILLEMS, P., VAN DE VEERDONK, F. L., VAN DER MEER, J. W., NG, A., JOOSTEN, L. A., WIJMENGA, C., STUNNENBERG, H. G., XAVIER, R. J. & NETEA, M. G. 2014. mTOR- and HIF-1α-mediated aerobic glycolysis as metabolic basis for trained immunity. *Science,* 345**,** 1250684.

CLAUDITZ, A., RESCH, A., WIELAND, K. P., PESCHEL, A. & GOTZ, F. 2006. Staphyloxanthin plays a role in the fitness of *Staphylococcus aureus* and its ability to cope with oxidative stress. *Infect Immun,* 74**,** 4950-3.

COMMONER, B., TOWNSEND, J. & PAKE, G. E. 1954. Free radicals in biological materials. *Nature,* 174**,** 689-91.

CORNISH, E. J., HURTGEN, B. J., MCINNERNEY, K., BURRITT, N. L., TAYLOR, R. M., JARVIS, J. N., WANG, S. Y. & BURRITT, J. B. 2008. Reduced nicotinamide adenine dinucleotide phosphate oxidase-independent resistance to *Aspergillus fumigatus* in alveolar macrophages. *J Immunol,* 180**,** 6854-67.

CORTES, C., RZOMP, K. A., TVINNEREIM, A., SCIDMORE, M. A. & WIZEL, B. 2007. *Chlamydia pneumoniae* inclusion membrane protein Cpn0585 interacts with multiple Rab GTPases. *Infect Immun,* 75**,** 5586-96.

COVARRUBIAS, A. J., AKSOYLAR, H. I. & HORNG, T. 2015. Control of macrophage metabolism and activation by mTOR and Akt signaling. *Semin Immunol,* 27**,** 286-96.

DAGENAIS, T. R. & KELLER, N. P. 2009. Pathogenesis of *Aspergillus fumigatus* in invasive aspergillosis. *Clin Microbiol Rev,* 22**,** 447-65.

DATTA, S. R., DUDEK, H., TAO, X., MASTERS, S., FU, H., GOTOH, Y. & GREENBERG, M. E. 1997. Akt phosphorylation of BAD couples survival signals to the cell-intrinsic death machinery. *Cell,* 91**,** 231-41.

DERMINE, J. F., DUCLOS, S., GARIN, J., ST-LOUIS, F., REA, S., PARTON, R. G. & DESJARDINS, M. 2001. Flotillin-1-enriched lipid raft domains accumulate on maturing phagosomes. *J Biol Chem,* 276**,** 18507-12.

DESJARDINS, M. 1995. Biogenesis of phagolysosomes: the 'kiss and run' hypothesis. *Trends Cell Biol,* 5**,** 183-6.

DESJARDINS, M., HUBER, L. A., PARTON, R. G. & GRIFFITHS, G. 1994. Biogenesis of phagolysosomes proceeds through a sequential series of interactions with the endocytic apparatus. *J Cell Biol,* 124**,** 677-88.

DESJARDINS, M., NZALA, N. N., CORSINI, R. & RONDEAU, C. 1997. Maturation of phagosomes is accompanied by changes in their fusion properties and size-selective acquisition of solute materials from endosomes. *J Cell Sci,* 110 (Pt 18)**,** 2303-14.

DIAMOND, R. D. 1993. Invasive aspergillosis: host defenses. *Recent Results Cancer Res,* 132**,** 109-15.

DIAO, J., LIU, R., RONG, Y., ZHAO, M., ZHANG, J., LAI, Y., ZHOU, Q., WILZ, L. M., LI, J., VIVONA, S., PFUETZNER, R. A., BRUNGER, A. T. & ZHONG, Q. 2015. ATG14 promotes membrane tethering and fusion of autophagosomes to endolysosomes. *Nature,* 520**,** 563-6.

DILL, B. D., GIERLINSKI, M., HARTLOVA, A., ARANDILLA, A. G., GUO, M., CLARKE, R. G. & TROST, M. 2015. Quantitative proteome analysis of temporally resolved phagosomes following uptake *via* key phagocytic receptors. *Mol Cell Proteomics,* 14**,** 1334-49.

DOERING, T. L., NOSANCHUK, J. D., ROBERTS, W. K. & CASADEVALL, A. 1999. Melanin as a potential cryptococcal defence against microbicidal proteins. *Med Mycol,* 37**,** 175-81.

DUBOURDEAU, M., ATHMAN, R., BALLOY, V., HUERRE, M., CHIGNARD, M., PHILPOTT, D. J., LATGE, J. P. & IBRAHIM-GRANET, O. 2006. *Aspergillus fumigatus* induces innate immune responses in alveolar macrophages through the MAPK pathway independently of TLR2 and TLR4. *J Immunol,* 177**,** 3994-4001.

DURINCK, S., SPELLMAN, P. T., BIRNEY, E. & HUBER, W. 2009. Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. *Nat Protoc,* 4**,** 1184-91.

EISENMAN, H. C. & CASADEVALL, A. 2012. Synthesis and assembly of fungal melanin. *Appl Microbiol Biotechnol,* 93**,** 931-40.

ERWIG, L. P. & GOW, N. A. 2016. Interactions of fungal pathogens with phagocytes. *Nat Rev Microbiol,* 14**,** 163-76.

FALCON, S. & GENTLEMAN, R. 2007. Using GOstats to test gene lists for GO term association. *Bioinformatics,* 23**,** 257-8.

FELDMESSER, M. 2006. Role of neutrophils in invasive aspergillosis. *Infect Immun,* 74**,** 6514-6.

FERREIRA, M. E., COLOMBO, A. L., PAULSEN, I., REN, Q., WORTMAN, J., HUANG, J., GOLDMAN, M. H. & GOLDMAN, G. H. 2005. The ergosterol biosynthesis pathway, transporter genes, and azole resistance in *Aspergillus fumigatus*. *Med Mycol,* 43 Suppl 1**,** S313-9.

FLANNAGAN, R. S., COSIO, G. & GRINSTEIN, S. 2009. Antimicrobial mechanisms of phagocytes and bacterial evasion strategies. *Nat Rev Microbiol,* 7**,** 355-66.

FORGAC, M. 2007. Vacuolar ATPases: rotary proton pumps in physiology and pathophysiology. *Nat Rev Mol Cell Biol,* 8**,** 917-29.

GARIN, J., DIEZ, R., KIEFFER, S., DERMINE, J. F., DUCLOS, S., GAGNON, E., SADOUL, R., RONDEAU, C. & DESJARDINS, M. 2001. The phagosome proteome: insight into phagosome functions. *J Cell Biol,* 152**,** 165-80.

GARLANDA, C., HIRSCH, E., BOZZA, S., SALUSTRI, A., DE ACETIS, M., NOTA, R., MACCAGNO, A., RIVA, F., BOTTAZZI, B., PERI, G., DONI, A., VAGO, L., BOTTO, M., DE SANTIS, R., CARMINATI, P., SIRACUSA, G., ALTRUDA, F., VECCHI, A., ROMANI, L. & MANTOVANI, A. 2002. Non-redundant role of the long pentraxin PTX3 in anti-fungal innate immune response. *Nature,* 420**,** 182-6.

GE, Z., DUDOIT, S. & SPEED, T. P. 2003. Resampling-based multiple testing for microarray data analysis. *Test,* 12**,** 1-77.

GERSUK, G. M., UNDERHILL, D. M., ZHU, L. & MARR, K. A. 2006. Dectin-1 and TLRs permit macrophages to distinguish between different *Aspergillus fumigatus* cellular states. *J Immunol,* 176**,** 3717-24.

GHIGO, E., CAPO, C., TUNG, C. H., RAOULT, D., GORVEL, J. P. & MEGE, J. L. 2002. *Coxiella burnetii* survival in THP-1 monocytes involves the impairment of phagosome maturation: IFN-γ mediates its restoration and bacterial killing. *J Immunol,* 169**,** 4488-95.

GILBERTI, R. M. & KNECHT, D. A. 2015. Macrophages phagocytose nonopsonized silica particles using a unique microtubule-dependent pathway. *Mol Biol Cell,* 26**,** 518-29.

GOODRIDGE, H. S., UNDERHILL, D. M. & TOURET, N. 2012. Mechanisms of Fc receptor and dectin-1 activation for phagocytosis. *Traffic,* 13**,** 1062-71.

GOYETTE, G., BOULAIS, J., CARRUTHERS, N. J., LANDRY, C. R., JUTRAS, I., DUCLOS, S., DERMINE, J. F., MICHNICK, S. W., LABOISSIERE, S., LAJOIE, G., BARREIRO, L., THIBAULT, P. & DESJARDINS, M. 2012. Proteomic characterization of phagosomal membrane microdomains during phagolysosome biogenesis and evolution. *Mol Cell Proteomics,* 11**,** 1365-77.

GRESNIGT, M. S., NETEA, M. G. & VAN DE VEERDONK, F. L. 2012. Pattern recognition receptors and their role in invasive aspergillosis. *Ann N Y Acad Sci,* 1273**,** 60-7.

GRIMM, M. J., VETHANAYAGAM, R. R., ALMYROUDIS, N. G., DENNIS, C. G., KHAN, A. N., D'AURIA, A. C., SINGEL, K. L., DAVIDSON, B. A., KNIGHT, P. R., BLACKWELL, T. S., HOHL, T. M., MANSOUR, M. K., VYAS, J. M., ROHM, M., URBAN, C. F., KELKKA, T., HOLMDAHL, R. & SEGAL, B. H. 2013. Monocyte- and macrophage-targeted NADPH oxidase mediates antifungal host defense and regulation of acute inflammation in mice. *J Immunol,* 190**,** 4175-84.

GUO, M., HARTLOVA, A., DILL, B. D., PRESCOTT, A. R., GIERLINSKI, M. & TROST, M. 2015. High-resolution quantitative proteome analysis reveals substantial differences between phagosomes of RAW 264.7 and bone marrow derived macrophages. *Proteomics,* 15**,** 3169-74.

HAAS, A. 2007. The phagosome: compartment with a license to kill. *Traffic,* 8**,** 311-30.

HAAS, H. 2012. Iron - a key nexus in the virulence of *Aspergillus fumigatus*. *Front Microbiol,* 3**,** 28.

HAINES, J. 1995. *Aspergillus* in compost: Straw man or fatal flaw. *BioCycle,* 6**,** 32-35.

HASENBERG, M., BEHNSEN, J., KRAPPMANN, S., BRAKHAGE, A. A. & GUNZER, M. 2011. Phagocyte responses towards *Aspergillus fumigatus*. *Int J Med Microbiol,* 301**,** 436-44.

HECTOR, R. F., YEE, E. & COLLINS, M. S. 1990. Use of DBA/2N mice in models of systemic candidasis and pulmonary and systemic aspergillosis. *Infect Immun,* 58**,** 1476 - 1478.

HEINEKAMP, T., SCHMIDT, H., LAPP, K., PAHTZ, V., SHOPOVA, I., KOSTER-EISERFUNKE, N., KRUGER, T., KNIEMEYER, O. & BRAKHAGE, A. A. 2015. Interference of *Aspergillus fumigatus* with the immune response. *Semin Immunopathol,* 37**,** 141-52.

HEINEKAMP, T., THYWISSEN, A., MACHELEIDT, J., KELLER, S., VALIANTE, V. & BRAKHAGE, A. A. 2012. *Aspergillus fumigatus* melanins: interference with the host endocytosis pathway and impact on virulence. *Front Microbiol,* 3**,** 440.

HENWICK, S., HETHERINGTON, S. V. & PATRICK, C. C. 1993. Complement binding to *Aspergillus* conidia correlates with pathogenicity. *J Lab Clin Med,* 122**,** 27-35.

HILL, T. W. & KAFER, E. 2001. Improved protocols for *Aspergillus* minimal medium: trace element and minimal medium salt stock solutions *Fungal Genetics Newsletter.* Fungal Genetics Stock Center (http://www.fgsc.net/fgn48/hill.htm).

HOFFMANN, C., FINSEL, I. & HILBI, H. 2012. Purification of pathogen vacuoles from *Legionella*-infected phagocytes. *J Vis Exp*.

HUANG, J., CANADIEN, V., LAM, G. Y., STEINBERG, B. E., DINAUER, M. C., MAGALHAES, M. A., GLOGAUER, M., GRINSTEIN, S. & BRUMELL, J. H. 2009. Activation of antibacterial autophagy by NADPH oxidases. *Proc Natl Acad Sci U S A,* 106**,** 6226-31.

IBATA-OMBETTA, S., IDZIOREK, T., TRINEL, P. A., POULAIN, D. & JOUAULT, T. 2003. *Candida albicans* phospholipomannan promotes survival of phagocytosed yeasts through modulation of bad phosphorylation and macrophage apoptosis. *J Biol Chem,* 278**,** 13086-93.

INFANTINO, V., IACOBAZZI, V., PALMIERI, F. & MENGA, A. 2013. ATP-citrate lyase is essential for macrophage inflammatory response. *Biochem Biophys Res Commun,* 440**,** 105-11.

JACOBSON, E. S. 2000. Pathogenic roles for fungal melanins. *Clin Microbiol Rev,* 13**,** 708-17.

JACOBSON, M. D. 1996. Reactive oxygen species and programmed cell death. *Trends Biochem Sci,* 21**,** 83-6.

JAHN, B., BOUKHALLOUK, F., LOTZ, J., LANGFELDER, K., WANNER, G. & BRAKHAGE, A. A. 2000. Interaction of human phagocytes with pigmentless *Aspergillus* conidia. *Infect Immun,* 68**,** 3736-9.

JAHN, B., KOCH, A., SCHMIDT, A., WANNER, G., GEHRINGER, H., BHAKDI, S. & BRAKHAGE, A. A. 1997. Isolation and characterization of a pigmentless-conidium mutant of *Aspergillus fumigatus* with altered conidial surface and reduced virulence. *Infect Immun,* 65**,** 5110-7.

JAHN, B., LANGFELDER, K., SCHNEIDER, U., SCHINDEL, C. & BRAKHAGE, A. A. 2002. PKSP-dependent reduction of phagolysosome fusion and intracellular kill of *Aspergillus fumigatus* conidia by human monocyte-derived macrophages. *Cell Microbiol,* 4**,** 793-803.

JANEWAY, C. A. J., TRAVERS, P., WALPORT, M. & *AL., E.* 2001. Part I, Chapter 2: The complement system and innate immunity. *In:* JANEWAY, C. (ed.) *Immunobiology: The Immune System in Health and Disease.* 5th edition ed. New York: Garland Science.

JUNG, C. H., RO, S. H., CAO, J., OTTO, N. M. & KIM, D. H. 2010. mTOR regulation of autophagy. *FEBS Lett,* 584**,** 1287-95.

KANEHISA, M., FURUMICHI, M., TANABE, M., SATO, Y. & MORISHIMA, K. 2017. KEGG: new perspectives on genomes, pathways, diseases and drugs. *Nucleic Acids Res,* 45**,** D353-D361.

KAPLAN, C. D. & KAPLAN, J. 2009. Iron acquisition and transcriptional regulation. *Chem Rev,* 109**,** 4536-52.

KIM, E. 2009. Mechanisms of amino acid sensing in mTOR signaling pathway. *Nutr Res Pract,* 3**,** 64-71.

KINSELLA, R. J., KAHARI, A., HAIDER, S., ZAMORA, J., PROCTOR, G., SPUDICH, G., ALMEIDA-KING, J., STAINES, D., DERWENT, P., KERHORNOU, A., KERSEY, P. & FLICEK, P. 2011. Ensembl BioMarts: a hub for data retrieval across taxonomic space. *Database,* Vol. 2011**,** Article ID bar030.

KNIEMEYER, O., SCHMIDT, A. D., VODISCH, M., WARTENBERG, D. & BRAKHAGE, A. A. 2011. Identification of virulence determinants of the human pathogenic fungi *Aspergillus fumigatus* and *Candida albicans* by proteomics. *Int J Med Microbiol,* 301**,** 368-77.

KOUL, A., HERGET, T., KLEBL, B. & ULLRICH, A. 2004. Interplay between *Mycobacteria* and host signalling pathways. *Nat Rev Microbiol,* 2**,** 189-202.

KOUSHA, M., TADI, R. & SOUBANI, A. O. 2011. Pulmonary aspergillosis: a clinical review. *Eur Respir Rev,* 20**,** 156-74.

KOZAKIEWICZ, Z. & SMITH, D. 1994. Physiology of *Aspergillus*. *In:* SMITH, J. E. (ed.) *Aspergillus.* Boston, MA: Springer US.

KOZEL, T. R., WILSON, M. A., FARRELL, T. P. & LEVITZ, S. M. 1989. Activation of C3 and binding to *Aspergillus fumigatus* conidia and hyphae. *Infect Immun,* 57**,** 3412-7.

KRAJCOVIC, M., KRISHNA, S., AKKARI, L., JOYCE, J. A. & OVERHOLTZER, M. 2013. mTOR regulates phagosome and entotic vacuole fission. *Mol Biol Cell,* 24**,** 3736-45.

KRAUS, P. R., HOFMANN, A. F. & HARRIS, S. D. 2002. Characterization of the *Aspergillus nidulans* 14-3-3 homologue, ArtA. *FEMS Microbiol Lett,* 210**,** 61-6.

KWON-CHUNG, K. J. & SUGUI, J. A. 2013. *Aspergillus fumigatus* - what makes the species a ubiquitous human fungal pathogen? *PLoS Pathog,* 9**,** e1003743.

KYRMIZI, I., GRESNIGT, M. S., AKOUMIANAKI, T., SAMONIS, G., SIDIROPOULOS, P., BOUMPAS, D., NETEA, M. G., VAN DE VEERDONK, F. L., KONTOYIANNIS, D. P. & CHAMILOS, G. 2013. Corticosteroids block autophagy protein recruitment in *Aspergillus fumigatus* phagosomes via targeting Dectin-1/Syk kinase signaling. *J Immunol,* 191**,** 1287-99.

LAFOURCADE, C., SOBO, K., KIEFFER-JAQUINOD, S., GARIN, J. & VAN DER GOOT, F. G. 2008. Regulation of the V-ATPase along the endocytic pathway occurs through reversible subunit association and membrane localization. *PLoS One,* 3**,** e2758.

LANGFELDER, K., JAHN, B., GEHRINGER, H., SCHMIDT, A., WANNER, G. & BRAKHAGE, A. A. 1998. Identification of a polyketide synthase gene (*pksP*) of *Aspergillus fumigatus* involved in conidial pigment biosynthesis and virulence. *Med Microbiol Immunol,* 187**,** 79-89.

LATGE, J. P. 1999. *Aspergillus fumigatus* and aspergillosis. *Clin Microbiol Rev,* 12**,** 310-50.

LAU, G. W., HASSETT, D. J., RAN, H. & KONG, F. 2004. The role of pyocyanin in *Pseudomonas aeruginosa* infection. *Trends Mol Med,* 10**,** 599-606.

LEE, B. Y., JETHWANEY, D., SCHILLING, B., CLEMENS, D. L., GIBSON, B. W. & HORWITZ, M. A. 2010. The *Mycobacterium bovis* bacille Calmette-Guerin phagosome proteome. *Mol Cell Proteomics,* 9**,** 32-53.

LEVITZ, S. M., SELSTED, M. E., GANZ, T., LEHRER, R. I. & DIAMOND, R. D. 1986. In vitro killing of spores and hyphae of *Aspergillus fumigatus* and *Rhizopus oryzae* by rabbit neutrophil cationic peptides and bronchoalveolar macrophages. *J Infect Dis,* 154**,** 483-9.

LIM, M. X., PNG, C. W., TAY, C. Y., TEO, J. D., JIAO, H., LEHMING, N., TAN, K. S. & ZHANG, Y. 2014. Differential regulation of proinflammatory cytokine expression by mitogen-activated protein kinases in macrophages in response to intestinal parasite infection. *Infect Immun,* 82**,** 4789-801.

LIN, S. J., SCHRANZ, J. & TEUTSCH, S. M. 2001. Aspergillosis case-fatality rate: systematic review of the literature. *Clin Infect Dis,* 32**,** 358-66.

LIU, G. Y., ESSEX, A., BUCHANAN, J. T., DATTA, V., HOFFMAN, H. M., BASTIAN, J. F., FIERER, J. & NIZET, V. 2005. *Staphylococcus aureus* golden pigment impairs neutrophil killing and promotes virulence through its antioxidant activity. *J Exp Med,* 202**,** 209-15.

LIU, G. Y. & NIZET, V. 2009. Color me bad: microbial pigments as virulence factors. *Trends Microbiol,* 17**,** 406-13.

LU, H., ZHU, Y. F., XIONG, J., WANG, R. & JIA, Z. 2015. Potential extra-ribosomal functions of ribosomal proteins in *Saccharomyces cerevisiae*. *Microbiol Res,* 177**,** 28-33.

MA, J., BECKER, C., LOWELL, C. A. & UNDERHILL, D. M. 2012. Dectin-1-triggered recruitment of light chain 3 protein to phagosomes facilitates major histocompatibility complex class II presentation of fungal-derived antigens. *J Biol Chem,* 287**,** 34149-56.

MA, J., BECKER, C., REYES, C. & UNDERHILL, D. M. 2014. Cutting edge: FYCO1 recruitment to dectin-1 phagosomes is accelerated by light chain 3 protein and regulates phagosome maturation and reactive oxygen production. *J Immunol,* 192**,** 1356-60.

MA, J. & UNDERHILL, D. M. 2013. β-Glucan signaling connects phagocytosis to autophagy. *Glycobiology,* 23**,** 1047-51.

MADAN, T., EGGLETON, P., KISHORE, U., STRONG, P., AGGRAWAL, S. S., SARMA, P. U. & REID, K. B. 1997. Binding of pulmonary surfactant proteins A and D to *Aspergillus fumigatus* conidia enhances phagocytosis and killing by human neutrophils and alveolar macrophages. *Infect Immun,* 65**,** 3171-9.

MANSOUR, M. K., TAM, J. M., KHAN, N. S., SEWARD, M., DAVIDS, P. J., PURANAM, S., SOKOLOVSKA, A., SYKES, D. B., DAGHER, Z., BECKER, C., TANNE, A., REEDY, J. L., STUART, L. M. & VYAS, J. M. 2013. Dectin-1 activation controls maturation of β-1,3-glucan-containing phagosomes. *J Biol Chem,* 288**,** 16043-54.

MARTINEZ, J., MALIREDDI, R. K., LU, Q., DIAS CUNHA, L., PELLETIER, S., GINGRAS, S., ORCHARD, R., GUAN, J. L., TAN, H., PENG, J., KANNEGANTI, T. D., VIRGIN, H. W. & GREEN, D. R. 2015. Molecular characterization of LC3-associated phagocytosis reveals distinct roles for Rubicon, NOX2 and autophagy proteins. *Nat Cell Biol,* 17**,** 893-906.

MATSUZAWA, T., KIM, B. H., SHENOY, A. R., KAMITANI, S., MIYAKE, M. & MACMICKING, J. D. 2012. IFN-γ elicits macrophage autophagy via the p38 MAPK signaling pathway. *J Immunol,* 189**,** 813-8.

MEGGER, D. A., POTT, L. L., AHRENS, M., PADDEN, J., BRACHT, T., KUHLMANN, K., EISENACHER, M., MEYER, H. E. & SITEK, B. 2014. Comparison of label-free and label-based strategies for proteome analysis of hepatoma cell lines. *Biochim Biophys Acta,* 1844**,** 967-76.

MEIER, A., KIRSCHNING, C. J., NIKOLAUS, T., WAGNER, H., HEESEMANN, J. & EBEL, F. 2003. Toll-like receptor (TLR) 2 and TLR4 are essential for *Aspergillus*-induced activation of murine macrophages. *Cell Microbiol,* 5**,** 561-70.

MERESSE, S., STEELE-MORTIMER, O., MORENO, E., DESJARDINS, M., FINLAY, B. & GORVEL, J. P. 1999. Controlling the maturation of pathogen-containing vacuoles: a matter of life and death. *Nat Cell Biol,* 1**,** E183-8.

MIRCESCU, M. M., LIPUMA, L., VAN ROOIJEN, N., PAMER, E. G. & HOHL, T. M. 2009. Essential role for neutrophils but not alveolar macrophages at early time points following *Aspergillus fumigatus* infection. *J Infect Dis,* 200**,** 647-56.

MOLINARI, M., GALLI, C., NORAIS, N., TELFORD, J. L., RAPPUOLI, R., LUZIO, J. P. & MONTECUCCO, C. 1997. Vacuoles induced by *Helicobacter pylori* toxin contain both late endosomal and lysosomal markers. *J Biol Chem,* 272**,** 25339-44.

MOODLEY, L., PILLAY, J. & DHEDA, K. 2014. Aspergilloma and the surgeon. *J Thorac Dis,* 6**,** 202-9.

MUKHERJEE, S., ZHA, X., TABAS, I. & MAXFIELD, F. R. 1998. Cholesterol distribution in living cells: fluorescence imaging using dehydroergosterol as a fluorescent cholesterol analog. *Biophys J,* 75**,** 1915-25.

NOSANCHUK, J. D. & CASADEVALL, A. 2003. The contribution of melanin to microbial pathogenesis. *Cell Microbiol,* 5**,** 203-23.

O'GORMAN, C. M., FULLER, H. & DYER, P. S. 2009. Discovery of a sexual cycle in the opportunistic fungal pathogen *Aspergillus fumigatus*. *Nature,* 457**,** 471-4.

OKAI, B., LYALL, N., GOW, N. A., BAIN, J. M. & ERWIG, L. P. 2015. Rab14 regulates maturation of macrophage phagosomes containing the fungal pathogen *Candida albicans* and outcome of the host-pathogen interaction. *Infect Immun,* 83**,** 1523-35.

OLIVEROS, J. C. 2007 - 2015. Venny. An interactive tool for comparing lists with Venn's diagrams. (http://bioinfogp.cnb.csic.es/tools/venny/index.html).

PAEHTZ, V. 2015. *Mechanismen der Wirtsadaptation von Aspergillus fumigatus.* Dissertation, Friedrich Schiller Universität Jena.

PAL, A. K., GAJJAR, D. U. & VASAVADA, A. R. 2014. DOPA and DHN pathway orchestrate melanin synthesis in *Aspergillus* species. *Med Mycol,* 52**,** 10-8.

PARIS, S., BOISVIEUX-ULRICH, E., CRESTANI, B., HOUCINE, O., TARAMELLI, D., LOMBARDI, L. & LATGE, J. P. 1997. Internalization of *Aspergillus fumigatus* conidia by epithelial and endothelial cells. *Infect Immun,* 65**,** 1510-4.

PARIS, S., DEBEAUPUIS, J. P., CRAMERI, R., CAREY, M., CHARLES, F., PREVOST, M. C., SCHMITT, C., PHILIPPE, B. & LATGE, J. P. 2003a. Conidial hydrophobins of *Aspergillus fumigatus*. *Appl Environ Microbiol,* 69**,** 1581-8.

PARIS, S., WYSONG, D., DEBEAUPUIS, J. P., SHIBUYA, K., PHILIPPE, B., DIAMOND, R. D. & LATGE, J. P. 2003b. Catalases of *Aspergillus fumigatus*. *Infect Immun,* 71**,** 3551-62.

PARK, S. J. & MEHRAD, B. 2009. Innate immunity to *Aspergillus* species. *Clin Microbiol Rev,* 22**,** 535-51.

PÉREZ-SÁEZ, M. J., MIR, M., MONTERO, M. M., CRESPO, M., MONTERO, N., GÓMEZ, J., HORCAJADA, J. P. & PASCUAL, J. 2014. Invasive aspergillosis in kidney transplant recipients: a cohort study. *Exp Clin Transplant,* 12**,** 101-105.

PHILIPPE, B., IBRAHIM-GRANET, O., PREVOST, M. C., GOUGEROT-POCIDALO, M. A., SANCHEZ PEREZ, M., VAN DER MEEREN, A. & LATGE, J. P. 2003. Killing of *Aspergillus fumigatus* by alveolar macrophages is mediated by reactive oxidant intermediates. *Infect Immun,* 71**,** 3034-42.

PUERTOLLANO, R. 2014. mTOR and lysosome regulation. *F1000Prime Rep,* 6**,** 52.

PUGAZHENTHI, S., NESTEROVA, A., SABLE, C., HEIDENREICH, K. A., BOXER, L. M., HEASLEY, L. E. & REUSCH, J. E. 2000. Akt/protein kinase B up-regulates Bcl-2 expression through cAMP-response element-binding protein. *J Biol Chem,* 275**,** 10761-6.

RAMAPRAKASH, H., ITO, T., STANDIFORD, T. J., KUNKEL, S. L. & HOGABOAM, C. M. 2009. Toll-like receptor 9 modulates immune responses to *Aspergillus fumigatus* conidia in immunodeficient and allergic mice. *Infect Immun,* 77**,** 108-19.

RAMBACH, G., DUM, D., MOHSENIPOUR, I., HAGLEITNER, M., WURZNER, R., LASS-FLORL, C. & SPETH, C. 2010. Secretion of a fungal protease represents a complement evasion mechanism in cerebral aspergillosis. *Mol Immunol,* 47**,** 1438-49.

RAMBACH, G., MAIER, H., VAGO, G., MOHSENIPOUR, I., LASS-FLORL, C., DEFANT, A., WURZNER, R., DIERICH, M. P. & SPETH, C. 2008. Complement induction and complement evasion in patients with cerebral aspergillosis. *Microbes Infect,* 10**,** 1567-76.

RAUNIYAR, N. & YATES, J. R., 3RD 2014. Isobaric labeling-based relative quantification in shotgun proteomics. *J Proteome Res,* 13**,** 5293-309.

REMMELE, C. W., LUTHER, C. H., BALKENHOL, J., DANDEKAR, T., MULLER, T. & DITTRICH, M. T. 2015. Integrated inference and evaluation of host-fungi interaction networks. *Front Microbiol,* 6**,** 764.

RINK, J., GHIGO, E., KALAIDZIDIS, Y. & ZERIAL, M. 2005. Rab conversion as a mechanism of progression from early to late endosomes. *Cell,* 122**,** 735-49.

RODRIGUEZ-PRADOS, J. C., TRAVES, P. G., CUENCA, J., RICO, D., ARAGONES, J., MARTIN-SANZ, P., CASCANTE, M. & BOSCA, L. 2010. Substrate fate in activated macrophages: a comparison between innate, classic, and alternative activation. *J Immunol,* 185**,** 605-14.

ROGERS, L. D. & FOSTER, L. J. 2007. The dynamic phagosomal proteome and the contribution of the endoplasmic reticulum. *Proc Natl Acad Sci U S A,* 104**,** 18520-5.

RUBINO, I., COSTE, A., LE ROY, D., ROGER, T., JATON, K., BOECKH, M., MONOD, M., LATGE, J. P., CALANDRA, T. & BOCHUD, P. Y. 2012. Species-specific recognition of *Aspergillus fumigatus* by Toll-like receptor 1 and Toll-like receptor 6. *J Infect Dis,* 205**,** 944-54.

RUHLAND, A., LEAL, N. & KIMA, P. E. 2007. *Leishmania promastigotes* activate PI3K/Akt signalling to confer host cell resistance to apoptosis. *Cell Microbiol,* 9**,** 84-96.

SANJUAN, M. A., DILLON, C. P., TAIT, S. W., MOSHIACH, S., DORSEY, F., CONNELL, S., KOMATSU, M., TANAKA, K., CLEVELAND, J. L., WITHOFF, S. & GREEN, D. R. 2007. Toll-like receptor signalling in macrophages links the autophagy pathway to phagocytosis. *Nature,* 450**,** 1253-7.

SATO, I., SHIMIZU, M., HOSHINO, T. & TAKAYA, N. 2009. The glutathione system of *Aspergillus nidulans* involves a fungus-specific glutathione S-transferase. *J Biol Chem,* 284**,** 8042-53.

SCAPINI, P., LAPINET-VERA, J. A., GASPERINI, S., CALZETTI, F., BAZZONI, F. & CASSATELLA, M. A. 2000. The neutrophil as a cellular source of chemokines. *Immunol Rev,* 177**,** 195-203.

SCHAFFNER, A., DOUGLAS, H., BRAUDE, A. I. & DAVIS, C. E. 1983. Killing of *Aspergillus* spores depends on the anatomical source of the macrophage. *Infect Immun,* 42**,** 1109-15.

SEGAL, A. W. 2005. How neutrophils kill microbes. *Annu Rev Immunol,* 23**,** 197-223.

SEIDER, K., BRUNKE, S., SCHILD, L., JABLONOWSKI, N., WILSON, D., MAJER, O., BARZ, D., HAAS, A., KUCHLER, K., SCHALLER, M. & HUBE, B. 2011. The facultative intracellular pathogen *Candida glabrata* subverts macrophage cytokine production and phagolysosome maturation. *J Immunol,* 187**,** 3072-86.

SERRANO-GOMEZ, D., DOMINGUEZ-SOTO, A., ANCOCHEA, J., JIMENEZ-HEFFERNAN, J. A., LEAL, J. A. & CORBI, A. L. 2004. Dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin mediates binding and internalization of *Aspergillus fumigatus* conidia by dendritic cells and macrophages. *J Immunol,* 173**,** 5635-43.

SHUI, W., PETZOLD, C. J., REDDING, A., LIU, J., PITCHER, A., SHEU, L., HSIEH, T., KEASLING, J. D. & BERTOZZI, C. R. 2011. Organelle membrane proteomics reveals differential influence of mycobacterial lipoglycans on macrophage phagosome maturation and autophagosome accumulation. *J Proteome Res,* 339**,** 339-348.

SHUI, W., SHEU, L., LIU, J., SMART, B., PETZOLD, C. J., HSIEH, T. Y., PITCHER, A., KEASLING, J. D. & BERTOZZI, C. R. 2008. Membrane proteomics of phagosomes suggests a connection to autophagy. *Proc Natl Acad Sci U S A,* 105**,** 16952-7.

SILVA, P. M., GONCALVES, S. & SANTOS, N. C. 2014. Defensins: antifungal lessons from eukaryotes. *Front Microbiol,* 5**,** 97.

SINGH, N. & HUSAIN, S. 2013. Aspergillosis in solid organ transplantation. *Am J Transplant,* 13 Suppl 4**,** 228-41.

SLESIONA, S., GRESSLER, M., MIHLAN, M., ZAEHLE, C., SCHALLER, M., BARZ, D., HUBE, B., JACOBSEN, I. D. & BROCK, M. 2012. Persistence versus escape: *Aspergillus terreus* and *Aspergillus fumigatus* employ different strategies during interactions with macrophages. *PLoS One,* 7**,** e31223.

SMITH, A. C., HEO, W. D., BRAUN, V., JIANG, X., MACRAE, C., CASANOVA, J. E., SCIDMORE, M. A., GRINSTEIN, S., MEYER, T. & BRUMELL, J. H. 2007. A network of Rab GTPases controls phagosome maturation and is modulated by *Salmonella enterica* serovar Typhimurium. *J Cell Biol,* 176**,** 263-8.

STEELE, C., RAPAKA, R. R., METZ, A., POP, S. M., WILLIAMS, D. L., GORDON, S., KOLLS, J. K. & BROWN, G. D. 2005. The β-glucan receptor dectin-1 recognizes specific morphologies of *Aspergillus fumigatus*. *PLoS Pathog,* 1**,** e42.

STEINHAUSER, C., HEIGL, U., TCHIKOV, V., SCHWARZ, J., GUTSMANN, T., SEEGER, K., BRANDENBURG, J., FRITSCH, J., SCHROEDER, J., WIESMULLER, K. H., ROSENKRANDS, I., WALTHER, P., POTT, J., KRAUSE, E., EHLERS, S., SCHNEIDER-BRACHERT, W., SCHUTZE, S. & REILING, N. 2013. Lipid-labeling facilitates a novel magnetic isolation procedure to characterize pathogen-containing phagosomes. *Traffic,* 14**,** 321-36.

STEVENS, D. A., B., M. R., KURUP, V. P., KNUTSEN, A. P., GREENBERGER, P., JUDSON, M. A., DENNING, D. W., CRAMERI, R., BRODY, A. S., LIGHT, M., SKOV, M., MAISH, W. & MASTELLA, G. 2003. Allergic bronchopulmonary aspergillosis in cystic fibrosis - state of the art: cystic fibrosis foundation consensus conference. *Clin Infect Dis,* 37 (Suppl. 3)**,** S225-S264.

STURTEVANT, J. & LATGE, J. P. 1992a. Participation of complement in the phagocytosis of the conidia of *Aspergillus fumigatus* by human polymorphonuclear cells. *J Infect Dis,* 166**,** 580-6.

STURTEVANT, J. E. & LATGE, J. P. 1992b. Interactions between conidia of *Aspergillus fumigatus* and human complement component C3. *Infect Immun,* 60**,** 1913-8.

SUMMERS, C., RANKIN, S. M., CONDLIFFE, A. M., SINGH, N., PETERS, A. M. & CHILVERS, E. R. 2010. Neutrophil kinetics in health and disease. *Trends Immunol,* 31**,** 318-24.

SUN-WADA, G. H., TABATA, H., KAWAMURA, N., AOYAMA, M. & WADA, Y. 2009. Direct recruitment of H^+-ATPase from lysosomes for phagosomal acidification. *J Cell Sci,* 122**,** 2504-13.

SVIRSHCHEVSKAYA, E. V., SHEVCHENKO, M. A., HUET, D., FEMENIA, F., LATGE, J. P., BOIREAU, P. & BERKOVA, N. P. 2009. Susceptibility of mice to invasive aspergillosis correlates with delayed cell influx into the lungs. *Int J Immunogenet,* 36**,** 289-99.

SZKLARCZYK, D., FRANCESCHINI, A., WYDER, S., FORSLUND, K., HELLER, D., HUERTA-CEPAS, J., SIMONOVIC, M., ROTH, A., SANTOS, A., TSAFOU, K. P., KUHN, M., BORK, P., JENSEN, L. J. & VON MERING, C. 2015. STRING v10: protein-protein interaction networks, integrated over the tree of life. *Nucleic Acids Res,* 43**,** D447-52.

TEUTSCHBEIN, J., ALBRECHT, D., POTSCH, M., GUTHKE, R., AIMANIANDA, V., CLAVAUD, C., LATGE, J. P., BRAKHAGE, A. A. & KNIEMEYER, O. 2010. Proteome profiling and functional classification of intracellular proteins from conidia of the human-pathogenic mold *Aspergillus fumigatus*. *J Proteome Res,* 9**,** 3427-42.

THI, E. P., LAMBERTZ, U. & REINER, N. E. 2012. Sleeping with the enemy: how intracellular pathogens cope with a macrophage lifestyle. *PLoS Pathog,* 8**,** e1002551.

THYWISSEN, A. 2012. *Molekulare Mechansimen der Interaktion von Aspergillus fumigatus mit Makrophagen.* Dissertation, Friedrich-Schiller Universität Jena.

THYWISSEN, A., HEINEKAMP, T., DAHSE, H. M., SCHMALER-RIPCKE, J., NIETZSCHE, S., ZIPFEL, P. F. & BRAKHAGE, A. A. 2011. Conidial dihydroxynaphthalene melanin of the human pathogenic fungus *Aspergillus fumigatus* interferes with the host endocytosis pathway. *Front Microbiol,* 2**,** 96.

TOMEE, J. F., WIERENGA, A. T., HIEMSTRA, P. S. & KAUFFMAN, H. K. 1997. Proteases from *Aspergillus fumigatus* induce release of proinflammatory cytokines and cell detachment in airway epithelial cell lines. *J Infect Dis,* 176**,** 300-3.

TOWBIN, H., STAEHELIN, T. & GORDON, J. 1979. Electrophoretic transfer of proteins from polyacrylamide gels to nitrocellulose sheets: procedure and some applications. *Proc Natl Acad Sci U S A,* 76**,** 4350-4.

TROST, M., ENGLISH, L., LEMIEUX, S., COURCELLES, M., DESJARDINS, M. & THIBAULT, P. 2009. The phagosomal proteome in interferon-γ-activated macrophages. *Immunity,* 30**,** 143-54.

TSURUTA, F., MASUYAMA, N. & GOTOH, Y. 2002. The phosphatidylinositol 3-kinase (PI3K)-Akt pathway suppresses Bax translocation to mitochondria. *J Biol Chem,* 277**,** 14040-7.

UPADHYAY, S., XU, X., LOWRY, D., JACKSON, J. C., ROBERSON, R. W. & LIN, X. 2016. Subcellular compartmentalization and trafficking of the biosynthetic machinery for fungal melanin. *Cell Rep,* 14**,** 2511-8.

VENABLE, J. H. & COGGESHALL, R. 1965. A simplified lead citrate stain for use in electron microscopy. *J Cell Biol,* 25**,** 407-8.

VIA, L. E., DERETIC, D., ULMER, R. J., HIBLER, N. S., HUBER, L. A. & DERETIC, V. 1997. Arrest of mycobacterial phagosome maturation is caused by a block in vesicle fusion between stages controlled by Rab5 and Rab7. *J Biol Chem,* 272**,** 13326-31.

VODISCH, M., SCHERLACH, K., WINKLER, R., HERTWECK, C., BRAUN, H. P., ROTH, M., HAAS, H., WERNER, E. R., BRAKHAGE, A. A. & KNIEMEYER, O. 2011. Analysis of the *Aspergillus fumigatus* proteome reveals metabolic changes and the activation of the pseurotin A biosynthesis gene cluster in response to hypoxia. *J Proteome Res,* 10**,** 2508-24.

VOGL, G., LESIAK, I., JENSEN, D. B., PERKHOFER, S., ECK, R., SPETH, C., LASS-FLORL, C., ZIPFEL, P. F., BLOM, A. M., DIERICH, M. P. & WURZNER, R. 2008. Immune evasion by acquisition of complement inhibitors: the mould *Aspergillus* binds both factor H and C4b binding protein. *Mol Immunol,* 45**,** 1485-93.

VOLLING, K., BRAKHAGE, A. A. & SALUZ, H. P. 2007. Apoptosis inhibition of alveolar macrophages upon interaction with conidia of *Aspergillus fumigatus*. *FEMS Microbiol Lett,* 275**,** 250-4.

VOLLING, K., THYWISSEN, A., BRAKHAGE, A. A. & SALUZ, H. P. 2011. Phagocytosis of melanized *Aspergillus* conidia by macrophages exerts cytoprotective effects by sustained PI3K/Akt signalling. *Cell Microbiol,* 13**,** 1130-48.

WANG, Y., AISEN, P. & CASADEVALL, A. 1995. *Cryptococcus neoformans* melanin and virulence: mechanism of action. *Infect Immun,* 63**,** 3131-6.

WANG, Y. & CASADEVALL, A. 1994. Growth of *Cryptococcus neoformans* in presence of L-dopa decreases its susceptibility to amphotericin B. *Antimicrob Agents Chemother,* 38**,** 2648-50.

WARNER, J. R. & MCINTOSH, K. B. 2009. How common are extraribosomal functions of ribosomal proteins? *Mol Cell,* 34**,** 3-11.

WASHBURN, R. G., DEHART, D. J., AGWU, D. E., BRYANT-VARELA, B. J. & JULIAN, N. C. 1990. *Aspergillus fumigatus* complement inhibitor: production, characterization, and purification by hydrophobic interaction and thin-layer chromatography. *Infect Immun,* 58**,** 3508-15.

WASYLNKA, J. A. & MOORE, M. M. 2003. *Aspergillus fumigatus* conidia survive and germinate in acidic organelles of A549 epithelial cells. *J Cell Sci,* 116**,** 1579-87.

WEIDNER, G., D'ENFERT, C., KOCH, A., MOL, P. C. & BRAKHAGE, A. A. 1998. Development of a homologous transformation system for the human pathogenic fungus *Aspergillus fumigatus* based on the *pyrG* gene encoding orotidine 5'-monophosphate decarboxylase. *Curr Genet,* 33**,** 378-85.

WELLEN, K. E., HATZIVASSILIOU, G., SACHDEVA, U. M., BUI, T. V., CROSS, J. R. & THOMPSON, C. B. 2009. ATP-citrate lyase links cellular metabolism to histone acetylation. *Science,* 324**,** 1076-80.

WESSEL, D. & FLUGGE, U. I. 1984. A method for the quantitative recovery of protein in dilute solution in the presence of detergents and lipids. *Anal Biochem,* 138**,** 141-3.

WEST, A. P., BRODSKY, I. E., RAHNER, C., WOO, D. K., ERDJUMENT-BROMAGE, H., TEMPST, P., WALSH, M. C., CHOI, Y., SHADEL, G. S. & GHOSH, S. 2011. TLR signalling augments macrophage bactericidal activity through mitochondrial ROS. *Nature,* 472**,** 476-80.

YOUNGCHIM, S., MORRIS-JONES, R., HAY, R. J. & HAMILTON, A. J. 2004. Production of melanin by *Aspergillus fumigatus*. *J Med Microbiol,* 53**,** 175-81.

ZAREMBER, K. A., SUGUI, J. A., CHANG, Y. C., KWON-CHUNG, K. J. & GALLIN, J. I. 2007. Human polymorphonuclear leukocytes inhibit *Aspergillus fumigatus* conidial growth by lactoferrin-mediated iron depletion. *J Immunol,* 178**,** 6367-73.

ZHONG, Y., WANG, Q. J., LI, X., YAN, Y., BACKER, J. M., CHAIT, B. T., HEINTZ, N. & YUE, Z. 2009. Distinct regulation of autophagic activity by Atg14L and Rubicon associated with Beclin 1-phosphatidylinositol-3-kinase complex. *Nat Cell Biol,* 11**,** 468-76.

ZHOU, Y. Y., LI, Y., JIANG, W. Q. & ZHOU, L. F. 2015. MAPK/JNK signalling: a potential autophagy regulation pathway. *Biosci Rep,* 35.

ZIPFEL, P. F. & SKERKA, C. 2009. Complement regulators and inhibitory proteins. *Nat Rev Immunol,* 9**,** 729-40.

Figures and tables

List of figures

List of tables

Table of abbreviations

° C	Degree Celsius
A.	*Aspergillus*
ABPA	Allergic bronchopulmonary aspergillosis
Acly	ATP citrate lyase
AGC	Automatic gain control
AMM	*Aspergillus* minimal medium
AspGD	*Aspergillus* genome database
ATCC	American Type Culture Collection
ATP	Adenosine triphosphate
BMDM	Bone marrow-derived macrophage
BP	Biological process
BSA	Bovine serum albumin
C.	*Candida*
CC	Cellular compartment
CD	Cluster of differentiation
CF	Cystic fibrosis
CFW	Calcofluor white
CGD	Chronic granulomatous disease
CLSM	Confocal laser scanning microscopy
CoA	Coenzyme A
COX4	Cytochrome c oxidase subunit 4
CR3	Complement receptor 3
CTB	Cholera toxin B
Cys	Cysteine
DC-SIGN	Dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin
DHN	1,8-dihydroxynaphthalene
DMEM	Dulbecco’s modified eagle medium
DNA	Deoxyribonucleic acid
DRM	Detergent-resistant membrane
DSM	Detergent-soluble membrane
EEA1	Early endosomal antigen 1
e.g.	*exempli gratia,* for example
EH	Eps15 homology
EMZ	Elektronenmikroskopisches Zentrum
EPS	Epidermal growth factor receptor pathway substrate 15
ER	Endoplasmic reticulum
ERK	Extracellular signal-regulated kinase
FcγR	Fragment, crystallisable gamma receptor
FDR	False discovery rate
FH	Factor H
FITC	Fluorescein isothiocyanate
GAG	Galactosaminoglycan
G-CSF	Granulocyte colony-stimulating factor
GAP	GTPase-activating protein
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
GDP	Guanine diphosphate
GEF	GTP-exchange factor
GM-CSF	Granulocyte-macrophage colony-stimulating factor
GM1	Monosialotetrahexosylganglioside
GO	Gene ontology
GPI	Glycosylphosphatidylinositol
GTP	Guanine triphosphate
h	Hour
HIV	Human immunodeficiency virus
HRP	Horseradish peroxidase
i.e.	*id est,* that is
IA	Invasive aspergillosis
IFN	Interferon
IgG	Immunoglobulin G
IL	Interleukin
ITAM	Immunoreceptor tyrosine-based activation motif
KEGG	Kyoto Encyclopedia of Genes and Genomes

Lamp1	Lysosomal-associated membrane protein 1
Lamtor	Late endosomal/lysosomal adaptor, MAPK and mTOR activator
LAP	LC3B-associated phagocytosis
LC-MS/MS	Liquid chromatography-tandem mass spectrometry
LC3B	Microtubule-associated protein 1 light chain 3 beta
LCV	*Legionella*-containing vacuoles
L-DOPA	L-3,4-dihydroxyphenylalanine
M.	*Mus*
m/z	Mass/charge
min	Minute
MAPK	Mitogen-activated protein kinase
Met	Methionine
MF	Molecular function
MHC	Major histocompatibility complex
MIP	Macrophage inflammatory protein
MOI	Multiplicity of infection
MPO	Myeloperoxidase
mRNA	Messenger ribonucleic acid
mTOR	Molecular target of rapamycin
MW	Molecular weight
NAD	Nicotinamide adenine dinucleotide
NADP	Nicotinamide adenine dinucleotide phosphate
Ncf	Neutrophil cytosolic factor
Nduf	NADH dehydrogenase
NET	Neutrophil extracellular traps
NFκB	Nuclear factor kappa b
NHS	N-hydroxysulfosuccinimide
NOX	NADPH oxidase
OXPHOS	Oxidative phosphorylation
PAGE	Polyacrylamide gel electrophoresis
PAMP	Pathogen-associated molecular pattern
PBS	Phosphate buffered saline
PE	Phosphatidylethanolamine
pH	Lat. *Potential Hydrogenii*
PI3K	Phosphatidylinositol-3 kinase
Pks	Polyketide synthase
PL	Phagolysosome
PMN	Polymorphonuclear neutrophil
PPI	Protein-protein interaction
Ppm	Parts per million
PPP	Pentose phosphate pathway
PRR	Pathogen recognition receptor
PSM	Peptide spectrum match
Ptx3	Pentraxin 3
RNA	Ribonucleic acid
ROS	Reactive oxygen species
Rubicon	Run domain Beclin-1-interacting and cysteine-rich domain-containing protein
SDS	Sodium dodecyl sulfate
SNAP	Synaptosomal-associated protein
SNARE	Soluble N-ethylmaleimide-sensitive-factor attachment receptor
TCEP	Tris(2-carboxyethyl)phosphine
TEAB	Triethylammonium bicarbonate
TEM	Transmission electron microscopy
TFA	Trifluoric acid
TLR	Toll-like receptor
TMT	Tandem mass tag
TNF	Tumor necrosis factor
UV	Ultraviolet
v/v	Volume per volume; Volume fraction
Vamp	Vesicle-associated membrane protein
vATPase	Vacuolar ATPase
Vti	Vesicle transport through interaction with t-SNARE
w/v	Weight per volume; Mass fraction
wt	Wild-type

Appendix

List of publications

Heinekamp T, **Schmidt H**, Lapp K, Pähtz V, Shopova I, Köster-Eiserfunke N, Krüger T, Kniemeyer O, Brakhage AA (2015) Interference of *Aspergillus fumigatus* with the immune response. *Semin Immunopathol* 37(2), 141-152. (Review)

Krüger T, Luo T, **Schmidt H**, Shopova I, Kniemeyer O (2015) Challenges and strategies for proteome analysis of the interaction of human pathogenic fungi with host immune cells. *Proteomes* 3(4), 467-495. (Review)

Johns A, Scharf DH, Gsaller F, **Schmidt H**, Heinekamp T, Straßburger M, Oliver JD, Gilsenan J, Rash B, Bignell E, Brakhage AA, Bromley MJ (2017) A non-redundant phosphopantetheinyl transferase, PptA, is a novel antifungal target that directs secondary metabolite, siderophore and lysine biosynthesis in *Aspergillus fumigatus* and is critical for pathogenicity. *eBio*. *Manuscript in revision*

Schmidt F*, **Schmidt H***, Thywißen A*, Röcker M, Westermann M, Gräler M, Cseresnyés Z, Chamilos G, Figge MT, Heinekamp T, Filler SG, Brakhage AA (2017) Fungal strategy of virulence by counteracting lipid raft formation of phagolysosomes. *Manuscript in preparation*; *shared first authorship

Schmidt H, Vlaic S, Krüger T, Balkenhol J, Thywißen A, Dandekar T, Guthke R, Kniemeyer O, Heinekamp T, Brakhage AA. Phagolysosomal proteomics identifies DHN-melanin-regulated processes in activated macrophages in response to *Aspergillus fumigatus* conidia. *Manuscript in preparation*

Mattern DJ, Raguz L, **Schmidt H**, Kraibooj K, Schoeler H, Weber J, Viediernikova I, Scherlach K, Thywißen A, Hillmann F, Hertweck C, Valiante V, Figge MT, Beemelmanns C, Brakhage AA. Identification of the biosynthetic gene cluster for the sphingolipid inhibitor, sphingofungin, in *Aspergillus fumigatus*. *Manuscript in preparation*

Atanasova Shopova I, Krüger T, Dasari P, Petzold S, Belyaev I, Svensson C-M, Medyukhina A, Figge MT, Szeifert V, Nietzsche S, **Schmidt H**, Conrad T, Guthke R, von Lilienfeld-Toal M, Zipfel P, Ligeti E, Brakhage AA. *Aspergillus fumigatus* melanin manipulates the cargo and kinetics of neutrophil-derived microvesicles. *Manuscript in preparation*

Conference contributions

Hella Schmidt, Thorsten Heinekamp, Andreas Thywißen, Axel A Brakhage
Aspergillus fumigatus interferes with the maturation of macrophage phagolysosomes
JSMC Symposium (2013) Jena, Germany, oral presentation

Hella Schmidt, Andreas Thywißen, Axel A Brakhage
Aspergillus fumigatus interferes with the maturation of macrophage phagosomes
48th Annual Scientific Meeting of the European Society for Clinical Investigation (ESCI) (2014), Utrecht, The Netherlands, poster presentation

Hella Schmidt, Thorsten Heinekamp, Andreas Thywißen, Axel A Brakhage
Aspergillus fumigatus interferes with the maturation of macrophage phagolysosomes
JSMC Symposium (2014) Jena, Germany, oral presentation

Hella Schmidt, Andreas Thywißen, Scott G Filler, Thorsten Heinekamp, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Axel A Brakhage
The fungal pathogen *Aspergillus fumigatus* interferes with the maturation of macrophage phagolysosomes
5th International Conference on Microbial Communication (MiCom) (2015) Jena, Germany, oral presentation

Hella Schmidt, Andreas Thywißen, Scott G Filler, Thorsten Heinekamp, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Axel A Brakhage
Conidia of the human pathogenic fungus *Aspergillus fumigatus* interfere with the maturation of macrophage phagolysosomes
49th Annual Scientific Meeting of the European Society for Clinical Investigation (ESCI) (2015), Cluj-Napoca, Romania, poster presentation

Hella Schmidt, Andreas Thywißen, Scott G Filler, Thorsten Heinekamp, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Axel A Brakhage
Conidia of the human pathogenic fungus *Aspergillus fumigatus* interfere with the maturation of macrophage phagolysosomes
49th Scientific Conference of the German speaking Mycological Society e.V. (DMykG Tagung) (2015), Jena, Germany, poster presentation

Hella Schmidt, Andreas Thywißen, Scott G Filler, Thorsten Heinekamp, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Axel A Brakhage
The fungal pathogen *Aspergillus fumigatu*s interferes with the maturation of macrophage phagolysosomes
67th Annual Meeting of the German Society for Hygiene and Microbiology (Jahrestagung der Deutschen Gesellschaft für Hygiene und Mikrobiologie, DGHM) (2015), Münster, Germany, oral presentation

Hella Schmidt, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Thorsten Heinekamp, Scott G Filler, Axel A Brakhage
Interaction of the human pathogenic fungus *Aspergillus fumigatus* with alveolar macrophages
Annual Meeting of the Association for General and Applied Microbiology. (Jahrestagung der Vereinigung für Allgemeine und Angewandte Mikrobiologie, VAAM) (2016), Jena; Germany, poster presentation

Hella Schmidt, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Thorsten Heinekamp, Axel A Brakhage
Interference of *Aspergillus fumigatus* conidia with the maturation of macrophage phagolysosomes
50th Annual Scientific Meeting of the European Society for Clinical Investigation (ESCI) (2015), Paris, France, oral presentation

Hella Schmidt, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Scott G. Filler, Thorsten Heinekamp, Olaf Kniemeyer, Axel A Brakhage
Interaction of the human pathogenic fungus *Aspergillus fumigatus* with alveolar macrophages
50th Scientific Conference of the German speaking Mycological Society e.V. (DMyk Tagung) (2016), Essen, Germany, poster presentation

Hella Schmidt, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Scott G. Filler, Thorsten Heinekamp, Olaf Kniemeyer, Axel A Brakhage
Interaction of the human pathogenic fungus *Aspergillus fumigatus* with alveolar macrophages
IFoFun – Virulence Mechanisms of Phyto- and Human-Pathogenic Fungi (2016), Erlangen, Germany, poster presentation

Hella Schmidt, Franziska Schmidt, Thomas Krüger, Sebastian Vlaic, Thorsten Heinekamp, Axel A Brakhage
A proteomic study of *Aspergillus fumigatus* conidia-containing phagolysosomes
JSMC Symposium (2016) Jena, Germany, oral presentation

Awards
'Best Poster Communication' Prize of the ESCI Annual Scientific Meeting in Cluj-Napoca, Romania (2015)

Posterprize of the DMyK Scientific Conference, Jena, Germany (2015)

Extracurricular Activities
Head of Organization Committee of the 4th International Conference on Microbial Communication (MiCom), 2014 in Jena

Curriculum Vitae

Personal Details

Name	Hella Schmidt
Date and place of birth	19. September 1986, Burgstädt

Education

Since November 2012	*PhD position* Leibniz-Institute for Natural Product Research and Infection Biology – Hans Knöll Institute Jena, Department of Molecular and Applied Microbiology, supervised by Prof. Dr. Axel A. Brakhage
October/2012	*Diplom* (Grade ‘Very Good’)
November/2011 – October/2012	*Diploma Thesis* ‘Diplomarbeit’ University of Stuttgart – Institute of Microbiology, supervised by Prof. Dr. Georg Sprenger; Bayer Technology Services GmbH, Enzyme and Fermentation Technology, supervised by Dr. Jorgen Magnus Title: ’Metabolic engineering of *Escherichia coli* to produce aromatic compounds’
October/2010 – March/2011	*Student Paper Thesis*, ‘Studienarbeit’ University of Stuttgart – Institute of Cell Biology and Immunology, supervised by Prof. Dr. Peter Scheurich; ProImmune Ltd., Oxford, UK, Cellular Analysis Services, supervised by Dr. Helen Barnby-Porritt Title: ’Evaluation of peptides used for a basic CFSE-based T Cell proliferation assay’ (Grade ‘Very Good’)
October(2008)	*Intermediate Exam* ‘Vordiplom’
October/2006 – September/2012	*University of Stuttgart, Technical Biology*
June/2006	*Abitur* (Grade ‘Very Good’)
August/1999 –June/2006	Cato Bontjes van Beek Gymnasium, Achim

Scholarship

Since November/2012	Fellow of the excellence initiative of the Jena School of Microbial Communication (JSMC)

Danksagung

Das Bearbeiten und Erstellen dieser Doktorarbeit wäre allein nicht möglich gewesen. Aus diesem Grund möchte ich an dieser Stelle denjenigen danken, die mir über die letzten gut vier Jahre beratend, unterstützend, helfend und motivierend zur Seite gestanden haben.

An erster Stelle möchte ich mich hier bei meinem Doktorvater Prof. Dr. Axel Brakhage für sein Vertrauen, mir dieses Projekt zur Bearbeitung und Entwicklung in die Hände zu legen und für die vielen konstruktiven und motivierenden Diskussionen während meiner gesamten Zeit als Doktorand in seinem Labor bedanken. Außerdem bedanke ich mich für die Korrektur und die Begutachtung dieser Arbeit. In diesem Zuge danke ich natürlich auch den weiteren Gutachtern für die Durchsicht meiner Arbeit.

Einen besonderen Dank möchte ich auch Dr. Thorsten Heinekamp aussprechen, der mir als zweiter Betreuer stetig zur Seite stand und mein erster Ansprechpartner war, wenn sich während der Arbeit Probleme experimenteller Natur ergeben haben oder Diskussionsbedarf existierte. Genauso danke ich Prof. Dr. Peter Zipfel, dem dritten Betreuer dieser Arbeit für seine Unterstützung und seine Bereitschaft mir die Zellkultur, das CLSM und FACS Gerät in seinem Labor für Experimente zur Verfügung zu stellen. In diesem Zusammenhang danke ich Dr. Hans-Martin Dahse, der anfänglich die Zellkultur bereitstellte und die Grundlage für die Etablierung eines eigenen Zellkultur-Labors in unserem Labor lieferte, sowie Andrea Hartmann für die Einweisung und Nutzung des dort vorhandenen CLSM.

Dr. Andreas Thywißen legte mit den Ergebnissen seiner Doktorarbeit die wissenschaftliche Grundlage einer proteomischen Untersuchung von Phagolysosomen und zeigte mir relevante zytologische Assays und vor allem den Umgang mit dem CLSM. Insbesondere zu Beginn meiner Arbeit leistete er einen großen Beitrag mich mit dem Projekt vertraut zu machen und gab Starthilfe für das anfängliche, experimentelle Vorgehen anhand zahlreicher Diskussionen.

Außerdem möchte ich mich bei Carmen Schult bedanken, die mir grundlegende mikrobielle Techniken zeigte und Birgit Schikowski, die immer zuverlässig die Betreuung der Zellkultur übernahm und diverse Immunofluoreszenzexperimente vorbereitete. Die Etablierung der Zellkultur in unserem Labor ist im Wesentlichen auch Franziska Schmidt zu verdanken, die sich zunächst als studentische Hilfswissenschaftskraft und später als Masterstudentin und Doktorandin mit viel Engagement der Zellkultur widmete. Ihrer Arbeit verdanke ich einen Großteil der zytologischen Experimente.

Bei der Entwicklung eines Protokolls zur Isolierung von Konidien-beinhaltenden Phagolysosomen waren die Diskussionen mit Anna C Geffken vom Forschungszentrum Borstel sehr hilfreich. Im Zuge der Arbeit an ihrer Doktorarbeit isolierte sie *Mycobakterien*-beinhaltenden Phagolysosomen und ihre

Erfahrungen waren wichtige Anhaltspunkte für mich zur Optimierung des Protokolls für A. fumigatus Konidien.

Einen großen Dank möchte ich Dr. Thomas Krüger für die LC-MS/MS Messungen und seine Expertise auf dem Gebiet der proteomischen Methoden aussprechen, die wesentlich zur Optimierung des Aufreinigungsprotokolls und dem Erfolg der Arbeit beitrugen.

Alle bioinformatischen Analysen wurden in Kooperation mit der Abteilung für Bioinformatik und Systembiologie unseres Instituts unter Leitung von Prof. Dr. Reinhard Guthke von Dr. Sebastian Vlaic durchgeführt. Seinen Bemühungen verdanke ich die Berechnung und Erstellung des regulatorischen Moduls auf Grundlage der umfangreichen Proteom-Informationen, sowie zahlreiche ausführliche Gespräche über die Interpretation der Analyse.

Weiterhin möchte ich Dr. Olaf Kniemeyer für wertvolle Tipps und Hinweise hinsichtlich des *A. fumigatus* Proteoms danken und der Fungal Septomics Arbeitsgruppe von Prof. Dr. Oliver Kurzai für die Bereitstellung ihres QuadroMacs Magneten für meine zahlreichen Phagolysosom-Aufreinigungexperimente. Ein besonderer Dank geht auch an Dr. Amelia Barber für die Hilfe mit der englischen Sprache.

Bei meinen vielen ehemaligen und aktuellen Kollegen bedanke ich mich herzlich für die gute Atmosphäre im Labor, im Büro und auch außerhalb der Arbeit. Ich habe die Hilfsbereitschaft, das wissenschaftliche Umfeld aber auch die vielen Doktorandenaktionen immer sehr zu schätzen gewusst.

Weiterhin danke ich der Jena School for Microbial Communication (JSMC) für die Aufnahme in das Graduiertenprogramm und das Stipendium, das ich drei Jahre lang für exzellente Forschung verwenden konnte. Weiterhin waren diverse Symposien, Konferenzen und Kolloquien im Rahmen der JSMC immer eine gute Möglichkeit, sich mit anderen Doktoranden auszutauschen.

Letztendlich danke ich meiner Familie dafür, dass sie mich immer auf meinem Weg unterstützt haben und hinter mir standen. Besonders danke ich Petru für das letzte Jahr, die moralische Unterstützung und die viele Geduld.

Ehrenwörtliche Erklärung

Hiermit versichere ich, dass mir die Promotionsordnung der Biologisch-Pharmazeutische Fakultät der Friedrich-Schiller Universität Jena bekannt ist.

Diese Arbeit habe ich eigeständig verfasst. Keiner der Textabschnitte wurde aus einer anderen, eigenen Prüfungsarbeit oder von Dritten ohne Kennzeichnung übernommen.

Alle verwendeten Hilfsmittel, Quellen oder Informationen aus persönlicher Kommunikation wurden vermerkt.

Jegliche Personen, die mich bei der Auswahl und Auswertung von Material sowie bei der Herstellung des Manuskripts unterstützt haben, wurden in den in den entsprechenden Abschnitten oder in der Danksagung genannt. Personen, die an Publikationen beteiligt waren, sind in der Publikationsliste erwähnt.

Die Hilfe eines Promotionsberaters wurde nicht in Anspruch genommen und Dritte haben weder unmittelbar noch mittelbar geldwerte Leistungen von mir für Arbeiten erhalten, die im Zusammenhang mit dem Inhalt der Dissertation stehen.

Diese Dissertation wurde nicht bereits als Prüfungsarbeit für eine andere staatliche oder wissenschaftliche Prüfung eingereicht. Außerdem habe ich diese Arbeit, eine in wesentlichen Teilen ähnliche oder eine andere Abhandlung nicht als Dissertation bei einer anderen Hochschule verwendet.

Jena, den

____

Hella Schmidt

List of supplemental tables

Table S1: List of host regulatory module poteins. [1] log2-fold change of protein quantities in *pksP* mutant versus wild-type conidia-containing phagolysosomes. Log2 *pksP*/wt > 2, enriched on *pksP* mutant and < 0,5 on wild-type conidia-containing phagolysosomes; '-' not detected in LC-MS/MS [2]Most enriched GO or KEGG pathway terms of the module BP – biological process, CC – cellular compartment, MF – molecular function.

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Submodule 1: Electron Transport Chain				
P56391	Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	1,82	oxidation-reduction process (BP)
A2RSV8	Cox4i1	cytochrome c oxidase subunit IV isoform 1	0,33	electron transport chain (BP)
Q9CXV1	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	-	respiratory electron transport chain (BP)
Q7JCZ3	mt-Cytb	mitochondrially encoded cytochrome b	-	
P99028	Uqcrh	ubiquinol-cytochrome c reductase hinge protein	-	NADH dehydrogenase activity (MF)
Q9CQ68	1700029P11Rik	RIKEN cDNA 1700029P11 gene	-	oxidoreductase activity (MF)
Q5NCJ9	Uqcr10	ubiquinol-cytochrome c reductase, complex III subunit X	-	electron carrier activity (MF)
Q9CR68	Uqcrfs1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0,83	
Q9DB77	Uqcrc2	ubiquinol cytochrome c reductase core protein 2	0,35	mitochondrial membrane (CC)
Q9CZ13	Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	0,23	
Q9D0M3	Cyc1	cytochrome c-1	0,08	Oxidative phosphorylation (KEGG)
Q9CQB4	Uqcrb	ubiquinol-cytochrome c reductase binding protein	-	
P48771	Cox7a2	cytochrome c oxidase subunit VIIa 2	-	
Q9CPX8	Uqcr11	ubiquinol-cytochrome c reductase, complex III subunit XI	-	
Q3UD06	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	0,27	
Q9CZB0	Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	1,73	
G3X9L6	Gm10250	predicted pseudogene 10250	1,51	
Q9D881	Gm11273	predicted gene 11273	-	
P12787	Cox5a	cytochrome c oxidase subunit Va	1,47	
Q78IK2	Usmg5	upregulated during skeletal muscle growth 5	1,33	
Q9CPQ8	Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	-0,24	
Q99LY9	Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	1,12	
Q9DB20	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	0,61	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
J3QNM7	Gm5426	predicted pseudogene 5426	-	
P56135	Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	-	
P17665	Cox7c	cytochrome c oxidase subunit VIIc	-2,09	
F7C106	Cox5b	cytochrome c oxidase subunit Vb	-	
Q9CQ69	Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	0,83	
Q06185	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit E	0,21	
Q9DCW5	Cox6a1	cytochrome c oxidase subunit VIa polypeptide 1	-	
Q9DCX2	Atp5h	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D	-	
P97450	Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	-	
Q545F5	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	-0,03	
Q9CPQ1	Cox6c	cytochrome c oxidase subunit VIc	0,49	
Q4FK74	Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	0,29	
J3QPT4	Gm4076	predicted gene 4076	-	
A0A0R4J275	Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	0,85	
Q59J78	Ndufaf2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	0,04	
Q9D6J6	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	1,10	
Q9CQH3	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	1,39	
Q9CPU2	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	-	
O09111	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	-	
Q9ERS2	Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	1,34	
A2AP31	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	-	
A0A0R3P9C8	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	1,12	
Q7JCY4	mt-Nd6	mitochondrially encoded NADH dehydrogenase 6	-	
Q9MD82	mt-Nd5	mitochondrially encoded NADH dehydrogenase 5	-1,07	
Q7GIP5	mt-Nd3	mitochondrially encoded NADH dehydrogenase 3	-	
Q9MD59	mt-Nd2	mitochondrially encoded NADH dehydrogenase 2	-	
Q4JFN6	mt-Nd1	mitochondrially encoded NADH dehydrogenase 1	-	
Q9CQ91	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	3,53	
Q5M9P5	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0,61	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q9JKL4	Ndufaf3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3	0,19	
Q9DCJ5	Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	0,56	
Q3U422	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3	-	
Q9DCS9	Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	0,81	
Q91YT0	Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	-0,33	
Q4FZG9	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	-	
Q9Z1P6	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	0,99	
Q9CQY9	Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	-	
Q9CR61	Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	2,26	
Q569N0	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-	
Q9CQ54	Ndufc2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	0,30	
A0A0N4SVQ1	Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	0,94	
Q9D1H6	Ndufaf4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	-0,15	
A0A0R4J081	Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	-2,56	
Q99LC3	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	0,22	
Q9CQZ6	Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	0,40	
Q91VD9	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	0,16	
Q9D6J5	Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	-	
Q9CPP6	Ndufa5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	1,17	
Q9CQC7	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4,NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4,NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	0,50	
Q9CQZ5	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	1,21	
Q9CQJ8	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	2,43	
E9QPX3	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	1,16	
P52503	Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	1,12	
Q9DC70	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0,36	
Q545K0	Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	-	
Q9CQ75	Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	0,46	
Q91WD5	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	-0,03	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q9DCT2	Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	1,54	
G5E814	Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11,NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	-	
Submodule 2: RNA transport				
Q3UYV9	Ncbp1	nuclear cap binding protein subunit 1	0,49	RNA transport (BP)
K9J7E2	Gm4301	predicted gene 4301	-	RNA localization (BP)
E9Q5E2	BC005561	cDNA sequence BC005561	-	nuclear export (BP)
Q8BG81	Poldip3	polymerase (DNA-directed), delta interacting protein 3	-2,09	
E9Q4V5	Gm4308	predicted gene 4308	-	RNA binding (MF)
Q8VDW0	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-0,28	
Q3TIV5	Zc3h15	zinc finger CCCH-type containing 15	-	transcription export complex (CC)
E9Q6R7	Utrn	utrophin	-	THO complex (CC)
G3X9I4	Alyref2	Aly/REF export factor 2	-	
Q9Z1N5	Ddx39b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	-0,41	Spliceosome (KEGG)
Q7TMY4	Thoc7	THO complex 7	2,00	mRNA surveillance pathway (KEGG)
A0A0R4J0J6	Thoc5	THO complex 5	-1,10	
B1AZI6	Thoc2	THO complex 2	-1,56	
Q5U4D9	Thoc6	THO complex 6	-1,03	
Q8VE80	Thoc3	THO complex 3	-1,27	
O08583	Alyref	Aly/REF export factor	0,06	
Q8R3N6	Thoc1	THO complex 1	0,14	
Submodule 3: Iron homeostasis				
Q8R0Z5	Slc25a28	solute carrier family 25, member 28	-	iron-sulfur cluster assembly (BP)
Q9D924	Isca1	iron-sulfur cluster assembly 1	-	iron ion homeostasis (BP)
Q3TV21	Fxn	frataxin	4,83	
A0A0R4J069	Scly	selenocysteine lyase	-	iron ion binding (MF)
A0A0R4J0T0	Hscb	HscB iron-sulfur cluster co-chaperone	-	
Q8K215	Lyrm4	LYR motif containing 4	7,39	mitochondrion (CC)
Q545P3	Fdx1	ferredoxin 1	1,76	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q9Z1J3	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	0,04	Sulfur relay system (KEGG)
Q9D7P6	Iscu	iron-sulfur cluster assembly enzyme	1,13	Thiamine metabolism (KEGG)
Q9DCB8	Isca2	iron-sulfur cluster assembly 2	-	
Submodule 4: Translation				
Q60737	Csnk2a1	casein kinase 2, alpha 1 polypeptide	2,57	basal transcription machinery binding (MF)
Q08943	Ssrp1	structure specific recognition protein 1	0,45	
Q5XJE5	Leo1	Leo1, Paf1/RNA polymerase II complex component	-	transcription elongation factor complex (CC)
A2AQ19	Rtf1	RTF1, Paf1/RNA polymerase II complex component	-	
Q62018	Ctr9	CTR9 homolog, Paf1/RNA polymerase II complex component	4,57	Ribosome biogenesis in eukaryotes (KEGG)
Q8K2T8	Paf1	Paf1, RNA polymerase II complex component	3,92	
Submodule 5: Stress response				
Q9Z2D6	Mecp2	methyl CpG binding protein 2	2,39	negative regulation of transcription from RNA polymerase II promoter (BP)
Q3ULN2	Gtf2b	general transcription factor IIB	2,17	
Q790L7	Ccnd1	cyclin D1	4,56	regulatory region DNA binding (MF)
F8WID3	Myc	myelocytomatosis oncogene	-	
A0A0R4J008	Hdac2	histone deacetylase 2	0,28	histone methyltransferase complex (CC)
P23798	Pcgf2	polycomb group ring finger 2	-	
Q02395	Mtf2	metal response element binding transcription factor 2	-	Cell cycle (KEGG)
Q9CXG9	Phf19	PHD finger protein 19	-	
Q9DBY5	Cbx6	chromobox 6	-	
A0A0R4J1C0	Ezh1	enhancer of zeste 1 polycomb repressive complex 2 subunit	-	
Q921E6	Eed	embryonic ectoderm development	-1,19	
Q61188	Ezh2	enhancer of zeste 2 polycomb repressive complex 2 subunit	-1,94	
Q9Z1B8	Phf1	PHD finger protein 1	-	
Q00899	Yy1	YY1 transcription factor	-1,29	
Q80U70	Suz12	suppressor of zeste 12 homolog (Drosophila)	-0,27	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
		Submodule 6: vATPase-dependent acidification		
Q9CR84	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	-	energy coupled proton transmembrane transport, against electrochemical gradient (BP)
P15920	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	-	ATP hydrolysis coupled proton transport (BP)
Q920R6	Atp6v0a4	ATPase, H+ transporting, lysosomal V0 subunit A4	-	
Q3U861	Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	1,56	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances (MF)
Q14BC2	Atp5g3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	-	transmembrane transporter activity (MF)
Q9D1K2	Atp6v1f	ATPase, H+ transporting, lysosomal V1 subunit F	1,61	
Q8BVE3	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	2,09	proton-transporting V-type ATPase complex (CC)
Q1XID4	Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	-0,31	proton-transporting two-sector ATPase complex (CC)
Q9Z1G4	Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	0,72	
P50516	Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	1,20	Phagosome (KEGG)
Q9D593	Atp6v1e2	ATPase, H+ transporting, lysosomal V1 subunit E2	-	Oxidative phosphorylation (KEGG)
Q3U889	Atp6v0b	ATPase, H+ transporting, lysosomal V0 subunit B	-	Lysosome (KEGG)
Q80SY3	Atp6v0d2	ATPase, H+ transporting, lysosomal V0 subunit D2	-	
Q8BMC1	Atp6v1g3	ATPase, H+ transporting, lysosomal V1 subunit G3	-	
A3KML5	Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	-	
Q9Z1G3	Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	1,63	
Q4FK49	Ppa1	pyrophosphatase (inorganic) 1	0,63	
P50518	Atp6v1e1	ATPase, H+ transporting, lysosomal V1 subunit E1	3,59	
Q3TWN7	Atp6ap1	ATPase, H+ transporting, lysosomal accessory protein 1	1,51	
P51863	Atp6v0d1	ATPase, H+ transporting, lysosomal V0 subunit D1	1,36	
P62814	Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	1,75	
Q91YH6	Atp6v1b1	ATPase, H+ transporting, lysosomal V1 subunit B1	-	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
		Submodule 7: Endocytosis		
P17047	Lamp2	lysosomal-associated membrane protein 2	1,35	endocytosis (BP)
Q549D0	Cd63	CD63 antigen	3,94	
Q3TM70	Ehd4	EH-domain containing 4	1,37	GTP binding (MF)
Q80ZZ0	Ehd1	EH-domain containing 1	1,14	
Q4FJQ0	Rab7	RAB7, member RAS oncogene family	0,71	endosome (CC)
Q8BL66	Eea1	early endosome antigen 1	-2,74	
Q3TA96	Lamp1	lysosomal-associated membrane protein 1	1,94	Endocytosis (KEGG)
Q9CQD1	Rab5a	RAB5A, member RAS oncogene family	1,28	Phagosome (KEGG)
		Submodule 8: Vesicle transport		
O35166	Gosr2	golgi SNAP receptor complex member 2	-	vesicle-mediated transport (BP)
Q791P0	Vamp5	vesicle-associated membrane protein 5	-	membrane fusion (BP)
Q80W45	Stx2	syntaxin 2	-	membrane organization (BP)
P56371	Rab4a	RAB4A, member RAS oncogene family	-	
Q8BH40	Stx7	syntaxin 7	-	SNARE binding (MF)
P61264	Stx1b	syntaxin 1B	-	SNAP receptor activity (MF)
O08599	Stxbp1	syntaxin binding protein 1	0,50	syntaxin binding (MF)
H6RXZ1	Syt1	synaptotagmin I	-	
Q8R1Q0	Stx19	syntaxin 19	-	SNARE complex (CC)
Q8BXT9	Sec22c	SEC22 homolog C, vesicle trafficking protein	-	endomembrane system (CC)
B2RSR2	Sec22a	SEC22 homolog A, vesicle trafficking protein	-	cytoplasmic vesicle (CC)
O88983	Stx8	syntaxin 8	0,62	
Q9CQW1	Ykt6	YKT6 v-SNARE homolog (S. cerevisiae)	0,98	SNARE interactions in vesicular transport (KEGG)
Q9D3L3	Snap23	synaptosomal-associated protein 23	-	
P46460	Nsf	N-ethylmaleimide sensitive fusion protein	0,75	
Q91XH6	Vti1b	vesicle transport through interaction with t-SNAREs 1B	-	
Q3U5V8	Stx11	syntaxin 11	-	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q9D0I4	Stx17	syntaxin 17	-	
P63040	Cplx1	complexin 1	-	
P70452	Stx4a	syntaxin 4A (placental)	3,64	
Q9ER00	Stx12	syntaxin 12	1,69	
P84086	Cplx2	complexin 2	-	
Q497P1	Stx1a	syntaxin 1A (brain)	-	
Q548T0	Stxbp2	syntaxin binding protein 2	-1,39	
Q8K1E0	Stx5a	syntaxin 5A	-	
Q64704	Stx3	syntaxin 3	-	
A0A0R4J0R1	Vamp8	vesicle-associated membrane protein 8	1,49	
P70280	Vamp7	vesicle-associated membrane protein 7	0,08	
Q8BSN6	Vamp4	vesicle-associated membrane protein 4	1,33	
P63024	Vamp3	vesicle-associated membrane protein 3	1,06	
P28663	Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	-	
P60879	Snap25	synaptosomal-associated protein 25	-	
Q9JKK1	Stx6	syntaxin 6	-	
Q9ERB0	Snap29	synaptosomal-associated protein 29	0,04	
Q8CHR4	Vamp2	vesicle-associated membrane protein 2	-	
Q9DB05	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	1,25	
		Submodule 9: Carboxylic acid metabolism		
Q3UAT9	Impdh2	inosine 5'-phosphate dehydrogenase 2	1,49	organic acid metabolic process (BP)
Q3V3R1	Mthfd1l	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	-0,34	carboxylic acid metabolic process (BP)
Q922D8	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	-1,76	
B2RQC6	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	-0,19	catalytic activity (MF)
Q921H8	Acaa1a	acetyl-Coenzyme A acyltransferase 1A	1,24	ligase activity (MF)
Q8QZT1	Acat1	acetyl-Coenzyme A acetyltransferase 1	-0,06	
Q9DBM2	Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	-	peroxisome (CC)

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q9DBL1	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	1,05	microbody (CC)
Q8CAY6	Acat2	acetyl-Coenzyme A acetyltransferase 2	-	nucleolus (CC)
P70700	Polr1b	polymerase (RNA) I polypeptide B	-2,00	
E9QN31	Nop2	NOP2 nucleolar protein	-	Valine, leucine and isoleucine degradation (KEGG)
Q8BHY2	Noc4l	NOC4 like	1,71	Propanoate metabolism (KEGG)
P35550	Fbl	fibrillarin	-0,33	Glyoxylate and dicarboxylate metabolism (KEGG)
Q64737	Gart	phosphoribosylglycinamide formyltransferase	1,04	
A0A0M3HEQ0	Txnrd2	thioredoxin reductase 2	2,30	
A2ATU0	Dhtkd1	dehydrogenase E1 and transketolase domain containing 1	-	
P16332	Mut	methylmalonyl-Coenzyme A mutase	2,23	
Q9EQ20	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	-1,40	
Q9D1I5	Mcee	methylmalonyl CoA epimerase	-	
Q3UGC8	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	0,58	
Q99MN9	Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	1,97	
E9Q4Z2	Acacb	acetyl-Coenzyme A carboxylase beta	-	
Q5SWU9	Acaca	acetyl-Coenzyme A carboxylase alpha	-	
Q3V117	Acly	ATP citrate lyase	-3,56	
Q8BMF4	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	0,71	
P47791	Gsr	glutathione reductase	1,07	
E9Q7L0	Ogdhl	oxoglutarate dehydrogenase-like	-	
Q8BKZ9	Pdhx	pyruvate dehydrogenase complex, component X	2,29	
Submodule 10: Ribosome				
Q9DCI9	Mrpl32	mitochondrial ribosomal protein L32	-	translation (BP)
Q9CZ83	Mrpl55	mitochondrial ribosomal protein L55	2,63	peptide biosynthetic process (BP)
Q9CY16	Mrps28	mitochondrial ribosomal protein S28	2,56	
Q9D1P0	Mrpl13	mitochondrial ribosomal protein L13	0,35	structural constituent of ribosome (MF)
Q99N93	Mrpl16	mitochondrial ribosomal protein L16	0,72	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q9D8P4	Mrpl17	mitochondrial ribosomal protein L17	-0,49	ribosome (CC)
Q9CPR5	Mrpl15	mitochondrial ribosomal protein L15	1,66	ribonucleoprotein complex (CC)
Q99N91	Mrpl34	mitochondrial ribosomal protein L34	-	
Q9DB15	Mrpl12	mitochondrial ribosomal protein L12	1,04	
Q99N95	Mrpl3	mitochondrial ribosomal protein L3	0,95	
Q9D338	Mrpl19	mitochondrial ribosomal protein L19	-0,18	
Q9CQF0	Mrpl11	mitochondrial ribosomal protein L11	1,14	
Q99N92	Mrpl27	mitochondrial ribosomal protein L27	3,85	
Q3UKS6	Mrpl40	mitochondrial ribosomal protein L40	2,33	
Q99N90	Mrpl36	mitochondrial ribosomal protein L36	-	
Q8BU88	Mrpl22	mitochondrial ribosomal protein L22	1,00	
Q9CQ06	Mrpl24	mitochondrial ribosomal protein L24	0,60	
Q9DCU6	Mrpl4	mitochondrial ribosomal protein L4	-	
Q9D773	Mrpl2	mitochondrial ribosomal protein L2	-1,20	
Submodule 11: RNA processing				
P62309	Gm8186	predicted gene 8186	-6,27	mRNA splicing, via spliceosome (BP)
P62305	Snrpe	small nuclear ribonucleoprotein E	-1,00	nucleic acid binding (MF)
P62309	Snrpg	small nuclear ribonucleoprotein polypeptide G	-6,27	small nuclear ribonucleoprotein complex (CC)
P62876	Polr2l	polymerase (RNA) II (DNA directed) polypeptide L	1,68	Spliceosome (KEGG)
Q497K3	Snrpf	small nuclear ribonucleoprotein polypeptide F	0,54	RNA polymerase (KEGG)
Q3UI46	Nedd8	neural precursor cell expressed, developmentally down-regulated gene 8	-	
Submodule 12: NADPH oxidase-dependent ROS production				
Q8CIZ9	Nox1	NADPH oxidase 1	-	reactive oxygen species metabolic process (BP)
Q3UPN1	Vcam1	vascular cell adhesion molecule 1	-	superoxide-generating NADPH oxidase activity (MF)
Q09014	Ncf1	neutrophil cytosolic factor 1	1,01	NADPH oxidase complex (CC)
A2AQ92	Duox1	dual oxidase 1	-	Phagosome (KEGG)
P97369	Ncf4	neutrophil cytosolic factor 4	1,15	

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q4FJK0	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	-	
O70145	Ncf2	neutrophil cytosolic factor 2	-1,37	
B3VQI8	Cyba	cytochrome b-245, alpha polypeptide	0,41	
Submodule 13: Immune response				
E9QN37	Mpeg1	macrophage expressed gene 1	1,73	immune response (BP)
A0A0R4J1C8	Cd68	CD68 antigen	1,37	response to stimulus (BP)
A0A077S2U6	Lyz2	lysozyme 2	0,95	signaling receptor activity (MF)
P14106	C1qb	complement component 1, q subcomponent, beta polypeptide	-	cell surface (CC)
Q3U419	Tyrobp	TYRO protein tyrosine kinase binding protein	-	
Q0P635	Csf1r	colony stimulating factor 1 receptor	1,38	Complement and coagulation cascades (KEGG)
Q3U9R0	Adgre1	adhesion G protein-coupled receptor E1	-	Cytokine-cytokine receptor interaction (KEGG)
Submodule 14: Signaling				
Q9QXX3	Pla2g10	phospholipase A2, group X	-	intracellular signal transduction (BP)
Q01279	Egfr	epidermal growth factor receptor	-	regulation of intracellular signal transduction (BP)
P12025	Mdk	midkine	-	
Q4VAE6	Rhoa	ras homolog family member A	-0,25	phospholipase A2 activity (MF)
P97819	Pla2g6	phospholipase A2, group VI	-	receptor signaling protein serine/threonine kinase activity (MF)
Q6GTW1	Pla2g5	phospholipase A2, group V	-	MAP kinase activity (MF)
Q8R3U1	Pla2g16	phospholipase A2, group XVI	-	
Q3UMQ1	Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-dependent)	1,37	membrane raft (CC)
Q05769	Ptgs2	prostaglandin-endoperoxide synthase 2	0,52	caveola (CC)
Q5J7N1	Kras	Kirsten rat sarcoma viral oncogene homolog	-	microtubule cytoskeleton (CC)
Q9WVS8	Mapk7	mitogen-activated protein kinase 7	-	
O08911	Mapk12	mitogen-activated protein kinase 12	-	Chemokine signaling pathway (KEGG)
Q61526	Erbb3	erb-b2 receptor tyrosine kinase 3	-	Glycerophospholipid metabolism (KEGG)
Q63844	Mapk3	mitogen-activated protein kinase 3	-1,78	Toll-like receptor signaling pathway (KEGG)

UNIPROT ACCESSION	GENE NAME	DESCRIBTION	log2FC[1]	GO TERMS[2]
Q6PB44	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	-0,04	
P63085	Mapk1	mitogen-activated protein kinase 1	-1,19	
Q3U5I5	Grb2	growth factor receptor bound protein 2	1,35	
Q5U421	Mapk14	mitogen-activated protein kinase 14	-	
		Submodule 15 Microtubule Movement		
Q9QWT9	Kifc1	kinesin family member C1	-1,30	mitotic sister chromatid segregation (BP)
Q8BH30	Kpna6	karyopherin (importin) alpha 6	1,02	motor activity (MF)
E9PUA5	Kifc5b	kinesin family member C5B	-1,30	kinesin complex (CC)
		Submodule 16: tRNA metabolism		
E9QB02	Mars	methionine-tRNA synthetase	-1,69	translational initiation (BP)
Q642K5	Gm9843	predicted gene 9843	-	translation factor activity, RNA binding
Q8JZQ9	Eif3b	eukaryotic translation initiation factor 3, subunit B	1,20	eukaryotic translation initiation factor 3 complex (CC)
Q3UHY8	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	-0,33	RNA transport (KEGG)
Q8R1B4	Eif3c	eukaryotic translation initiation factor 3, subunit C	1,06	Aminoacyl-tRNA biosynthesis (KEGG)
		Submodule 17: DNA replication		
Q6ZQJ5	Dna2	DNA replication helicase/nuclease 2	-	DNA-dependent DNA replication (BP)
E9QPB3	Wdhd1	WD repeat and HMG-box DNA binding protein 1	-2,90	double-strand break repair (BP)
Q3U4X8	Lig1	ligase I, DNA, ATP-dependent	-1,63	DNA binding (MF)
Q3URU4	Mre11a	MRE11A homolog A, double strand break repair nuclease	-3,46	condensed chromosome (CC)
Q08297	Rad51	RAD51 recombinase	-	Homologous recombination (KEGG)

Table S2: Murine proteins detected in the label-free LC-MS/MS measurement of purified conidia-containing phagolysosomes. Protein quantities were calculated with the 'Top Three' method. [1]Proteins with a *pksP/*wt ratio ≥ 2 were considered as enriched on *pksP* mutant conidia (green) and proteins with a *pksP*/wt ≤ 0.5 were considered as enriched on wild-type conidia-containing phagolysosomes (red). n.a.- not available; protein values only detected in one condition.

Accession	**Gene**	**Description**	**Σcover-age**	**Σ# Unique Peptides**	**Σ# Peptides**	**Σ# PSMs**	**[1]*pksP*/wt**
P45878	Fkbp2	Peptidyl-prolyl cis-trans isomerase FKBP2	13.57	3	3	6	n.a.
Q9Z0J0	Npc2	Epididymal secretory protein E1	32.21	6	6	51	n.a.
Q9JII6	Akr1a1	Alcohol dehydrogenase [NADP(+)]	7.08	2	2	6	n.a.
Q3UDF0	Slc2a6	Protein Slc2a6	7.44	3	3	20	n.a.
O35405	Pld3	Phospholipase D3	4.51	2	2	12	n.a.
Q8BWH0	Slc38a7	Putative sodium-coupled neutral amino acid transporter 7	7.56	3	3	15	n.a.
Q91WM2	Cecr5	Cat eye syndrome critical region protein 5 homolog	4.77	2	2	4	n.a.
Q8R3Q6	Ccdc58	Coiled-coil domain-containing protein 58	25.69	3	3	10	n.a.
Q9CQX8	Mrps36	28S ribosomal protein S36, mitochondrial	36.27	2	2	9	n.a.
P40201	Chd1	Chromodomain-helicase-DNA-binding protein 1	1.05	3	3	3	n.a.
Q9CS00	Cactin	Cactin	2.07	2	2	4	n.a.
Q5XJE5	Leo1	RNA polymerase-associated protein LEO1	2.85	2	2	6	n.a.
Q60648	Gm2a	Ganglioside GM2 activator	14.51	3	3	16	n.a.
Q9DCU6	Mrpl4	39S ribosomal protein L4, mitochondrial	5.78	2	2	4	n.a.
P62311	Lsm3	U6 snRNA-associated Sm-like protein LSm3	17.65	2	2	2	n.a.
P51569	Gla	Alpha-galactosidase A	5.25	2	2	12	n.a.
Q91VA6	Poldip2	Polymerase delta-interacting protein 2	6.25	2	2	6	n.a.
Q3TKY6	Cwc27	Peptidyl-prolyl cis-trans isomerase CWC27 homolog	7.04	2	2	6	n.a.
Q8R317	Ubqln1	Ubiquilin-1	6.87	2	3	20	n.a.
O88188	Ly86	Lymphocyte antigen 86	9.26	2	2	8	n.a.
Q62393	Tpd52	Tumor protein D52	17.41	3	3	12	n.a.
Q9WU28	Pfdn5	Prefoldin subunit 5	14.94	2	2	4	n.a.
Q8K442	Abca8a	ATP-binding cassette sub-family A member 8-A	0.74	1	2	3	n.a.
Q9CQF8	Mrpl57	Ribosomal protein 63, mitochondrial	27.45	3	3	8	n.a.
P21279	Gnaq	Guanine nucleotide-binding protein G(q) subunit alpha	10.86	3	3	10	n.a.
Q8C7V8	Ccdc134	Coiled-coil domain-containing protein 134	9.61	2	2	2	n.a.
Q9JK48	Sh3glb1	Endophilin-B1	7.95	3	3	14	n.a.
Q60770	Stxbp3	Syntaxin-binding protein 3	3.38	2	2	2	n.a.
O89116	Vti1a	Vesicle transport through interaction with t-SNAREs homolog 1A	13.82	3	3	4	n.a.
Q3U3R4	Lmf1	Lipase maturation factor 1	4.01	2	2	4	n.a.
Q9CQV7	Dnajc19	Mitochondrial import inner membrane translocase subunit TIM14	18.97	2	2	2	n.a.
Q8VE88	Fam114a2	Protein FAM114A2	3.22	2	2	2	n.a.
Q9D162	Ccdc167	Coiled-coil domain-containing protein 167	26.80	2	2	12	n.a.
Q3UMR5	Mcu	Calcium uniporter protein, mitochondrial	6.00	2	2	6	n.a.

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q9D1C1	Ube2c	Ubiquitin-conjugating enzyme E2 C	13.41	2	2	6	n.a.
P70699	Gaa	Lysosomal alpha-glucosidase	2.94	2	2	6	n.a.
Q9D8S9	Bola1	BolA-like protein 1	25.55	3	3	17	n.a.
Q3TWL2	Tmem55b	Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase	7.39	2	2	2	n.a.
Q6Y685	Tacc1	Transforming acidic coiled-coil-containing protein 1	2.58	2	2	4	n.a.
P52875	Tmem165	Transmembrane protein 165	13.62	3	3	21	n.a.
Q8VD58	Evi2b	Protein EVI2B	5.86	2	2	4	n.a.
A2AGH6	Med12	Mediator of RNA polymerase II transcription subunit 12	0.91	2	2	2	n.a.
Q62426	Cstb	Cystatin-B	32.65	2	2	4	n.a.
O54782	Man2b2	Epididymis-specific alpha-mannosidase	1.47	2	2	4	n.a.
Q3UMW8	Cln5	Ceroid-lipofuscinosis neuronal protein 5 homolog	5.87	2	2	6	n.a.
Q8BVF2	Pdcl3	Phosducin-like protein 3	9.58	2	2	6	n.a.
Q80X71	Tmem106b	Transmembrane protein 106B	8.36	2	2	12	n.a.
Q6NXK9	Man1c1	alpha-1,2-Mannosidase	5.44	2	2	6	n.a.
Q8BY89	Slc44a2	Choline transporter-like protein 2	3.97	2	2	18	n.a.
Q8BN82	Slc17a5	Sialin	7.88	3	3	15	n.a.
Q9D7X3	Dusp3	Dual specificity protein phosphatase 3	15.68	2	2	6	n.a.
Q3USZ8	N/A	Deleted in autism protein 1 homolog	5.35	2	2	6	n.a.
Q5KU39	Vps41	Vacuolar protein sorting-associated protein 41 homolog	1.64	2	2	2	n.a.
Q91VW5	Golga4	Golgin subfamily A member 4	2.01	5	5	15	n.a.
Q8K1E0	Stx5	Syntaxin-5	6.48	3	3	6	n.a.
Q8K358	Pigu	Phosphatidylinositol glycan anchor biosynthesis class U protein	4.84	2	2	6	n.a.
O55102	Bloc1s1	Biogenesis of lysosome-related organelles complex 1 subunit 1	16.80	2	2	6	n.a.
Q8K3A0	Hscb	Iron-sulfur cluster co-chaperone protein HscB, mitochondrial	9.83	2	2	4	n.a.
J3QP80	Gm5814	MCG15559	24.80	2	2	4	n.a.
Q9DBG5	Plin3	Perilipin-3	9.38	3	3	18	n.a.
B2RXC6	Polr3a	DNA-directed RNA polymerase	2.45	2	3	12	n.a.
Q8BS35	Agmo	Alkylglycerol monooxygenase	5.82	2	2	4	n.a.
Q64674	Srm	Spermidine synthase	5.96	2	2	6	n.a.
Q8BV66	Ifi44	Interferon-induced protein 44	4.98	2	2	4	n.a.
Q7TMB8	Cyfip1	Cytoplasmic FMR1-interacting protein 1	1.92	2	2	6	n.a.
Q9CYZ2	Tpd52l2	Tumor protein D54	11.82	2	2	6	n.a.
Q3V009	Tmed1	Transmembrane emp24 domain-containing protein 1	9.69	2	2	2	n.a.
Q61609	Slc20a1	Sodium-dependent phosphate transporter 1	2.64	1	2	2	n.a.
O54774	Ap3d1	AP-3 complex subunit delta-1	2.00	1	2	2	n.a.
Q9CR21	Ndufab1	Acyl carrier protein, mitochondrial	9.62	2	2	2	n.a.
A2AQ19	Rtf1	RNA polymerase-associated protein RTF1 homolog	4.76	3	3	8	n.a.
Q6A0D4	Rftn1	Raftlin	6.50	3	3	10	n.a.
Q7TMQ7	Wdr91	WD repeat-containing protein 91	3.61	2	2	6	n.a.
Q9Z0V7	Timm17b	Mitochondrial import inner membrane translocase subunit Tim17-B	12.79	2	2	4	n.a.

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q6DID3	Scaf8	Protein SCAF8	1.89	1	2	6	n.a.
Q9EQC5	Scyl1	N-terminal kinase-like protein	2.85	2	2	12	n.a.
Q9DCI3	Stard3nl	MLN64 N-terminal domain homolog	8.94	2	2	6	n.a.
Q9CQG2	Mettl16	Methyltransferase-like protein 16	7.05	3	3	15	n.a.
Q921M7	Fam49b	Protein FAM49B	9.26	2	2	10	n.a.
Q9CQ80	Vps25	Vacuolar protein-sorting-associated protein 25	11.36	2	2	4	n.a.
Q6PFF0	Scaf4	Protein Scaf4	1.90	1	2	8	n.a.
Q8BFP9	Pdk1	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	2.76	2	2	2	n.a.
Q9D902	Gtf2e2	General transcription factor IIE subunit 2	7.53	2	2	4	n.a.
Q62447	Ccnc	Cyclin-C	6.01	1	2	2	n.a.
E9Q3L4	AI607873	Protein AI607873	1.53	2	2	2	n.a.
Q8BJU0	Sgta	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	8.89	2	2	6	n.a.
P70704	Atp8a1	Phospholipid-transporting ATPase IA	1.72	2	2	2	n.a.
P0C0A3	Chmp6	Charged multivesicular body protein 6	16.50	3	3	14	n.a.
Q78RX3	Smim12	Small integral membrane protein 12	18.48	2	2	4	n.a.
P83093	Stim2	Stromal interaction molecule 2	3.08	2	2	4	n.a.
Q80VQ0	Aldh3b1	Aldehyde dehydrogenase family 3 member B1	4.70	2	2	6	n.a.
Q9JLQ2	Git2	ARF GTPase-activating protein GIT2	2.26	2	2	6	n.a.
O54950	Prkag1	5'-AMP-activated protein kinase subunit gamma-1	8.18	3	3	12	n.a.
Q6NVG1	Lpcat4	Lysophospholipid acyltransferase LPCAT4	4.77	2	2	6	n.a.
Q922Q2	Riok1	Serine/threonine-protein kinase RIO1	3.70	2	2	10	n.a.
Q91XL9	Osbpl1a	Oxysterol-binding protein-related protein 1	2.00	2	2	6	n.a.
Q810B6	Ankfy1	Rabankyrin-5	1.97	2	2	4	n.a.
P70268	Pkn1	Serine/threonine-protein kinase N1	2.33	2	2	6	n.a.
P30415	Nktr	NK-tumor recognition protein	1.65	2	2	6	n.a.
Q91UZ1	Plcb4	Phosphoinositide phospholipase C	4.60	3	3	12	n.a.
Q8K194	Snrnp27	U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein	10.32	2	2	12	n.a.
Q8VI93	Oas3	2'-5'-oligoadenylate synthase 3	3.08	3	3	12	n.a.
Q99MK8	Adrbk1	Beta-adrenergic receptor kinase 1	2.03	2	2	4	n.a.
Q8K268	Abcf3	ATP-binding cassette sub-family F member 3	2.12	2	2	2	n.a.
Q8R349	Cdc16	Cell division cycle protein 16 homolog	2.90	2	2	4	n.a.
Q8R5L3	Vps39	Vam6/Vps39-like protein	2.93	2	2	6	n.a.
Q60953	Pml	Protein PML	2.94	2	2	6	n.a.
Q8CAS9	Parp9	Poly [ADP-ribose] polymerase 9	2.66	1	2	2	n.a.
Q3U1F9	Pag1	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1	6.76	2	2	4	n.a.
A2AGT5	Ckap5	Cytoskeleton-associated protein 5	1.18	2	2	4	n.a.
Q8BG94	Commd7	COMM domain-containing protein 7	12.00	2	2	4	n.a.
Q3TRM4	Pnpla6	Neuropathy target esterase	1.99	2	2	2	n.a.
E9Q5G3	Kif23	Kinesin-like protein KIF23	1.78	2	2	2	n.a.
Q80VI1	Trim56	E3 ubiquitin-protein ligase TRIM56	2.45	2	2	4	n.a.

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8R570	Snap47	Synaptosomal-associated protein 47	4.36	2	2	4	n.a.
Q91ZJ5	Ugp2	UTP--glucose-1-phosphate uridylyltransferase	3.35	2	2	6	n.a.
E9Q9B7	Kidins220	Protein Kidins220	1.23	2	2	4	n.a.
Q8CFE4	Scyl2	SCY1-like protein 2	3.01	2	2	6	n.a.
Q99MS7	Ehbp1l1	EH domain-binding protein 1-like protein 1	1.69	2	2	6	n.a.
P13597	Icam1	Intercellular adhesion molecule 1	6.89	4	4	10	634.43
Q8K021	Scamp1	Secretory carrier-associated membrane protein 1	10.65	2	2	6	189.59
O08992	Sdcbp	Syntenin-1	12.04	4	5	27	176.68
Q8K215	Lyrm4	LYR motif-containing protein 4	41.76	4	4	22	167.36
Q9D198	Syf2	Pre-mRNA-splicing factor SYF2	11.57	3	3	10	137.30
Q8BIP0	Dars2	Aspartate--tRNA ligase, mitochondrial	6.74	4	4	18	123.82
Q9Z1T1	Ap3b1	AP-3 complex subunit beta-1	11.22	12	12	67	108.59
Q2EMV9	Parp14	Poly [ADP-ribose] polymerase 14	2.92	4	5	11	106.35
Q6ZWR6	Syne1	Nesprin-1	0.16	2	2	2	95.31
Q61703	Itih2	Inter-alpha-trypsin inhibitor heavy chain H2	2.54	2	2	4	66.05
Q8CJ40	Crocc	Rootletin	2.04	5	5	5	42.56
Q9D125	Mrps25	28S ribosomal protein S25, mitochondrial	11.11	3	3	8	39.34
Q8VEK0	Tmem30a	Cell cycle control protein 50A	6.87	2	2	6	37.22
Q9D8Y1	Tmem126a	Transmembrane protein 126A	10.71	2	2	6	36.97
Q9D6K8	Fundc2	FUN14 domain-containing protein 2	27.81	6	6	44	33.64
O35943	Fxn	Frataxin, mitochondrial	16.91	3	3	15	28.49
Q61542	Stard3	StAR-related lipid transfer protein 3	3.59	2	2	2	27.10
P28667	Marcksl1	MARCKS-related protein	14.00	2	2	6	24.18
Q62018	Ctr9	RNA polymerase-associated protein CTR9 homolog	2.73	4	4	10	23.74
P25322	Ccnd1	G1/S-specific cyclin-D1	8.14	2	2	18	23.57
Q80UZ2	Sdad1	Protein SDA1 homolog	5.97	4	4	25	21.22
P83741	Wnk1	Serine/threonine-protein kinase WNK1	2.10	3	5	10	20.39
Q8VDP6	Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	9.86	2	2	18	19.24
Q8VDD9	Phip	PH-interacting protein	9.72	15	15	169	18.93
Q9R020	Zranb2	Zinc finger Ran-binding domain-containing protein 2	23.64	7	7	61	18.93
Q9JI11	Stk4	Serine/threonine-protein kinase 4	3.90	2	2	6	17.73
Q8R322	Gle1	Nucleoporin GLE1	3.43	2	2	6	17.68
O88736	Hsd17b7	3-keto-steroid reductase	8.08	2	2	6	17.41
Q07797	Lgals3bp	Galectin-3-binding protein	12.13	6	6	80	15.69
Q6NWW9	Fndc3b	Fibronectin type III domain-containing protein 3B	6.13	6	6	37	15.40
P41731	Cd63	CD63 antigen	7.56	2	2	6	15.38
Q8K2T8	Paf1	RNA polymerase II-associated factor 1 homolog	14.39	6	6	51	15.14
O08756	Hsd17b10	3-hydroxyacyl-CoA dehydrogenase type-2	25.67	7	7	130	14.91
Q9CQ22	Lamtor1	Ragulator complex protein LAMTOR1	40.99	5	5	30	14.67
Q99N92	Mrpl27	39S ribosomal protein L27, mitochondrial	14.19	2	2	6	14.40

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q80YD1	Supv3l1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	6.80	4	4	21	13.20
Q8BTV2	Cpsf7	Cleavage and polyadenylation specificity factor subunit 7	8.92	4	4	36	12.89
Q80TY0	Fnbp1	Formin-binding protein 1	2.76	2	2	2	12.89
Q9Z1F9	Uba2	SUMO-activating enzyme subunit 2	4.23	2	3	5	12.88
Q9WUA2	Farsb	Phenylalanine--tRNA ligase beta subunit	8.32	4	5	35	12.87
P70452	Stx4	Syntaxin-4	16.78	4	4	18	12.49
Q6P8X1	Snx6	Sorting nexin-6	9.61	3	5	16	12.32
P50518	Atp6v1e1	V-type proton ATPase subunit E 1	40.71	10	10	181	12.05
Q925J9	Med1	Mediator of RNA polymerase II transcription subunit 1	2.92	4	4	28	11.67
Q9CQ91	Ndufa3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	28.57	3	3	10	11.57
O88466	Znf106	Zinc finger protein 106	1.69	3	3	18	11.55
P49452	Cenpc	Centromere protein C	2.43	2	2	4	11.54
B1AY13	Usp24	Ubiquitin carboxyl-terminal hydrolase 24	0.50	1	2	7	11.25
P98195	Atp9b	Probable phospholipid-transporting ATPase IIB	2.97	3	3	16	11.11
P61022	Chp1	Calcineurin B homologous protein 1	17.95	3	3	8	10.97
P49722	Psma2	Proteasome subunit alpha type-2	14.96	4	4	45	10.86
Q9D379	Ephx1	Epoxide hydrolase 1	7.25	4	4	10	10.43
O54988	Slk	STE20-like serine/threonine-protein kinase	2.76	2	3	10	10.40
Q9WVA2	Timm8a1	Mitochondrial import inner membrane translocase subunit Tim8 A	22.68	2	2	6	10.18
P06797	Ctsl	Cathepsin L1	12.28	3	3	23	10.12
Q9CWU2	Zdhhc13	Palmitoyltransferase ZDHHC13	3.54	2	2	10	9.62
Q3UHX2	Pdap1	28 kDa heat- and acid-stable phosphoprotein	6.08	2	2	6	9.59
Q8BH43	Wasf2	Wiskott-Aldrich syndrome protein family member 2	5.03	2	2	12	9.39
Q9CQY6	Uqcc2	Ubiquinol-cytochrome-c reductase complex assembly factor 2	22.79	3	3	20	9.31
Q9DBU0	Tm9sf1	Transmembrane 9 superfamily member 1	4.29	1	2	4	8.99
O35143	Atpif1	ATPase inhibitor, mitochondrial	8.49	2	2	24	8.97
Q9JHS3	Lamtor2	Ragulator complex protein LAMTOR2	28.80	3	3	39	8.72
Q03347	Runx1	Runt-related transcription factor 1	9.76	4	4	26	8.40
Q9ET22	Dpp7	Dipeptidyl peptidase 2	8.89	4	4	27	8.26
P24063	Itgal	Integrin alpha-L	2.49	3	3	18	8.26
Q9CXJ4	Abcb8	ATP-binding cassette sub-family B member 8, mitochondrial	3.07	2	2	4	8.09
Q9Z2I0	Letm1	LETM1 and EF-hand domain-containing protein 1, mitochondrial	16.67	13	13	109	7.78
P32261	Serpinc1	Antithrombin-III	8.82	5	5	41	7.68
Q99K23	Ufsp2	Ufm1-specific protease 2	4.34	2	2	6	7.49
Q9D3B1	Hacd2	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	12.20	3	3	21	7.42
Q80UP3	Dgkz	Diacylglycerol kinase zeta	3.12	2	2	4	7.39
Q9WUQ2	Preb	Prolactin regulatory element-binding protein	10.55	3	3	18	7.38
O35114	Scarb2	Lysosome membrane protein 2	8.37	5	5	15	7.33
Q9CRA8	Exosc5	Exosome complex component RRP46	15.32	3	3	10	7.24
Q8BG07	Pld4	Phospholipase D4	13.12	6	6	75	7.14

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q4VAA2	Cdv3	Protein CDV3	13.88	3	3	13	7.04
Q9R1Q6	Tmem176b	Transmembrane protein 176B	8.75	2	2	12	7.03
Q91XB0	Trex1	Three-prime repair exonuclease 1	13.69	3	3	30	7.02
Q9D4J7	Phf6	PHD finger protein 6	4.40	2	2	4	6.97
Q8R1Q8	Dync1li1	Cytoplasmic dynein 1 light intermediate chain 1	9.75	4	4	14	6.95
Q61249	Igbp1	Immunoglobulin-binding protein 1	16.18	4	4	24	6.78
Q9ESY9	Ifi30	Gamma-interferon-inducible lysosomal thiol reductase	9.68	2	2	6	6.64
Q64310	Surf4	Surfeit locus protein 4	6.69	2	2	12	6.61
P21956	Mfge8	Lactadherin	6.48	3	3	10	6.58
Q8K124	Plekho2	Pleckstrin homology domain-containing family O member 2	15.96	5	5	34	6.51
Q62241	Snrpc	U1 small nuclear ribonucleoprotein C	16.98	2	2	6	6.46
Q91V81	Rbm42	RNA-binding protein 42	3.16	2	2	2	6.45
Q9Z2Q2	Knop1	Lysine-rich nucleolar protein 1	10.04	4	4	25	6.33
Q80X98	Dhx38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	4.97	5	5	26	6.33
E9Q166	Atad2b	Protein Atad2b	3.29	3	5	25	6.31
Q3TFD2	Lpcat1	Lysophosphatidylcholine acyltransferase 1	4.31	2	2	4	6.28
Q9CZ83	Mrpl55	39S ribosomal protein L55, mitochondrial	25.20	3	3	8	6.19
P07724	Alb	Serum albumin	5.43	3	3	84	6.13
Q61210	Arhgef1	Rho guanine nucleotide exchange factor 1	6.41	5	5	13	6.05
Q3UJU9	Rmdn3	Regulator of microtubule dynamics protein 3	5.53	2	2	4	6.02
Q6P4S8	Ints1	Integrator complex subunit 1	2.23	5	5	30	6.02
Q60737	Csnk2a1	Casein kinase II subunit alpha	3.32	2	2	2	5.93
Q3TYA6	Mphosph8	M-phase phosphoprotein 8	3.15	2	2	6	5.92
Q9CY16	Mrps28	28S ribosomal protein S28, mitochondrial	16.13	3	3	8	5.90
Q8R420	Abca3	ATP-binding cassette sub-family A member 3	2.17	4	4	7	5.84
Q2TBE6	Pi4k2a	Phosphatidylinositol 4-kinase type 2-alpha	10.44	4	5	12	5.82
P54823	Ddx6	Probable ATP-dependent RNA helicase DDX6	8.70	3	4	20	5.77
Q922B9	Ssfa2	Sperm-specific antigen 2 homolog	3.12	3	3	15	5.68
Q8R149	Bud13	BUD13 homolog	5.81	3	3	12	5.66
Q8C147	Dock8	Dedicator of cytokinesis protein 8	4.00	9	9	47	5.53
Q61081	Cdc37	Hsp90 co-chaperone Cdc37	16.09	5	5	31	5.50
Q9DCS3	Mecr	Trans-2-enoyl-CoA reductase, mitochondrial	5.63	2	2	7	5.44
Q8R4H9	Slc30a5	Zinc transporter 5	3.02	2	2	4	5.42
Q9CQJ8	Ndufb9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	8.38	2	2	2	5.40
Q9CR51	Atp6v1g1	V-type proton ATPase subunit G 1	23.73	2	2	48	5.29
P97371	Psme1	Proteasome activator complex subunit 1	23.69	5	5	41	5.29
Q9Z2D6	Mecp2	Methyl-CpG-binding protein 2	22.93	9	9	80	5.24
Q62192	Cd180	CD180 antigen	6.81	3	3	42	5.24
O35900	Lsm2	U6 snRNA-associated Sm-like protein LSm2	18.95	2	2	6	5.19
Q8BIJ7	Rufy1	RUN and FYVE domain-containing protein 1	9.55	6	6	16	5.11

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q9CPR8	Ndnl2	Melanoma-associated antigen G1	6.81	2	2	12	5.07
Q9JIK9	Mrps34	28S ribosomal protein S34, mitochondrial	17.89	4	4	8	5.04
Q5SSL4	Abr	Active breakpoint cluster region-related protein	2.56	2	2	4	5.03
Q9Z2Q5	Mrpl40	39S ribosomal protein L40, mitochondrial	23.79	4	4	42	5.01
O09110	Map2k3	Dual specificity mitogen-activated protein kinase kinase 3	10.09	3	3	12	5.01
Q5SS80	Dhrs13	Dehydrogenase/reductase SDR family member 13	7.45	2	2	6	4.99
O88325	Naglu	Alpha-N-acetylglucosaminidase	14.07	10	10	88	4.97
Q9JIG8	Praf2	PRA1 family protein 2	12.36	2	2	12	4.96
Q9D6M3	Slc25a22	Mitochondrial glutamate carrier 1	16.10	4	5	37	4.95
P97300	Nptn	Neuroplastin	13.10	5	5	26	4.92
Q9JLT4	Txnrd2	Thioredoxin reductase 2, mitochondrial	4.20	2	2	6	4.91
Q8BKZ9	Pdhx	Pyruvate dehydrogenase protein X component, mitochondrial	12.97	7	7	35	4.89
P97822	Anp32e	Acidic leucine-rich nuclear phosphoprotein 32 family member E	10.38	3	3	18	4.87
Q8R4N0	Clybl	Citrate lyase subunit beta-like protein, mitochondrial	16.57	5	5	18	4.84
Q69ZK0	Prex1	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	1.33	2	2	2	4.82
Q9CR61	Ndufb7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	25.55	3	3	53	4.78
Q80YV2	Zc3hc1	Nuclear-interacting partner of ALK	4.59	2	2	4	4.71
P16332	Mut	Methylmalonyl-CoA mutase, mitochondrial	10.70	7	7	81	4.70
P81117	Nucb2	Nucleobindin-2	11.67	4	4	36	4.69
Q9WTU0	Phf2	Lysine-specific demethylase PHF2	2.55	3	3	8	4.69
O08734	Bak1	Bcl-2 homologous antagonist/killer	22.97	4	4	34	4.68
P29416	Hexa	Beta-hexosaminidase subunit alpha	13.07	7	7	85	4.65
Q3UQN2	Fcho2	F-BAR domain only protein 2	1.85	1	2	2	4.64
Q8VI33	Taf9	Transcription initiation factor TFIID subunit 9	15.53	4	4	29	4.62
Q8VDG3	Parn	Poly(A)-specific ribonuclease PARN	8.49	5	5	14	4.60
Q8CG46	Smc5	Structural maintenance of chromosomes protein 5	1.45	1	2	2	4.53
P62915	Gtf2b	Transcription initiation factor IIB	7.59	2	2	6	4.49
Q9CQV1	Pam16	Mitochondrial import inner membrane translocase subunit TIM16	24.80	3	3	19	4.48
Q80Y14	Glrx5	Glutaredoxin-related protein 5, mitochondrial	17.11	2	2	6	4.48
Q8BQ30	Ppp1r18	Phostensin	5.72	3	3	36	4.47
Q9CQ60	Pgls	6-phosphogluconolactonase	19.84	4	4	46	4.46
O55131	Sep-07	Septin-7	13.53	5	5	28	4.40
P42208	Sep-02	Septin-2	13.57	4	4	40	4.39
Q3ULF4	Spg7	Paraplegin	4.35	2	4	10	4.39
Q9WV54	Asah1	Acid ceramidase	14.72	7	7	150	4.37
P28063	Psmb8	Proteasome subunit beta type-8	13.04	3	3	12	4.37
Q99KY4	Gak	Cyclin-G-associated kinase	3.60	5	5	20	4.32
Q9CQ40	Mrpl49	39S ribosomal protein L49, mitochondrial	20.48	4	4	15	4.32
Q8C3X2	Ccdc90b	Coiled-coil domain-containing protein 90B, mitochondrial	6.25	2	2	18	4.31
Q920A5	Scpep1	Retinoid-inducible serine carboxypeptidase	8.85	5	5	32	4.27

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8BVE3	Atp6v1h	V-type proton ATPase subunit H	16.56	7	7	83	4.26
Q9QXT0	Cnpy2	Protein canopy homolog 2	21.43	3	3	12	4.26
Q9JIW9	Ralb	Ras-related protein Ral-B	13.59	2	3	60	4.24
Q05D44	Eif5b	Eukaryotic translation initiation factor 5B	1.73	2	2	4	4.23
Q8K385	FRRS1	Ferric-chelate reductase 1	3.72	2	2	2	4.18
Q99K70	Rragc	Ras-related GTP-binding protein C	6.53	2	2	15	4.17
P48725	Pcnt	Pericentrin	0.72	1	3	6	4.14
Q8CIM5	Gpr84	G-protein coupled receptor 84	2.78	2	2	18	4.12
P09528	Fth1	Ferritin heavy chain	16.48	3	3	18	4.11
Q80UK8	Ints2	Integrator complex subunit 2	2.00	2	3	18	4.10
O08603	Raet1b	Retinoic acid early-inducible protein 1-beta	8.70	1	2	10	4.07
Q7TMY4	Thoc7	THO complex subunit 7 homolog	25.49	6	6	28	3.99
Q9JHZ2	Ankh	Progressive ankylosis protein	10.77	5	5	58	3.99
Q3UW53	Fam129a	Protein Niban	6.91	7	7	39	3.99
Q8R1N4	Nudcd3	NudC domain-containing protein 3	4.68	2	2	10	3.94
Q99MN9	Pccb	Propionyl-CoA carboxylase beta chain, mitochondrial	13.86	6	6	28	3.93
Q99J99	Mpst	3-mercaptopyruvate sulfurtransferase	6.73	2	2	6	3.92
P36371	Tap2	Antigen peptide transporter 2	2.56	2	2	6	3.88
P63073	Eif4e	Eukaryotic translation initiation factor 4E	12.90	2	3	29	3.87
Q9CT10	Ranbp3	Ran-binding protein 3	6.31	2	2	9	3.86
Q9JKF7	Mrpl39	39S ribosomal protein L39, mitochondrial	16.07	6	6	22	3.85
P11438	Lamp1	Lysosome-associated membrane glycoprotein 1	13.30	5	5	439	3.84
Q8R0G7	Spns1	Protein spinster homolog 1	3.79	2	2	6	3.82
Q8BFR4	Gns	N-acetylglucosamine-6-sulfatase	10.11	6	6	83	3.82
Q6ZPY7	Kdm3b	Lysine-specific demethylase 3B	1.54	2	2	6	3.82
Q9DCH4	Eif3f	Eukaryotic translation initiation factor 3 subunit F	18.28	5	5	61	3.74
Q8VEA4	Chchd4	Mitochondrial intermembrane space import and assembly protein 40	41.01	4	4	29	3.74
P34884	Mif	Macrophage migration inhibitory factor	17.39	2	2	8	3.72
Q9D023	Mpc2	Mitochondrial pyruvate carrier 2	11.81	2	2	6	3.69
P03930	Mtatp8	ATP synthase protein 8	55.22	5	5	43	3.68
P63271	Supt4h1a	Transcription elongation factor SPT4-A	27.35	3	3	12	3.67
Q64133	Maoa	Amine oxidase [flavin-containing] A	13.69	7	7	30	3.66
A6H611	Mipep	Mitochondrial intermediate peptidase	3.09	2	2	2	3.66
P63158	Hmgb1	High mobility group protein B1	27.44	4	5	85	3.65
Q9R0M6	Rab9a	Ras-related protein Rab-9A	11.44	2	2	6	3.61
Q8BMC4	Nop9	Nucleolar protein 9	6.92	4	4	26	3.61
Q8VDC0	Lars2	Probable leucine--tRNA ligase, mitochondrial	5.32	5	5	17	3.60
B1AQP7	Apol7b	Protein Apol7b	3.79	1	2	3	3.60
P54116	Stom	Erythrocyte band 7 integral membrane protein	47.89	13	13	916	3.56
Q924S8	Spred1	Sprouty-related, EVH1 domain-containing protein 1	6.53	2	2	6	3.53

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
P56391	Cox6b1	Cytochrome c oxidase subunit 6B1	32.56	4	4	38	3.53
Q91X21	Kiaa2013	Uncharacterized protein KIAA2013	6.47	4	4	24	3.53
P57716	Ncstn	Nicastrin	9.75	7	7	125	3.52
Q922Q4	Pycr2	Pyrroline-5-carboxylate reductase 2	43.13	12	12	293	3.51
E9PYB0	Ahnak2	Protein Ahnak2 (Fragment)	22.20	5	5	67	3.49
P61087	Ube2k	Ubiquitin-conjugating enzyme E2 K	24.00	4	4	40	3.49
Q9JJZ4	Ube2j1	Ubiquitin-conjugating enzyme E2 J1	20.75	5	5	40	3.49
Q80YV3	Trrap	Transformation/transcription domain-associated protein	2.92	6	8	74	3.48
P30993	C5ar1	C5a anaphylatoxin chemotactic receptor 1	9.97	4	4	44	3.48
Q8K2H1	Pphln1	Periphilin-1	3.94	2	2	4	3.47
P70362	Ufd1l	Ubiquitin fusion degradation protein 1 homolog	10.10	3	3	13	3.47
Q61207	Psap	Prosaposin	18.31	10	10	120	3.43
Q6IRU2	Tpm4	Tropomyosin alpha-4 chain	25.00	4	7	74	3.42
O88829	St3gal5	Lactosylceramide alpha-2,3-sialyltransferase	4.59	2	2	20	3.41
Q9JJF9	Sppl2a	Signal peptide peptidase-like 2A	3.06	2	2	12	3.41
Q9JMA1	Usp14	Ubiquitin carboxyl-terminal hydrolase 14	10.55	4	4	19	3.41
E9Q3T0	Gm10073	Uncharacterized protein	19.30	2	2	3	3.41
Q9JHF5	Tcirg1	V-type proton ATPase subunit a	25.90	18	18	506	3.40
Q8CFE3	Rcor1	REST corepressor 1	7.34	3	3	18	3.38
P46656	Fdx1	Adrenodoxin, mitochondrial	13.83	3	3	12	3.38
P62814	Atp6v1b2	V-type proton ATPase subunit B, brain isoform	34.44	15	15	377	3.36
P28798	Grn	Granulins	26.66	12	12	180	3.35
P01896	N/A	H-2 class I histocompatibility antigen, alpha chain (Fragment)	27.03	3	4	49	3.33
Q9CZB0	Sdhc	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	17.16	2	2	6	3.32
A1L314	Mpeg1	Macrophage-expressed gene 1 protein	15.85	11	11	262	3.32
Q9R0E2	Plod1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	3.57	3	3	7	3.31
Q99JW4	Lims1	LIM and senescent cell antigen-like-containing domain protein 1	5.54	2	2	2	3.31
Q9DB25	Alg5	Dolichyl-phosphate beta-glucosyltransferase	17.59	6	6	42	3.27
Q8BHY2	Noc4l	Nucleolar complex protein 4 homolog	3.10	2	2	12	3.27
Q9WUR2	Eci2	Enoyl-CoA delta isomerase 2, mitochondrial	6.65	2	2	6	3.25
O55126	Gbas	Protein NipSnap homolog 2	12.10	3	4	13	3.24
Q9ER00	Stx12	Syntaxin-12	24.09	5	5	58	3.24
Q9QXY6	Ehd3	EH domain-containing protein 3	8.22	2	5	67	3.21
Q9CQ45	Nenf	Neudesin	17.54	3	3	6	3.21
P62876	Polr2l	DNA-directed RNA polymerases I, II, and III subunit RPABC5	22.39	2	2	4	3.21
Q9JKW0	Arl6ip1	ADP-ribosylation factor-like protein 6-interacting protein 1	7.88	2	2	6	3.20
Q6ZQ03	Fnbp4	Formin-binding protein 4	2.13	2	2	2	3.19
Q68ED3	Papd5	Non-canonical poly(A) RNA polymerase PAPD5	3.95	3	3	20	3.18
P31651	Slc6a12	Sodium- and chloride-dependent betaine transporter	7.49	3	4	114	3.17
Q9CPR5	Mrpl15	39S ribosomal protein L15, mitochondrial	22.37	6	6	36	3.17

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q60649	Clpb	Caseinolytic peptidase B protein homolog	9.45	5	6	34	3.16
Q8BGC4	Zadh2	Zinc-binding alcohol dehydrogenase domain-containing protein 2	12.20	4	4	24	3.14
Q61187	Tsg101	Tumor susceptibility gene 101 protein	9.46	4	4	12	3.11
Q9D1H8	Mrpl53	39S ribosomal protein L53, mitochondrial	26.27	3	3	33	3.10
Q9Z1G3	Atp6v1c1	V-type proton ATPase subunit C 1	28.01	13	14	150	3.10
Q8R0F5	Rbmx2	RNA-binding motif protein, X-linked 2	6.75	2	2	6	3.09
Q9D1L0	Chchd2	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	22.22	2	2	30	3.09
P24788	Cdk11b	Cyclin-dependent kinase 11B	6.38	6	6	31	3.08
Q9D1K2	Atp6v1f	V-type proton ATPase subunit F	26.89	3	3	20	3.05
P47856	Gfpt1	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	6.17	3	3	8	3.04
P62849	Rps24	40S ribosomal protein S24	9.77	2	2	4	3.03
Q6TEK5	Vkorc1l1	Vitamin K epoxide reductase complex subunit 1-like protein 1	9.66	2	2	6	3.01
P62843	Rps15	40S ribosomal protein S15	17.24	2	2	47	3.01
E9Q4N7	Arid1b	Protein Arid1b	3.39	6	7	37	3.01
B2RQG2	Phf3	PHD finger protein 3	2.07	4	4	13	3.00
Q9WVB0	Rbpms	RNA-binding protein with multiple splicing	26.90	5	5	59	3.00
Q61666	Hira	Protein HIRA	1.67	2	2	4	2.99
Q9JJN2	Zfhx4	Zinc finger homeobox protein 4	1.41	4	4	13	2.96
Q91VC9	Ghitm	Growth hormone-inducible transmembrane protein	9.25	3	3	65	2.95
P57746	Atp6v1d	V-type proton ATPase subunit D	16.19	4	4	28	2.95
O35638	Stag2	Cohesin subunit SA-2	5.44	3	8	35	2.93
Q91YN9	Bag2	BAG family molecular chaperone regulator 2	27.62	6	6	39	2.92
Q9DCT2	Ndufs3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	18.25	4	4	108	2.90
P13020	Gsn	Gelsolin	8.08	6	6	70	2.89
P50136	Bckdha	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	5.43	2	2	10	2.89
Q9QWR8	Naga	Alpha-N-acetylgalactosaminidase	8.67	4	4	24	2.88
P40336	Vps26a	Vacuolar protein sorting-associated protein 26A	5.50	2	2	4	2.87
O70370	Ctss	Cathepsin S	19.41	6	6	154	2.86
Q8R2Q8	Bst2	Bone marrow stromal antigen 2	15.70	3	3	8	2.85
Q8VCF0	Mavs	Mitochondrial antiviral-signaling protein	11.13	4	4	36	2.84
Q9R1Q9	Atp6ap1	V-type proton ATPase subunit S1	11.66	5	5	37	2.84
G3X9L6	Gm10250	MCG55033	50.63	9	9	299	2.84
Q8VD75	Hip1	Huntingtin-interacting protein 1	3.01	2	3	8	2.83
Q5XG73	Acbd5	Acyl-CoA-binding domain-containing protein 5	5.51	3	3	6	2.82
O70404	Vamp8	Vesicle-associated membrane protein 8	40.59	5	5	132	2.81
P24547	Impdh2	Inosine-5'-monophosphate dehydrogenase 2	24.51	12	12	160	2.81
Q9CZX9	Emc4	ER membrane protein complex subunit 4	15.30	2	2	6	2.80
A2AJ88	Pnpla7	Patatin-like phospholipase domain-containing protein 7	2.59	4	4	8	2.79
Q9JKP7	Pole3	DNA polymerase epsilon subunit 3	11.72	1	2	8	2.77
D3Z081	Gm7353	Protein Gm7353	3.05	2	2	4	2.77

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
P05627	Jun	Transcription factor AP-1	6.89	2	2	4	2.77
Q8VC65	Nrm	Nurim	5.73	2	2	6	2.77
P12787	Cox5a	Cytochrome c oxidase subunit 5A, mitochondrial	30.14	5	6	121	2.77
O88696	Clpp	ATP-dependent Clp protease proteolytic subunit, mitochondrial	23.16	5	5	56	2.76
Q9D2R6	Coa3	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	25.93	3	3	24	2.74
Q9Z210	Pex11b	Peroxisomal membrane protein 11B	15.83	4	4	32	2.74
P26516	Psmd7	26S proteasome non-ATPase regulatory subunit 7	9.66	3	4	17	2.74
Q9WTQ8	Timm23	Mitochondrial import inner membrane translocase subunit Tim23	13.40	2	2	12	2.74
F6QL70	Gm17669	Protein Gm17669	28.57	5	5	71	2.73
Q14C51	Ptcd3	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	13.43	9	9	59	2.72
Q9CQE7	Ergic3	Endoplasmic reticulum-Golgi intermediate compartment protein 3	11.23	5	5	37	2.72
Q8BP92	Rcn2	Reticulocalbin-2	11.56	3	4	25	2.69
Q62446	Fkbp3	Peptidyl-prolyl cis-trans isomerase FKBP3	13.39	3	3	6	2.69
Q99LH1	Gnl2	Nucleolar GTP-binding protein 2	12.50	9	9	44	2.68
P97797	Sirpa	Tyrosine-protein phosphatase non-receptor type substrate 1	20.08	8	8	61	2.68
Q6GQT1	A2mp	Alpha-2-macroglobulin-P	1.02	2	2	20	2.64
Q9JHJ0	Tmod3	Tropomodulin-3	19.32	6	7	56	2.62
Q80XR2	Atp2c1	Calcium-transporting ATPase type 2C member 1	2.72	2	3	21	2.62
Q9CQH3	Ndufb5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	21.16	4	4	34	2.62
Q80X85	Mrps7	28S ribosomal protein S7, mitochondrial	31.82	6	6	31	2.61
Q01730	Rsu1	Ras suppressor protein 1	10.83	3	3	26	2.60
P09581	Csf1r	Macrophage colony-stimulating factor 1 receptor	10.64	11	11	134	2.60
P21460	Cst3	Cystatin-C	37.14	5	5	59	2.60
P18242	Ctsd	Cathepsin D	36.10	13	13	887	2.59
Q9ESZ8	Gtf2i	General transcription factor II-I	5.21	5	5	19	2.59
Q80SZ7	Gng5	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	33.82	4	4	32	2.59
P47713	Pla2g4a	Cytosolic phospholipase A2	17.38	12	12	115	2.58
P28658	Atxn10	Ataxin-10	11.16	5	5	31	2.58
Q9EQP2	Ehd4	EH domain-containing protein 4	29.94	13	15	211	2.58
P50429	Arsb	Arylsulfatase B	11.42	7	7	179	2.58
P31996	Cd68	Macrosialin	14.42	4	4	281	2.58
Q8CH25	Sltm	SAFB-like transcription modulator	14.06	12	13	86	2.58
Q9DBT5	Ampd2	AMP deaminase 2	8.15	8	8	64	2.58
Q91VK1	Bzw2	Basic leucine zipper and W2 domain-containing protein 2	10.50	4	5	25	2.58
P51863	Atp6v0d1	V-type proton ATPase subunit d 1	22.22	9	9	383	2.57
P97868	Rbbp6	E3 ubiquitin-protein ligase RBBP6	7.15	9	10	57	2.57
P39054	Dnm2	Dynamin-2	6.90	6	6	23	2.57
P97742	Cpt1a	Carnitine O-palmitoyltransferase 1, liver isoform	3.75	3	3	8	2.56
Q9D1C9	Rrp7a	Ribosomal RNA-processing protein 7 homolog A	23.21	5	5	24	2.56

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
P97808	Fxyd5	FXYD domain-containing ion transport regulator 5	33.71	4	4	30	2.55
Q60631	Grb2	Growth factor receptor-bound protein 2	11.06	2	2	4	2.55
P17047	Lamp2	Lysosome-associated membrane glycoprotein 2	12.05	5	5	150	2.54
Q8QZS1	Hibch	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	12.47	4	4	17	2.54
Q8BGT7	Smndc1	Survival of motor neuron-related-splicing factor 30	18.07	3	3	12	2.54
Q9ERS2	Ndufa13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	29.17	4	5	97	2.54
Q8K4I3	Arhgef6	Rho guanine nucleotide exchange factor 6	2.46	1	2	4	2.54
Q78IK2	Usmg5	Up-regulated during skeletal muscle growth protein 5	44.83	3	3	32	2.52
O70480	Vamp4	Vesicle-associated membrane protein 4	18.44	2	2	46	2.51
O88384	Vti1b	Vesicle transport through interaction with t-SNAREs homolog 1B	17.24	4	4	146	2.51
Q9Z2E1	Mbd2	Methyl-CpG-binding domain protein 2	14.73	4	5	28	2.51
Q9QZH6	Ecsit	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	4.60	2	2	2	2.49
Q5M8N0	Cnrip1	CB1 cannabinoid receptor-interacting protein 1	9.15	1	2	3	2.48
Q3TIX9	Usp39	U4/U6.U5 tri-snRNP-associated protein 2	3.55	2	2	4	2.47
Q61464	Znf638	Zinc finger protein 638	7.50	14	14	101	2.47
Q80ZK0	Mrps10	28S ribosomal protein S10, mitochondrial	30.00	4	4	36	2.46
Q9D168	Ints12	Integrator complex subunit 12	3.04	2	2	2	2.46
Q64337	Sqstm1	Sequestosome-1	17.19	5	5	22	2.45
P56395	Cyb5a	Cytochrome b5	45.52	5	5	105	2.45
Q60974	Ncor1	Nuclear receptor corepressor 1	3.83	8	8	20	2.45
P99029	Prdx5	Peroxiredoxin-5, mitochondrial	27.14	6	6	62	2.45
P58021	Tm9sf2	Transmembrane 9 superfamily member 2	10.57	6	7	151	2.45
Q9CQD1	Rab5a	Ras-related protein Rab-5A	30.70	3	6	162	2.43
Q9DBP5	Cmpk1	UMP-CMP kinase	17.86	3	3	10	2.43
Q61768	Kif5b	Kinesin-1 heavy chain	12.46	7	9	54	2.43
P70404	Idh3g	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	10.69	5	5	85	2.41
Q9D710	Tmx2	Thioredoxin-related transmembrane protein 2	8.81	3	3	12	2.41
Q9WVM1	Racgap1	Rac GTPase-activating protein 1	4.14	2	2	12	2.40
Q5SSZ5	Tns3	Tensin-3	2.01	2	3	19	2.40
E9PVA8	Gcn1l1	Protein Gcn1l1	4.23	11	11	72	2.39
Q9JIS8	Slc12a4	Solute carrier family 12 member 4	5.07	6	6	17	2.39
P56399	Usp5	Ubiquitin carboxyl-terminal hydrolase 5	3.03	2	2	6	2.38
Q9DB05	Napa	Alpha-soluble NSF attachment protein	50.51	12	12	173	2.38
Q9CXI5	Manf	Mesencephalic astrocyte-derived neurotrophic factor	45.81	11	11	235	2.37
P30999	Ctnnd1	Catenin delta-1	8.64	9	9	54	2.37
Q921H8	Acaa1a	3-ketoacyl-CoA thiolase A, peroxisomal	67.22	21	22	844	2.37
P53996	Cnbp	Cellular nucleic acid-binding protein	43.82	6	6	178	2.37
O89086	Rbm3	RNA-binding protein 3	30.72	5	5	57	2.37
Q8BH07	Arl6ip6	ADP-ribosylation factor-like protein 6-interacting protein 6	7.96	1	2	13	2.36
Q9D5V5	Cul5	Cullin-5	2.56	2	2	6	2.36

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
P63280	Ube2i	SUMO-conjugating enzyme UBC9	14.56	3	3	18	2.36
O35226	Psmd4	26S proteasome non-ATPase regulatory subunit 4	7.18	2	2	12	2.35
Q9R049	Amfr	E3 ubiquitin-protein ligase AMFR	3.58	2	2	18	2.35
Q8VCN9	Tbcc	Tubulin-specific chaperone C	4.69	2	2	12	2.35
Q9CQV4	Fam134c	Protein FAM134C	4.51	2	2	2	2.35
Q8VE22	Mrps23	28S ribosomal protein S23, mitochondrial	47.46	7	7	97	2.33
Q9Z1Q5	Clic1	Chloride intracellular channel protein 1	23.24	5	5	71	2.33
Q91VN4	Chchd6	MICOS complex subunit Mic25	31.14	7	7	77	2.33
Q91WN1	Dnajc9	DnaJ homolog subfamily C member 9	28.57	9	10	121	2.33
P97304	Polr1d	DNA-directed RNA polymerases I and III subunit RPAC2	26.32	3	3	14	2.32
Q9QZ23	Nfu1	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	16.47	3	3	45	2.31
Q9CQZ5	Ndufa6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	33.59	4	4	60	2.31
O88531	Ppt1	Palmitoyl-protein thioesterase 1	22.88	7	7	79	2.31
P15247	Il9	Interleukin-9	11.11	1	2	3	2.31
Q4FZF3	Ddx49	Probable ATP-dependent RNA helicase DDX49	3.54	2	2	4	2.30
Q8JZQ9	Eif3b	Eukaryotic translation initiation factor 3 subunit B	20.67	14	14	109	2.29
P50516	Atp6v1a	V-type proton ATPase catalytic subunit A	32.25	19	19	536	2.29
Q9CZE3	Rab32	Ras-related protein Rab-32	41.26	8	8	226	2.29
Q9DBY1	Syvn1	E3 ubiquitin-protein ligase synoviolin	2.61	2	2	4	2.29
P99027	Rplp2	60S acidic ribosomal protein P2	77.39	7	7	287	2.28
A2AJ15	Man1b1	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	3.04	2	2	2	2.28
Q61733	Mrps31	28S ribosomal protein S31, mitochondrial	20.83	9	10	89	2.28
Q64430	Atp7a	Copper-transporting ATPase 1	1.74	2	3	13	2.27
Q9CPW5	Ssr2	Translocon-associated protein subunit beta	7.65	3	3	148	2.27
Q99LP6	Grpel1	GrpE protein homolog 1, mitochondrial	48.85	11	11	161	2.27
Q61550	Rad21	Double-strand-break repair protein rad21 homolog	19.84	10	10	99	2.27
P56542	Dnase2	Deoxyribonuclease-2-alpha	4.53	2	2	10	2.25
Q9Z0M5	Lipa	Lysosomal acid lipase/cholesteryl ester hydrolase	14.86	6	6	102	2.25
Q9CPP6	Ndufa5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	38.79	6	6	111	2.24
Q99J93	Ifitm2	Interferon-induced transmembrane protein 2	16.67	1	2	143	2.23
Q9CX00	Ist1	IST1 homolog	11.88	5	5	31	2.23
Q9CXZ1	Ndufs4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	40.57	7	7	127	2.23
P41105	Rpl28	60S ribosomal protein L28	50.36	9	10	404	2.23
P22892	Ap1g1	AP-1 complex subunit gamma-1	8.76	8	8	41	2.23
P97369	Ncf4	Neutrophil cytosol factor 4	13.57	4	4	10	2.22
Q9JL26	Fmnl1	Formin-like protein 1	19.84	21	21	290	2.22
Q91VZ6	Smap1	Stromal membrane-associated protein 1	9.77	4	4	24	2.22
P61021	Rab5b	Ras-related protein Rab-5B	25.12	2	5	165	2.22
B9EJ86	Osbpl8	Oxysterol-binding protein	13.72	11	11	65	2.21
Q9CWW7	Cxxc1	CXXC-type zinc finger protein 1	4.09	2	2	6	2.21

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q9CQF0	Mrpl11	39S ribosomal protein L11, mitochondrial	44.79	8	8	82	2.21
Q8CEE7	Rdh13	Retinol dehydrogenase 13	7.78	3	3	10	2.20
Q9WVK4	Ehd1	EH domain-containing protein 1	14.04	7	9	116	2.20
Q9CR62	Slc25a11	Mitochondrial 2-oxoglutarate/malate carrier protein	28.34	9	9	214	2.19
Q9JIY5	Htra2	Serine protease HTRA2, mitochondrial	7.86	3	3	32	2.19
Q9Z1M8	Ik	Protein Red	22.98	14	14	176	2.19
Q9JKB3	Ybx3	Y-box-binding protein 3	24.93	3	8	359	2.19
Q9D7P6	Iscu	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	29.76	5	5	71	2.19
Q8BY02	Nkrf	NF-kappa-B-repressing factor	10.43	8	8	34	2.19
P14685	Psmd3	26S proteasome non-ATPase regulatory subunit 3	26.42	14	14	154	2.19
Q8CIN4	Pak2	Serine/threonine-protein kinase PAK 2	24.24	11	11	119	2.18
Q8BUE4	Aifm2	Apoptosis-inducing factor 2	11.80	4	5	27	2.18
Q69ZK6	Jmjd1c	Probable JmjC domain-containing histone demethylation protein 2C	0.98	2	2	2	2.18
O35855	Bcat2	Branched-chain-amino-acid aminotransferase, mitochondrial	15.27	6	6	78	2.18
Q8VCG3	Wdr74	WD repeat-containing protein 74	7.81	3	3	11	2.18
O35593	Psmd14	26S proteasome non-ATPase regulatory subunit 14	6.45	2	2	58	2.18
P52503	Ndufs6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	41.38	4	4	109	2.18
Q9DC69	Ndufa9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	18.57	7	7	101	2.17
Q8JZN5	Acad9	Acyl-CoA dehydrogenase family member 9, mitochondrial	24.48	15	15	159	2.17
Q8BGC0	Htatsf1	HIV Tat-specific factor 1 homolog	2.51	2	2	6	2.17
Q99LY9	Ndufs5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	34.91	4	4	59	2.17
Q9QY06	Myo9b	Unconventional myosin-IXb	1.37	3	3	6	2.16
P35278	Rab5c	Ras-related protein Rab-5C	48.61	6	9	358	2.16
P24668	M6pr	Cation-dependent mannose-6-phosphate receptor	25.90	9	9	248	2.16
Q9D855	Uqcrb	Cytochrome b-c1 complex subunit 7	42.34	5	5	88	2.15
P68254	Ywhaq	14-3-3 protein theta	32.24	3	8	153	2.15
Q8VCW8	Acsf2	Acyl-CoA synthetase family member 2, mitochondrial	3.74	2	2	6	2.15
Q9D6J6	Ndufv2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	33.06	8	8	92	2.14
A2ABV5	Med14	Mediator of RNA polymerase II transcription subunit 14	1.37	2	2	2	2.14
Q9CQ49	Ncbp2	Nuclear cap-binding protein subunit 2	19.23	3	3	23	2.14
Q99N89	Mrpl43	39S ribosomal protein L43, mitochondrial	17.49	4	4	38	2.12
Q9JMD0	Znf207	BUB3-interacting and GLEBS motif-containing protein ZNF207	5.25	2	2	18	2.11
Q62093	Srsf2	Serine/arginine-rich splicing factor 2	28.96	7	7	238	2.11
Q93092	Taldo1	Transaldolase	31.45	11	12	127	2.11
P47791	Gsr	Glutathione reductase, mitochondrial	10.40	4	4	32	2.10
P24638	Acp2	Lysosomal acid phosphatase	3.78	2	2	2	2.10
P53994	Rab2a	Ras-related protein Rab-2A	37.74	7	7	228	2.10
O55125	Nipsnap1	Protein NipSnap homolog 1	18.66	4	5	33	2.09
P09671	Sod2	Superoxide dismutase [Mn], mitochondrial	23.42	5	5	172	2.09

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q8R1B4	Eif3c	Eukaryotic translation initiation factor 3 subunit C	13.17	10	10	120	2.09
Q8BJ48	Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	10.25	4	4	35	2.09
P63024	Vamp3	Vesicle-associated membrane protein 3	38.83	3	3	27	2.08
P63323	Rps12	40S ribosomal protein S12	28.79	5	5	190	2.08
Q9D0F6	Rfc5	Replication factor C subunit 5	15.04	5	5	32	2.08
Q8C854	Myef2	Myelin expression factor 2	27.41	18	18	217	2.07
Q9DBL1	Acadsb	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	12.27	5	5	65	2.07
Q8K411	Pitrm1	Presequence protease, mitochondrial	19.21	17	18	198	2.07
Q9D964	Gatm	Glycine amidinotransferase, mitochondrial	11.82	5	5	148	2.07
P19973	Lsp1	Lymphocyte-specific protein 1	18.48	4	4	21	2.07
Q9ERG0	Lima1	LIM domain and actin-binding protein 1	5.84	4	4	31	2.07
Q9D024	Ccdc47	Coiled-coil domain-containing protein 47	19.67	10	10	81	2.07
Q8CH02	Sugp1	SURP and G-patch domain-containing protein 1	10.89	5	5	28	2.07
O35381	Anp32a	Acidic leucine-rich nuclear phosphoprotein 32 family member A	10.93	1	4	76	2.07
Q8BK08	Tmem11	Transmembrane protein 11, mitochondrial	17.37	3	3	16	2.06
Q9D0L7	Armc10	Armadillo repeat-containing protein 10	14.38	4	4	53	2.06
Q8BHJ9	Slu7	Pre-mRNA-splicing factor SLU7	5.64	3	3	20	2.06
Q3TWW8	Srsf6	Serine/arginine-rich splicing factor 6	30.68	11	14	458	2.06
P55302	Lrpap1	Alpha-2-macroglobulin receptor-associated protein	38.89	15	15	131	2.06
Q9DB15	Mrpl12	39S ribosomal protein L12, mitochondrial	23.38	6	6	108	2.06
Q64737	Gart	Trifunctional purine biosynthetic protein adenosine-3	8.32	9	9	70	2.06
Q8BJY1	Psmd5	26S proteasome non-ATPase regulatory subunit 5	3.37	2	2	6	2.06
Q91VU0	Fam3c	Protein FAM3C	8.81	2	2	6	2.05
Q9CQC6	Bzw1	Basic leucine zipper and W2 domain-containing protein 1	17.18	7	8	50	2.05
P10923	Spp1	Osteopontin	21.77	5	5	67	2.04
Q8C407	Yipf4	Protein YIPF4	8.13	2	2	23	2.03
Q9D6U8	Fam162a	Protein FAM162A	20.65	3	3	15	2.03
P30204	Msr1	Macrophage scavenger receptor types I and II	14.19	7	7	217	2.03
Q80X90	Flnb	Filamin-B	7.30	15	17	102	2.03
O35345	Kpna6	Importin subunit alpha-7	8.40	4	5	33	2.02
Q9WUU7	Ctsz	Cathepsin Z	30.07	8	8	547	2.02
Q9D7N3	Mrps9	28S ribosomal protein S9, mitochondrial	17.18	6	6	56	2.02
Q8VBT6	Apobr	Apolipoprotein B receptor	19.85	15	15	160	2.01
P29391	Ftl1	Ferritin light chain 1	39.89	5	5	78	2.01
Q09014	Ncf1	Neutrophil cytosol factor 1	32.82	12	12	209	2.01
Q8BU88	Mrpl22	39S ribosomal protein L22, mitochondrial	36.41	8	8	95	2.01
Q9ES28	Arhgef7	Rho guanine nucleotide exchange factor 7	10.44	8	9	40	2.00
Q9R0Q7	Ptges3	Prostaglandin E synthase 3	17.50	3	3	33	2.00
Q8BGA9	Oxa1l	Mitochondrial inner membrane protein OXA1L	4.39	2	2	12	2.00
Q9JKK7	Tmod2	Tropomodulin-2	4.27	1	2	17	1.99

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q9Z1P6	Ndufa7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	54.87	6	6	100	1.99
Q8C6L5	Mb21d1	Cyclic GMP-AMP synthase	13.81	6	6	32	1.98
Q9CQW1	Ykt6	Synaptobrevin homolog YKT6	30.30	7	7	53	1.98
P21855	Cd72	B-cell differentiation antigen CD72	10.45	3	3	57	1.98
Q99LD4	Gps1	COP9 signalosome complex subunit 1	4.46	2	2	6	1.98
Q9CQV8	Ywhab	14-3-3 protein beta/alpha	43.50	4	10	296	1.98
Q9DB34	Chmp2a	Charged multivesicular body protein 2a	17.57	6	6	12	1.97
Q9D883	U2af1	Splicing factor U2AF 35 kDa subunit	21.76	6	6	179	1.97
Q9CSU0	Rprd1b	Regulation of nuclear pre-mRNA domain-containing protein 1B	16.56	4	4	36	1.97
Q9JM76	Arpc3	Actin-related protein 2/3 complex subunit 3	13.48	3	3	16	1.97
Q62465	Vat1	Synaptic vesicle membrane protein VAT-1 homolog	18.97	8	8	104	1.96
P15092	Ifi204	Interferon-activable protein 204	3.75	2	3	26	1.96
Q8K1M6	Dnm1l	Dynamin-1-like protein	5.80	4	5	19	1.96
Q9CPT4	Mydgf	Myeloid-derived growth factor	19.28	3	3	23	1.96
Q8R0K4	Ccdc137	Coiled-coil domain-containing protein 137	9.31	3	3	11	1.95
O08715	Akap1	A-kinase anchor protein 1, mitochondrial	4.32	2	2	4	1.95
Q99M87	Dnaja3	DnaJ homolog subfamily A member 3, mitochondrial	12.29	5	5	145	1.95
O35604	Npc1	Niemann-Pick C1 protein	4.31	6	6	37	1.95
P25976	Ubtf	Nucleolar transcription factor 1	30.85	26	26	422	1.95
Q9CWK8	Snx2	Sorting nexin-2	16.57	7	8	99	1.95
Q61599	Arhgdib	Rho GDP-dissociation inhibitor 2	35.00	6	6	84	1.94
Q6P3A8	Bckdhb	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	5.90	2	2	6	1.94
Q6NVF9	Cpsf6	Cleavage and polyadenylation specificity factor subunit 6	15.06	6	6	111	1.94
P20060	Hexb	Beta-hexosaminidase subunit beta	19.40	10	10	157	1.94
Q9DAU1	Cnpy3	Protein canopy homolog 3	23.91	6	6	169	1.94
Q6PFR5	Tra2a	Transformer-2 protein homolog alpha	10.68	2	3	52	1.93
Q99N95	Mrpl3	39S ribosomal protein L3, mitochondrial	8.05	3	3	46	1.93
Q6A4J8	Usp7	Ubiquitin carboxyl-terminal hydrolase 7	7.98	9	9	38	1.93
O88587	Comt	Catechol O-methyltransferase	14.72	5	5	40	1.93
Q61466	Smarcd1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	13.01	6	7	54	1.93
P08905	Lyz2	Lysozyme C-2	50.68	8	8	584	1.93
P16675	Ctsa	Lysosomal protective protein	23.00	12	12	289	1.92
Q9CXW3	Cacybp	Calcyclin-binding protein	10.48	3	3	18	1.92
O88456	Capns1	Calpain small subunit 1	11.52	3	3	11	1.92
Q6P1H6	Ankle2	Ankyrin repeat and LEM domain-containing protein 2	6.02	5	5	37	1.92
Q9WU81	Slc37a2	Sugar phosphate exchanger 2	8.38	3	3	57	1.92
Q9QYI4	Dnajb12	DnaJ homolog subfamily B member 12	10.90	4	4	35	1.92
A2AR02	Ppig	Peptidyl-prolyl cis-trans isomerase G	5.98	4	4	10	1.92
Q91VT4	Cbr4	Carbonyl reductase family member 4	10.59	3	3	14	1.92

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q3UVK0	Ermp1	Endoplasmic reticulum metallopeptidase 1	9.69	7	7	98	1.92
Q99K51	Pls3	Plastin-3	10.63	3	7	192	1.91
Q62425	Ndufa4	Cytochrome c oxidase subunit NDUFA4	56.10	6	6	288	1.91
Q9Z0R6	Itsn2	Intersectin-2	3.01	4	5	30	1.91
Q80X95	Rraga	Ras-related GTP-binding protein A	8.31	3	3	13	1.91
Q61425	Hadh	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	19.43	7	8	131	1.91
P39098	Man1a2	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB	5.46	2	3	10	1.91
Q925H1	Trps1	Zinc finger transcription factor Trps1	1.72	2	2	4	1.90
P21107	Tpm3	Tropomyosin alpha-3 chain	32.28	2	11	260	1.90
Q9QY76	Vapb	Vesicle-associated membrane protein-associated protein B	36.21	8	9	377	1.90
Q8R5J9	Arl6ip5	PRA1 family protein 3	17.02	4	4	95	1.89
P59999	Arpc4	Actin-related protein 2/3 complex subunit 4	27.98	5	5	158	1.89
P35282	Rab21	Ras-related protein Rab-21	15.32	5	5	86	1.88
O35326	Srsf5	Serine/arginine-rich splicing factor 5	30.48	8	9	275	1.88
Q8BXA1	Golim4	Golgi integral membrane protein 4	10.23	5	6	23	1.88
Q921Y2	Imp3	U3 small nucleolar ribonucleoprotein protein IMP3	35.33	6	6	42	1.88
Q9CVB6	Arpc2	Actin-related protein 2/3 complex subunit 2	26.33	9	9	124	1.88
Q6DID7	Wls	Protein wntless homolog	1.85	2	2	14	1.88
A0A0A6YVU8	Gm9774	MCG119397	5.41	2	2	6	1.87
Q3UDW8	Hgsnat	Heparan-alpha-glucosaminide N-acetyltransferase	3.66	2	2	76	1.87
Q99PU8	Dhx30	Putative ATP-dependent RNA helicase DHX30	4.60	4	4	8	1.87
Q61655	Ddx19a	ATP-dependent RNA helicase DDX19A	11.51	5	5	25	1.87
Q99JI6	Rap1b	Ras-related protein Rap-1b	39.13	3	8	446	1.87
P68181	Prkacb	cAMP-dependent protein kinase catalytic subunit beta	5.13	2	2	6	1.87
Q3TMP1	Gtf3c3	General transcription factor IIIC, polypeptide 3	2.49	2	2	4	1.87
Q91YE7	Rbm5	RNA-binding protein 5	13.62	9	11	128	1.87
Q9Z148	Ehmt2	Histone-lysine N-methyltransferase EHMT2	1.98	2	2	4	1.86
Q9DC61	Pmpca	Mitochondrial-processing peptidase subunit alpha	15.84	9	9	138	1.86
Q7TPR4	Actn1	Alpha-actinin-1	5.94	3	5	91	1.86
Q8VCB1	Ndc1	Nucleoporin NDC1	18.57	10	10	132	1.86
Q8JZM7	Cdc73	Parafibromin	21.09	11	11	85	1.86
Q3UPF5	Zc3hav1	Zinc finger CCCH-type antiviral protein 1	8.14	7	8	42	1.85
P10605	Ctsb	Cathepsin B	47.79	15	15	726	1.85
Q9ESU6	Brd4	Bromodomain-containing protein 4	3.50	4	5	26	1.85
P10107	Anxa1	Annexin A1	38.44	11	13	249	1.85
Q9WVG6	Carm1	Histone-arginine methyltransferase CARM1	3.95	3	3	14	1.85
Q8VE97	Srsf4	Serine/arginine-rich splicing factor 4	13.09	3	7	239	1.84
O70439	Stx7	Syntaxin-7	30.27	7	7	215	1.84
Q8BK72	Mrps27	28S ribosomal protein S27, mitochondrial	16.39	6	6	54	1.84
Q99MN1	Kars	Lysine--tRNA ligase	14.12	7	7	44	1.84

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q9Z2I8	Suclg2	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	26.10	11	11	265	1.84
Q8CDN6	Txnl1	Thioredoxin-like protein 1	21.80	4	4	42	1.83
Q9DBJ1	Pgam1	Phosphoglycerate mutase 1	48.03	10	11	186	1.83
Q3TVI8	Pbxip1	Pre-B-cell leukemia transcription factor-interacting protein 1	4.13	2	2	6	1.83
P57759	Erp29	Endoplasmic reticulum resident protein 29	28.24	8	8	531	1.83
Q9D7Z3	Nol7	Nucleolar protein 7	6.30	3	3	7	1.83
P00405	Mtco2	Cytochrome c oxidase subunit 2	10.57	3	3	135	1.83
Q6ZQM8	Ugt1a7c	UDP-glucuronosyltransferase 1-7C	16.95	9	9	261	1.83
P62835	Rap1a	Ras-related protein Rap-1A	27.17	1	6	392	1.83
Q64433	Hspe1	10 kDa heat shock protein, mitochondrial	74.51	8	8	782	1.83
Q91VN6	Ddx41	Probable ATP-dependent RNA helicase DDX41	19.77	13	13	69	1.82
Q9DC71	Mrps15	28S ribosomal protein S15, mitochondrial	25.97	7	7	45	1.82
Q9DC51	Gnai3	Guanine nucleotide-binding protein G(k) subunit alpha	29.66	5	10	335	1.82
P70295	Aup1	Ancient ubiquitous protein 1	25.12	8	8	85	1.82
Q9Z0H4	Celf2	CUGBP Elav-like family member 2	11.22	7	7	144	1.81
Q6NZN0	Rbm26	RNA-binding protein 26	4.25	2	3	38	1.81
D0QMC3	Mndal	Myeloid cell nuclear differentiation antigen-like protein	7.06	2	3	9	1.81
Q497V5	Srbd1	S1 RNA-binding domain-containing protein 1	4.14	4	5	21	1.81
Q9DAA6	Exosc1	Exosome complex component CSL4	11.79	2	2	24	1.81
A2RSY6	Trmt1l	TRMT1-like protein	5.49	4	4	17	1.81
Q60855	Ripk1	Receptor-interacting serine/threonine-protein kinase 1	8.69	6	6	51	1.81
Q8BWT1	Acaa2	3-ketoacyl-CoA thiolase, mitochondrial	26.95	10	10	210	1.81
Q8R5M8	Cadm1	Cell adhesion molecule 1	4.17	2	2	12	1.81
P17426	Ap2a1	AP-2 complex subunit alpha-1	11.16	7	11	82	1.81
Q9D3E6	Stag1	Cohesin subunit SA-1	5.96	3	9	51	1.80
Q7TMF3	Ndufa12	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	34.48	4	4	44	1.80
P63325	Rps10	40S ribosomal protein S10	55.76	10	11	406	1.80
Q8K4Q8	Colec12	Collectin-12	14.42	12	12	244	1.79
Q3THE2	Myl12b	Myosin regulatory light chain 12B	29.65	5	5	235	1.79
P28656	Nap1l1	Nucleosome assembly protein 1-like 1	6.91	1	2	21	1.79
E9PVZ8	Golgb1	Protein Golgb1	9.39	27	28	189	1.79
Q9CQW0	Emc6	ER membrane protein complex subunit 6	20.00	2	2	32	1.79
P70388	Rad50	DNA repair protein RAD50	6.55	8	9	46	1.79
Q7JJ13	Brd2	Bromodomain-containing protein 2	8.40	6	7	51	1.79
Q9DB85	Rrp8	Ribosomal RNA-processing protein 8	19.47	8	8	141	1.78
Q8BKC5	Ipo5	Importin-5	5.65	6	6	50	1.78
Q9CR68	Uqcrfs1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	31.39	9	9	228	1.78
O88630	Gosr1	Golgi SNAP receptor complex member 1	15.60	5	5	24	1.78
Q8BH86	N/A	UPF0317 protein C14orf159 homolog, mitochondrial	16.86	9	9	70	1.78
Q9CQ69	Uqcrq	Cytochrome b-c1 complex subunit 8	39.02	5	5	84	1.78

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8JZQ2	Afg3l2	AFG3-like protein 2	18.20	13	16	114	1.77
P09055	Itgb1	Integrin beta-1	13.53	9	9	55	1.77
P16045	Lgals1	Galectin-1	39.26	5	5	158	1.77
Q60875	Arhgef2	Rho guanine nucleotide exchange factor 2	12.18	12	12	151	1.77
P61982	Ywhag	14-3-3 protein gamma	42.91	4	10	266	1.77
Q99P91	Gpnmb	Transmembrane glycoprotein NMB	14.81	8	8	170	1.77
Q80WW9	Ddrgk1	DDRGK domain-containing protein 1	13.97	4	4	49	1.77
Q9CQ92	Fis1	Mitochondrial fission 1 protein	24.34	4	4	70	1.76
P59708	Sf3b6	Splicing factor 3B subunit 6	45.60	6	6	84	1.76
P08752	Gnai2	Guanine nucleotide-binding protein G(i) subunit alpha-2	38.31	7	12	588	1.76
B2RXS4	Plxnb2	Plexin-B2	10.37	19	19	218	1.76
Q99JI4	Psmd6	26S proteasome non-ATPase regulatory subunit 6	23.91	9	9	28	1.76
Q8BJ05	Zc3h14	Zinc finger CCCH domain-containing protein 14	11.43	7	7	81	1.76
Q9WU40	Lemd3	Inner nuclear membrane protein Man1	14.55	10	10	138	1.76
O09167	Rpl21	60S ribosomal protein L21	23.75	6	6	95	1.76
P35486	Pdha1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	23.08	10	10	183	1.75
Q9QYB1	Clic4	Chloride intracellular channel protein 4	14.62	4	4	13	1.75
Q9DCS9	Ndufb10	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	41.48	6	6	56	1.75
Q9D1Q6	Erp44	Endoplasmic reticulum resident protein 44	35.22	13	14	297	1.75
Q9JHU4	Dync1h1	Cytoplasmic dynein 1 heavy chain 1	7.64	36	37	243	1.75
P62259	Ywhae	14-3-3 protein epsilon	34.51	7	10	235	1.75
P68510	Ywhah	14-3-3 protein eta	52.85	8	13	246	1.75
Q9D7S9	Chmp5	Charged multivesicular body protein 5	10.50	2	2	26	1.75
D3Z2H9	Tpm3-rs7	Protein Tpm3-rs7	45.56	7	16	352	1.74
Q9R0X4	Acot9	Acyl-coenzyme A thioesterase 9, mitochondrial	16.63	8	8	132	1.74
P54227	Stmn1	Stathmin	36.24	6	6	27	1.73
Q9D938	Tmem160	Transmembrane protein 160	10.64	2	2	16	1.73
Q6ZWM4	Lsm8	U6 snRNA-associated Sm-like protein LSm8	19.79	2	2	24	1.73
Q9CQA6	Chchd1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 1	39.83	3	3	15	1.73
Q9CY73	Mrpl44	39S ribosomal protein L44, mitochondrial	12.31	4	4	27	1.73
A0A087WRH0	Zfp951	Protein Zfp951	19.07	1	3	13	1.73
Q8BHF7	Pgs1	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, mitochondrial	3.62	1	2	13	1.73
Q9QUJ7	Acsl4	Long-chain-fatty-acid--CoA ligase 4	13.64	8	10	125	1.73
P45952	Acadm	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	25.18	9	10	183	1.73
Q60960	Kpna1	Importin subunit alpha-5	12.83	5	6	58	1.72
Q6P9J9	Ano6	Anoctamin-6	2.41	2	2	4	1.72
Q8VEE4	Rpa1	Replication protein A 70 kDa DNA-binding subunit	20.39	13	13	170	1.72
Q04447	Ckb	Creatine kinase B-type	4.20	2	2	2	1.72

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8BUV8	Gpr107	Protein GPR107	3.99	2	3	9	1.72
Q9CX56	Psmd8	26S proteasome non-ATPase regulatory subunit 8	11.33	5	5	41	1.72
Q63932	Map2k2	Dual specificity mitogen-activated protein kinase kinase 2	12.47	4	5	49	1.71
O88307	Sorl1	Sortilin-related receptor	7.36	15	15	70	1.71
Q9ES97	Rtn3	Reticulon-3	1.97	1	2	62	1.70
Q8CCF0	Prpf31	U4/U6 small nuclear ribonucleoprotein Prp31	18.04	9	9	125	1.70
Q9Z2D8	Mbd3	Methyl-CpG-binding domain protein 3	17.19	4	5	46	1.70
Q64522	Hist2h2ab	Histone H2A type 2-B	67.69	1	8	2399	1.70
Q8K2C9	Hacd3	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	5.52	3	3	34	1.70
P62852	Rps25	40S ribosomal protein S25	40.80	7	7	414	1.70
Q6NV83	U2surp	U2 snRNP-associated SURP motif-containing protein	21.67	21	21	365	1.69
O55242	Sigmar1	Sigma non-opioid intracellular receptor 1	12.11	3	3	70	1.69
Q9JJF3	No66	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	16.09	9	9	78	1.69
Q6PGF3	Med16	Mediator of RNA polymerase II transcription subunit 16	4.47	4	4	38	1.68
P46460	Nsf	Vesicle-fusing ATPase	31.45	23	24	514	1.68
P47740	Aldh3a2	Fatty aldehyde dehydrogenase	16.12	7	8	41	1.68
Q4FK66	Prpf38a	Pre-mRNA-splicing factor 38A	14.74	4	4	70	1.68
Q8BL97	Srsf7	Serine/arginine-rich splicing factor 7	29.96	8	9	197	1.68
O70251	Eef1b	Elongation factor 1-beta	25.33	6	6	72	1.68
Q8BRF7	Scfd1	Sec1 family domain-containing protein 1	18.00	10	10	61	1.68
Q8K0H5	Taf10	Transcription initiation factor TFIID subunit 10	15.14	2	2	6	1.67
O08579	Emd	Emerin	39.77	10	10	310	1.67
Q9D7S7	Rpl22l1	60S ribosomal protein L22-like 1	25.41	3	3	36	1.67
Q8R2Y0	Abhd6	Monoacylglycerol lipase ABHD6	7.14	2	2	6	1.67
Q9D1B9	Mrpl28	39S ribosomal protein L28, mitochondrial	12.84	3	3	22	1.67
Q99NH8	Trem2	Triggering receptor expressed on myeloid cells 2	11.01	2	2	6	1.66
P08556	Nras	GTPase NRas	16.93	3	3	18	1.66
Q60864	Stip1	Stress-induced-phosphoprotein 1	23.39	12	12	123	1.66
Q3UHX0	Nol8	Nucleolar protein 8	9.15	9	9	82	1.66
P14901	Hmox1	Heme oxygenase 1	22.84	5	5	92	1.66
Q9DC37	Mfsd1	Major facilitator superfamily domain-containing protein 1	6.90	3	3	45	1.66
Q91WS0	Cisd1	CDGSH iron-sulfur domain-containing protein 1	44.44	5	5	112	1.65
Q8R164	Bphl	Valacyclovir hydrolase	14.09	5	5	15	1.65
Q9Z1G4	Atp6v0a1	V-type proton ATPase 116 kDa subunit a isoform 1	4.77	4	4	35	1.65
Q9D0B0	Srsf9	Serine/arginine-rich splicing factor 9	42.34	8	9	215	1.65
P62754	Rps6	40S ribosomal protein S6	34.94	11	11	580	1.65
P56480	Atp5b	ATP synthase subunit beta, mitochondrial	61.44	24	24	1787	1.65
P12265	Gusb	Beta-glucuronidase	23.92	16	16	547	1.65
Q60865	Caprin1	Caprin-1	11.74	11	11	165	1.64
Q99N93	Mrpl16	39S ribosomal protein L16, mitochondrial	7.97	2	2	4	1.64

Accession	**Gene**	**Description**	**Σcover-age**	**Σ# Unique Peptides**	**Σ# Peptides**	**Σ# PSMs**	**[1]*pksP*/wt**
Q9DCZ4	Apoo	MICOS complex subunit Mic26	13.13	2	2	31	1.64
Q8BMF4	Dlat	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	22.59	12	12	422	1.64
Q8R2E9	Ero1lb	ERO1-like protein beta	7.71	2	4	90	1.64
O08795	Prkcsh	Glucosidase 2 subunit beta	28.02	17	17	477	1.64
Q3UUQ7	Pgap1	GPI inositol-deacylase	5.53	6	6	35	1.64
P51410	Rpl9	60S ribosomal protein L9	44.79	9	9	130	1.64
Q9CZ44	Nsfl1c	NSFL1 cofactor p47	22.43	6	6	45	1.64
P18052	Ptpra	Receptor-type tyrosine-protein phosphatase alpha	3.14	2	3	26	1.64
P51150	Rab7a	Ras-related protein Rab-7a	82.61	17	17	814	1.64
P01942	Hba	Hemoglobin subunit alpha	16.90	3	3	458	1.63
P54822	Adsl	Adenylosuccinate lyase	8.06	4	4	36	1.63
P29341	Pabpc1	Polyadenylate-binding protein 1	37.11	17	27	495	1.63
Q9DBC7	Prkar1a	cAMP-dependent protein kinase type I-alpha regulatory subunit	12.07	4	4	23	1.63
Q8R050	Gspt1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	9.12	7	7	16	1.63
O08547	Sec22b	Vesicle-trafficking protein SEC22b	45.58	10	10	354	1.63
Q91VH2	Snx9	Sorting nexin-9	6.89	4	4	40	1.62
Q5U458	Dnajc11	DnaJ homolog subfamily C member 11	9.84	6	6	62	1.62
P12382	Pfkl	ATP-dependent 6-phosphofructokinase, liver type	8.85	4	6	43	1.62
Q80Y81	Elac2	Zinc phosphodiesterase ELAC protein 2	4.69	3	3	14	1.62
Q61827	Mafk	Transcription factor MafK	14.74	1	3	39	1.62
O08528	Hk2	Hexokinase-2	21.70	17	19	161	1.62
Q9CR59	Gadd45gip1	Growth arrest and DNA damage-inducible proteins-interacting protein 1	13.06	2	2	4	1.62
Q9EST5	Anp32b	Acidic leucine-rich nuclear phosphoprotein 32 family member B	25.74	6	9	171	1.61
P01897	H2-L	H-2 class I histocompatibility antigen, L-D alpha chain	22.65	5	7	119	1.61
Q9CY58	Serbp1	Plasminogen activator inhibitor 1 RNA-binding protein	32.19	13	13	321	1.61
P21126	Ubl4a	Ubiquitin-like protein 4A	33.12	6	6	36	1.61
Q80VL1	Tdrkh	Tudor and KH domain-containing protein	11.96	6	6	48	1.61
Q99JB2	Stoml2	Stomatin-like protein 2, mitochondrial	32.58	12	12	405	1.61
Q3TCH7	Cul4a	Cullin-4A	3.03	2	2	6	1.61
O35295	Purb	Transcriptional activator protein Pur-beta	20.37	4	6	69	1.60
Q810V0	Mphosph10	U3 small nucleolar ribonucleoprotein protein MPP10	23.35	15	15	162	1.60
P62274	Rps29	40S ribosomal protein S29	58.93	5	5	19	1.60
P14115	Rpl27a	60S ribosomal protein L27a	32.43	6	6	334	1.60
E9PUR0	Ankhd1	Protein Ankhd1	0.82	2	2	6	1.60
P35279	Rab6a	Ras-related protein Rab-6A	32.21	6	7	226	1.60
Q9QYJ0	Dnaja2	DnaJ homolog subfamily A member 2	24.03	11	11	317	1.59
P26350	Ptma	Prothymosin alpha	23.42	5	5	158	1.59
P63028	Tpt1	Translationally-controlled tumor protein	17.44	4	4	38	1.59
Q9WTI7	Myo1c	Unconventional myosin-Ic	8.75	11	11	85	1.59

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q3UDR8	Yipf3	Protein YIPF3	8.07	3	3	8	1.59
P49717	Mcm4	DNA replication licensing factor MCM4	11.60	9	10	61	1.59
A2BE28	Las1l	Ribosomal biogenesis protein LAS1L	10.95	7	7	53	1.59
Q9D1M7	Fkbp11	Peptidyl-prolyl cis-trans isomerase FKBP11	14.43	3	3	15	1.59
Q9EQU5	Set	Protein SET	28.72	8	8	256	1.59
Q921S7	Mrpl37	39S ribosomal protein L37, mitochondrial	23.64	10	10	97	1.58
Q9D0I9	Rars	Arginine--tRNA ligase, cytoplasmic	15.76	10	10	110	1.58
Q9D1A2	Cndp2	Cytosolic non-specific dipeptidase	19.16	8	8	60	1.58
P47754	Capza2	F-actin-capping protein subunit alpha-2	25.52	4	6	70	1.58
Q5SYH2	Tmem199	Transmembrane protein 199	25.96	5	5	66	1.58
Q02819	Nucb1	Nucleobindin-1	22.00	10	10	151	1.58
P30681	Hmgb2	High mobility group protein B2	50.48	10	11	165	1.58
Q8R092	N/A	Uncharacterized protein C1orf43 homolog	4.74	1	2	4	1.58
Q9QXV1	Cbx8	Chromobox protein homolog 8	5.25	2	2	9	1.57
P83917	Cbx1	Chromobox protein homolog 1	10.27	2	2	2	1.57
Q8CFX1	H6pd	GDH/6PGL endoplasmic bifunctional protein	3.80	2	3	16	1.57
Q8BKE6	Cyp20a1	Cytochrome P450 20A1	29.22	12	12	147	1.57
Q8CGY8	Ogt	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	7.07	7	7	42	1.57
Q9QWH1	Phc2	Polyhomeotic-like protein 2	1.65	2	2	6	1.57
P97496	Smarcc1	SWI/SNF complex subunit SMARCC1	17.66	15	19	348	1.57
O70252	Hmox2	Heme oxygenase 2	22.22	6	6	134	1.56
O08788	Dctn1	Dynactin subunit 1	1.48	1	3	28	1.56
Q9QZI9	Serinc3	Serine incorporator 3	2.54	2	2	6	1.56
P53395	Dbt	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	13.49	7	7	71	1.56
Q99L48	Nmd3	60S ribosomal export protein NMD3	5.17	2	2	24	1.56
O55100	Syngr1	Synaptogyrin-1	10.26	2	2	22	1.56
O35685	Nudc	Nuclear migration protein nudC	31.63	9	9	181	1.56
Q9CXK8	Nip7	60S ribosome subunit biogenesis protein NIP7 homolog	16.11	3	3	36	1.56
Q00651	Itga4	Integrin alpha-4	18.19	19	19	395	1.56
P58242	Smpdl3b	Acid sphingomyelinase-like phosphodiesterase 3b	12.28	6	6	52	1.56
Q9WV55	Vapa	Vesicle-associated membrane protein-associated protein A	44.58	11	12	484	1.56
Q9CWZ7	Napg	Gamma-soluble NSF attachment protein	20.83	6	7	59	1.56
P36536	Sar1a	GTP-binding protein SAR1a	18.18	1	4	76	1.56
Q99KK9	Hars2	Probable histidine--tRNA ligase, mitochondrial	10.89	4	5	45	1.55
Q91YI4	Arrb2	Beta-arrestin-2	6.83	3	3	9	1.55
Q9Z1R2	Bag6	Large proline-rich protein BAG6	6.85	5	6	10	1.55
O35129	Phb2	Prohibitin-2	68.56	22	22	1044	1.55
Q9D819	Ppa1	Inorganic pyrophosphatase	17.30	6	6	51	1.55

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8K0T0	Rtn1	Reticulon-1	2.44	1	2	4	1.55
P01887	B2m	Beta-2-microglobulin	21.01	3	3	71	1.55
Q9CQC9	Sar1b	GTP-binding protein SAR1b	15.15	1	3	80	1.55
Q8VDD5	Myh9	Myosin-9	52.35	110	114	3263	1.54
Q9EQK5	Mvp	Major vault protein	15.91	12	12	83	1.54
Q9DBA9	Gtf2h1	General transcription factor IIH subunit 1	2.74	2	2	4	1.54
Q8VCW4	Unc93b1	Protein unc-93 homolog B1	8.36	4	4	168	1.54
P35293	Rab18	Ras-related protein Rab-18	36.41	6	7	110	1.54
Q3TAS6	Emc10	ER membrane protein complex subunit 10	6.98	1	2	2	1.54
O88983	Stx8	Syntaxin-8	16.95	4	4	27	1.54
P61027	Rab10	Ras-related protein Rab-10	59.50	10	14	598	1.54
F6YVP7	Gm10260	Protein Gm10260	58.55	16	16	842	1.54
Q9QZD8	Slc25a10	Mitochondrial dicarboxylate carrier	18.47	5	5	95	1.53
Q9JIX8	Acin1	Apoptotic chromatin condensation inducer in the nucleus	17.64	24	24	509	1.53
P61205	Arf3	ADP-ribosylation factor 3	56.35	5	9	522	1.53
O88668	Creg1	Protein CREG1	5.91	2	2	3	1.53
Q8VBZ3	Clptm1	Cleft lip and palate transmembrane protein 1 homolog	29.67	13	13	277	1.53
O54962	Banf1	Barrier-to-autointegration factor	15.73	3	3	24	1.53
Q9QZH3	Ppie	Peptidyl-prolyl cis-trans isomerase E	23.59	7	7	29	1.53
Q8CGZ0	Cherp	Calcium homeostasis endoplasmic reticulum protein	13.25	14	14	186	1.53
P63101	Ywhaz	14-3-3 protein zeta/delta	54.29	8	12	285	1.53
P61082	Ube2m	NEDD8-conjugating enzyme Ubc12	32.79	6	6	58	1.53
Q8K3J1	Ndufs8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	21.23	4	4	45	1.53
Q9DB20	Atp5o	ATP synthase subunit O, mitochondrial	41.78	11	11	434	1.52
Q8R366	Igsf8	Immunoglobulin superfamily member 8	3.93	2	2	6	1.52
Q80ZS3	Mrps26	28S ribosomal protein S26, mitochondrial	28.50	6	6	61	1.52
P42232	Stat5b	Signal transducer and activator of transcription 5B	1.91	1	2	6	1.52
E9Q6E5	Srsf11	Protein Srsf11	5.68	3	3	6	1.52
Q9CQ06	Mrpl24	39S ribosomal protein L24, mitochondrial	25.00	6	6	58	1.51
Q9CRD0	Ociad1	OCIA domain-containing protein 1	29.15	7	7	166	1.51
Q78IK4	Apool	MICOS complex subunit Mic27	30.19	8	8	192	1.51
Q8BU30	Iars	Isoleucine--tRNA ligase, cytoplasmic	9.43	12	13	66	1.51
Q8C5H8	Nadk2	NAD kinase 2, mitochondrial	8.63	4	4	8	1.50
P07901	Hsp90aa1	Heat shock protein HSP 90-alpha	36.29	12	31	1634	1.50
P49138	Mapkapk2	MAP kinase-activated protein kinase 2	12.95	5	5	21	1.50
Q5FWK3	Arhgap1	Rho GTPase-activating protein 1	15.03	7	8	127	1.50
Q8BWW4	Larp4	La-related protein 4	12.24	8	8	54	1.50
Q91ZA3	Pcca	Propionyl-CoA carboxylase alpha chain, mitochondrial	14.36	10	10	95	1.50
Q8C5N3	Cwc22	Pre-mRNA-splicing factor CWC22 homolog	8.04	8	8	36	1.49
P61028	Rab8b	Ras-related protein Rab-8B	57.49	7	14	543	1.49

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q99LE6	Abcf2	ATP-binding cassette sub-family F member 2	18.79	13	13	190	1.49
Q8BP40	Acp6	Lysophosphatidic acid phosphatase type 6	13.64	6	6	45	1.49
Q62318	Trim28	Transcription intermediary factor 1-beta	21.58	18	18	528	1.49
Q8C7V3	Utp15	U3 small nucleolar RNA-associated protein 15 homolog	31.63	17	17	202	1.49
P14576	Srp54	Signal recognition particle 54 kDa protein	21.43	13	13	209	1.49
O55201	Supt5h	Transcription elongation factor SPT5	16.08	15	15	98	1.49
Q62029	Pabpc2	Polyadenylate-binding protein	16.56	2	10	198	1.48
P54728	Rad23b	UV excision repair protein RAD23 homolog B	8.41	4	4	37	1.48
P30355	Alox5ap	Arachidonate 5-lipoxygenase-activating protein	11.80	2	2	54	1.48
Q9JL62	Gltp	Glycolipid transfer protein	10.05	2	2	6	1.48
P55258	Rab8a	Ras-related protein Rab-8A	60.87	8	16	625	1.48
P28867	Prkcd	Protein kinase C delta type	4.90	4	4	26	1.48
Q9R0Q9	Mpdu1	Mannose-P-dolichol utilization defect 1 protein	8.10	2	2	12	1.47
Q6PDM2	Srsf1	Serine/arginine-rich splicing factor 1	58.06	15	16	989	1.47
P97429	Anxa4	Annexin A4	19.75	6	6	58	1.47
Q9DCJ5	Ndufa8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	47.67	7	7	128	1.47
P49710	Hcls1	Hematopoietic lineage cell-specific protein	21.19	10	10	166	1.47
Q8BH95	Echs1	Enoyl-CoA hydratase, mitochondrial	25.86	7	8	141	1.47
P62334	Psmc6	26S protease regulatory subunit 10B	20.31	8	8	52	1.47
Q60715	P4ha1	Prolyl 4-hydroxylase subunit alpha-1	29.03	15	15	305	1.47
Q9DBD5	Pelp1	Proline-, glutamic acid- and leucine-rich protein 1	11.58	10	10	159	1.47
Q8BX10	Pgam5	Serine/threonine-protein phosphatase PGAM5, mitochondrial	33.33	10	11	253	1.47
Q80T69	Rsbn1	Round spermatid basic protein 1	9.94	8	8	41	1.46
Q63850	Nup62	Nuclear pore glycoprotein p62	12.17	7	7	140	1.46
P40630	Tfam	Transcription factor A, mitochondrial	22.63	7	8	140	1.46
P54071	Idh2	Isocitrate dehydrogenase [NADP], mitochondrial	42.04	18	19	735	1.46
Q61335	Bcap31	B-cell receptor-associated protein 31	29.39	11	12	323	1.46
P62307	Snrpf	Small nuclear ribonucleoprotein F	24.42	2	2	63	1.46
Q8JZU2	Slc25a1	Tricarboxylate transport protein, mitochondrial	18.97	6	6	93	1.46
Q9CWV6	Prkrip1	PRKR-interacting protein 1	7.53	2	2	8	1.46
Q80XL6	Acad11	Acyl-CoA dehydrogenase family member 11	2.57	2	2	4	1.46
P59110	Senp1	Sentrin-specific protease 1	10.78	6	6	39	1.45
P26039	Tln1	Talin-1	33.06	74	74	1663	1.45
P58064	Mrps6	28S ribosomal protein S6, mitochondrial	46.40	7	7	100	1.45
O88967	Yme1l1	ATP-dependent zinc metalloprotease YME1L1	13.57	10	10	134	1.45
Q8BMD8	Slc25a24	Calcium-binding mitochondrial carrier protein SCaMC-1	15.79	7	8	110	1.45
Q05920	Pc	Pyruvate carboxylase, mitochondrial	1.53	2	2	6	1.45
P11370	Fv4	Retrovirus-related Env polyprotein from Fv-4 locus	6.48	2	5	260	1.45
Q9WVA4	Tagln2	Transgelin-2	33.67	7	7	134	1.45
Q9CQU0	Txndc12	Thioredoxin domain-containing protein 12	18.24	3	3	39	1.45

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q9JKX4	Aatf	Protein AATF	20.72	9	9	80	1.45
P11152	Lpl	Lipoprotein lipase	22.15	10	10	96	1.44
Q9D8U8	Snx5	Sorting nexin-5	26.73	9	11	123	1.44
P70399	Tp53bp1	Tumor suppressor p53-binding protein 1	7.77	10	10	84	1.44
O54941	Smarce1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	26.03	8	9	135	1.44
Q9CRB9	Chchd3	MICOS complex subunit Mic19	46.26	11	11	325	1.44
Q64092	Tfe3	Transcription factor E3	18.88	5	8	78	1.44
Q05769	Ptgs2	Prostaglandin G/H synthase 2	14.57	7	7	40	1.44
Q61164	Ctcf	Transcriptional repressor CTCF	9.65	6	6	25	1.44
Q924Z4	Cers2	Ceramide synthase 2	8.95	3	3	226	1.43
Q9DCM0	Ethe1	Persulfide dioxygenase ETHE1, mitochondrial	17.72	4	4	28	1.43
Q62086	Pon2	Serum paraoxonase/arylesterase 2	13.28	4	4	38	1.43
P50544	Acadvl	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	31.86	18	18	223	1.43
Q9CQW9	Ifitm3	Interferon-induced transmembrane protein 3	32.85	3	4	376	1.43
Q5SVQ0	Kat7	Histone acetyltransferase KAT7	8.16	4	4	17	1.43
Q78ZA7	Nap1l4	Nucleosome assembly protein 1-like 4	10.13	2	3	30	1.43
Q9D5T0	Atad1	ATPase family AAA domain-containing protein 1	25.76	8	8	70	1.43
Q9WV30	Nfat5	Nuclear factor of activated T-cells 5	7.17	9	9	76	1.43
Q61093	Cybb	Cytochrome b-245 heavy chain	37.19	20	20	419	1.43
Q3TXS7	Psmd1	26S proteasome non-ATPase regulatory subunit 1	8.29	7	7	38	1.42
P18155	Mthfd2	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	25.71	7	7	90	1.42
Q80W00	Ppp1r10	Serine/threonine-protein phosphatase 1 regulatory subunit 10	4.62	3	3	10	1.42
Q9CQC7	Ndufb4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	26.36	3	3	22	1.42
P61750	Arf4	ADP-ribosylation factor 4	48.89	4	7	327	1.42
P63276	Rps17	40S ribosomal protein S17	45.93	8	8	223	1.42
P18572	Bsg	Basigin	23.39	9	9	384	1.42
O70152	Dpm1	Dolichol-phosphate mannosyltransferase subunit 1	14.23	3	3	69	1.42
Q99KN9	Clint1	Clathrin interactor 1	22.66	14	14	260	1.41
Q07813	Bax	Apoptosis regulator BAX	22.92	3	3	12	1.41
O08599	Stxbp1	Syntaxin-binding protein 1	6.40	3	3	15	1.41
P70248	Myo1f	Unconventional myosin-If	7.55	6	9	86	1.41
Q6PHN9	Rab35	Ras-related protein Rab-35	24.88	2	6	319	1.41
Q91W50	Csde1	Cold shock domain-containing protein E1	17.29	12	12	118	1.41
Q9DAV9	Tmem38b	Trimeric intracellular cation channel type B	26.71	8	8	274	1.41
O55128	Sap18	Histone deacetylase complex subunit SAP18	59.48	13	13	407	1.41
Q7TQK1	Ints7	Integrator complex subunit 7	10.66	10	10	75	1.41
Q9CPQ1	Cox6c	Cytochrome c oxidase subunit 6C	46.05	7	7	233	1.41
Q3URS9	Ccdc51	Coiled-coil domain-containing protein 51	4.43	2	2	6	1.40

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q99KP6	Prpf19	Pre-mRNA-processing factor 19	34.72	15	15	671	1.40
P62245	Rps15a	40S ribosomal protein S15a	47.69	8	8	308	1.40
Q8VE99	Ccdc115	Coiled-coil domain-containing protein 115	35.56	5	5	177	1.40
Q3UYV9	Ncbp1	Nuclear cap-binding protein subunit 1	8.61	8	8	123	1.40
O35887	Calu	Calumenin	38.41	10	10	232	1.40
Q8VEJ4	Nle1	Notchless protein homolog 1	4.12	2	2	12	1.40
Q8CIE6	Copa	Coatomer subunit alpha	11.11	12	13	138	1.40
P58681	Tlr7	Toll-like receptor 7	4.29	5	5	47	1.40
Q80XI3	Eif4g3	Eukaryotic translation initiation factor 4 gamma 3	1.71	2	3	43	1.40
Q8VCH8	Ubxn4	UBX domain-containing protein 4	12.25	5	5	114	1.40
P10810	Cd14	Monocyte differentiation antigen CD14	31.69	9	9	299	1.40
D3YZZ5	Tmed7	Protein Tmed7	30.36	7	8	80	1.40
Q6PDG5	Smarcc2	SWI/SNF complex subunit SMARCC2	7.09	5	9	121	1.39
Q8BG51	Rhot1	Mitochondrial Rho GTPase 1	4.91	3	3	22	1.39
Q920Q2	Rev1	DNA repair protein REV1	1.52	1	2	4	1.39
Q69ZQ2	Isy1	Pre-mRNA-splicing factor ISY1 homolog	22.81	8	8	64	1.39
P0C0S6	H2afz	Histone H2A.Z	58.59	5	7	3362	1.39
Q9CWZ3	Rbm8a	RNA-binding protein 8A	26.44	5	5	140	1.39
P80316	Cct5	T-complex protein 1 subunit epsilon	23.66	13	13	264	1.39
P62821	Rab1A	Ras-related protein Rab-1A	70.73	6	15	801	1.39
Q9D1G1	Rab1b	Ras-related protein Rab-1B	57.21	2	11	656	1.39
Q91V41	Rab14	Ras-related protein Rab-14	70.70	11	12	512	1.39
Q6ZQ38	Cand1	Cullin-associated NEDD8-dissociated protein 1	7.24	10	10	65	1.39
Q6URW6	Myh14	Myosin-14	3.90	4	9	252	1.38
Q3U186	Rars2	Probable arginine--tRNA ligase, mitochondrial	6.23	4	4	24	1.38
P17710	Hk1	Hexokinase-1	20.02	18	20	232	1.38
Q9DCN2	Cyb5r3	NADH-cytochrome b5 reductase 3	34.88	10	10	293	1.38
Q8HWB2	H2-Q4	Protein H2-Q4	14.41	3	5	100	1.38
Q9QXZ0	Macf1	Microtubule-actin cross-linking factor 1	12.69	87	88	953	1.38
Q3UQ84	Tars2	Threonine--tRNA ligase, mitochondrial	11.48	9	9	60	1.38
Q8K1R3	Pnpt1	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	11.88	10	10	111	1.38
P27661	H2afx	Histone H2AX	72.73	4	12	3321	1.38
Q99KE1	Me2	NAD-dependent malic enzyme, mitochondrial	11.38	6	6	187	1.38
Q5SFM8	Rbm27	RNA-binding protein 27	4.06	3	4	71	1.38
Q8R180	Ero1l	ERO1-like protein alpha	31.03	12	14	331	1.38
P62281	Rps11	40S ribosomal protein S11	50.63	12	12	712	1.37
Q8BGS0	Mak16	Protein MAK16 homolog	21.28	7	7	81	1.37
Q62167	Ddx3x	ATP-dependent RNA helicase DDX3X	44.56	28	29	725	1.37
Q80VA0	Galnt7	N-acetylgalactosaminyltransferase 7	31.20	21	21	586	1.37
Q9CQ75	Ndufa2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	56.57	7	7	102	1.37

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
P14131	Rps16	40S ribosomal protein S16	62.33	11	11	570	1.37
O08807	Prdx4	Peroxiredoxin-4	46.35	9	11	503	1.37
P01901	H2-K1	H-2 class I histocompatibility antigen, K-B alpha chain	7.05	1	3	68	1.37
Q08943	Ssrp1	FACT complex subunit SSRP1	21.89	14	14	233	1.37
P47226	Tes	Testin	18.44	9	9	116	1.37
P62702	Rps4x	40S ribosomal protein S4, X isoform	61.98	20	20	1093	1.37
Q91VA7	Idh3b	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	34.90	13	13	267	1.37
P68368	Tuba4a	Tubulin alpha-4A chain	37.95	4	16	624	1.37
Q8BSP2	Ncaph2	Condensin-2 complex subunit H2	2.97	2	2	6	1.37
Q80YR5	Safb2	Scaffold attachment factor B2	22.81	12	22	315	1.37
P67778	Phb	Prohibitin	77.57	18	18	1094	1.37
Q8BXZ1	Tmx3	Protein disulfide-isomerase TMX3	23.68	11	11	123	1.37
Q8BFY9	Tnpo1	Transportin-1	9.35	7	7	81	1.37
Q6ZWX6	Eif2s1	Eukaryotic translation initiation factor 2 subunit 1	34.60	11	11	175	1.37
O88441	Mtx2	Metaxin-2	12.93	3	3	22	1.36
D3Z7P3	Gls	Glutaminase kidney isoform, mitochondrial	16.47	8	8	283	1.36
P48962	Slc25a4	ADP/ATP translocase 1	45.97	7	15	1374	1.36
P31938	Map2k1	Dual specificity mitogen-activated protein kinase kinase 1	18.58	6	7	94	1.36
Q9Z2K1	Krt16	Keratin, type I cytoskeletal 16	9.17	2	5	177	1.36
P31266	Rbpj	Recombining binding protein suppressor of hairless	16.92	8	8	98	1.36
P39749	Fen1	Flap endonudease 1	6.35	3	3	10	1.36
Q8BMK4	Ckap4	Cytoskeleton-associated protein 4	46.96	29	29	684	1.36
Q61171	Prdx2	Peroxiredoxin-2	30.30	6	6	110	1.36
Q9CPW4	Arpc5	Actin-related protein 2/3 complex subunit 5	11.92	2	2	15	1.36
P70296	Pebp1	Phosphatidylethanolamine-binding protein 1	32.62	4	4	47	1.36
Q6ZWV3	Rpl10	60S ribosomal protein L10	39.72	12	12	343	1.36
Q9CZW5	Tomm70a	Mitochondrial import receptor subunit TOM70	25.04	16	16	402	1.35
P62960	Ybx1	Nuclease-sensitive element-binding protein 1	55.90	8	13	559	1.35
Q0GNC1	Inf2	Inverted formin-2	5.89	8	8	57	1.35
P68037	Ube2l3	Ubiquitin-conjugating enzyme E2 L3	37.01	4	5	42	1.35
Q08288	Lyar	Cell growth-regulating nucleolar protein	35.05	13	14	245	1.35
P08030	Aprt	Adenine phosphoribosyltransferase	21.67	3	3	18	1.35
Q99JR1	Sfxn1	Sideroflexin-1	25.47	7	8	246	1.35
Q8BI84	Mia3	Melanoma inhibitory activity protein 3	6.99	13	13	81	1.35
P26369	U2af2	Splicing factor U2AF 65 kDa subunit	28.00	11	11	215	1.35
O35704	Sptlc1	Serine palmitoyltransferase 1	12.68	6	6	111	1.35
Q9CPR4	Rpl17	60S ribosomal protein L17	42.93	10	10	419	1.34
Q8CGK3	Lonp1	Lon protease homolog, mitochondrial	26.13	24	25	541	1.34
Q9CYX7	Rrp15	RRP15-like protein	24.91	9	9	118	1.34
P32067	Ssb	Lupus La protein homolog	34.46	18	18	358	1.34

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q62203	Sf3a2	Splicing factor 3A subunit 2	13.26	6	6	133	1.34
Q5SYD0	Myo1d	Unconventional myosin-Id	8.65	9	9	53	1.34
Q80ZW2	Them6	Protein THEM6	27.05	6	6	46	1.34
P25206	Mcm3	DNA replication licensing factor MCM3	19.83	15	15	114	1.34
P47962	Rpl5	60S ribosomal protein L5	47.81	17	17	504	1.34
B1AQJ2	Usp36	Ubiquitin carboxyl-terminal hydrolase 36	8.74	9	10	53	1.34
Q9CYA0	Creld2	Cysteine-rich with EGF-like domain protein 2	16.86	5	5	48	1.34
P46638	Rab11b	Ras-related protein Rab-11B	40.37	9	10	406	1.34
O35316	Slc6a6	Sodium- and chloride-dependent taurine transporter	8.21	5	6	22	1.33
Q9CY50	Ssr1	Translocon-associated protein subunit alpha	11.89	3	3	198	1.33
Q61941	Nnt	NAD(P) transhydrogenase, mitochondrial	18.97	20	20	235	1.33
Q99PT1	Arhgdia	Rho GDP-dissociation inhibitor 1	61.27	13	13	179	1.33
P38647	Hspa9	Stress-70 protein, mitochondrial	70.40	49	50	3379	1.33
P57776	Eef1d	Elongation factor 1-delta	28.47	6	6	79	1.33
Q9CZX8	Rps19	40S ribosomal protein S19	58.62	13	13	742	1.33
P98078	Dab2	Disabled homolog 2	24.80	15	15	221	1.33
P43406	Itgav	Integrin alpha-V	3.16	4	4	10	1.33
Q791V5	Mtch2	Mitochondrial carrier homolog 2	27.06	7	7	104	1.33
Q60749	Khdrbs1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	27.31	15	16	445	1.33
Q61462	Cyba	Cytochrome b-245 light chain	34.90	5	5	205	1.33
P84084	Arf5	ADP-ribosylation factor 5	45.00	3	7	297	1.33
Q60596	Xrcc1	DNA repair protein XRCC1	6.34	4	4	30	1.33
Q01147	Creb1	Cyclic AMP-responsive element-binding protein 1	8.80	3	3	18	1.33
Q9D0I8	Mrto4	mRNA turnover protein 4 homolog	39.75	10	10	255	1.33
Q8BYB9	Poglut1	Protein O-glucosyltransferase 1	9.18	4	4	12	1.32
P09103	P4hb	Protein disulfide-isomerase	65.82	39	40	3183	1.32
Q91XE8	Tmem205	Transmembrane protein 205	17.46	3	3	44	1.32
Q925I1	Atad3	ATPase family AAA domain-containing protein 3	26.90	17	18	221	1.32
Q9CQZ6	Ndufb3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	17.31	2	2	58	1.32
E9Q634	Myo1e	Unconventional myosin-Ie	11.20	11	15	162	1.32
Q91VX2	Ubap2	Ubiquitin-associated protein 2	11.48	10	10	178	1.32
Q921V5	Mgat2	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	5.88	3	3	15	1.32
P70670	Naca	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	1.92	3	3	85	1.32
P62301	Rps13	40S ribosomal protein S13	56.95	11	11	695	1.32
Q9DB43	Zfpl1	Zinc finger protein-like 1	5.48	2	2	2	1.32
P67984	Rpl22	60S ribosomal protein L22	35.16	4	4	364	1.32
Q61584	Fxr1	Fragile X mental retardation syndrome-related protein 1	6.65	5	5	95	1.32
Q61598	Gdi2	Rab GDP dissociation inhibitor beta	22.47	9	9	154	1.32
P84091	Ap2m1	AP-2 complex subunit mu	15.86	8	8	89	1.32
P55096	Abcd3	ATP-binding cassette sub-family D member 3	8.80	6	6	33	1.31

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
P57780	Actn4	Alpha-actinin-4	17.00	11	13	176	1.31
Q8BXQ2	Pigt	GPI transamidase component PIG-T	17.01	11	11	143	1.31
P58281	Opa1	Dynamin-like 120 kDa protein, mitochondrial	11.88	11	11	161	1.31
F8WIX8	Hist1h2al	Histone H2A	76.00	2	12	4338	1.31
Q920E5	Fdps	Farnesyl pyrophosphate synthase	18.13	5	5	33	1.31
Q8CGP5	Hist1h2af	Histone H2A type 1-F	74.62	2	13	4484	1.31
Q8CGP6	Hist1h2ah	Histone H2A type 1-H	74.22	1	13	4314	1.31
Q9CU62	Smc1a	Structural maintenance of chromosomes protein 1A	30.98	40	40	671	1.31
Q8BLF1	Nceh1	Neutral cholesterol ester hydrolase 1	14.71	5	5	119	1.31
Q9WVJ2	Psmd13	26S proteasome non-ATPase regulatory subunit 13	28.99	13	13	198	1.31
Q80VD1	Fam98b	Protein FAM98B	7.69	3	3	22	1.31
P51174	Acadl	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	29.53	13	13	316	1.31
Q8K009	Aldh1l2	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	16.90	13	14	84	1.31
Q8VH51	Rbm39	RNA-binding protein 39	33.02	12	12	230	1.31
Q9Z130	Hnrnpdl	Heterogeneous nuclear ribonucleoprotein D-like	23.59	5	7	547	1.31
P70460	Vasp	Vasodilator-stimulated phosphoprotein	21.87	7	7	136	1.31
P11835	Itgb2	Integrin beta-2	37.22	25	25	879	1.31
P42932	Cct8	T-complex protein 1 subunit theta	47.81	23	23	583	1.31
Q8C172	Cers6	Ceramide synthase 6	8.07	4	4	141	1.30
Q68FD5	Cltc	Clathrin heavy chain 1	27.46	41	41	960	1.30
Q99L04	Dhrs1	Dehydrogenase/reductase SDR family member 1	26.52	8	8	116	1.30
Q8CAQ8	Immt	MICOS complex subunit Mic60	54.16	42	42	1211	1.30
P16627	Hspa1l	Heat shock 70 kDa protein 1-like	14.82	2	9	1069	1.30
Q99M04	Lias	Lipoyl synthase, mitochondrial	4.02	2	2	4	1.30
P61358	Rpl27	60S ribosomal protein L27	53.68	8	8	494	1.30
Q6PIC6	Atp1a3	Sodium/potassium-transporting ATPase subunit alpha-3	23.99	5	23	884	1.30
Q499M4	Tigd5	Tigger transposable element derived 5	1.87	1	2	4	1.30
Q8BK64	Ahsa1	Activator of 90 kDa heat shock protein ATPase homolog 1	11.83	4	4	19	1.30
P59325	Eif5	Eukaryotic translation initiation factor 5	4.20	2	2	2	1.29
P24452	Capg	Macrophage-capping protein	26.14	9	9	415	1.29
Q9Z2G6	Sel1l	Protein sel-1 homolog 1	8.10	5	5	29	1.29
Q9D0T1	Nhp2l1	NHP2-like protein 1	46.09	5	5	665	1.29
Q5F2E7	Nufip2	Nuclear fragile X mental retardation-interacting protein 2	8.53	5	5	18	1.29
Q9CYI4	Luc7l	Putative RNA-binding protein Luc7-like 1	24.26	4	8	171	1.29
D3YYI8	Gm10093	Histone deacetylase	17.84	5	9	207	1.29
Q9D1D4	Tmed10	Transmembrane emp24 domain-containing protein 10	28.77	6	6	436	1.29
Q8C7X2	Emc1	ER membrane protein complex subunit 1	21.97	21	21	349	1.29
Q91ZX7	Lrp1	Prolow-density lipoprotein receptor-related protein 1	17.87	76	76	1111	1.29
A2A4P0	Dhx8	ATP-dependent RNA helicase DHX8	6.75	8	8	40	1.29
P61211	Arl1	ADP-ribosylation factor-like protein 1	9.39	2	2	2	1.29

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
P62204	Calm1	Calmodulin	32.89	4	4	42	1.29
Q921J2	Rheb	GTP-binding protein Rheb	26.09	5	5	40	1.29
Q5XJY5	Arcn1	Coatomer subunit delta	22.50	12	12	120	1.29
P61804	Dad1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	35.40	4	4	47	1.29
P14211	Calr	Calreticulin	56.49	26	26	2738	1.29
P62983	Rps27a	Ubiquitin-40S ribosomal protein S27a	66.03	11	11	2549	1.28
P15379	Cd44	CD44 antigen	7.46	5	5	38	1.28
P12970	Rpl7a	60S ribosomal protein L7a	52.63	23	23	1030	1.28
Q8K297	Colgalt1	Procollagen galactosyltransferase 1	15.88	10	10	197	1.28
Q8R0X7	Sgpl1	Sphingosine-1-phosphate lyase 1	29.40	19	19	647	1.28
Q9D8Y0	Efhd2	EF-hand domain-containing protein D2	39.58	11	11	392	1.28
Q9D6R2	Idh3a	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	39.89	15	15	557	1.28
Q9DC70	Ndufs7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	20.54	6	6	135	1.28
Q9D735	N/A	Uncharacterized protein C19orf43 homolog	12.72	2	2	4	1.28
Q8VDJ3	Hdlbp	Vigilin	14.98	19	19	186	1.28
Q9D1P0	Mrpl13	39S ribosomal protein L13, mitochondrial	28.09	5	5	20	1.28
P56183	Rrp1	Ribosomal RNA processing protein 1 homolog A	15.59	7	7	104	1.28
P27601	Gna13	Guanine nucleotide-binding protein subunit alpha-13	5.04	1	2	4	1.28
Q9QWL7	Krt17	Keratin, type I cytoskeletal 17	18.94	7	10	212	1.28
E9Q616	Ahnak	Protein Ahnak	52.25	132	135	3193	1.28
Q61035	Hars	Histidine--tRNA ligase, cytoplasmic	9.82	4	5	25	1.28
Q569Z5	Ddx46	Probable ATP-dependent RNA helicase DDX46	18.02	18	18	278	1.27
P63038	Hspd1	60 kDa heat shock protein, mitochondrial	75.74	46	46	4061	1.27
Q9DB77	Uqcrc2	Cytochrome b-c1 complex subunit 2, mitochondrial	39.29	17	17	701	1.27
Q9DCW4	Etfb	Electron transfer flavoprotein subunit beta	51.76	13	13	681	1.27
Q61696	Hspa1a	Heat shock 70 kDa protein 1A	17.78	4	10	840	1.27
Q61543	Glg1	Golgi apparatus protein 1	24.43	30	30	740	1.27
Q9ERK4	Cse1l	Exportin-2	9.89	9	9	111	1.27
Q921T2	Tor1aip1	Torsin-1A-interacting protein 1	31.43	16	16	517	1.27
Q9EPR4	Slc23a2	Solute carrier family 23 member 2	3.24	2	2	4	1.27
Q62193	Rpa2	Replication protein A 32 kDa subunit	14.81	4	4	49	1.27
Q3TW96	Uap1l1	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	6.71	3	3	12	1.27
Q8K2C7	Os9	Protein -9	8.63	5	6	80	1.27
P51881	Slc25a5	ADP/ATP translocase 2	48.32	10	18	2084	1.27
Q69ZN6	Gnptab	N-acetylglucosamine-1-phosphotransferase subunits alpha/beta	1.54	2	2	2	1.26
O35963	Rab33b	Ras-related protein Rab-33B	12.23	1	3	57	1.26
P62830	Rpl23	60S ribosomal protein L23	50.00	7	7	353	1.26
Q7TNC4	Luc7l2	Putative RNA-binding protein Luc7-like 2	27.30	7	10	369	1.26
O35857	Timm44	Mitochondrial import inner membrane translocase subunit TIM44	24.12	12	12	141	1.26
Q05816	Fabp5	Fatty acid-binding protein, epidermal	42.22	5	5	50	1.26

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q9CQB5	Cisd2	CDGSH iron-sulfur domain-containing protein 2	47.41	6	6	146	1.26
Q9Z1Z0	Uso1	General vesicular transport factor p115	6.57	5	5	48	1.26
Q8C129	Lnpep	Leucyl-cystinyl aminopeptidase	8.78	8	9	93	1.26
G5E829	Atp2b1	Plasma membrane calcium-transporting ATPase 1	12.21	15	15	157	1.26
P10711	Tcea1	Transcription elongation factor A protein 1	9.63	3	3	10	1.26
Q9QYA2	Tomm40	Mitochondrial import receptor subunit TOM40 homolog	36.01	9	9	136	1.26
Q8BMS1	Hadha	Trifunctional enzyme subunit alpha, mitochondrial	21.23	16	17	651	1.26
Q9D4H9	Phf14	PHD finger protein 14	2.61	2	2	6	1.26
Q9QYE6	Golga5	Golgin subfamily A member 5	21.81	15	15	100	1.25
P19783	Cox4i1	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	46.75	9	9	492	1.25
A2ARR7	Gm14412	Protein Gm14412	31.56	1	4	42	1.25
Q8BTT6	Diexf	Digestive organ expansion factor homolog	11.14	8	8	51	1.25
Q07113	Igf2r	Cation-independent mannose-6-phosphate receptor	2.70	6	6	29	1.25
P50580	Pa2g4	Proliferation-associated protein 2G4	33.76	12	12	184	1.25
P19253	Rpl13a	60S ribosomal protein L13a	56.65	17	17	574	1.25
P62806	Hist1h4a	Histone H4	61.17	14	14	7711	1.25
Q99KI3	Emc3	ER membrane protein complex subunit 3	24.90	5	5	20	1.25
P62900	Rpl31	60S ribosomal protein L31	44.80	6	6	290	1.24
O54790	Mafg	Transcription factor MafG	38.27	5	7	77	1.24
E9Q137	Tex264	Protein Tex264	6.80	2	2	2	1.24
Q9D2G2	Dlst	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	23.35	10	10	292	1.24
Q8BJW6	Eif2a	Eukaryotic translation initiation factor 2A	11.19	6	6	56	1.24
Q6PIE5	Atp1a2	Sodium/potassium-transporting ATPase subunit alpha-2	20.39	1	20	891	1.24
Q9JJT0	Rcl1	RNA 3'-terminal phosphate cyclase-like protein	22.25	8	8	153	1.24
P62267	Rps23	40S ribosomal protein S23	30.07	6	6	289	1.24
Q8BMA6	Srp68	Signal recognition particle subunit SRP68	13.92	8	8	73	1.24
Q9CQT2	Rbm7	RNA-binding protein 7	12.45	3	3	14	1.24
D3Z5L4	5430403G16Rik	Protein 5430403G16Rik	16.19	1	3	37	1.24
Q8BH74	Nup107	Nuclear pore complex protein Nup107	18.14	16	16	337	1.24
Q5SUF2	Luc7l3	Luc7-like protein 3	13.43	5	5	93	1.24
Q7TMK9	Syncrip	Heterogeneous nuclear ribonucleoprotein Q	24.24	8	15	479	1.24
Q9Z277	Baz1b	Tyrosine-protein kinase BAZ1B	30.56	47	47	553	1.24
Q8R332	Nupl1	Nucleoporin p58/p45	10.05	6	6	91	1.23
P46471	Psmc2	26S protease regulatory subunit 7	28.64	14	14	170	1.23
P20108	Prdx3	Thioredoxin-dependent peroxide reductase, mitochondrial	36.19	7	7	149	1.23
P42125	Eci1	Enoyl-CoA delta isomerase 1, mitochondrial	18.34	4	4	45	1.23
P10852	Slc3a2	4F2 cell-surface antigen heavy chain	23.00	12	12	268	1.23
O70503	Hsd17b12	Very-long-chain 3-oxoacyl-CoA reductase	44.23	15	15	386	1.23
Q8QZV7	Asun	Protein asunder homolog	5.60	4	4	15	1.23

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
O35343	Kpna4	Importin subunit alpha-3	9.40	3	4	63	1.23
Q91W90	Txndc5	Thioredoxin domain-containing protein 5	27.10	10	10	287	1.23
Q9CQ54	Ndufc2	NADH dehydrogenase [ubiquinone] 1 subunit C2	24.17	3	3	25	1.23
Q99K28	Arfgap2	ADP-ribosylation factor GTPase-activating protein 2	13.85	7	7	100	1.23
P63166	Sumo1	Small ubiquitin-related modifier 1	27.72	3	3	9	1.23
O89017	Lgmn	Legumain	8.51	3	3	23	1.23
Q9D824	Fip1l1	Pre-mRNA 3'-end-processing factor FIP1	15.49	7	7	191	1.23
P04441	Cd74	H-2 class II histocompatibility antigen gamma chain	20.79	5	5	128	1.23
Q9WTP6	Ak2	Adenylate kinase 2, mitochondrial	39.33	9	9	335	1.23
Q60930	Vdac2	Voltage-dependent anion-selective channel protein 2	49.83	12	13	932	1.23
Q8BX90	Fndc3a	Fibronectin type-III domain-containing protein 3A	2.67	2	2	4	1.23
Q99LL5	Pwp1	Periodic tryptophan protein 1 homolog	11.98	6	6	83	1.23
Q99LC5	Etfa	Electron transfer flavoprotein subunit alpha, mitochondrial	50.45	13	13	676	1.23
Q60597	Ogdh	2-oxoglutarate dehydrogenase, mitochondrial	18.18	19	19	348	1.23
E9Q5K9	Ythdc1	YTH domain-containing protein 1	3.26	3	3	43	1.22
P24369	Ppib	Peptidyl-prolyl cis-trans isomerase B	55.56	13	14	902	1.22
Q9D8S4	Rexo2	Oligoribonuclease, mitochondrial	10.13	3	3	20	1.22
Q9D3D9	Atp5d	ATP synthase subunit delta, mitochondrial	17.26	3	3	361	1.22
P23198	Cbx3	Chromobox protein homolog 3	30.60	7	7	133	1.22
Q99020	Hnrnpab	Heterogeneous nuclear ribonucleoprotein A/B	47.37	15	16	1060	1.22
P11499	Hsp90ab1	Heat shock protein HSP 90-beta	45.86	18	39	2496	1.22
P09405	Ncl	Nucleolin	55.02	51	51	3289	1.22
Q60870	Reep5	Receptor expression-enhancing protein 5	14.59	3	3	78	1.22
Q9CZU6	Cs	Citrate synthase, mitochondrial	27.80	13	13	579	1.22
P61255	Rpl26	60S ribosomal protein L26	48.97	10	10	489	1.22
Q9R0Q3	Tmed2	Transmembrane emp24 domain-containing protein 2	21.39	5	5	151	1.22
Q8BP67	Rpl24	60S ribosomal protein L24	39.49	8	8	228	1.22
Q64516	Gk	Glycerol kinase	6.80	4	4	22	1.21
Q9D6K9	Cers5	Ceramide synthase 5	3.38	1	2	2	1.21
P14148	Rpl7	60S ribosomal protein L7	51.85	24	25	980	1.21
P70288	Hdac2	Histone deacetylase 2	16.19	4	8	135	1.21
Q62087	Pon3	Serum paraoxonase/lactonase 3	23.45	6	6	195	1.21
Q9DCD2	Xab2	Pre-mRNA-splicing factor SYF1	19.18	18	18	136	1.21
E9Q070	Gm8730	Uncharacterized protein	53.31	2	15	673	1.21
P14869	Rplp0	60S acidic ribosomal protein P0	52.05	2	15	692	1.21
Q91VR2	Atp5c1	ATP synthase subunit gamma, mitochondrial	40.60	13	13	565	1.21
Q8K202	Polr1e	DNA-directed RNA polymerase I subunit RPA49	19.09	9	9	90	1.21
P47802	Mtx1	Metaxin-1	36.91	14	14	316	1.21
Q8CGC7	Eprs	Bifunctional glutamate/proline--tRNA ligase	11.77	18	18	276	1.20
Q5XKN4	Jagn1	Protein jagunal homolog 1	13.11	2	2	9	1.20

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q3UMC0	Spata5	Spermatogenesis-associated protein 5	3.58	2	3	6	1.20
Q99KG3	Rbm10	RNA-binding protein 10	16.24	11	13	186	1.20
P10404	N/A	MLV-related proviral Env polyprotein	13.42	7	10	571	1.20
Q8BH59	Slc25a12	Calcium-binding mitochondrial carrier protein Aralar1	27.62	13	19	423	1.20
Q60668	Hnrnpd	Heterogeneous nuclear ribonucleoprotein D0	35.49	12	14	840	1.20
Q6NZJ6	Eif4g1	Eukaryotic translation initiation factor 4 gamma 1	18.31	25	26	365	1.20
P57784	Snrpa1	U2 small nuclear ribonucleoprotein A'	48.63	13	13	420	1.20
Q9D8B3	Chmp4b	Charged multivesicular body protein 4b	17.41	4	4	69	1.20
P97765	Wbp2	WW domain-binding protein 2	21.84	6	7	189	1.20
Q9CXT8	Pmpcb	Mitochondrial-processing peptidase subunit beta	18.20	8	9	219	1.20
O35609	Scamp3	Secretory carrier-associated membrane protein 3	25.21	7	7	133	1.20
P62242	Rps8	40S ribosomal protein S8	52.40	11	11	765	1.20
Q9CYG7	Tomm34	Mitochondrial import receptor subunit TOM34	24.27	7	7	62	1.19
P15532	Nme1	Nucleoside diphosphate kinase A	43.42	2	6	206	1.19
Q9WV80	Snx1	Sorting nexin-1	17.24	7	9	141	1.19
Q07417	Acads	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	25.49	9	9	229	1.19
Q9CQN1	Trap1	Heat shock protein 75 kDa, mitochondrial	31.59	22	23	1013	1.19
Q9JKN1	Slc30a7	Zinc transporter 7	9.52	3	3	74	1.19
Q8JZR0	Acsl5	Long-chain-fatty-acid--CoA ligase 5	19.62	12	14	274	1.19
Q9WU78	Pdcd6ip	Programmed cell death 6-interacting protein	33.60	29	29	525	1.19
Q01853	Vcp	Transitional endoplasmic reticulum ATPase	43.80	28	29	678	1.19
P02535	Krt10	Keratin, type I cytoskeletal 10	13.33	7	9	602	1.19
Q99JY0	Hadhb	Trifunctional enzyme subunit beta, mitochondrial	31.58	16	16	538	1.19
G5E8V9	Arfip1	MCG18094	10.19	3	3	32	1.19
Q8VDN2	Atp1a1	Sodium/potassium-transporting ATPase subunit alpha-1	41.84	28	45	1791	1.19
Q9CQA3	Sdhb	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	43.26	17	17	364	1.19
P40142	Tkt	Transketolase	29.86	19	19	374	1.19
P53566	Cebpa	CCAAT/enhancer-binding protein alpha	7.80	3	3	6	1.19
P53564	Cux1	Homeobox protein cut-like 1	24.69	32	32	582	1.19
Q9JIF7	Copb1	Coatomer subunit beta	13.22	11	11	60	1.19
Q569Z6	Thrap3	Thyroid hormone receptor-associated protein 3	22.08	21	22	525	1.19
Q9DC48	Cdc40	Pre-mRNA-processing factor 17	10.19	6	6	71	1.19
Q08874	Mitf	Microphthalmia-associated transcription factor	7.60	2	5	41	1.19
P47738	Aldh2	Aldehyde dehydrogenase, mitochondrial	51.45	23	24	1485	1.19
Q9CPS7	Pno1	RNA-binding protein PNO1	10.48	2	2	6	1.19
P20029	Hspa5	78 kDa glucose-regulated protein	63.82	46	49	5276	1.19
P63017	Hspa8	Heat shock cognate 71 kDa protein	67.49	34	41	4008	1.18
Q9JHS4	Clpx	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	12.30	7	7	89	1.18
P18760	Cfl1	Cofilin-1	65.06	12	12	345	1.18
Q8C1B7	Sep-11	Septin-11	16.94	6	6	19	1.18

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
P35564	Canx	Calnexin	43.82	34	34	1926	1.18
Q9D0W5	Ppil1	Peptidyl-prolyl cis-trans isomerase-like 1	35.54	5	5	38	1.18
Q9QVP9	Ptk2b	Protein-tyrosine kinase 2-beta	5.75	6	6	49	1.18
P61620	Sec61a1	Protein transport protein Sec61 subunit alpha isoform 1	15.13	9	9	403	1.18
Q9ESP1	Sdf2l1	Stromal cell-derived factor 2-like protein 1	20.36	3	3	46	1.18
Q02053	Uba1	Ubiquitin-like modifier-activating enzyme 1	16.26	15	15	202	1.18
Q3UL36	Arglu1	Arginine and glutamate-rich protein 1	15.13	5	6	51	1.18
Q9CQY5	Magt1	Magnesium transporter protein 1	15.22	7	7	109	1.18
Q99KI0	Aco2	Aconitate hydratase, mitochondrial	46.79	32	32	1284	1.18
Q80UM7	Mogs	Mannosyl-oligosaccharide glucosidase	19.66	15	15	417	1.18
P80314	Cct2	T-complex protein 1 subunit beta	31.40	16	16	433	1.18
Q69ZN7	Myof	Myoferlin	14.45	28	29	385	1.18
Q5PSV9	Mdc1	Mediator of DNA damage checkpoint protein 1	6.85	10	10	55	1.18
Q61699	Hsph1	Heat shock protein 105 kDa	13.40	9	10	82	1.18
Q9EPU0	Upf1	Regulator of nonsense transcripts 1	4.63	5	5	48	1.18
Q9D0R2	Tars	Threonine--tRNA ligase, cytoplasmic	6.79	5	5	18	1.17
P61967	Ap1s1	AP-1 complex subunit sigma-1A	14.56	2	2	4	1.17
P63037	Dnaja1	DnaJ homolog subfamily A member 1	23.43	8	9	159	1.17
Q9D8M4	Rpl7l1	60S ribosomal protein L7-like 1	39.02	10	10	106	1.17
Q9CZ13	Uqcrc1	Cytochrome b-c1 complex subunit 1, mitochondrial	39.58	15	16	588	1.17
P62751	Rpl23a	60S ribosomal protein L23a	46.15	13	13	744	1.17
P97461	Rps5	40S ribosomal protein S5	42.65	11	11	548	1.17
Q9CQQ7	Atp5f1	ATP synthase F(0) complex subunit B1, mitochondrial	30.08	9	9	209	1.17
Q52KI8	Srrm1	Serine/arginine repetitive matrix protein 1	10.15	7	7	80	1.17
Q922R8	Pdia6	Protein disulfide-isomerase A6	48.41	21	21	1027	1.17
Q9QUM9	Psma6	Proteasome subunit alpha type-6	26.83	6	6	66	1.17
P97287	Mcl1	Induced myeloid leukemia cell differentiation protein Mcl-1 homolog	25.68	6	6	127	1.16
P26638	Sars	Serine--tRNA ligase, cytoplasmic	12.70	6	6	67	1.16
Q9D0F3	Lman1	Protein ERGIC-53	23.98	12	12	191	1.16
Q99N96	Mrpl1	39S ribosomal protein L1, mitochondrial	17.26	5	5	37	1.16
P62911	Rpl32	60S ribosomal protein L32	40.74	6	6	136	1.16
Q61578	Fdxr	NADPH:adrenodoxin oxidoreductase, mitochondrial	17.41	8	8	34	1.16
Q99KF1	Tmed9	Transmembrane emp24 domain-containing protein 9	27.66	6	8	278	1.16
Q9CYR0	Ssbp1	Single-stranded DNA-binding protein, mitochondrial	46.71	8	8	197	1.16
P60766	Cdc42	Cell division control protein 42 homolog	20.94	3	4	168	1.16
Q9D753	Exosc8	Exosome complex component RRP43	24.64	6	6	98	1.16
Q99LC3	Ndufa10	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	21.69	8	8	259	1.16
P03966	Mycn	N-myc proto-oncogene protein	3.46	2	2	2	1.16
Q8K0D5	Gfm1	Elongation factor G, mitochondrial	23.30	18	18	213	1.16

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q3TMX7	Qsox2	Sulfhydryl oxidase 2	2.46	2	2	4	1.16
O08810	Eftud2	116 kDa U5 small nuclear ribonucleoprotein component	31.31	27	28	923	1.16
O35658	C1qbp	Complement component 1 Q subcomponent-binding protein, mitochondrial	34.17	5	5	207	1.16
Q99JR8	Smarcd2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	19.96	10	11	153	1.16
Q9Z0X1	Aifm1	Apoptosis-inducing factor 1, mitochondrial	26.47	15	15	329	1.16
Q99PL5	Rrbp1	Ribosome-binding protein 1	50.78	49	51	1307	1.16
P47963	Rpl13	60S ribosomal protein L13	43.13	11	11	533	1.16
O70493	Snx12	Sorting nexin-12	9.70	1	2	44	1.16
Q06185	Atp5i	ATP synthase subunit e, mitochondrial	43.66	4	4	65	1.16
Q61792	Lasp1	LIM and SH3 domain protein 1	44.49	14	14	177	1.16
Q9JKR6	Hyou1	Hypoxia up-regulated protein 1	42.44	42	42	1377	1.16
Q9D0K2	Oxct1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	25.96	13	13	482	1.16
P32020	Scp2	Non-specific lipid-transfer protein	15.90	12	12	419	1.16
P23116	Eif3a	Eukaryotic translation initiation factor 3 subunit A	13.69	19	20	157	1.15
P84099	Rpl19	60S ribosomal protein L19	34.18	8	8	359	1.15
Q9DCL9	Paics	Multifunctional protein ADE2	39.53	15	16	263	1.15
P09450	Junb	Transcription factor jun-B	21.51	5	5	59	1.15
Q62351	Tfrc	Transferrin receptor protein 1	35.52	27	28	971	1.15
O55023	Impa1	Inositol monophosphatase 1	12.27	2	3	8	1.15
P08113	Hsp90b1	Endoplasmin	48.75	44	46	3558	1.15
P62082	Rps7	40S ribosomal protein S7	50.00	11	11	248	1.15
P63005	Pafah1b1	Platelet-activating factor acetylhydrolase IB subunit alpha	5.37	1	2	47	1.15
Q9CR67	Tmem33	Transmembrane protein 33	18.62	5	5	94	1.15
Q8CJF7	Ahctf1	Protein ELYS	18.19	32	32	306	1.15
P17742	Ppia	Peptidyl-prolyl cis-trans isomerase A	68.29	12	14	500	1.15
Q9CPT5	Nop16	Nucleolar protein 16	46.63	8	8	205	1.15
Q8CCJ3	Ufl1	E3 UFM1-protein ligase 1	18.41	12	13	133	1.15
Q91WK2	Eif3h	Eukaryotic translation initiation factor 3 subunit H	18.75	7	7	144	1.15
Q8K4Z5	Sf3a1	Splicing factor 3A subunit 1	38.05	31	31	1165	1.15
P03975	Iap	IgE-binding protein	21.18	13	13	89	1.15
Q8R4R6	Nup35	Nucleoporin NUP53	32.31	8	8	232	1.15
Q91W98	Slc15a4	Solute carrier family 15 member 4	6.97	4	4	21	1.15
Q9R1P0	Psma4	Proteasome subunit alpha type-4	22.22	6	6	64	1.15
Q61233	Lcp1	Plastin-2	54.23	29	33	1175	1.15
Q9Z110	Aldh18a1	Delta-1-pyrroline-5-carboxylate synthase	30.31	23	23	583	1.15
Q3TDN2	Faf2	FAS-associated factor 2	6.29	3	3	12	1.15
Q99P72	Rtn4	Reticulon-4	25.82	22	22	749	1.14
E9PZF0	Gm20390	Nucleoside diphosphate kinase	49.81	4	8	268	1.14
Q9D1M0	Sec13	Protein SEC13 homolog	18.63	5	5	70	1.14

Accession	**Gene**	**Description**	**Σcover-age**	**Σ# Unique Peptides**	**Σ# Peptides**	**Σ# PSMs**	**[1]*pksP*/wt**
Q9JHI7	Exosc9	Exosome complex component RRP45	10.05	4	4	31	1.14
P46978	Stt3a	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	18.30	14	16	486	1.14
P62320	Snrpd3	Small nuclear ribonucleoprotein Sm D3	36.51	4	4	144	1.14
Q8BTM8	Flna	Filamin-A	20.21	42	44	603	1.14
Q99JY9	Actr3	Actin-related protein 3	22.25	9	9	215	1.14
E9PYL9	Gm10036	Protein Gm10036	41.01	9	9	489	1.14
Q9JKL4	Ndufaf3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	10.27	2	2	2	1.14
P47964	Rpl36	60S ribosomal protein L36	29.52	4	4	186	1.14
P97370	Atp1b3	Sodium/potassium-transporting ATPase subunit beta-3	30.58	8	8	359	1.14
P20491	Fcer1g	High affinity immunoglobulin epsilon receptor subunit gamma	33.72	4	4	236	1.14
P19096	Fasn	Fatty acid synthase	9.86	23	24	251	1.14
Q6PAQ4	Rexo4	RNA exonuclease 4	45.37	17	17	286	1.14
P37040	Por	NADPH--cytochrome P450 reductase	35.40	25	25	599	1.14
P62874	Gnb1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	27.35	4	10	203	1.14
Q9D0G0	Mrps30	28S ribosomal protein S30, mitochondrial	11.31	4	4	35	1.14
Q61127	Nab2	NGFI-A-binding protein 2	7.05	4	4	10	1.13
Q62433	Ndrg1	Protein NDRG1	11.68	3	3	24	1.13
Q9D8M7	Phf10	PHD finger protein 10	3.42	2	2	6	1.13
O89023	Tpp1	Tripeptidyl-peptidase 1	3.74	2	2	10	1.13
Q9D1N9	Mrpl21	39S ribosomal protein L21, mitochondrial	14.83	3	3	69	1.13
Q8K078	Slco4a1	Solute carrier organic anion transporter family member 4A1	10.93	7	7	111	1.13
P13864	Dnmt1	DNA (cytosine-5)-methyltransferase 1	32.53	48	48	999	1.13
P47911	Rpl6	60S ribosomal protein L6	52.70	20	20	1088	1.13
Q8BI72	Cdkn2aip	CDKN2A-interacting protein	9.24	4	4	14	1.13
P97807	Fh	Fumarate hydratase, mitochondrial	43.79	22	22	662	1.13
Q9D1R9	Rpl34	60S ribosomal protein L34	36.75	6	6	321	1.13
Q9JIK5	Ddx21	Nucleolar RNA helicase 2	59.46	51	52	3065	1.13
Q99N87	Mrps5	28S ribosomal protein S5, mitochondrial	17.36	7	7	116	1.13
P35979	Rpl12	60S ribosomal protein L12	76.97	11	11	595	1.13
A2BH40	Arid1a	AT-rich interactive domain-containing protein 1A	11.26	20	21	247	1.13
Q922H2	Pdk3	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	12.05	5	5	31	1.13
Q501J6	Ddx17	Probable ATP-dependent RNA helicase DDX17	33.08	13	21	1023	1.13
P62918	Rpl8	60S ribosomal protein L8	38.52	11	11	618	1.13
Q8CG76	Akr7a2	Aflatoxin B1 aldehyde reductase member 2	6.27	2	2	12	1.13
Q3TLH4	Prrc2c	Protein PRRC2C	5.34	12	14	113	1.13
Q921L3	Tmco1	Transmembrane and coiled-coil domain-containing protein 1	32.45	7	7	206	1.12
P33174	Kif4	Chromosome-associated kinesin KIF4	1.87	2	2	6	1.12
Q6P542	Abcf1	ATP-binding cassette sub-family F member 1	8.60	6	6	29	1.12
Q9JIG7	Ccdc22	Coiled-coil domain-containing protein 22	6.22	3	3	36	1.12
Q9CXL3	N/A	Uncharacterized protein C7orf50 homolog	13.33	2	2	18	1.12

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
P84089	Erh	Enhancer of rudimentary homolog	32.69	3	3	51	1.12
P35980	Rpl18	60S ribosomal protein L18	44.15	8	8	670	1.12
Q61656	Ddx5	Probable ATP-dependent RNA helicase DDX5	49.19	27	36	2013	1.12
Q922F4	Tubb6	Tubulin beta-6 chain	33.33	5	13	574	1.12
Q8K2A7	Ints10	Integrator complex subunit 10	2.68	2	2	4	1.12
Q9WUM5	Suclg1	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	24.28	7	7	240	1.12
Q9CQS8	Sec61b	Protein transport protein Sec61 subunit beta	52.08	5	5	322	1.12
P56959	Fus	RNA-binding protein FUS	18.34	9	9	411	1.12
Q9JJ80	Rpf2	Ribosome production factor 2 homolog	24.18	10	11	186	1.12
Q9R1P3	Psmb2	Proteasome subunit beta type-2	22.89	5	5	38	1.12
P19536	Cox5b	Cytochrome c oxidase subunit 5B, mitochondrial	31.25	5	5	156	1.12
Q60520	Sin3a	Paired amphipathic helix protein Sin3a	9.18	12	12	121	1.12
Q60787	Lcp2	Lymphocyte cytosolic protein 2	3.56	2	2	4	1.12
Q8BGH2	Samm50	Sorting and assembly machinery component 50 homolog	18.98	11	11	159	1.12
Q9D662	Sec23b	Protein transport protein Sec23B	4.30	3	3	36	1.12
Q91VD9	Ndufs1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	34.11	25	25	796	1.12
Q64FW2	Retsat	All-trans-retinol 13,14-reductase	6.90	5	5	15	1.11
Q3U1J4	Ddb1	DNA damage-binding protein 1	17.37	18	18	266	1.11
P08249	Mdh2	Malate dehydrogenase, mitochondrial	67.75	19	19	1914	1.11
P84228	Hist1h3b	Histone H3.2	83.09	17	17	6497	1.11
Q3UEB3	Puf60	Poly(U)-binding-splicing factor PUF60	29.43	16	16	326	1.11
Q3TZZ7	Esyt2	Extended synaptotagmin-2	3.55	3	3	10	1.11
Q8VEM8	Slc25a3	Phosphate carrier protein, mitochondrial	28.57	14	14	1079	1.11
Q8R323	Rfc3	Replication factor C subunit 3	25.84	9	9	121	1.11
P70195	Psmb7	Proteasome subunit beta type-7	10.47	3	3	57	1.11
Q8K2C8	Agpat6	Glycerol-3-phosphate acyltransferase 4	4.82	2	2	4	1.11
Q9R210	Tfeb	Transcription factor EB	6.53	1	4	39	1.11
P11440	Cdk1	Cyclin-dependent kinase 1	26.60	8	9	205	1.11
Q9R233	Tapbp	Tapasin	14.84	7	7	176	1.11
Q60973	Rbbp7	Histone-binding protein RBBP7	25.41	6	11	260	1.11
P35283	Rab12	Ras-related protein Rab-12	20.16	3	4	164	1.11
Q99KV1	Dnajb11	DnaJ homolog subfamily B member 11	32.68	14	14	322	1.11
P25444	Rps2	40S ribosomal protein S2	46.42	16	16	684	1.11
O08585	Clta	Clathrin light chain A	17.02	4	5	65	1.11
P63321	Rala	Ras-related protein Ral-A	12.14	1	2	32	1.11
Q8C4J7	Tbl3	Transducin beta-like protein 3	24.09	17	17	208	1.11
Q9JI44	Dmap1	DNA methyltransferase 1-associated protein 1	13.68	5	5	28	1.11
O35216	Cenpa	Histone H3-like centromeric protein A	22.39	4	4	15	1.11
O35465	Fkbp8	Peptidyl-prolyl cis-trans isomerase FKBP8	24.13	9	9	135	1.11
O08749	Dld	Dihydrolipoyl dehydrogenase, mitochondrial	27.70	14	14	633	1.11

Accession	**Gene**	**Description**	**Σcover-age**	**Σ# Unique Peptides**	**Σ# Peptides**	**Σ# PSMs**	**[1]*pksP*/wt**
Q9DBR1	Xrn2	5'-3' exoribonuclease 2	17.56	17	17	168	1.10
Q9CSN1	Snw1	SNW domain-containing protein 1	35.26	19	19	411	1.10
Q9QZQ8	H2afy	Core histone macro-H2A.1	51.88	17	17	1032	1.10
Q8BWY3	Etf1	Eukaryotic peptide chain release factor subunit 1	14.42	6	6	145	1.10
O08602	Raet1a	Retinoic acid early-inducible protein 1-alpha	11.07	2	3	29	1.10
Q3UGC7	Eif3j1	Eukaryotic translation initiation factor 3 subunit J-A	19.54	5	5	43	1.10
Q09200	B4galnt1	Beta-1,4 N-acetylgalactosaminyltransferase 1	24.39	13	13	298	1.10
O70492	Snx3	Sorting nexin-3	29.01	4	5	105	1.10
Q8R3N6	Thoc1	THO complex subunit 1	25.57	17	17	213	1.10
Q4VBE8	Wdr18	WD repeat-containing protein 18	14.15	6	6	57	1.10
Q9CPY7	Lap3	Cytosol aminopeptidase	29.48	13	13	150	1.10
Q05144	Rac2	Ras-related C3 botulinum toxin substrate 2	44.27	5	10	612	1.10
Q3UBX0	Tmem109	Transmembrane protein 109	14.81	4	4	102	1.10
Q80WJ7	Mtdh	Protein LYRIC	39.38	20	20	791	1.10
Q9Z2I9	Sucla2	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	25.92	14	14	388	1.09
Q9QXS1	Plec	Plectin	48.11	230	235	6125	1.09
P62889	Rpl30	60S ribosomal protein L30	76.52	9	9	365	1.09
Q9CX86	Hnrnpa0	Heterogeneous nuclear ribonucleoprotein A0	40.66	10	12	1199	1.09
P62264	Rps14	40S ribosomal protein S14	39.74	7	7	474	1.09
Q80UU2	Rpp38	Ribonuclease P protein subunit p38	8.57	2	2	24	1.09
O89053	Coro1a	Coronin-1A	30.15	13	14	472	1.09
Q9CWL8	Ctnnbl1	Beta-catenin-like protein 1	3.37	2	2	12	1.09
Q9D7N9	Apmap	Adipocyte plasma membrane-associated protein	22.41	9	9	148	1.09
Q6P5B0	Rrp12	RRP12-like protein	26.10	32	32	788	1.09
P27659	Rpl3	60S ribosomal protein L3	42.93	22	22	1075	1.09
P83882	Rpl36a	60S ribosomal protein L36a	25.47	4	4	122	1.09
Q8CEC0	Nup88	Nuclear pore complex protein Nup88	23.77	14	14	177	1.08
O55029	Copb2	Coatomer subunit beta'	13.70	13	13	128	1.08
Q8K019	Bclaf1	Bcl-2-associated transcription factor 1	21.11	19	20	295	1.08
P84104	Srsf3	Serine/arginine-rich splicing factor 3	51.83	12	13	207	1.08
P41216	Acsl1	Long-chain-fatty-acid--CoA ligase 1	8.58	4	6	96	1.08
P11983	Tcp1	T-complex protein 1 subunit alpha	38.31	19	20	339	1.08
P16858	Gapdh	Glyceraldehyde-3-phosphate dehydrogenase	60.36	20	20	1438	1.08
Q6ZWN5	Rps9	40S ribosomal protein S9	60.82	17	17	764	1.08
Q99MD9	Nasp	Nuclear autoantigenic sperm protein	8.93	6	7	36	1.08
O55135	Eif6	Eukaryotic translation initiation factor 6	22.86	4	4	191	1.08
P57787	Slc16a3	Monocarboxylate transporter 4	15.11	7	7	63	1.08
Q8R1V4	Tmed4	Transmembrane emp24 domain-containing protein 4	22.03	5	7	96	1.08
Q99J62	Rfc4	Replication factor C subunit 4	23.35	9	9	75	1.08
Q31125	Slc39a7	Zinc transporter SLC39A7	7.56	3	3	48	1.08

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q922Q8	Lrrc59	Leucine-rich repeat-containing protein 59	47.88	11	12	647	1.08
Q9D8E6	Rpl4	60S ribosomal protein L4	52.27	27	27	993	1.08
Q8BUI3	LRWD1	Leucine-rich repeat and WD repeat-containing protein 1	7.10	4	4	28	1.08
P30416	Fkbp4	Peptidyl-prolyl cis-trans isomerase FKBP4	25.55	12	12	173	1.08
Q921M4	Golga2	Golgin subfamily A member 2	11.11	10	10	98	1.07
Q9QYI3	Dnajc7	DnaJ homolog subfamily C member 7	23.89	14	14	140	1.07
Q9QZE5	Copg1	Coatomer subunit gamma-1	3.78	2	3	15	1.07
Q8BH04	Pck2	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	16.09	9	9	140	1.07
P62313	Lsm6	U6 snRNA-associated Sm-like protein LSm6	56.25	5	5	49	1.07
Q9JHK5	Plek	Pleckstrin	7.71	2	2	20	1.07
Q9CQI6	Cotl1	Coactosin-like protein	28.17	6	6	36	1.07
Q8VDM4	Psmd2	26S proteasome non-ATPase regulatory subunit 2	14.65	14	14	159	1.07
Q99KC8	Vwa5a	von Willebrand factor A domain-containing protein 5A	10.47	8	8	60	1.07
Q8BG32	Psmd11	26S proteasome non-ATPase regulatory subunit 11	25.83	11	11	162	1.07
Q6PB66	Lrpprc	Leucine-rich PPR motif-containing protein, mitochondrial	32.69	49	49	1008	1.07
Q8CI51	Pdlim5	PDZ and LIM domain protein 5	9.48	4	4	18	1.07
Q03265	Atp5a1	ATP synthase subunit alpha, mitochondrial	61.48	35	35	2476	1.07
Q14B01	Rnf113a2	Protein Rnf113a2	12.76	4	4	40	1.07
P29758	Oat	Ornithine aminotransferase, mitochondrial	31.21	14	15	469	1.07
A2A8U2	Tmem201	Transmembrane protein 201	3.61	3	3	8	1.07
Q6R5N8	Tlr13	Toll-like receptor 13	2.42	3	3	12	1.07
Q9CWT6	Ddx28	Probable ATP-dependent RNA helicase DDX28	9.07	5	5	20	1.07
P06869	Plau	Urokinase-type plasminogen activator	17.09	6	6	33	1.07
Q9QYG0	Ndrg2	Protein NDRG2	6.47	2	2	12	1.07
Q6ZQL4	Wdr43	WD repeat-containing protein 43	26.29	21	21	482	1.07
Q9QXX4	Slc25a13	Calcium-binding mitochondrial carrier protein Aralar2	21.60	9	15	410	1.06
Q9QYF1	Rdh11	Retinol dehydrogenase 11	30.38	8	8	136	1.06
P06800	Ptprc	Receptor-type tyrosine-protein phosphatase C	14.02	16	16	165	1.06
Q9QUN7	Tlr2	Toll-like receptor 2	7.14	6	6	21	1.06
P11103	Parp1	Poly [ADP-ribose] polymerase 1	30.01	32	32	654	1.06
Q80X50	Ubap2l	Ubiquitin-associated protein 2-like	24.57	20	20	706	1.06
P97855	G3bp1	Ras GTPase-activating protein-binding protein 1	27.31	8	9	258	1.06
Q00612	G6pdx	Glucose-6-phosphate 1-dehydrogenase X	24.08	14	14	194	1.06
Q9CY27	Tecr	Very-long-chain enoyl-CoA reductase	30.19	12	12	289	1.06
Q921E2	Rab31	Ras-related protein Rab-31	29.38	6	6	94	1.06
P97351	Rps3a	40S ribosomal protein S3a	68.94	24	24	1158	1.06
P53702	Hccs	Cytochrome c-type heme lyase	18.38	4	4	61	1.06
Q9Z315	Sart1	U4/U6.U5 tri-snRNP-associated protein 1	25.81	20	21	404	1.06
Q8K2B3	Sdha	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	35.84	22	22	809	1.06
Q9D0M3	Cyc1	Cytochrome c1, heme protein, mitochondrial	17.23	6	6	76	1.06

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q9WTP7	Ak3	GTP:AMP phosphotransferase AK3, mitochondrial	27.31	6	6	94	1.06
Q61316	Hspa4	Heat shock 70 kDa protein 4	23.90	17	18	216	1.06
Q6KCD5	Nipbl	Nipped-B-like protein	4.93	13	13	121	1.06
P70280	Vamp7	Vesicle-associated membrane protein 7	10.91	2	2	6	1.05
P60867	Rps20	40S ribosomal protein S20	33.61	4	5	439	1.05
Q9CR47	Nsa2	Ribosome biogenesis protein NSA2 homolog	29.23	8	8	105	1.05
Q9D172	D10Jhu81e	ES1 protein homolog, mitochondrial	10.53	3	3	41	1.05
Q6ZWV7	Rpl35	60S ribosomal protein L35	31.71	5	5	136	1.05
Q8BJS4	Sun2	SUN domain-containing protein 2	21.89	14	14	223	1.05
Q6PGH2	Hn1l	Hematological and neurological expressed 1-like protein	14.74	2	2	6	1.05
P61089	Ube2n	Ubiquitin-conjugating enzyme E2 N	23.68	4	4	94	1.05
E9Q555	Rnf213	E3 ubiquitin-protein ligase RNF213	0.83	3	3	8	1.05
Q76MZ3	Ppp2r1a	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	23.43	13	13	185	1.05
Q62189	Snrpa	U1 small nuclear ribonucleoprotein A	25.09	5	7	227	1.05
Q9D517	Agpat3	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	9.84	4	4	28	1.05
Q8BU03	Pwp2	Periodic tryptophan protein 2 homolog	10.45	9	9	191	1.05
P63001	Rac1	Ras-related C3 botulinum toxin substrate 1	36.46	3	8	440	1.05
Q9QXK7	Cpsf3	Cleavage and polyadenylation specificity factor subunit 3	11.40	7	7	83	1.05
Q60972	Rbbp4	Histone-binding protein RBBP4	42.12	8	14	473	1.05
Q4PJX1	Odr4	Protein odr-4 homolog	3.80	2	2	4	1.05
Q6R0H7	Gnas	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	4.41	3	4	130	1.05
O08583	Alyref	THO complex subunit 4	23.53	5	5	307	1.04
Q9WTX8	Mad1l1	Mitotic spindle assembly checkpoint protein MAD1	23.99	15	15	172	1.04
Q9EP72	Emc7	ER membrane protein complex subunit 7	26.14	6	6	43	1.04
Q64525	Hist2h2bb	Histone H2B type 2-B	81.75	2	19	8090	1.04
P10853	Hist1h2bf	Histone H2B type 1-F/J/L	81.75	2	19	7999	1.04
Q62481	Vps72	Vacuolar protein sorting-associated protein 72 homolog	9.51	3	3	12	1.04
Q8VHM5	Hnrnpr	Heterogeneous nuclear ribonucleoprotein R	33.86	13	21	742	1.04
D4AFX7	Dnajc13	Protein Dnajc13	4.05	7	7	24	1.04
P60229	Eif3e	Eukaryotic translation initiation factor 3 subunit E	15.06	6	6	103	1.04
P30285	Cdk4	Cyclin-dependent kinase 4	4.62	1	2	65	1.04
Q9CQI7	Snrpb2	U2 small nuclear ribonucleoprotein B''	23.11	4	6	367	1.04
Q80UU9	Pgrmc2	Membrane-associated progesterone receptor component 2	37.33	8	8	220	1.04
Q921G7	Etfdh	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	19.64	11	11	223	1.04
Q91VM5	Rbmxl1	RNA binding motif protein, X-linked-like-1	60.57	30	30	1278	1.04
P68372	Tubb4b	Tubulin beta-4B chain	46.29	2	17	1554	1.04
Q78PY7	Snd1	Staphylococcal nuclease domain-containing protein 1	34.95	32	32	651	1.04
Q9JLJ2	Aldh9a1	4-trimethylaminobutyraldehyde dehydrogenase	26.11	12	13	153	1.04
Q8K1S6	Spire2	Protein spire homolog 2	1.95	1	2	4	1.04

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q9CQ56	Use1	Vesicle transport protein USE1	24.81	6	6	57	1.04
P07742	Rrm1	Ribonucleoside-diphosphate reductase large subunit	8.84	6	6	56	1.04
Q9CQM9	Glrx3	Glutaredoxin-3	14.84	5	5	17	1.04
P29351	Ptpn6	Tyrosine-protein phosphatase non-receptor type 6	27.39	15	15	311	1.03
O08784	Tcof1	Treacle protein	23.33	27	28	742	1.03
Q9CQU1	Mfap1	Microfibrillar-associated protein 1	11.62	5	5	66	1.03
P05202	Got2	Aspartate aminotransferase, mitochondrial	57.21	25	25	1215	1.03
Q921F2	Tardbp	TAR DNA-binding protein 43	29.95	14	15	907	1.03
P97930	Dtymk	Thymidylate kinase	24.06	5	5	30	1.03
Q9R0U0	Srsf10	Serine/arginine-rich splicing factor 10	18.70	6	6	136	1.03
O55143	Atp2a2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	36.88	32	40	1766	1.03
O35218	Cpsf2	Cleavage and polyadenylation specificity factor subunit 2	14.45	11	11	142	1.03
Q8R1K1	Ubac2	Ubiquitin-associated domain-containing protein 2	8.41	3	3	24	1.03
Q99PV0	Prpf8	Pre-mRNA-processing-splicing factor 8	26.90	66	66	1459	1.03
P67871	Csnk2b	Casein kinase II subunit beta	9.30	2	2	16	1.03
P08003	Pdia4	Protein disulfide-isomerase A4	49.84	34	35	1374	1.03
P10126	Eef1a1	Elongation factor 1-alpha 1	51.08	25	25	1900	1.03
Q8BM55	Tmem214	Transmembrane protein 214	20.38	13	13	251	1.03
A2A432	Cul4b	Cullin-4B	2.37	2	2	6	1.03
P61079	Ube2d3	Ubiquitin-conjugating enzyme E2 D3	16.33	2	3	34	1.03
Q9ERB0	Snap29	Synaptosomal-associated protein 29	32.31	8	8	106	1.03
Q9Z1J3	Nfs1	Cysteine desulfurase, mitochondrial	23.09	10	10	147	1.03
O35598	Adam10	Disintegrin and metalloproteinase domain-containing protein 10	10.41	7	7	78	1.03
Q920B9	Supt16h	FACT complex subunit SPT16	23.69	24	24	393	1.03
Q9QZK7	Dok3	Docking protein 3	12.39	5	5	24	1.03
P26041	Msn	Moesin	29.46	16	23	405	1.03
Q9ER69	Wtap	Pre-mRNA-splicing regulator WTAP	19.70	7	7	44	1.03
Q9CZD3	Gars	Glycine--tRNA ligase	6.86	5	5	27	1.03
Q9EP69	Sacm1l	Phosphatidylinositide phosphatase SAC1	25.04	16	16	287	1.03
Q59J78	Ndufaf2	Mimitin, mitochondrial	20.83	3	3	8	1.02
P45376	Akr1b1	Aldose reductase	16.14	6	6	72	1.02
Q8BSY0	Asph	Aspartyl/asparaginyl beta-hydroxylase	32.25	21	21	640	1.02
Q9D0D4	Dimt1	Probable dimethyladenosine transferase	8.31	3	3	23	1.02
Q9EP89	Lactb	Serine beta-lactamase-like protein LACTB, mitochondrial	11.62	5	6	37	1.02
Q8K2K6	Agfg1	Arf-GAP domain and FG repeat-containing protein 1	14.62	6	8	124	1.02
Q61937	Npm1	Nucleophosmin	64.38	22	22	2129	1.02
Q9CZN7	Shmt2	Serine hydroxymethyltransferase	48.02	26	26	1411	1.02
Q80UW8	Polr2e	DNA-directed RNA polymerases I, II, and III subunit RPABC1	34.29	7	7	181	1.02
P58468	Fam207a	Protein FAM207A	29.68	5	5	89	1.02
P40124	Cap1	Adenylyl cyclase-associated protein 1	41.14	19	19	523	1.02

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q0VBL3	Rbm15	Protein Rbm15	22.56	20	20	203	1.02
E9Q784	Zc3h13	Protein Zc3h13	1.97	3	3	14	1.02
Q9Z0H1	Wdr46	WD repeat-containing protein 46	17.36	9	10	125	1.02
Q9D823	Rpl37	60S ribosomal protein L37	22.68	3	3	8	1.02
O70126	Aurkb	Aurora kinase B	15.94	5	5	28	1.02
Q9CQF3	Nudt21	Cleavage and polyadenylation specificity factor subunit 5	22.91	5	5	42	1.02
P51660	Hsd17b4	Peroxisomal multifunctional enzyme type 2	23.67	16	16	498	1.02
O88665	Brd7	Bromodomain-containing protein 7	3.69	2	2	18	1.02
Q8VDF2	Uhrf1	E3 ubiquitin-protein ligase UHRF1	31.97	25	25	765	1.02
P00920	Ca2	Carbonic anhydrase 2	31.54	8	8	274	1.01
Q9Z0N2	Eif2s3y	Eukaryotic translation initiation factor 2 subunit 3, Y-linked	22.03	2	9	109	1.01
Q80WR5	N/A	UPF0688 protein C1orf174 homolog	11.74	2	2	6	1.01
Q80U93	Nup214	Nuclear pore complex protein Nup214	14.82	26	27	546	1.01
E9Q0Q3	2610021A01Rik	Protein 2610021A01Rik	8.63	1	2	35	1.01
Q9D8N0	Eef1g	Elongation factor 1-gamma	32.04	17	17	512	1.01
Q6DIC0	Smarca2	Probable global transcription activator SNF2L2	6.98	9	11	130	1.01
Q8K4L0	Ddx54	ATP-dependent RNA helicase DDX54	19.79	17	17	169	1.01
O55142	Rpl35a	60S ribosomal protein L35a	52.73	7	7	456	1.01
P62908	Rps3	40S ribosomal protein S3	67.49	18	18	1279	1.01
Q8R326	Pspc1	Paraspeckle component 1	30.02	12	15	211	1.01
Q9CXE7	Tmed5	Transmembrane emp24 domain-containing protein 5	27.95	7	7	179	1.01
Q6ZWU9	Rps27	40S ribosomal protein S27	39.29	2	4	256	1.01
Q3UFY8	Trmt10c	Mitochondrial ribonuclease P protein 1	11.11	3	3	12	1.01
Q640M1	Utp14a	U3 small nucleolar RNA-associated protein 14 homolog A	32.99	26	26	445	1.01
Q99NB9	Sf3b1	Splicing factor 3B subunit 1	32.21	42	42	1326	1.00
Q9CW46	Raver1	Ribonucleoprotein PTB-binding 1	11.10	7	7	201	1.00
Q8BGD9	Eif4b	Eukaryotic translation initiation factor 4B	11.46	5	5	52	1.00
Q60766	Irgm1	Immunity-related GTPase family M protein 1	15.16	6	6	59	1.00
Q9Z1X4	Ilf3	Interleukin enhancer-binding factor 3	32.96	24	26	660	1.00
Q9QY81	Nup210	Nuclear pore membrane glycoprotein 210	17.07	29	30	595	1.00
Q8BVK9	Sp110	Sp110 nuclear body protein	30.79	14	15	129	1.00
Q9CR57	Rpl14	60S ribosomal protein L14	35.48	10	10	521	1.00
Q6PD26	Pigs	GPI transamidase component PIG-S	8.65	5	5	57	1.00
P80313	Cct7	T-complex protein 1 subunit eta	35.11	20	20	388	1.00
P62880	Gnb2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	29.41	5	11	268	1.00
Q9Z0N1	Eif2s3x	Eukaryotic translation initiation factor 2 subunit 3, X-linked	30.51	5	12	130	1.00
Q3UV17	Krt76	Keratin, type II cytoskeletal 2 oral	8.92	3	7	163	1.00
Q3V1V3	Esf1	ESF1 homolog	9.47	8	8	66	1.00
P04104	Krt1	Keratin, type II cytoskeletal 1	7.06	4	6	404	0.99
Q9CY57	Chtop	Chromatin target of PRMT1 protein	23.29	5	5	162	0.99

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q8VHR5	Gatad2b	Transcriptional repressor p66-beta	31.48	13	13	187	0.99
Q62383	Supt6h	Transcription elongation factor SPT6	7.18	10	10	113	0.99
Q8CG48	Smc2	Structural maintenance of chromosomes protein 2	18.39	20	20	207	0.99
Q99JX3	Gorasp2	Golgi reassembly-stacking protein 2	15.96	6	6	108	0.99
P62717	Rpl18a	60S ribosomal protein L18a	47.16	9	9	468	0.99
Q8QZY9	Sf3b4	Splicing factor 3B subunit 4	8.96	4	4	83	0.99
P07356	Anxa2	Annexin A2	46.61	15	15	454	0.99
Q8C6B9	Rps19bp1	Active regulator of SIRT1	41.26	5	5	67	0.99
P27773	Pdia3	Protein disulfide-isomerase A3	70.30	43	43	3251	0.99
P17918	Pcna	Proliferating cell nuclear antigen	52.87	12	12	437	0.99
Q9WUR9	Ak4	Adenylate kinase 4, mitochondrial	23.32	5	5	35	0.99
Q8R5K4	Nol6	Nucleolar protein 6	14.58	17	17	328	0.99
Q9CRB2	Nhp2	H/ACA ribonucleoprotein complex subunit 2	41.18	4	4	153	0.99
Q61753	Phgdh	D-3-phosphoglycerate dehydrogenase	32.65	17	17	546	0.99
Q9R0P6	Sec11a	Signal peptidase complex catalytic subunit SEC11A	11.73	3	3	34	0.99
Q9WUK4	Rfc2	Replication factor C subunit 2	26.36	9	9	204	0.99
P22437	Ptgs1	Prostaglandin G/H synthase 1	14.62	9	9	164	0.99
Q9WV70	Noc2l	Nucleolar complex protein 2 homolog	13.52	11	11	262	0.99
P12815	Pdcd6	Programmed cell death protein 6	8.90	2	2	11	0.98
Q9Z0H3	Smarcb1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	18.18	6	6	85	0.98
Q8BFZ9	Erlin2	Erlin-2	30.59	7	10	374	0.98
Q9R0Q8	Clec4e	C-type lectin domain family 4 member E	12.15	2	2	12	0.98
Q8CHY6	Gatad2a	Transcriptional repressor p66 alpha	27.50	14	14	214	0.98
O88685	Psmc3	26S protease regulatory subunit 6A	6.33	3	3	21	0.98
P62192	Psmc1	26S protease regulatory subunit 4	12.05	4	5	106	0.98
Q9DBG7	Srpr	Signal recognition particle receptor subunit alpha	25.16	16	16	233	0.98
P56382	Atp5e	ATP synthase subunit epsilon, mitochondrial	57.69	4	4	141	0.98
P58742	Aaas	Aladin	9.52	5	5	109	0.98
P80318	Cct3	T-complex protein 1 subunit gamma	40.73	23	23	481	0.98
Q7M6Y3	Picalm	Phosphatidylinositol-binding clathrin assembly protein	22.42	14	14	400	0.98
Q9WTK3	Gpaa1	Glycosylphosphatidylinositol anchor attachment 1 protein	4.35	3	3	22	0.98
Q9Z1D1	Eif3g	Eukaryotic translation initiation factor 3 subunit G	9.06	3	3	65	0.98
P09411	Pgk1	Phosphoglycerate kinase 1	48.92	21	21	628	0.98
Q61595	Ktn1	Kinectin	9.42	12	12	167	0.98
Q91WD5	Ndufs2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	14.69	7	7	107	0.98
Q9ES52	Inpp5d	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	10.66	10	12	93	0.98
Q8BIG7	Comtd1	Catechol O-methyltransferase domain-containing protein 1	14.50	3	3	72	0.98
Q8BVY0	Rsl1d1	Ribosomal L1 domain-containing protein 1	47.79	26	26	1158	0.98
Q6PB44	Ptpn23	Tyrosine-protein phosphatase non-receptor type 23	2.42	3	3	9	0.98

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q9D8V7	Sec11c	Signal peptidase complex catalytic subunit SEC11C	11.98	3	3	20	0.98
Q8BHN3	Ganab	Neutral alpha-glucosidase AB	25.64	24	24	583	0.97
Q9D6T0	Nosip	Nitric oxide synthase-interacting protein	12.96	3	3	12	0.97
Q61490	Alcam	CD166 antigen	10.63	7	7	107	0.97
Q9DB73	Cyb5r1	NADH-cytochrome b5 reductase 1	22.95	6	6	88	0.97
Q9CXY6	Ilf2	Interleukin enhancer-binding factor 2	36.92	13	13	457	0.97
Q8BMG7	Rab3gap2	Rab3 GTPase-activating protein non-catalytic subunit	2.78	3	3	9	0.97
P35700	Prdx1	Peroxiredoxin-1	60.80	10	12	1093	0.97
Q6A0A9	FAM120A	Constitutive coactivator of PPAR-gamma-like protein 1	2.79	2	2	6	0.97
Q9D0Q7	Mrpl45	39S ribosomal protein L45, mitochondrial	11.44	4	4	36	0.97
Q4G0F8	Ubn1	Ubinuclein-1	1.76	2	2	7	0.97
O08912	Galnt1	Polypeptide N-acetylgalactosaminyltransferase 1	8.05	4	4	48	0.97
Q8BTS4	Nup54	Nuclear pore complex protein Nup54	26.86	12	12	281	0.97
O35375	Nrp2	Neuropilin-2	10.10	8	8	138	0.97
P53569	Cebpz	CCAAT/enhancer-binding protein zeta	17.11	19	19	260	0.97
Q5RJH6	Smg7	Protein SMG7	1.76	2	2	4	0.97
Q9D903	Ebna1bp2	Probable rRNA-processing protein EBP2	49.67	18	18	587	0.97
P70168	Kpnb1	Importin subunit beta-1	26.71	20	20	592	0.97
Q8R3N1	Nop14	Nucleolar protein 14	22.79	19	21	256	0.97
P05213	Tuba1b	Tubulin alpha-1B chain	48.12	3	18	922	0.96
P68373	Tuba1c	Tubulin alpha-1C chain	47.88	3	18	888	0.96
Q8CIM8	Ints4	Integrator complex subunit 4	10.89	10	10	40	0.96
Q61686	Cbx5	Chromobox protein homolog 5	27.75	5	6	76	0.96
Q9WUM4	Coro1c	Coronin-1C	14.35	6	7	69	0.96
Q8BTW3	Exosc6	Exosome complex component MTR3	34.07	8	8	121	0.96
P46061	Rangap1	Ran GTPase-activating protein 1	35.31	20	20	533	0.96
Q6PGH1	Bud31	Protein BUD31 homolog	30.10	3	3	93	0.96
Q91WM1	Strbp	Spermatid perinuclear RNA-binding protein	10.57	5	7	61	0.96
Q9Z2U1	Psma5	Proteasome subunit alpha type-5	23.65	4	5	96	0.96
P31001	Des	Desmin	13.65	2	9	1076	0.96
Q9JKF1	Iqgap1	Ras GTPase-activating-like protein IQGAP1	15.93	24	24	308	0.96
Q8QZT1	Acat1	Acetyl-CoA acetyltransferase, mitochondrial	51.89	18	18	741	0.96
P58252	Eef2	Elongation factor 2	34.03	31	32	1308	0.96
Q99MR6	Srrt	Serrate RNA effector molecule homolog	17.26	19	19	420	0.96
Q6A068	Cdc5l	Cell division cycle 5-like protein	33.17	26	26	464	0.96
Q61136	Prpf4b	Serine/threonine-protein kinase PRP4 homolog	6.85	8	8	67	0.96
Q3TAQ9	Wdr36	Protein Wdr36	18.80	14	15	270	0.95
Q8BGQ7	Aars	Alanine--tRNA ligase, cytoplasmic	3.10	3	3	14	0.95
P62996	Tra2b	Transformer-2 protein homolog beta	18.06	4	5	338	0.95
G3XA10	Gm28062	Heterogeneous nuclear ribonucleoprotein U, isoform CRA_b	42.12	41	42	2656	0.95

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q8CIB6	Tmem230	Transmembrane protein 230	15.00	2	2	6	0.95
P61327	Magoh	Protein mago nashi homolog	36.30	7	7	111	0.95
P51912	Slc1a5	Neutral amino acid transporter B(0)	11.57	6	6	182	0.95
Q9EQH3	Vps35	Vacuolar protein sorting-associated protein 35	11.43	8	8	46	0.95
Q9JIX0	Eny2	Transcription and mRNA export factor ENY2	13.86	2	2	4	0.95
P35821	Ptpn1	Tyrosine-protein phosphatase non-receptor type 1	24.07	10	11	80	0.95
Q99PM9	Uck2	Uridine-cytidine kinase 2	12.64	3	3	41	0.95
A2AIX1	Sec16a	Protein Sec16a	1.51	4	4	22	0.95
O54734	Ddost	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	36.28	15	15	723	0.95
Q80SW1	Ahcyl1	Putative adenosylhomocysteinase 2	6.79	3	4	15	0.95
Q9WTR1	Trpv2	Transient receptor potential cation channel subfamily V member 2	12.04	8	8	86	0.95
P99024	Tubb5	Tubulin beta-5 chain	52.48	4	18	1888	0.95
Q9EPJ9	Arfgap1	ADP-ribosylation factor GTPase-activating protein 1	17.15	6	6	24	0.94
Q8BLN5	Lss	Lanosterol synthase	15.42	11	11	154	0.94
Q6QD59	Bnip1	Vesicle transport protein SEC20	28.95	7	7	47	0.94
Q8BTI8	Srrm2	Serine/arginine repetitive matrix protein 2	18.72	43	43	1026	0.94
Q6PR54	Rif1	Telomere-associated protein RIF1	11.16	24	24	309	0.94
Q91YQ5	Rpn1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	49.84	31	31	1804	0.94
Q8CIL4	N/A	Uncharacterized protein C1orf131 homolog	9.61	2	2	10	0.94
Q9WTM5	Ruvbl2	RuvB-like 2	36.07	18	18	543	0.94
Q922B2	Dars	Aspartate--tRNA ligase, cytoplasmic	26.95	13	13	122	0.94
Q8C898	C130026I21Rik	Protein C130026I21Rik	21.99	6	7	151	0.94
Q8K1B8	Fermt3	Fermitin family homolog 3	21.80	13	13	214	0.94
P38060	Hmgcl	Hydroxymethylglutaryl-CoA lyase, mitochondrial	16.00	5	5	82	0.94
Q9EQH2	Erap1	Endoplasmic reticulum aminopeptidase 1	13.12	13	13	183	0.94
Q9R0L6	Pcm1	Pericentriolar material 1 protein	0.94	2	2	4	0.94
Q9ERY9	ORF11	Probable ergosterol biosynthetic protein 28	30.00	4	4	11	0.94
Q9R0E1	Plod3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	8.77	6	6	67	0.94
Q8BKS9	Kiaa0020	Pumilio domain-containing protein KIAA0020	23.49	16	16	370	0.94
Q61166	Mapre1	Microtubule-associated protein RP/EB family member 1	22.39	7	7	44	0.94
Q62159	Rhoc	Rho-related GTP-binding protein RhoC	12.95	1	3	73	0.94
Q6DVA0	Lemd2	LEM domain-containing protein 2	14.87	7	7	98	0.94
Q64518	Atp2a3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	12.72	5	13	460	0.94
Q9D2M8	Ube2v2	Ubiquitin-conjugating enzyme E2 variant 2	31.03	2	5	58	0.94
Q8BIJ6	Iars2	Isoleucine--tRNA ligase, mitochondrial	6.03	5	6	59	0.94
Q9DBS5	Klc4	Kinesin light chain 4	7.75	4	4	17	0.94
Q64727	Vcl	Vinculin	3.28	3	3	10	0.94
Q99J47	Dhrs7b	Dehydrogenase/reductase SDR family member 7B	17.03	6	6	20	0.94
Q8BIQ5	Cstf2	Cleavage stimulation factor subunit 2	12.41	7	7	216	0.94
D3Z0M9	Ddx23	MCG18410, isoform CRA_a	24.54	21	21	310	0.93

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q91ZR1	Rab4b	Ras-related protein Rab-4B	19.25	3	4	155	0.93
Q8BG05	Hnrnpa3	Heterogeneous nuclear ribonucleoprotein A3	44.06	18	23	2675	0.93
Q9CRD2	Emc2	ER membrane protein complex subunit 2	21.89	7	7	179	0.93
Q04750	Top1	DNA topoisomerase 1	38.46	31	31	1103	0.93
Q91YK2	Rrp1b	Ribosomal RNA processing protein 1 homolog B	41.02	26	27	393	0.93
Q9D554	Sf3a3	Splicing factor 3A subunit 3	22.55	12	12	334	0.93
P17751	Tpi1	Triosephosphate isomerase	53.85	12	12	369	0.93
Q64511	Top2b	DNA topoisomerase 2-beta	28.16	33	47	1167	0.93
P00493	Hprt1	Hypoxanthine-guanine phosphoribosyltransferase	14.68	3	3	29	0.93
O54984	Asna1	ATPase Asna1	13.79	5	5	15	0.93
Q3TZX8	Nol9	Polynucleotide 5'-hydroxyl-kinase NOL9	6.30	5	5	26	0.93
Q0P678	Zc3h18	Zinc finger CCCH domain-containing protein 18	14.56	10	10	91	0.93
Q8VE37	Rcc1	Regulator of chromosome condensation	33.97	13	13	646	0.93
Q8BHS3	Rbm22	Pre-mRNA-splicing factor RBM22	14.29	6	6	133	0.93
Q8BU14	Sec62	Translocation protein SEC62	13.57	6	6	181	0.93
Q922K7	Nop2	Probable 28S rRNA (cytosine-C(5))-methyltransferase	38.34	26	26	863	0.93
P35276	Rab3d	Ras-related protein Rab-3D	20.55	2	5	182	0.93
P43275	Hist1h1a	Histone H1.1	35.68	9	12	1305	0.92
P62317	Snrpd2	Small nuclear ribonucleoprotein Sm D2	61.86	7	7	353	0.92
Q9DBE9	Ftsj3	pre-rRNA processing protein FTSJ3	33.29	27	27	540	0.92
Q8K4P0	Wdr33	pre-mRNA 3' end processing protein WDR33	9.92	11	12	120	0.92
Q9CZX5	Pinx1	PIN2/TERF1-interacting telomerase inhibitor 1	11.14	3	3	8	0.92
P70227	Itpr3	Inositol 1,4,5-trisphosphate receptor type 3	5.13	14	14	130	0.92
P59235	Nup43	Nucleoporin Nup43	17.11	5	5	36	0.92
P62962	Pfn1	Profilin-1	72.14	9	9	283	0.92
O35639	Anxa3	Annexin A3	17.96	4	6	26	0.92
P80315	Cct4	T-complex protein 1 subunit delta	38.03	20	20	397	0.92
P60335	Pcbp1	Poly(rC)-binding protein 1	49.44	8	12	966	0.92
P10639	Txn	Thioredoxin	20.95	2	2	27	0.92
E9Q411	Nbas	Protein Nbas	2.29	6	6	9	0.92
Q9CTH6	Fcf1	rRNA-processing protein FCF1 homolog	14.65	3	3	51	0.92
Q99LX0	Park7	Protein deglycase DJ-1	27.51	6	6	82	0.92
Q6PHQ9	Pabpc4	Polyadenylate-binding protein	29.24	12	20	180	0.92
Q6PDQ2	Chd4	Chromodomain-helicase-DNA-binding protein 4	22.87	41	41	691	0.92
P05555	Itgam	Integrin alpha-M	11.36	12	12	193	0.92
Q61103	Dpf2	Zinc finger protein ubi-d4	15.86	5	5	64	0.92
Q7TPN9	Prr14	Proline-rich protein 14	3.59	2	2	6	0.92
P54775	Psmc4	26S protease regulatory subunit 6B	16.27	7	7	74	0.92
Q7TND5	Rpf1	Ribosome production factor 1	12.32	4	4	27	0.92
Q9R0I7	Ylpm1	YLP motif-containing protein 1	9.16	12	12	130	0.92

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8VDQ9	Kri1	Protein KRI1 homolog	11.36	8	8	116	0.91
Q9DBG6	Rpn2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	28.53	15	15	812	0.91
Q9R1C7	Prpf40a	Pre-mRNA-processing factor 40 homolog A	15.84	17	17	339	0.91
P50446	Krt6a	Keratin, type II cytoskeletal 6A	16.27	3	11	227	0.91
Q07076	Anxa7	Annexin A7	46.44	23	24	1020	0.91
P60843	Eif4a1	Eukaryotic initiation factor 4A-I	43.84	11	20	680	0.91
Q9CZU3	Skiv2l2	Superkiller viralicidic activity 2-like 2	15.87	17	17	333	0.91
O88952	Lin7c	Protein lin-7 homolog C	21.83	5	5	38	0.91
Q9ESV0	Ddx24	ATP-dependent RNA helicase DDX24	34.42	30	30	555	0.91
P70279	Surf6	Surfeit locus protein 6	30.99	14	14	245	0.91
Q9D2D7	Znf687	Zinc finger protein 687	4.77	5	5	23	0.91
O35344	Kpna3	Importin subunit alpha-4	8.45	3	4	40	0.90
Q9R059	Fhl3	Four and a half LIM domains protein 3	25.95	7	7	345	0.90
Q9CZ30	Ola1	Obg-like ATPase 1	5.05	2	2	6	0.90
G3UWG1	Gm10108	MCG115977	45.71	7	7	344	0.90
Q8R2M2	Dnttip2	Deoxynucleotidyltransferase terminal-interacting protein 2	25.99	19	19	350	0.90
Q80Y44	Ddx10	Probable ATP-dependent RNA helicase DDX10	14.63	13	13	221	0.90
P62196	Psmc5	26S protease regulatory subunit 8	21.18	7	8	84	0.90
Q9D1H6	Ndufaf4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	25.43	4	4	14	0.90
Q810A7	Ddx42	ATP-dependent RNA helicase DDX42	11.41	10	10	71	0.90
Q91WM3	Rrp9	U3 small nucleolar RNA-interacting protein 2	20.21	9	9	317	0.90
P47930	Fosl2	Fos-related antigen 2	7.36	2	2	34	0.90
P80317	Cct6a	T-complex protein 1 subunit zeta	29.19	17	17	501	0.90
Q3U1G5	Isg20l2	Interferon-stimulated 20 kDa exonuclease-like 2	19.84	7	7	56	0.90
A6ZI47	Aldoart2	Fructose-bisphosphate aldolase	18.41	2	10	519	0.90
Q3TKT4	Smarca4	Transcription activator BRG1	19.22	30	32	547	0.90
Q91VC3	Eif4a3	Eukaryotic initiation factor 4A-III	40.39	18	21	875	0.90
Q8BX70	Vps13c	Vacuolar protein sorting-associated protein 13C	11.85	39	40	420	0.90
Q9CXR1	Dhrs7	Dehydrogenase/reductase SDR family member 7	5.03	2	2	6	0.90
P05201	Got1	Aspartate aminotransferase, cytoplasmic	13.56	5	5	30	0.90
Q60872	Eif1a	Eukaryotic translation initiation factor 1A	14.58	2	2	13	0.90
P06151	Ldha	L-lactate dehydrogenase A chain	40.36	15	15	651	0.90
Q9R1P1	Psmb3	Proteasome subunit beta type-3	8.29	2	2	4	0.90
Q9QX47	Son	Protein SON	21.40	39	39	1004	0.90
Q8QZY1	Eif3l	Eukaryotic translation initiation factor 3 subunit L	10.46	6	6	39	0.90
Q921N6	Ddx27	Probable ATP-dependent RNA helicase DDX27	28.03	21	21	485	0.90
P26443	Glud1	Glutamate dehydrogenase 1, mitochondrial	48.21	25	25	1048	0.89
Q9JJ89	Ccdc86	Coiled-coil domain-containing protein 86	13.85	6	6	97	0.89
E9QAE3	Btaf1	Protein Btaf1	5.90	11	11	76	0.89
A2APB8	Tpx2	Targeting protein for Xklp2	17.45	13	13	123	0.89

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8CH18	Ccar1	Cell division cycle and apoptosis regulator protein 1	12.04	15	15	239	0.89
Q6NS46	Pdcd11	Protein RRP5 homolog	29.65	54	54	1009	0.89
P17225	Ptbp1	Polypyrimidine tract-binding protein 1	29.03	8	13	636	0.89
Q9WU62	Incenp	Inner centromere protein	13.98	11	11	119	0.89
P05064	Aldoa	Fructose-bisphosphate aldolase A	65.11	15	22	962	0.89
Q4FZC9	Syne3	Nesprin-3	21.95	20	20	279	0.89
Q9CYH6	Rrs1	Ribosome biogenesis regulatory protein homolog	30.14	14	14	298	0.89
F6ZDS4	Tpr	Nucleoprotein TPR	33.16	80	81	1738	0.89
Q64012	Raly	RNA-binding protein Raly	54.49	18	18	1084	0.89
P15864	Hist1h1c	Histone H1.2	56.13	8	23	3780	0.89
P43277	Hist1h1d	Histone H1.3	58.37	3	24	3772	0.89
Q9D8W5	Psmd12	26S proteasome non-ATPase regulatory subunit 12	28.51	14	14	123	0.89
P68040	Gnb2l1	Guanine nucleotide-binding protein subunit beta-2-like 1	44.16	14	14	479	0.89
Q62376	Snrnp70	U1 small nuclear ribonucleoprotein 70 kDa	29.46	17	17	301	0.89
B9EJ54	Nup205	MCG21756, isoform CRA_b	17.53	36	36	761	0.89
Q9Z0W3	Nup160	Nuclear pore complex protein Nup160	9.42	14	14	174	0.89
Q78YY6	Dnajc15	DnaJ homolog subfamily C member 15	22.15	3	3	11	0.89
O35134	Polr1a	DNA-directed RNA polymerase I subunit RPA1	8.56	11	12	115	0.89
Q00PI9	Hnrnpul2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	26.04	21	21	474	0.89
Q9CX34	Sugt1	Protein SGT1 homolog	21.43	7	7	125	0.89
P52480	Pkm	Pyruvate kinase PKM	65.16	34	34	2061	0.89
P48678	Lmna	Prelamin-A/C	80.30	62	65	8318	0.89
Q920L1	Fads1	Fatty acid desaturase 1	16.11	6	6	129	0.88
Q8CI11	Gnl3	Guanine nucleotide-binding protein-like 3	45.72	24	25	469	0.88
P48036	Anxa5	Annexin A5	28.53	10	10	260	0.88
Q8BPB0	Mob1b	MOB kinase activator 1B	8.33	2	2	13	0.88
O35691	Pnn	Pinin	26.48	21	21	460	0.88
Q922J9	Far1	Fatty acyl-CoA reductase 1	20.78	11	11	199	0.88
Q99LR1	Abhd12	Monoacylglycerol lipase ABHD12	19.85	7	7	67	0.88
Q9D338	Mrpl19	39S ribosomal protein L19, mitochondrial	9.93	3	3	55	0.88
Q9EQI8	Mrpl46	39S ribosomal protein L46, mitochondrial	15.19	4	4	51	0.88
P70372	Elavl1	ELAV-like protein 1	46.63	13	13	614	0.88
Q61334	Bcap29	B-cell receptor-associated protein 29	20.00	6	6	97	0.88
Q80X41	Vrk1	Serine/threonine-protein kinase VRK1	10.91	5	5	17	0.88
Q60605	Myl6	Myosin light polypeptide 6	30.46	4	4	39	0.88
Q9CQR2	Rps21	40S ribosomal protein S21	48.19	5	5	263	0.88
P21619	Lmnb2	Lamin-B2	56.04	28	37	1562	0.88
P61924	Copz1	Coatomer subunit zeta-1	11.86	2	2	18	0.88
P56960	Exosc10	Exosome component 10	16.12	15	15	86	0.88
Q8VDP4	Ccar2	Cell cycle and apoptosis regulator protein 2	22.13	16	16	258	0.88

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
B2RQC6	Cad	CAD protein	6.92	16	16	161	0.88
Q61687	Atrx	Transcriptional regulator ATRX	5.33	12	12	97	0.88
Q9D2V8	Mfsd10	Major facilitator superfamily domain-containing protein 10	8.77	4	4	98	0.88
P17182	Eno1	Alpha-enolase	51.15	23	23	1765	0.88
Q8K2P7	Slc38a1	Sodium-coupled neutral amino acid transporter 1	3.92	2	2	4	0.88
Q9CW03	Smc3	Structural maintenance of chromosomes protein 3	34.68	40	41	706	0.88
Q91VE6	Nifk	MKI67 FHA domain-interacting nucleolar phosphoprotein	51.74	15	15	459	0.88
Q5XG71	Utp20	Small subunit processome component 20 homolog	13.38	39	39	485	0.88
Q99JF8	Psip1	PC4 and SFRS1-interacting protein	43.94	20	20	260	0.88
O35286	Dhx15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	37.23	29	29	916	0.88
Q9CZR8	Tsfm	Elongation factor Ts, mitochondrial	15.12	5	5	30	0.88
Q8BU31	Rap2c	Ras-related protein Rap-2c	10.93	2	2	11	0.87
O70551	Srpk1	SRSF protein kinase 1	4.32	2	2	6	0.87
O08709	Prdx6	Peroxiredoxin-6	35.27	7	7	103	0.87
Q61990	Pcbp2	Poly(rC)-binding protein 2	31.22	5	9	754	0.87
Q9Z1N2	Orc1	Origin recognition complex subunit 1	9.64	7	7	45	0.87
P53026	Rpl10a	60S ribosomal protein L10a	47.47	13	13	574	0.87
Q91YU8	Ppan	Suppressor of SWI4 1 homolog	26.60	13	13	229	0.87
O70133	Dhx9	ATP-dependent RNA helicase A	34.28	51	52	2013	0.87
P27048	Snrpb	Small nuclear ribonucleoprotein-associated protein B	22.08	5	5	197	0.87
P70349	Hint1	Histidine triad nucleotide-binding protein 1	16.67	2	2	44	0.87
Q6GQT9	Nomo1	Nodal modulator 1	18.95	21	21	398	0.87
P60122	Ruvbl1	RuvB-like 1	41.01	15	15	358	0.87
Q9DBG3	Ap2b1	AP-2 complex subunit beta	20.92	10	19	199	0.87
Q99L47	St13	Hsc70-interacting protein	26.95	11	11	268	0.87
D3YVN7	Gm9755	Elongation factor Tu	53.10	23	24	1023	0.87
G3X9B1	Heatr1	HEAT repeat containing 1	18.99	42	43	944	0.87
Q9DCV7	Krt7	Keratin, type II cytoskeletal 7	8.75	2	6	380	0.87
Q91VI7	Rnh1	Ribonuclease inhibitor	30.70	12	12	145	0.87
A2ANY6	Mdn1	Protein Mdn1	6.57	35	36	281	0.87
Q64213	Sf1	Splicing factor 1	7.96	6	6	148	0.87
Q6ZWY3	Rps27l	40S ribosomal protein S27-like	38.10	1	3	181	0.87
Q9CYN2	Spcs2	Signal peptidase complex subunit 2	47.79	11	11	189	0.86
Q8K1Z0	Coq9	Ubiquinone biosynthesis protein COQ9, mitochondrial	19.17	5	5	62	0.86
Q01320	Top2a	DNA topoisomerase 2-alpha	37.24	52	65	2060	0.86
Q9QZD9	Eif3i	Eukaryotic translation initiation factor 3 subunit I	23.38	7	7	37	0.86
P48410	Abcd1	ATP-binding cassette sub-family D member 1	11.41	7	7	153	0.86
Q8BFV2	Pcid2	PCI domain-containing protein 2	12.28	4	4	33	0.86
E9PY39	Gm20431	Protein Gm20431	15.90	3	6	71	0.86
O88532	Zfr	Zinc finger RNA-binding protein	14.34	13	13	359	0.86

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q60932	Vdac1	Voltage-dependent anion-selective channel protein 1	70.27	16	18	1018	0.86
P47753	Capza1	F-actin-capping protein subunit alpha-1	32.17	5	7	178	0.86
Q99P88	Nup155	Nuclear pore complex protein Nup155	22.07	31	31	754	0.86
P60710	Actb	Actin, cytoplasmic 1	62.40	22	23	4750	0.86
P17095	Hmga1	High mobility group protein HMG-I/HMG-Y	66.36	9	9	474	0.86
Q9R112	Sqrdl	Sulfide:quinone oxidoreductase, mitochondrial	14.44	6	6	94	0.86
Q8C0L0	Tmx4	Thioredoxin-related transmembrane protein 4	8.96	2	2	12	0.86
Q6DFW4	Nop58	Nucleolar protein 58	41.98	19	19	869	0.86
Q922U1	Prpf3	U4/U6 small nuclear ribonucleoprotein Prp3	20.94	15	15	343	0.86
Q8K2M0	Mrpl38	39S ribosomal protein L38, mitochondrial	11.05	4	4	31	0.86
Q8BHD7	Ptbp3	Polypyrimidine tract-binding protein 3	24.47	9	14	489	0.86
Q924T2	Mrps2	28S ribosomal protein S2, mitochondrial	11.34	2	3	14	0.86
Q3U9G9	Lbr	Lamin-B receptor	23.16	18	18	836	0.86
Q8CFI7	Polr2b	DNA-directed RNA polymerase II subunit RPB2	17.04	18	18	212	0.86
Q8BYI6	Lpcat2	Lysophosphatidylcholine acyltransferase 2	9.19	5	5	117	0.86
Q3UJB0	Sf3b2	Protein Sf3b2	31.09	28	28	1024	0.86
P83870	Phf5a	PHD finger-like domain-containing protein 5A	62.73	7	7	242	0.86
Q99M28	Rnps1	RNA-binding protein with serine-rich domain 1	9.51	3	3	118	0.86
Q9QYS9	Qki	Protein quaking	15.84	5	5	35	0.86
P28033	Cebpb	CCAAT/enhancer-binding protein beta	23.31	6	6	133	0.86
Q8K310	Matr3	Matrin-3	43.50	39	39	1424	0.85
Q6PEB6	Mob4	MOB-like protein phocein	10.22	2	2	4	0.85
P24270	Cat	Catalase	37.57	19	19	428	0.85
P47758	Srprb	Signal recognition particle receptor subunit beta	46.47	12	12	440	0.85
E9Q5C9	Nolc1	Protein Nolc1	27.07	27	27	1311	0.85
Q3TTY5	Krt2	Keratin, type II cytoskeletal 2 epidermal	8.06	4	8	249	0.85
Q99K48	Nono	Non-POU domain-containing octamer-binding protein	45.88	22	26	1167	0.85
Q920A7	Afg3l1	AFG3-like protein 1	10.27	6	9	52	0.85
Q921M3	Sf3b3	Splicing factor 3B subunit 3	28.18	36	36	1208	0.85
P97363	Sptlc2	Serine palmitoyltransferase 2	17.68	10	10	157	0.85
Q8BH24	Tm9sf4	Transmembrane 9 superfamily member 4	8.86	6	7	166	0.85
Q60664	Lrmp	Lymphoid-restricted membrane protein	20.96	10	10	105	0.85
Q3TIU4	Pde12	2',5'-phosphodiesterase 12	3.62	2	2	2	0.85
Q91WC9	Daglb	Sn1-specific diacylglycerol lipase beta	8.97	7	7	48	0.85
E9PVX6	Mki67	Protein Mki67	42.90	127	127	3345	0.85
Q5NC05	Ttf2	Transcription termination factor 2	1.93	1	3	12	0.85
Q8BK67	Rcc2	Protein RCC2	24.62	12	12	171	0.85
Q8C2Q3	Rbm14	RNA-binding protein 14	36.47	25	25	1469	0.84
Q9JKP5	Mbnl1	Muscleblind-like protein 1	11.44	4	4	67	0.84
Q9CQW2	Arl8b	ADP-ribosylation factor-like protein 8B	36.02	1	6	470	0.84

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
P26043	Rdx	Radixin	13.38	3	10	160	0.84
Q9CPQ8	Atp5l	ATP synthase subunit g, mitochondrial	41.75	3	3	108	0.84
Q3UH06	Rreb1	Ras-responsive element-binding protein 1	1.18	2	2	6	0.84
Q9D1J3	Sarnp	SAP domain-containing ribonucleoprotein	27.62	5	5	111	0.84
Q3UHX9	D2Wsu81e	Putative methyltransferase C9orf114 homolog	19.22	6	7	82	0.84
Q8CGC6	Rbm28	RNA-binding protein 28	31.33	24	24	514	0.84
Q9ET30	Tm9sf3	Transmembrane 9 superfamily member 3	10.73	8	8	289	0.84
Q99KK2	Cmas	N-acylneuraminate cytidylyltransferase	15.28	7	7	100	0.84
Q9D051	Pdhb	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	21.17	8	8	137	0.84
O35130	Emg1	Ribosomal RNA small subunit methyltransferase NEP1	25.41	5	5	108	0.84
Q99LI2	Clcc1	Chloride channel CLIC-like protein 1	22.45	11	11	167	0.84
Q9Z2U0	Psma7	Proteasome subunit alpha type-7	32.26	7	7	166	0.84
P62075	Timm13	Mitochondrial import inner membrane translocase subunit Tim13	26.32	2	2	2	0.84
Q9QUI0	Rhoa	Transforming protein RhoA	22.28	3	5	125	0.84
P59326	Ythdf1	YTH domain-containing family protein 1	9.66	1	6	157	0.84
Q8K2Y7	Mrpl47	39S ribosomal protein L47, mitochondrial	8.33	2	2	18	0.84
Q8C570	Rae1	mRNA export factor	30.43	11	11	178	0.84
Q3TYS2	N/A	Uncharacterized protein C17orf62 homolog	11.76	3	3	89	0.84
Q9D0E1	Hnrnpm	Heterogeneous nuclear ribonucleoprotein M	69.96	55	55	3058	0.84
Q3TFK5	Gpatch4	G patch domain-containing protein 4	17.83	5	6	77	0.84
Q9EQ06	Hsd17b11	Estradiol 17-beta-dehydrogenase 11	11.74	4	4	54	0.84
Q9D0R4	Ddx56	Probable ATP-dependent RNA helicase DDX56	16.12	8	9	278	0.83
Q8VCM8	Ncln	Nicalin	14.92	9	9	268	0.83
Q922U2	Krt5	Keratin, type II cytoskeletal 5	19.14	9	17	394	0.83
Q9DBY8	Nvl	Nuclear valosin-containing protein-like	24.80	19	19	290	0.83
Q8BHB4	Wdr3	WD repeat-containing protein 3	14.76	12	12	165	0.83
Q9Z0R9	Fads2	Fatty acid desaturase 2	6.76	3	3	41	0.83
Q8K3Z9	Pom121	Nuclear envelope pore membrane protein POM 121	14.08	13	13	144	0.83
P61164	Actr1a	Alpha-centractin	7.71	3	4	105	0.83
Q9R099	Tbl2	Transducin beta-like protein 2	23.98	10	10	96	0.83
Q80U70	Suz12	Polycomb protein Suz12	6.61	5	5	30	0.83
Q99N69	Lpxn	Leupaxin	21.24	8	8	104	0.83
Q99K01	Pdxdc1	Pyridoxal-dependent decarboxylase domain-containing protein 1	4.57	3	3	8	0.83
Q922Q1	Marc2	Mitochondrial amidoxime reducing component 2	26.04	11	11	132	0.83
Q8BJ03	Cox15	Cytochrome c oxidase assembly protein COX15 homolog	5.33	2	2	18	0.83
Q8VIJ6	Sfpq	Splicing factor, proline- and glutamine-rich	44.21	31	33	2496	0.83
O55098	Stk10	Serine/threonine-protein kinase 10	2.17	2	2	4	0.83
G5E870	Trip12	E3 ubiquitin-protein ligase TRIP12	6.32	11	12	106	0.83
Q8K327	Champ1	Chromosome alignment-maintaining phosphoprotein 1	12.09	7	9	68	0.83
Q60931	Vdac3	Voltage-dependent anion-selective channel protein 3	59.36	11	13	336	0.83

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q6ZQ58	Larp1	La-related protein 1	8.02	8	8	63	0.83
O35841	Api5	Apoptosis inhibitor 5	16.67	9	9	84	0.83
Q8K2Q9	Kiaa1598	Shootin-1	10.78	6	6	31	0.83
P10630	Eif4a2	Eukaryotic initiation factor 4A-II	27.27	4	13	382	0.83
B2RY56	Rbm25	RNA-binding protein 25	26.85	20	20	458	0.83
Q80UM3	Naa15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	6.47	6	7	23	0.83
P52825	Cpt2	Carnitine O-palmitoyltransferase 2, mitochondrial	6.99	5	5	25	0.83
P61979	Hnrnpk	Heterogeneous nuclear ribonucleoprotein K	52.27	24	24	2012	0.83
E9QAZ2	Gm10020	Ribosomal protein L15	51.96	13	13	492	0.83
D3YXK2	Safb	Scaffold attachment factor B1	24.65	14	24	398	0.83
Q80VY9	Dhx33	Putative ATP-dependent RNA helicase DHX33	10.17	7	7	32	0.82
P84096	Rhog	Rho-related GTP-binding protein RhoG	41.88	7	8	260	0.82
Q5MJS3	Fam20c	Extracellular serine/threonine protein kinase FAM20C	3.28	2	2	2	0.82
Q8VDT9	Mrpl50	39S ribosomal protein L50, mitochondrial	22.01	3	3	21	0.82
Q3U0V1	Khsrp	Far upstream element-binding protein 2	47.99	29	33	1468	0.82
Q9CWK3	Cd2bp2	CD2 antigen cytoplasmic tail-binding protein 2	10.23	3	3	12	0.82
Q9Z2X1	Hnrnpf	Heterogeneous nuclear ribonucleoprotein F	51.81	15	18	1478	0.82
Q8VDL4	Adpgk	ADP-dependent glucokinase	18.55	7	7	243	0.82
Q8VDW0	Ddx39a	ATP-dependent RNA helicase DDX39A	29.04	6	15	265	0.82
P43276	Hist1h1b	Histone H1.5	59.64	17	24	2738	0.82
Q91ZN5	Slc35b2	Adenosine 3'-phospho 5'-phosphosulfate transporter 1	8.12	3	3	18	0.82
Q9ERA6	Tfip11	Tuftelin-interacting protein 11	5.97	5	5	20	0.82
Q9WV32	Arpc1b	Actin-related protein 2/3 complex subunit 1B	20.70	6	6	59	0.82
Q9CXW2	Mrps22	28S ribosomal protein S22, mitochondrial	20.61	8	8	139	0.82
Q8JZX4	Rbm17	Splicing factor 45	26.17	10	10	241	0.82
Q8R2Y8	Ptrh2	Peptidyl-tRNA hydrolase 2, mitochondrial	50.28	6	6	34	0.81
Q6P4T2	Snrnp200	U5 small nuclear ribonucleoprotein 200 kDa helicase	27.81	62	62	1490	0.81
Q6PFD9	Nup98	Nuclear pore complex protein Nup98-Nup96	15.69	25	26	568	0.81
Q05186	Rcn1	Reticulocalbin-1	12.92	4	4	19	0.81
Q9DAW6	Prpf4	U4/U6 small nuclear ribonucleoprotein Prp4	19.77	8	9	85	0.81
P43274	Hist1h1e	Histone H1.4	58.45	7	24	3625	0.81
Q9JIH2	Nup50	Nuclear pore complex protein Nup50	36.70	15	15	250	0.81
Q60692	Psmb6	Proteasome subunit beta type-6	13.03	3	3	22	0.81
Q64152	Btf3	Transcription factor BTF3	18.63	4	4	51	0.81
Q9ERU3	Znf22	Zinc finger protein 22	16.46	3	4	44	0.81
Q99JX7	Nxf1	Nuclear RNA export factor 1	16.50	12	12	151	0.81
Q9CYN9	Atp6ap2	Renin receptor	14.86	6	6	67	0.81
O54946	Dnajb6	DnaJ homolog subfamily B member 6	18.36	6	6	90	0.81
Q9CYA6	Zcchc8	Zinc finger CCHC domain-containing protein 8	6.06	4	5	14	0.81
P20152	Vim	Vimentin	88.63	43	50	7602	0.81

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q99MJ9	Ddx50	ATP-dependent RNA helicase DDX50	10.49	8	9	70	0.81
P70245	Ebp	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	9.57	2	2	12	0.81
Q6Y7W8	Gigyf2	PERQ amino acid-rich with GYF domain-containing protein 2	2.63	2	3	11	0.81
Q9CZJ1	Utp11l	Probable U3 small nucleolar RNA-associated protein 11	33.99	8	9	168	0.80
P63242	Eif5a	Eukaryotic translation initiation factor 5A-1	40.26	9	9	208	0.80
Q8R081	Hnrnpl	Heterogeneous nuclear ribonucleoprotein L	55.12	25	25	1463	0.80
O35643	Ap1b1	AP-1 complex subunit beta-1	13.68	4	13	129	0.80
Q9EPU4	Cpsf1	Cleavage and polyadenylation specificity factor subunit 1	10.20	16	16	163	0.80
Q6ZQI3	Mlec	Malectin	28.52	9	9	293	0.80
Q8CGF7	Tcerg1	Transcription elongation regulator 1	11.18	14	14	71	0.80
Q7TQH0	Atxn2l	Ataxin-2-like protein	9.72	10	10	101	0.80
O88844	Idh1	Isocitrate dehydrogenase [NADP] cytoplasmic	15.70	6	7	111	0.80
Q80V86	Ints8	Integrator complex subunit 8	6.23	6	6	30	0.80
Q9DBH5	Lman2	Vesicular integral-membrane protein VIP36	26.54	10	10	414	0.80
Q99J95	Cdk9	Cyclin-dependent kinase 9	9.41	1	4	79	0.79
Q9CY66	Gar1	H/ACA ribonucleoprotein complex subunit 1	19.91	6	6	243	0.79
Q8BW10	Nob1	RNA-binding protein NOB1	11.91	6	6	50	0.79
Q91YT0	Ndufv1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	21.77	11	11	277	0.79
Q91YR7	Prpf6	Pre-mRNA-processing factor 6	23.70	23	23	394	0.79
Q3U7R1	Esyt1	Extended synaptotagmin-1	9.43	10	11	85	0.79
P35550	Fbl	rRNA 2'-O-methyltransferase fibrillarin	61.47	19	19	1077	0.79
P61222	Abce1	ATP-binding cassette sub-family E member 1	14.19	9	9	49	0.79
Q91YT7	Ythdf2	YTH domain-containing family protein 2	16.23	5	10	252	0.79
Q99LI8	Hgs	Hepatocyte growth factor-regulated tyrosine kinase substrate	2.45	2	2	6	0.79
O55234	Psmb5	Proteasome subunit beta type-5	23.86	6	6	43	0.79
E9Q3G8	Nup153	Protein Nup153	23.19	27	27	647	0.79
Q8R3C6	Rbm19	Probable RNA-binding protein 19	20.17	17	17	320	0.79
Q6ZPV2	Ino80	DNA helicase INO80	1.48	2	2	6	0.79
Q9Z1Z2	Strap	Serine-threonine kinase receptor-associated protein	18.00	5	5	32	0.79
Q3V3R1	Mthfd1l	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	33.47	33	33	1061	0.79
Q91X78	Erlin1	Erlin-1	13.29	2	5	177	0.79
Q99LF4	Rtcb	tRNA-splicing ligase RtcB homolog	14.85	7	7	47	0.79
Q8C5L7	Rbm34	RNA-binding protein 34	25.87	9	9	39	0.78
Q9EPE9	Atp13a1	Manganese-transporting ATPase 13A1	13.00	16	16	292	0.78
O88569	Hnrnpa2b1	Heterogeneous nuclear ribonucleoproteins A2/B1	66.86	24	29	4408	0.78
Q8CC88	Vwa8	von Willebrand factor A domain-containing protein 8	3.15	6	6	18	0.78
Q14AX6	Cdk12	Cyclin-dependent kinase 12	1.68	1	3	70	0.78
Q6P9R1	Ddx51	ATP-dependent RNA helicase DDX51	17.21	9	9	82	0.78
P61965	Wdr5	WD repeat-containing protein 5	33.23	8	8	74	0.78
O88342	Wdr1	WD repeat-containing protein 1	10.73	7	7	60	0.78

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
E9Q4Y2	Rsf1	Protein Rsf1	9.23	10	10	101	0.78
Q99KR7	Ppif	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	17.48	4	5	123	0.78
P70333	Hnrnph2	Heterogeneous nuclear ribonucleoprotein H2	41.20	5	17	926	0.78
Q9D880	Timm50	Mitochondrial import inner membrane translocase subunit TIM50	26.06	10	10	165	0.78
Q80U78	Pum1	Pumilio homolog 1	3.87	1	5	89	0.78
Q91YY4	Atpaf2	ATP synthase mitochondrial F1 complex assembly factor 2	7.27	2	2	30	0.78
O35737	Hnrnph1	Heterogeneous nuclear ribonucleoprotein H	50.11	6	19	1205	0.78
Q8BX17	Gemin5	Gem-associated protein 5	2.13	3	3	8	0.78
Q99KJ8	Dctn2	Dynactin subunit 2	6.47	3	3	24	0.78
Q3TEA8	Hp1bp3	Heterochromatin protein 1-binding protein 3	28.34	19	19	716	0.78
Q91ZW3	Smarca5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	35.30	45	46	1424	0.78
Q9JHI5	Ivd	Isovaleryl-CoA dehydrogenase, mitochondrial	22.41	10	10	95	0.78
Q8BGA5	Krr1	KRR1 small subunit processome component homolog	21.05	10	10	171	0.78
Q60862	Orc2	Origin recognition complex subunit 2	8.68	6	6	26	0.78
Q05910	Adam8	Disintegrin and metalloproteinase domain-containing protein 8	9.81	6	7	58	0.77
Q80X82	Sympk	Symplekin	10.59	13	13	164	0.77
P25911	Lyn	Tyrosine-protein kinase Lyn	13.28	5	7	85	0.77
Q8VDS8	Stx18	Syntaxin-18	6.59	2	2	4	0.77
Q8BML9	Qars	Glutaminyl-tRNA synthetase	5.81	4	4	36	0.77
Q99K85	Psat1	Phosphoserine aminotransferase	29.46	11	11	131	0.77
Q9EQ61	Pes1	Pescadillo homolog	24.49	17	17	443	0.77
Q7TPV4	Mybbp1a	Myb-binding protein 1A	45.98	63	63	3289	0.77
Q8BXV2	Bri3bp	BRI3-binding protein	19.37	4	4	281	0.77
P52432	Polr1c	DNA-directed RNA polymerases I and III subunit RPAC1	17.63	5	5	28	0.77
Q8VHE0	Sec63	Translocation protein SEC63 homolog	18.03	12	12	120	0.77
Q8R2N2	Cirh1a	Cirhin	17.64	13	13	300	0.76
Q8CFQ3	Aqr	Intron-binding protein aquarius	6.89	11	12	129	0.76
P70428	Ext2	Exostosin-2	3.48	2	2	12	0.76
Q8K224	Nat10	N-acetyltransferase 10	34.08	32	33	828	0.76
Q01965	Ly9	T-lymphocyte surface antigen Ly-9	3.67	2	2	10	0.76
Q8K0C4	Cyp51a1	Lanosterol 14-alpha demethylase	21.47	10	10	160	0.76
Q9D0N7	Chaf1b	Chromatin assembly factor 1 subunit B	4.55	3	3	21	0.76
Q5RJG1	Nol10	Nucleolar protein 10	11.64	9	9	84	0.76
Q9R190	Mta2	Metastasis-associated protein MTA2	34.73	22	25	607	0.76
Q9CSH3	Dis3	Exosome complex exonuclease RRP44	3.44	2	3	13	0.76
Q9Z2Z6	Slc25a20	Mitochondrial carnitine/acylcarnitine carrier protein	8.31	3	3	16	0.76
Q923G2	Polr2h	DNA-directed RNA polymerases I, II, and III subunit RPABC3	36.67	5	5	60	0.76
P42669	Pura	Transcriptional activator protein Pur-alpha	9.35	2	4	36	0.76
Q9DB96	Ngdn	Neuroguidin	15.56	5	5	73	0.76

Accession	**Gene**	**Description**	**Σcover-age**	**Σ# Unique Peptides**	**Σ# Peptides**	**Σ# PSMs**	**[1]*pksP*/wt**
Q62186	Ssr4	Translocon-associated protein subunit delta	40.12	6	6	265	0.76
O09061	Psmb1	Proteasome subunit beta type-1	32.92	6	6	44	0.76
P97379	G3bp2	Ras GTPase-activating protein-binding protein 2	12.24	5	6	90	0.76
O88286	Wiz	Protein Wiz	4.33	6	6	66	0.76
Q62448	Eif4g2	Eukaryotic translation initiation factor 4 gamma 2	12.14	10	10	174	0.75
Q64521	Gpd2	Glycerol-3-phosphate dehydrogenase, mitochondrial	19.12	14	14	130	0.75
P14733	Lmnb1	Lamin-B1	70.58	43	52	3899	0.75
Q9D6Z1	Nop56	Nucleolar protein 56	54.31	30	30	1786	0.75
Q76KJ5	Cd3eap	DNA-directed RNA polymerase I subunit RPA34	13.78	4	4	18	0.75
Q9Z103	Adnp	Activity-dependent neuroprotector homeobox protein	14.13	10	10	58	0.75
Q9Z1N5	Ddx39b	Spliceosome RNA helicase Ddx39b	30.61	7	16	271	0.75
Q9QXK3	Copg2	Coatomer subunit gamma-2	4.36	3	4	13	0.75
P14069	S100a6	Protein S100-A6	16.85	2	2	4	0.75
O70194	Eif3d	Eukaryotic translation initiation factor 3 subunit D	8.03	4	4	33	0.75
P62855	Rps26	40S ribosomal protein S26	37.39	4	4	186	0.75
Q8VDM6	Hnrnpul1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	27.12	19	20	579	0.75
Q8C7Q4	Rbm4	RNA-binding protein 4	19.67	7	7	50	0.75
Q5SSI6	Utp18	U3 small nucleolar RNA-associated protein 18 homolog	31.16	16	16	363	0.75
Q3UXZ9	Kdm5a	Lysine-specific demethylase 5A	1.12	2	2	6	0.75
P13011	Scd2	Acyl-CoA desaturase 2	10.89	4	4	163	0.75
P52293	Kpna2	Importin subunit alpha-1	28.92	14	15	275	0.74
Q91VR5	Ddx1	ATP-dependent RNA helicase DDX1	16.35	13	13	136	0.74
Q9WVA3	Bub3	Mitotic checkpoint protein BUB3	26.38	8	8	253	0.74
Q9R0P3	Esd	S-formylglutathione hydrolase	15.60	4	4	69	0.74
O35955	Psmb10	Proteasome subunit beta type-10	7.69	2	2	12	0.74
Q9CWU9	Nup37	Nucleoporin Nup37	25.15	8	8	80	0.74
Q9D1I6	Mrpl14	39S ribosomal protein L14, mitochondrial	18.62	2	2	4	0.74
Q8R2U0	Seh1l	Nucleoporin SEH1	16.11	4	4	34	0.74
G3X972	Sec24c	Protein Sec24c	5.66	6	6	69	0.74
Q8BP47	Nars	Asparagine--tRNA ligase, cytoplasmic	10.38	7	7	30	0.74
Q6A026	Pds5a	Sister chromatid cohesion protein PDS5 homolog A	6.61	7	8	45	0.74
P99026	Psmb4	Proteasome subunit beta type-4	12.88	3	3	67	0.74
Q8BSQ9	Pbrm1	Protein polybromo-1	8.94	15	15	109	0.74
Q3TIX6	Fubp3	Protein Fubp3	31.48	17	19	359	0.74
Q91YW3	Dnajc3	DnaJ homolog subfamily C member 3	26.98	15	15	370	0.73
Q9DC16	Ergic1	Endoplasmic reticulum-Golgi intermediate compartment protein 1	24.48	7	7	116	0.73
Q99N85	Mrps18a	28S ribosomal protein S18a, mitochondrial	11.73	2	2	6	0.73
Q6P9R2	Oxsr1	Serine/threonine-protein kinase R1	8.35	4	5	37	0.73
P53986	Slc16a1	Monocarboxylate transporter 1	11.76	4	4	246	0.73
P62827	Ran	GTP-binding nuclear protein Ran	31.02	8	8	580	0.73

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q6PIJ4	Nfrkb	Nuclear factor related to kappa-B-binding protein	4.48	4	4	15	0.73
P49312	Hnrnpa1	Heterogeneous nuclear ribonucleoprotein A1	60.31	15	23	2309	0.73
Q99N94	Mrpl9	39S ribosomal protein L9, mitochondrial	13.21	3	3	22	0.72
Q99104	Myo5a	Unconventional myosin-Va	10.63	18	18	130	0.72
P14152	Mdh1	Malate dehydrogenase, cytoplasmic	19.46	5	6	119	0.72
Q61033	Tmpo	Lamina-associated polypeptide 2, isoforms alpha/zeta	40.69	22	22	781	0.72
Q91YH5	Atl3	Atlastin-3	15.53	8	8	193	0.72
Q6PE01	Snrnp40	U5 small nuclear ribonucleoprotein 40 kDa protein	31.28	10	11	213	0.72
Q9Z2N8	Actl6a	Actin-like protein 6A	27.51	9	9	119	0.72
Q5ND52	Rnmtl1	rRNA methyltransferase 3, mitochondrial	3.11	1	2	2	0.72
Q9R0G7	Zeb2	Zinc finger E-box-binding homeobox 2	7.82	7	7	22	0.72
Q8BJW5	Nol11	Nucleolar protein 11	22.13	18	18	351	0.72
Q99ME9	Gtpbp4	Nucleolar GTP-binding protein 1	33.91	23	23	574	0.72
Q9DCA5	Brix1	Ribosome biogenesis protein BRX1 homolog	15.30	5	5	33	0.72
Q8VI84	Noc3l	Nucleolar complex protein 3 homolog	11.15	10	10	140	0.72
Q9CXY9	Pigk	GPI-anchor transamidase	6.08	3	3	33	0.72
Q8BJZ4	Mrps35	28S ribosomal protein S35, mitochondrial	23.44	6	6	36	0.72
E9Q7G0	Numa1	Protein Numa1	21.49	41	41	485	0.72
P97329	Kif20a	Kinesin-like protein KIF20A	5.98	5	5	25	0.72
Q61191	Hcfc1	Host cell factor 1	10.81	20	20	238	0.71
Q8BYK6	Ythdf3	YTH domain-containing family protein 3	17.26	4	10	263	0.71
O88291	Znf326	DBIRD complex subunit ZNF326	11.21	6	6	98	0.71
P61514	Rpl37a	60S ribosomal protein L37a	52.17	5	5	243	0.71
P08775	Polr2a	DNA-directed RNA polymerase II subunit RPB1	17.66	31	31	447	0.71
P52912	Tia1	Nucleolysin TIA-1	11.92	3	5	230	0.71
Q9CQX2	Cyb5b	Cytochrome b5 type B	54.79	5	5	45	0.71
Q9D287	Bcas2	Pre-mRNA-splicing factor SPF27	17.78	5	5	78	0.71
Q9D8P4	Mrpl17	39S ribosomal protein L17, mitochondrial	23.30	5	5	19	0.71
Q6NZF1	Zc3h11a	Zinc finger CCCH domain-containing protein 11A	14.65	9	9	99	0.71
P50247	Ahcy	Adenosylhomocysteinase	18.52	6	7	80	0.71
Q91WJ8	Fubp1	Far upstream element-binding protein 1	34.25	16	20	1010	0.71
P06745	Gpi	Glucose-6-phosphate isomerase	16.49	9	9	133	0.70
Q9QZV9	Nxt1	NTF2-related export protein 1	10.71	2	2	6	0.70
Q9Z204	Hnrnpc	Heterogeneous nuclear ribonucleoproteins C1/C2	52.72	23	23	1866	0.70
Q8VEH3	Arl8a	ADP-ribosylation factor-like protein 8A	38.71	2	7	262	0.70
Q8BJ71	Nup93	Nuclear pore complex protein Nup93	44.81	36	36	731	0.70
P62315	Snrpd1	Small nuclear ribonucleoprotein Sm D1	36.97	4	4	107	0.70
P47757	Capzb	F-actin-capping protein subunit beta	24.91	6	6	83	0.70
Q8C0I1	Agps	Alkyldihydroxyacetonephosphate synthase, peroxisomal	17.36	11	11	240	0.70
P14206	Rpsa	40S ribosomal protein SA	41.69	9	10	533	0.70

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
P11031	Sub1	Activated RNA polymerase II transcriptional coactivator p15	28.35	5	5	62	0.70
Q9DBS1	Tmem43	Transmembrane protein 43	22.25	7	7	188	0.70
Q8K4B0	Mta1	Metastasis-associated protein MTA1	9.23	4	7	32	0.70
Q9ERU9	Ranbp2	E3 SUMO-protein ligase RanBP2	27.87	86	86	1772	0.70
Q91XD7	Creld1	Cysteine-rich with EGF-like domain protein 1	12.38	5	5	47	0.70
Q8K301	Ddx52	Probable ATP-dependent RNA helicase DDX52	19.57	11	11	114	0.70
P62869	Tceb2	Transcription elongation factor B polypeptide 2	13.56	2	2	6	0.70
O88455	Dhcr7	7-dehydrocholesterol reductase	4.46	2	2	78	0.70
Q9R1S3	Pign	GPI ethanolamine phosphate transferase 1	3.97	3	3	8	0.70
O54825	Bysl	Bystin	25.23	11	11	84	0.69
Q61881	Mcm7	DNA replication licensing factor MCM7	13.63	9	9	47	0.69
Q9DC23	Dnajc10	DnaJ homolog subfamily C member 10	2.02	2	2	6	0.69
Q922P9	Glyr1	Putative oxidoreductase GLYR1	14.10	8	8	131	0.69
Q920Q4	Vps16	Vacuolar protein sorting-associated protein 16 homolog	2.74	2	2	4	0.69
Q9ERE7	Mesdc2	LDLR chaperone MESD	13.39	3	3	27	0.69
Q9CWJ9	Atic	Bifunctional purine biosynthesis protein PURH	21.62	11	11	126	0.69
Q9CWX9	Ddx47	Probable ATP-dependent RNA helicase DDX47	16.26	7	7	120	0.69
O70435	Psma3	Proteasome subunit alpha type-3	16.47	5	5	54	0.69
Q9D1Q4	Dpm3	Dolichol-phosphate mannosyltransferase subunit 3	23.91	2	2	10	0.69
Q8C9B9	Dido1	Death-inducer obliterator 1	5.90	10	10	81	0.69
Q3TDQ1	Stt3b	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	11.54	8	10	146	0.69
Q8R0G9	Nup133	Nuclear pore complex protein Nup133	19.22	22	22	358	0.69
Q9R0A0	Pex14	Peroxisomal membrane protein PEX14	17.82	6	6	90	0.69
Q60848	Hells	Lymphocyte-specific helicase	10.23	7	8	101	0.69
Q7TQ95	Lnp	Protein lunapark	9.65	4	4	36	0.69
Q922B1	Macrod1	O-acetyl-ADP-ribose deacetylase MACROD1	6.50	2	2	4	0.69
Q91YX5	Lpgat1	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1	4.59	2	2	6	0.68
Q8R480	Nup85	Nuclear pore complex protein Nup85	18.29	12	13	157	0.68
Q9JII5	Dazap1	DAZ-associated protein 1	18.23	6	6	219	0.68
Q9WTL7	Lypla2	Acyl-protein thioesterase 2	6.93	2	2	10	0.68
Q6P5E4	Uggt1	UDP-glucose:glycoprotein glucosyltransferase 1	19.02	29	30	497	0.68
Q8BPU7	Elmo1	Engulfment and cell motility protein 1	6.19	5	5	61	0.68
Q61263	Soat1	Sterol O-acyltransferase 1	12.22	7	7	153	0.68
Q91XA2	Golm1	Golgi membrane protein 1	18.58	8	8	53	0.68
P50171	Hsd17b8	Estradiol 17-beta-dehydrogenase 8	17.37	4	4	44	0.67
Q4VA53	Pds5b	Sister chromatid cohesion protein PDS5 homolog B	14.52	17	19	183	0.67
Q9DBR0	Akap8	A-kinase anchor protein 8	15.57	11	11	285	0.67
Q923D5	Wbp11	WW domain-binding protein 11	12.01	8	8	96	0.67
Q9D8V0	Hm13	Minor histocompatibility antigen H13	9.26	4	4	325	0.67
P97386	Lig3	DNA ligase 3	12.81	13	13	104	0.67

Accession	**Gene**	**Description**	**Σcover-age**	**Σ# Unique Peptides**	**Σ# Peptides**	**Σ# PSMs**	**[1]*pksP*/wt**
P97384	Anxa11	Annexin A11	30.42	15	16	446	0.67
Q04899	Cdk18	Cyclin-dependent kinase 18	5.10	2	3	66	0.67
P39689	Cdkn1a	Cyclin-dependent kinase inhibitor 1	13.84	2	2	6	0.67
O70469	Dok2	Docking protein 2	7.52	3	3	18	0.67
Q8R2U2	BC027231	Protein BC027231	7.09	4	4	18	0.66
Q9JJL8	Sars2	Serine--tRNA ligase, mitochondrial	8.49	3	3	8	0.66
Q8R311	Ctage5	cTAGE family member 5	17.84	12	13	85	0.66
Q99L13	Hibadh	3-hydroxyisobutyrate dehydrogenase, mitochondrial	22.99	5	5	138	0.66
Q9D8T7	Slirp	SRA stem-loop-interacting RNA-binding protein, mitochondrial	36.61	4	4	20	0.66
P16110	Lgals3	Galectin-3	43.94	13	13	1797	0.66
P97452	Bop1	Ribosome biogenesis protein BOP1	18.85	12	12	202	0.66
Q8VHZ7	Imp4	U3 small nucleolar ribonucleoprotein protein IMP4	14.78	5	5	106	0.65
Q9JHS9	Cwc15	Spliceosome-associated protein CWC15 homolog	13.10	3	3	42	0.65
Q8R3Y5	2	Uncharacterized protein C19orf47 homolog	16.22	5	5	37	0.65
Q91YM4	Tbrg4	Protein TBRG4	8.89	5	5	65	0.65
Q9CZW4	Acsl3	Long-chain-fatty-acid--CoA ligase 3	15.83	9	11	145	0.65
Q80W54	Zmpste24	CAAX prenyl protease 1 homolog	13.68	7	7	76	0.65
Q571H0	Urb1	Nucleolar pre-ribosomal-associated protein 1	3.78	8	8	70	0.65
P63328	Ppp3ca	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	4.22	2	2	6	0.65
Q8BG15	Ctdspl2	CTD small phosphatase-like protein 2	13.55	7	7	55	0.64
Q9D8T2	Gsdmdc1	Gasdermin-D	13.35	6	7	92	0.64
O35633	Slc32a1	Vesicular inhibitory amino acid transporter	2.86	1	2	2	0.64
Q91Z96	Bmp2k	BMP-2-inducible protein kinase	1.49	2	2	2	0.64
O35495	Cdk14	Cyclin-dependent kinase 14	4.48	1	2	65	0.64
Q8BMQ2	Gtf3c4	General transcription factor 3C polypeptide 4	6.24	5	5	43	0.64
Q9CQE8	2	UPF0568 protein C14orf166 homolog	12.70	3	3	13	0.64
Q8BXA5	Clptm1l	Cleft lip and palate transmembrane protein 1-like protein	4.82	2	2	18	0.64
E9Q7E2	Arid2	Protein Arid2	0.98	2	2	2	0.64
Q9JJI8	Rpl38	60S ribosomal protein L38	32.86	4	4	137	0.64
Q6PAC3	Dcaf13	DDB1- and CUL4-associated factor 13	23.82	10	11	109	0.64
P52927	Hmga2	High mobility group protein HMGI-C	49.07	5	5	327	0.64
Q9ER88	Dap3	28S ribosomal protein S29, mitochondrial	20.97	8	8	54	0.64
Q9CXS4	Cenpv	Centromere protein V	34.13	8	8	83	0.63
Q6P3Y5	Znf280c	Zinc finger protein 280C	5.53	5	5	36	0.63
Q9WUA3	Pfkp	ATP-dependent 6-phosphofructokinase, platelet type	7.40	3	5	31	0.63
E9PZM7	Scaf11	Protein Scaf11	8.31	10	10	97	0.63
P08103	Hck	Tyrosine-protein kinase HCK	10.11	4	6	97	0.63
Q61074	Ppm1g	Protein phosphatase 1G	8.67	5	5	35	0.63
P06795	Abcb1b	Multidrug resistance protein 1B	4.62	6	6	43	0.63
A2A484	Zmynd8	Protein Zmynd8	7.61	8	8	84	0.63

Accession	**Gene**	**Description**	**Σcover-age**	**Σ# Unique Peptides**	**Σ# Peptides**	**Σ# PSMs**	**[1]*pksP*/wt**
P48999	Alox5	Arachidonate 5-lipoxygenase	3.56	3	3	25	0.63
Q8BGS7	Cept1	Choline/ethanolaminephosphotransferase 1	4.81	2	2	24	0.63
Q9JJA4	Wdr12	Ribosome biogenesis protein WDR12	20.57	8	8	135	0.62
P70318	Tial1	Nucleolysin TIAR	21.17	7	9	434	0.62
Q8BRG8	Tmem209	Transmembrane protein 209	10.70	6	6	66	0.62
Q80U62	Kiaa0226	Run domain Beclin-1 interacting and cysteine-rich containing protein	1.26	2	2	2	0.62
P20918	Plg	Plasminogen	2.71	3	3	14	0.62
Q3URQ0	Tex10	Testis-expressed sequence 10 protein	8.73	8	8	53	0.62
P10922	H1f0	Histone H1.0	31.96	7	7	288	0.62
Q8VCG1	Dut	Deoxyuridine triphosphatase, isoform CRA_b	19.50	3	3	30	0.61
O35459	Ech1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	6.73	3	3	10	0.61
Q9Z1Q2	Abhd16a	Abhydrolase domain-containing protein 16A	6.27	3	4	13	0.61
Q9DCD0	Pgd	6-phosphogluconate dehydrogenase, decarboxylating	30.85	15	15	221	0.60
Q3U319	Rnf40	E3 ubiquitin-protein ligase BRE1B	4.50	3	4	26	0.60
Q78WZ7	Twistnb	DNA-directed RNA polymerase I subunit RPA43	5.45	2	2	6	0.60
Q9ESX5	Dkc1	H/ACA ribonucleoprotein complex subunit 4	37.92	19	19	576	0.60
P63154	Crnkl1	Crooked neck-like protein 1	21.88	16	16	184	0.60
Q9D6K5	Synj2bp	Synaptojanin-2-binding protein	21.38	3	3	15	0.59
Q9ESW4	Agk	Acylglycerol kinase, mitochondrial	11.64	4	4	8	0.59
Q99K74	Med24	Mediator of RNA polymerase II transcription subunit 24	4.15	3	3	21	0.59
P61957	Sumo2	Small ubiquitin-related modifier 2	23.16	2	2	11	0.59
O88508	Dnmt3a	DNA (cytosine-5)-methyltransferase 3A	13.33	11	12	103	0.59
Q9Z2G9	Htatip2	Oxidoreductase HTATIP2	19.42	5	5	51	0.59
Q922M5	Cdca7l	Cell division cycle-associated 7-like protein	11.87	5	5	40	0.58
Q922V4	Plrg1	Pleiotropic regulator 1	24.37	10	11	163	0.58
Q9CQR4	Acot13	Acyl-coenzyme A thioesterase 13	20.00	3	3	23	0.58
Q61102	Abcb7	ATP-binding cassette sub-family B member 7, mitochondrial	10.37	8	8	72	0.58
P62858	Rps28	40S ribosomal protein S28	46.38	3	3	165	0.58
Q9Z1Q9	Vars	Valine--tRNA ligase	13.14	14	15	233	0.58
Q8VCY6	Utp6	U3 small nucleolar RNA-associated protein 6 homolog	22.95	16	17	246	0.57
Q9EP97	Senp3	Sentrin-specific protease 3	15.49	6	6	145	0.57
P35601	Rfc1	Replication factor C subunit 1	8.84	8	8	85	0.57
Q61545	Ewsr1	RNA-binding protein EWS	14.35	7	7	412	0.57
Q8K2Z4	Ncapd2	Condensin complex subunit 1	2.23	2	2	6	0.57
Q9D937	2	Uncharacterized protein C11orf98 homolog	42.28	4	5	33	0.57
O35892	Sp100	Nuclear autoantigen Sp-100	12.24	5	6	41	0.57
Q9CR95	Necap1	Adaptin ear-binding coat-associated protein 1	14.91	4	4	14	0.57
P28474	Adh5	Alcohol dehydrogenase class-3	4.01	2	2	4	0.57
D3Z3N4	Hnrnph3	MCG11326, isoform CRA_a	26.88	7	8	209	0.57
P97311	Mcm6	DNA replication licensing factor MCM6	16.44	14	14	116	0.57

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	^{1}*pksP*/wt
Q8K072	Reep4	Receptor expression-enhancing protein 4	6.61	2	2	4	0.56
Q6A028	Swap70	Switch-associated protein 70	4.44	3	3	40	0.56
Q8VBT0	Tmx1	Thioredoxin-related transmembrane protein 1	14.75	7	7	237	0.56
O54864	Suv39h1	Histone-lysine N-methyltransferase SUV39H1	15.78	6	6	49	0.56
Q8CDM1	Atad2	ATPase family AAA domain-containing protein 2	10.67	8	10	67	0.56
Q9DBZ5	Eif3k	Eukaryotic translation initiation factor 3 subunit K	17.89	3	3	10	0.56
Q9R1P4	Psma1	Proteasome subunit alpha type-1	31.18	8	8	103	0.56
Q1HFZ0	Nsun2	tRNA (cytosine(34)-C(5))-methyltransferase	12.02	10	10	58	0.56
P48193	Epb41	Protein 4.1	2.45	2	2	12	0.56
Q9JI13	Utp3	Something about silencing protein 10	24.31	9	9	163	0.55
Q8BYW1	Arhgap25	Rho GTPase-activating protein 25	9.10	5	5	33	0.55
Q91Z49	Fyttd1	UAP56-interacting factor	21.14	8	8	138	0.55
P42128	Foxk1	Forkhead box protein K1	5.01	4	4	15	0.55
Q9WUP7	Uchl5	Ubiquitin carboxyl-terminal hydrolase isozyme L5	5.78	2	2	6	0.55
D3Z6Q9	Bin2	Bridging integrator 2	4.29	2	2	6	0.55
Q8R0F3	Sumf1	Sulfatase-modifying factor 1	8.60	2	2	12	0.55
O88379	Baz1a	Bromodomain adjacent to zinc finger domain protein 1A	14.53	21	21	240	0.55
Q8BX09	Rbbp5	Retinoblastoma-binding protein 5	10.41	6	6	32	0.54
P49718	Mcm5	DNA replication licensing factor MCM5	20.19	15	15	89	0.54
Q6ZPR5	Smpd4	Sphingomyelin phosphodiesterase 4	12.27	9	9	73	0.54
Q6P5F9	Xpo1	Exportin-1	4.39	5	5	34	0.54
Q99LM2	Cdk5rap3	CDK5 regulatory subunit-associated protein 3	16.70	9	9	129	0.54
A2BDX3	Mocs3	Adenylyltransferase and sulfurtransferase MOCS3	3.48	2	2	49	0.54
Q03267	Ikzf1	DNA-binding protein Ikaros	10.64	6	6	72	0.54
Q9JHP7	Kdelc1	KDEL motif-containing protein 1	13.75	6	7	38	0.54
Q9D7B6	Acad8	Isobutyryl-CoA dehydrogenase, mitochondrial	5.81	2	2	2	0.54
Q3THK7	Gmps	GMP synthase [glutamine-hydrolyzing]	9.09	6	6	23	0.54
Q9ET26	Rnf114	E3 ubiquitin-protein ligase RNF114	8.73	2	2	4	0.54
Q9ER38	Tor3a	Torsin-3A	7.53	3	3	18	0.54
Q9CPY3	Cdca5	Sororin	13.64	3	3	9	0.54
Q8VI75	Ipo4	Importin-4	2.59	2	3	10	0.53
Q8VBZ0	Dhrsx	Dehydrogenase/reductase SDR family member on chromosome X homolog	11.04	3	3	8	0.53
Q8VI36	Pxn	Paxillin	9.98	4	5	34	0.53
Q8K284	Gtf3c1	General transcription factor 3C polypeptide 1	4.62	10	10	73	0.53
Q9EPL9	Acox3	Peroxisomal acyl-coenzyme A oxidase 3	13.29	8	8	68	0.53
P21958	Tap1	Antigen peptide transporter 1	6.08	5	5	17	0.53
Q9CY64	Blvra	Biliverdin reductase A	25.08	6	7	90	0.53
Q3U821	Wdr75	Protein Wdr75	17.23	16	16	326	0.53
A2A654	Bptf	Protein Bptf	5.43	14	14	94	0.53
Q91VJ5	Pqbp1	Polyglutamine-binding protein 1	13.31	3	3	10	0.53

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8CCS6	Pabpn1	Polyadenylate-binding protein 2	12.58	4	4	99	0.53
Q8BWG8	Arrb1	Beta-arrestin-1	6.22	3	3	7	0.52
P11157	Rrm2	Ribonucleoside-diphosphate reductase subunit M2	16.15	6	6	40	0.52
E9Q7L1	Urb2	Protein Urb2	2.23	3	4	31	0.52
P63087	Ppp1cc	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	19.81	2	6	65	0.52
Q6PGF5	Bms1	BMS1 homolog, ribosome assembly protein (Yeast)	13.24	16	16	157	0.51
Q69Z99	Znf512	Zinc finger protein 512	10.50	5	5	21	0.50
P62305	Snrpe	Small nuclear ribonucleoprotein E	25.00	2	2	35	0.50
P11928	Oas1a	2'-5'-oligoadenylate synthase 1A	18.53	5	5	77	0.50
Q9D666	Sun1	SUN domain-containing protein 1	12.49	9	9	63	0.49
Q58NB6	Dhrs9	Dehydrogenase/reductase SDR family member 9	9.72	3	3	8	0.49
P04202	Tgfb1	Transforming growth factor beta-1	14.10	4	4	14	0.49
Q5U4D9	Thoc6	THO complex subunit 6 homolog	20.23	7	7	73	0.49
O88544	Cops4	COP9 signalosome complex subunit 4	15.27	6	6	31	0.48
Q8R035	Ict1	Peptidyl-tRNA hydrolase ICT1, mitochondrial	14.08	3	3	24	0.48
Q8CIC2	Nupl2	Nucleoporin-like protein 2	10.71	3	3	21	0.48
Q8K363	Ddx18	ATP-dependent RNA helicase DDX18	26.06	17	17	532	0.48
P03921	Mtnd5	NADH-ubiquinone oxidoreductase chain 5	3.95	2	2	6	0.48
Q6P8I4	Pcnp	PEST proteolytic signal-containing nuclear protein	35.96	5	5	34	0.47
P27046	Man2a1	Alpha-mannosidase 2	3.39	4	4	21	0.47
Q9CZT6	Cmss1	Protein CMSS1	21.74	6	6	56	0.47
Q9CPQ3	Tomm22	Mitochondrial import receptor subunit TOM22 homolog	26.06	2	2	12	0.47
E9Q2I4	Elmsan1	Protein Elmsan1	6.80	6	6	26	0.47
Q8BKT7	Thoc5	THO complex subunit 5 homolog	17.57	13	13	104	0.47
Q9QXE7	Tbl1x	F-box-like/WD repeat-containing protein TBL1X	11.39	1	5	24	0.46
Q3UPL0	Sec31a	Protein transport protein Sec31A	1.79	2	2	4	0.46
O35379	Abcc1	Multidrug resistance-associated protein 1	1.44	2	2	6	0.46
Q9CQN7	Mrpl41	39S ribosomal protein L41, mitochondrial	39.26	5	5	51	0.46
P97310	Mcm2	DNA replication licensing factor MCM2	6.31	5	5	39	0.45
Q91W39	Ncoa5	Nuclear receptor coactivator 5	17.27	10	11	140	0.45
Q99LI7	Cstf3	Cleavage stimulation factor subunit 3	15.76	11	11	204	0.45
Q61624	Znf148	Zinc finger protein 148	2.02	2	2	6	0.45
Q6P069	Sri	Sorcin	20.71	4	4	84	0.45
P17427	Ap2a2	AP-2 complex subunit alpha-2	9.49	6	9	62	0.45
Q8K205	Pop1	Blood vessel epicardial substance	10.91	10	10	69	0.45
Q8CEC6	Ppwd1	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	4.49	3	3	18	0.44
Q80U58	Pum2	Pumilio homolog 2	3.75	1	4	69	0.44
Q8BFQ4	Wdr82	WD repeat-containing protein 82	10.54	5	5	22	0.44
Q921E6	Eed	Polycomb protein EED	12.24	5	5	20	0.44
P63085	Mapk1	Mitogen-activated protein kinase 1	17.32	4	7	84	0.44

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
P97760	Polr2c	DNA-directed RNA polymerase II subunit RPB3	24.36	6	6	62	0.43
Q9D773	Mrpl2	39S ribosomal protein L2, mitochondrial	7.19	2	2	6	0.43
P61161	Actr2	Actin-related protein 2	19.04	8	9	267	0.43
A2A791	Zmym4	Zinc finger MYM-type protein 4	1.55	2	2	12	0.43
P61290	Psme3	Proteasome activator complex subunit 3	12.20	4	4	39	0.43
Q7TPD0	Ints3	Integrator complex subunit 3	7.40	7	7	53	0.42
Q8CG47	Smc4	Structural maintenance of chromosomes protein 4	14.39	20	20	145	0.42
Q9QYR9	Acot2	Acyl-coenzyme A thioesterase 2, mitochondrial	11.92	5	5	12	0.42
P51859	Hdgf	Hepatoma-derived growth factor	8.02	2	2	6	0.42
Q8VE80	Thoc3	THO complex subunit 3	10.83	4	5	17	0.41
Q9R0Q4	Morf4l2	Mortality factor 4-like protein 2	7.29	2	2	6	0.41
Q00899	Yy1	Transcriptional repressor protein YY1	10.63	4	4	10	0.41
Q7TNV0	Dek	Protein DEK	29.21	11	11	98	0.41
Q7TSZ8	Nacc1	Nucleus accumbens-associated protein 1	4.47	2	2	6	0.41
O70378	Emc8	ER membrane protein complex subunit 8	21.74	5	5	194	0.41
Q9QWT9	Kifc1	Kinesin-like protein KIFC1	3.26	2	2	6	0.41
Q99MU3	Adar	Double-stranded RNA-specific adenosine deaminase	7.05	7	7	24	0.40
P62137	Ppp1ca	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	26.97	4	8	58	0.39
Q9CQF9	Pcyox1	Prenylcysteine oxidase	2.57	2	2	2	0.39
O35451	Atf6b	Cyclic AMP-dependent transcription factor ATF-6 beta	2.00	1	2	2	0.39
Q91WQ3	Yars	Tyrosine--tRNA ligase, cytoplasmic	17.23	9	10	52	0.39
Q8BHJ5	Tbl1xr1	F-box-like/WD repeat-containing protein TBL1XR1	11.28	1	5	21	0.39
Q9JIF0	Prmt1	Protein arginine N-methyltransferase 1	13.21	5	5	37	0.39
Q9CZ91	Srfbp1	Serum response factor-binding protein 1	12.70	4	4	29	0.39
O70145	Ncf2	Neutrophil cytosol factor 2	19.05	9	10	38	0.39
Q64324	Stxbp2	Syntaxin-binding protein 2	9.78	5	5	10	0.38
Q9JHU9	Isyna1	Inositol-3-phosphate synthase 1	2.87	2	2	12	0.38
Q9EQ20	Aldh6a1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	3.74	2	2	6	0.38
Q3TAA7	Stk11ip	Serine/threonine-protein kinase 11-interacting protein	1.96	2	2	2	0.37
Q99L45	Eif2s2	Eukaryotic translation initiation factor 2 subunit 2	21.45	6	6	27	0.37
E9PYH6	Setd1a	Protein Setd1a	1.63	3	3	12	0.37
Q9DCA2	Mrps11	28S ribosomal protein S11, mitochondrial	14.14	2	2	12	0.37
A2AMD0	Gm12666	Protein Gm12666 (Fragment)	20.08	2	4	28	0.36
Q6P5D8	Smchd1	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	6.98	14	14	101	0.36
Q9DBL7	Coasy	Bifunctional coenzyme A synthase	3.55	2	2	6	0.36
Q9R1J0	Nsdhl	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	20.44	7	7	93	0.36
Q3UKJ7	Smu1	WD40 repeat-containing protein SMU1	17.54	8	8	185	0.36
Q8BY71	Hat1	Histone acetyltransferase type B catalytic subunit	9.38	3	3	15	0.36
Q9ER72	Cars	Cysteine--tRNA ligase, cytoplasmic	5.05	4	4	19	0.36

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q8BL74	Gtf3c2	General transcription factor 3C polypeptide 2	5.18	4	5	35	0.35
Q9D1C8	Vps28	Vacuolar protein sorting-associated protein 28 homolog	13.57	3	3	8	0.35
Q8BU11	Tox4	TOX high mobility group box family member 4	7.27	4	4	35	0.35
Q9Z1B5	Mad2l1	Mitotic spindle assembly checkpoint protein MAD2A	19.51	5	5	43	0.34
B1AZI6	Thoc2	THO complex subunit 2	8.91	14	15	264	0.34
A2AIV2	Kiaa1429	Protein virilizer homolog	2.21	3	3	18	0.34
Q9WUU9	Mcm3ap	Germinal-center associated nuclear protein	2.44	4	4	36	0.34
Q05CL8	Larp7	La-related protein 7	15.26	5	7	44	0.34
P28352	Apex1	DNA-(apurinic or apyrimidinic site) lyase	22.08	6	6	57	0.34
Q6NZL1	Dhx37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	16.17	19	20	137	0.33
Q8CD15	Mina	Bifunctional lysine-specific demethylase and histidyl-hydroxylase MINA	4.73	2	2	4	0.33
V9GXJ1	Gm28036	Protein Gm28036	5.02	3	3	16	0.33
P05531	Xlr	X-linked lymphocyte-regulated protein PM1	14.90	3	3	8	0.33
Q6ZQ88	Kdm1a	Lysine-specific histone demethylase 1A	4.10	4	4	31	0.32
P37913	Lig1	DNA ligase 1	8.84	7	7	20	0.32
Q9CR16	Ppid	Peptidyl-prolyl cis-trans isomerase D	14.32	6	7	97	0.32
Q9Z0F8	Adam17	Disintegrin and metalloproteinase domain-containing protein 17	14.15	11	11	56	0.32
Q6ZQH8	Nup188	Nucleoporin NUP188 homolog	10.40	15	15	101	0.32
O70279	Dgcr14	Protein DGCR14	5.85	3	3	14	0.32
Q9JK30	Orc3	Origin recognition complex subunit 3	5.59	4	4	22	0.32
Q8BK35	Gltscr2	MCG2065, isoform CRA_c	13.43	5	5	57	0.32
Q61510	Trim25	E3 ubiquitin/ISG15 ligase TRIM25	6.78	3	3	29	0.31
Q5DW34	Ehmt1	Histone-lysine N-methyltransferase EHMT1	4.17	4	4	33	0.31
Q68FL6	Mars	Methionine--tRNA ligase, cytoplasmic	6.54	6	6	23	0.31
Q8BZR9	2	Uncharacterized protein C17orf85 homolog	3.74	2	2	6	0.31
P59017	Bcl2l13	Bcl-2-like protein 13	5.07	2	2	4	0.30
Q922D8	Mthfd1	C-1-tetrahydrofolate synthase, cytoplasmic	14.76	14	14	91	0.29
P62141	Ppp1cb	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	28.75	4	8	90	0.29
Q63844	Mapk3	Mitogen-activated protein kinase 3	11.84	2	5	57	0.29
Q62523	Zyx	Zyxin	9.93	5	5	36	0.29
Q6NXI6	Rprd2	Regulation of nuclear pre-mRNA domain-containing protein 2	11.50	13	13	159	0.28
Q9CS42	Prps2	Ribose-phosphate pyrophosphokinase 2	10.06	3	3	14	0.28
Q99LB2	Dhrs4	Dehydrogenase/reductase SDR family member 4	11.47	4	4	20	0.28
Q7TN29	Smap2	Stromal membrane-associated protein 2	3.50	2	2	6	0.28
Q61188	Ezh2	Histone-lysine N-methyltransferase EZH2	1.61	2	2	2	0.26
P09602	Hmgn2	Non-histone chromosomal protein HMG-17	44.44	5	5	44	0.26
S4R1W5	Rbm6	Protein Rbm6	7.60	7	9	42	0.26
Q62504	Spen	Msx2-interacting protein	1.18	4	4	10	0.25
Q8K114	Ints9	Integrator complex subunit 9	2.58	2	2	4	0.25
Q99KX1	Mlf2	Myeloid leukemia factor 2	8.50	2	2	6	0.25

Accession	Gene	Description	Σcoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q61024	Asns	Asparagine synthetase [glutamine-hydrolyzing]	3.39	2	2	4	0.25
P70700	Polr1b	DNA-directed RNA polymerase I subunit RPA2	7.67	8	9	72	0.25
Q3UJD6	Usp19	Ubiquitin carboxyl-terminal hydrolase 19	1.10	2	2	2	0.25
Q8BZH4	Pogz	Pogo transposable element with ZNF domain	6.46	8	8	41	0.25
Q9QZM0	Ubqln2	Ubiquilin-2	3.61	1	2	15	0.24
Q91V61	Sfxn3	Sideroflexin-3	15.89	3	4	24	0.24
Q8C0C7	Farsa	Phenylalanine--tRNA ligase alpha subunit	3.35	2	2	6	0.24
Q8BG81	Poldip3	Polymerase delta-interacting protein 3	18.33	7	7	46	0.23
P17665	Cox7c	Cytochrome c oxidase subunit 7C, mitochondrial	28.57	2	2	4	0.23
O70318	Epb41l2	Band 4.1-like protein 2	5.16	4	5	20	0.23
Q62311	Taf6	Transcription initiation factor TFIID subunit 6	2.95	2	2	6	0.23
P58404	Strn4	Striatin-4	2.63	2	2	4	0.22
E9QAP7	Taf4a	Protein Taf4a	1.92	2	2	2	0.21
Q3THS6	Mat2a	S-adenosylmethionine synthase isoform type-2	9.87	4	4	8	0.20
Q8VBV3	Exosc2	Exosome complex component RRP4	16.38	4	5	45	0.20
A2AUY4	Baz2b	Protein Baz2b	1.04	2	2	6	0.20
Q8C3J5	Dock2	Dedicator of cytokinesis protein 2	7.60	13	13	144	0.19
O09159	Man2b1	Lysosomal alpha-mannosidase	2.57	3	3	15	0.19
Q8BMJ2	Lars	Leucine--tRNA ligase, cytoplasmic	7.13	8	8	37	0.19
Q9WUK2	Eif4h	Eukaryotic translation initiation factor 4H	5.24	2	2	5	0.19
Q9JMG1	Edf1	Endothelial differentiation-related factor 1	13.51	2	2	4	0.18
O08553	Dpysl2	Dihydropyrimidinase-related protein 2	6.29	3	3	15	0.18
Q9DCE5	Pak1ip1	p21-activated protein kinase-interacting protein 1	20.94	7	7	66	0.18
Q9QXK2	Rad18	E3 ubiquitin-protein ligase RAD18	4.91	2	2	6	0.18
Q9CWX2	Ndufaf1	Complex I intermediate-associated protein 30, mitochondrial	4.88	2	2	6	0.17
F7BJB9	Morc3	Protein Morc3	2.23	2	2	4	0.16
Q810D6	Grwd1	Glutamate-rich WD repeat-containing protein 1	8.07	3	4	20	0.16
Q99LC2	Cstf1	Cleavage stimulation factor subunit 1	18.33	7	7	57	0.15
Q8BL66	Eea1	Early endosome antigen 1	1.13	2	2	3	0.15
P56546	Ctbp2	C-terminal-binding protein 2	11.46	3	5	42	0.15
P59328	Wdhd1	WD repeat and HMG-box DNA-binding protein 1	1.34	2	2	4	0.13
Q3V300	Kif22	Kinesin-like protein KIF22	3.03	2	2	2	0.12
Q3UFM5	Nom1	Nucleolar MIF4G domain-containing protein 1	5.74	3	3	7	0.12
Q99KQ4	Nampt	Nicotinamide phosphoribosyltransferase	3.05	2	2	4	0.12
O88712	Ctbp1	C-terminal-binding protein 1	6.58	2	4	20	0.12
Q9D4V7	Rabl3	Rab-like protein 3	9.32	2	2	4	0.11
Q9Z1A1	Tfg	Protein Tfg	4.03	2	2	15	0.10
Q921F4	Hnrnpll	Heterogeneous nuclear ribonucleoprotein L-like	3.21	2	2	6	0.09
P97449	Anpep	Aminopeptidase N	9.42	8	8	86	0.09
Q61216	Mre11a	Double-strand break repair protein MRE11A	3.12	2	2	6	0.09

Accession	Gene	Description	Σcover-age	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Q91V92	Acly	ATP-citrate synthase	3.94	4	4	20	0.08
Q9QWF0	Chaf1a	Chromatin assembly factor 1 subunit A	3.84	4	4	10	0.08
Q6ZQE4	Nemp1	Nuclear envelope integral membrane protein 1	5.49	3	3	9	0.08
O35864	Cops5	COP9 signalosome complex subunit 5	7.78	3	3	18	0.07
Q8R3L8	Cdk8	Cyclin-dependent kinase 8	3.23	2	2	2	0.07
Q78Y63	Pdcl2	Phosducin-like protein 2	7.92	1	2	2	0.07
E9Q6J5	Bod1l	Protein Bod1l	4.55	10	10	42	0.06
Q80WC1	Ubn2	Ubinuclein-2	1.22	2	2	6	0.05
P12367	Prkar2a	cAMP-dependent protein kinase type II-alpha regulatory subunit	4.24	2	2	4	0.05
Q8C7K6	Pcyox1l	Prenylcysteine oxidase-like	3.23	2	2	4	0.04
Q64735	Cr1l	Complement component receptor 1-like protein	6.00	3	3	6	0.04
P62309	Snrpg	Small nuclear ribonucleoprotein G	18.42	2	2	2	0.01
F8VQC1	Srp72	Signal recognition particle subunit SRP72	15.05	9	10	66	0.01
Q3UXZ6	Fam81a	Protein FAM81A	5.49	2	2	4	0.00
Q6PG16	Hjurp	Holliday junction recognition protein	3.60	2	2	4	0.00
Q80X32	N/A	UPF0461 protein C5orf24 homolog	13.30	2	2	6	0.00
Q9R1T2	Sae1	SUMO-activating enzyme subunit 1	5.43	2	2	2	0.00
O88942	Nfatc1	Nuclear factor of activated T-cells, cytoplasmic 1	2.23	2	2	4	0.00
P33611	Pola2	DNA polymerase alpha subunit B	4.00	2	2	2	0.00
Q80US4	Actr5	Actin-related protein 5	3.31	2	2	4	0.00
Q8VCC6	Ccm2l	Cerebral cavernous malformations 2 protein-like	3.74	2	2	2	0.00
P33175	Kif5a	Kinesin heavy chain isoform 5A	3.02	1	3	7	0.00
Q8BR65	Suds3	Sin3 histone deacetylase corepressor complex component SDS3	5.18	2	2	2	0.00
E9Q8I7	Nfxl1	Protein Nfxl1	2.40	2	2	2	0.00
B1AZA5	Tmem245	Transmembrane protein 245	2.28	2	2	2	0.00
Q9CR11	Yeats4	YEATS domain-containing protein 4	9.69	2	2	6	0.00
P56477	Irf5	Interferon regulatory factor 5	4.43	2	2	4	0.00
Q9JHR7	Ide	Insulin-degrading enzyme	1.86	2	2	6	0.00
A2AL36	Cntrl	Centriolin	1.03	2	2	2	0.00
Q8CIH5	Plcg2	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	1.11	2	2	4	0.00
Q9D1E6	Tbcb	Tubulin-folding cofactor B	7.79	2	2	6	0.00
Q64514	Tpp2	Tripeptidyl-peptidase 2	2.54	3	3	5	0.00
Q5DTT3	Fam208b	Protein FAM208B	0.55	2	2	2	0.00
Q8BJF9	Chmp2b	Charged multivesicular body protein 2b	9.39	2	2	4	0.00
P58137	Acot8	Acyl-coenzyme A thioesterase 8	6.25	1	2	2	0.00
Q9JMH6	Txnrd1	Thioredoxin reductase 1, cytoplasmic	3.43	2	2	6	0.00

Table S3*: A. fumigatus* proteins detected in the label-free LC-MS/MS measurement of purified conidia-containing phagolysosomes. Proteins with a pksP/wt ratio > 2 were considered as enriched on pksP mutant conidia (green) and proteins with pksP/wt < 0.5 were considered as enriched on wild-type conidia-containing phagolysosomes (red). N.a. – not available, protein values only detected in one condition.

Accession	Description	ΣCoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Afu5g03020	Uncharacterized ORF; 60S ribosomal protein L4	5,09	2	2	2	n.a.
Afu1g12070	Uncharacterized ORF; Ortholog(s) have glycine dehydrogenase (decarboxylating) activity, role in glycine catabolic process, one-carbon metabolic process, protein lipoylation and mitochondrion localization	31,43	4	4	81	33,56
Afu2g10750	Uncharacterized ORF; Putative RNA helicase; transcript induced by exposure to human airway epithelial cells	5,46	2	3	45	6,96
Afu5g09230	Verified ORF; Putative transaldolase; abundant protein in conidia and mycelia; protein induced by hydrogen peroxide and hypoxia	5,56	2	2	2	4,54
Afu4g08040	Uncharacterized ORF; Ortholog(s) have GTP binding activity	10,09	2	2	95	2,59
Afu2g00720	Uncharacterized ORF; Putative aldehyde dehydrogenase (NAD+)	3,05	1	2	21	2,26
Afu1g11730	Uncharacterized ORF; Ortholog(s) have GTPase activity, role in ER to Golgi vesicle-mediated transport, Golgi to plasma membrane transport, cellular response to drug, macroautophagy and Golgi apparatus, glyoxysome localization	17,49	2	2	50	2,19
Afu6g11430	Verified ORF; Putative aldehyde dehydrogenase; predicted gene pair with AFUA_7G01000; hypoxia repressed protein; transcript up-regulated in conidia exposed to neutrophils; immunoreactive protein	2,86	1	2	44	2,17
Afu2g13530	Verified ORF; Putative translation elongation factor EF-2 subunit; protein abundant in conidia; protein induced by heat shock	11,68	10	10	46	2,00
Afu3g08660	Uncharacterized ORF; Putative isocitrate dehydrogenase; protein induced by heat shock	3,79	2	2	20	1,80
Afu6g12930	Verified ORF; Mitochondrial aconitate hydratase; citric acid cycle enzyme; protein abundant in conidia; transcript induced in conidia exposed to neutrophils; reacts with rabbit immunosera exposed to A. fumigatus conidia; hypoxia induced	2,03	2	2	2	1,51
Afu1g02190	Uncharacterized ORF; Ras GTPase; hypoxia repressed protein	19,05	4	4	219	1,49
Afu2g15570	Uncharacterized ORF; Ortholog(s) have GTP binding activity, role in cellular response to osmotic stress, hyphal growth, intracellular protein transport, retrograde transport, endosome to Golgi and Golgi membrane, cytosol, nucleus, spitzenkorper localization	14,01	2	3	139	1,44
Afu6g07540	Uncharacterized ORF; Ortholog(s) have chaperonin-containing T-complex localization	4,01	2	2	2	1,43
Afu1g13780	Uncharacterized ORF; Has domain(s) with predicted DNA binding, protein heterodimerization activity, role in DNA-dependent transcription, initiation, nucleosome assembly and nucleosome, nucleus localization	33,01	5	5	2454	1,40
Afu5g12130	Uncharacterized ORF; Rab small monomeric GTPase	30,41	6	6	279	1,39
Afu4g07660	Uncharacterized ORF; ATP-dependent RNA helicase	6,38	3	4	196	1,38
Afu1g07440	Verified ORF; Molecular chaperone; conidia-enriched protein	21,47	14	15	593	1,35
Afu2g04620	Uncharacterized ORF; Hsp70 chaperone; protein enriched in dormant conidia	7,74	4	5	654	1,32
Afu5g04170	Verified ORF; Heat shock protein; allergen Asp f 12; likely essential; required for conidiation and cell wall integrity; transcript induced by growth on hydrogen peroxide; enters the nucleus in	9,77	7	7	425	1,30

Accession	Description	ΣCoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
	response to heat shock					
Afu2g03030	Verified ORF; Putative pre-mRNA splicing factor; intein-containing protein, inteins are protein intervening sequences that can self-excise through protein splicing	2,37	8	8	130	1,29
Afu2g10440	Uncharacterized ORF; Ortholog(s) have mRNA binding, small ribosomal subunit rRNA binding activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly	16,00	2	2	10	1,28
Afu3g07820	Uncharacterized ORF; Ortholog(s) have role in positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, positive regulation of protein catabolic process and proteasome regulatory particle assembly,	5,01	2	2	2	1,25
Afu5g04320	Uncharacterized ORF; Ortholog(s) have GTPase activity and role in ER to Golgi vesicle-mediated transport, Golgi organization, cellular response to drug, cellular response to nitrogen starvation, negative regulation of G0 to G1 transition, protein secretion	39,80	6	7	347	1,24
Afu5g10550	Uncharacterized ORF; ATP synthase F1, beta subunit; reacts with rabbit immunosera exposed to A. fumigatus conidia; hypoxia induced protein	17,53	8	8	258	1,24
Afu1g05630	Uncharacterized ORF; 40S ribosomal protein S3	31,58	8	8	114	1,23
Afu6g13250	Uncharacterized ORF; 60S ribosomal protein L31e; transcript induced by exposure to human airway epithelial cells	13,82	2	2	14	1,18
Afu2g09210	Uncharacterized ORF; 60S ribosomal protein L10; reacts with rabbit immunosera exposed to A. fumigatus conidia	16,59	4	4	28	1,18
Afu4g10350	Uncharacterized ORF; Polyubiquitin; calcium induced	39,49	4	4	1456	1,17
Afu1g15020	Uncharacterized ORF; 40S ribosomal protein S5; reacts with rabbit immunosera exposed to A. fumigatus conidia	20,93	6	6	175	1,03
Afu5g07050	Uncharacterized ORF; Proteasome regulatory particle subunit; transcript induced by exposure to human airway epithelial cells	5,18	2	2	2	0,98
Afu1g03920	Uncharacterized ORF; Ortholog(s) have role in negative regulation of helicase activity and MCM complex, cytosol, nucleus localization	2,02	2	2	2	0,96
Afu1g10910	Uncharacterized ORF; Beta-tubulin; predicted gene pair with AFUA_7G00250 (tubulin beta-2 subunit); protein induced by hydrogen peroxide	5,36	2	2	73	0,96
Afu3g05350	Uncharacterized ORF; Histone H2B	22,86	5	5	1933	0,95
Afu1g10130	Uncharacterized ORF; Putative adenosylhomocysteinase; protein induced by heat shock	4,48	2	2	8	0,92
Afu1g03390	Uncharacterized ORF; Putative 60S ribosomal protein L12	20,00	3	3	17	0,91
Afu1g02550	Uncharacterized ORF; Tubulin alpha-1 subunit; gene pair with AFUA_2G14990 (tubulin alpha-2 subunit	4,69	3	3	11	0,91
Afu6g12990	Uncharacterized ORF; Putative cytosolic large ribosomal subunit protein L7A	9,89	3	3	6	0,90
Afu6g04740	Verified ORF; Actin	24,43	10	10	1283	0,89
Afu1g12170	Uncharacterized ORF; Putative translation elongation factor EF-Tu; hypoxia induced protein	4,09	2	2	4	0,85
Afu2g10500	Uncharacterized ORF; 40S ribosomal protein Rps16	11,19	2	2	4	0,84
Afu3g06970	Uncharacterized ORF; 40S ribosomal protein S9; transcript induced by exposure to human airway epithelial cells	8,81	2	2	4	0,78
Afu6g13300	Uncharacterized ORF; GTP-Binding nuclear protein Ran	23,26	6	6	451	0,77
Afu2g09290	Verified ORF; Putative antigenic mitochondrial protein; reacts with rabbit immunosera exposed to	3,07	3	3	22	0,77

Accession	Description	ΣCoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
	A. fumigatus conidia; hypoxia induced protein					
Afu3g11390	Uncharacterized ORF; Ortholog(s) have role in positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, proteasome regulatory particle assembly, ubiquitin-dependent protein catabolic process	5,38	2	2	31	0,76
Afu5g11620	Uncharacterized ORF; Ortholog(s) have ATP-dependent RNA helicase activity	2,48	3	3	21	0,66
Afu6g07980	Uncharacterized ORF; Ortholog(s) have RNA polymerase II core binding, cyclin-dependent protein serine/threonine kinase activity, histone binding activity	5,88	2	2	11	0,62
Afu7g05290	Uncharacterized ORF; Cytosolic small ribosomal subunit S13/S15; transcript repressed by exposure to human airway epithelial cells	12,58	2	2	2	0,60
Afu8g05320	Verified ORF; Putative mitochondrial F1 ATPase subunit alpha; hypoxia induced protein	19,42	10	10	170	0,59
Afu1g06220	Uncharacterized ORF; Ortholog(s) have cytosol, nucleus localization	8,47	4	4	38	0,58
Afu1g06390	Verified ORF; Putative translation elongation factor EF-1 alpha subunit; protein abundant in conidia; protein induced by heat shock	24,90	10	10	118	0,52
Afu1g13790	Uncharacterized ORF; Histone H3	37,50	8	8	240	0,52
Afu6g03890	Verified ORF; Spore-specific catalase; abundant protein in conidia; calcium downregulated; predicted secretory signal sequence	12,80	8	8	30	0,48
Afu1g13900	Uncharacterized ORF; Ortholog(s) have DNA-directed RNA polymerase activity, role in mRNA export from nucleus, nucleolus organization, protein localization to nucleolar rDNA repeats and DNA-directed RNA polymerase I complex, cytosol localization	0,89	1	2	4	0,47
Afu1g14680	Uncharacterized ORF; Ortholog(s) have DNA binding activity and cytosol, nucleus localization	1,49	2	3	5	0,47
Afu3g05360	Uncharacterized ORF; Has domain(s) with predicted DNA binding, protein heterodimerization activity, role in nucleosome assembly and nucleosome, nucleus localization	8,68	4	4	89	0,41
Afu1g06280	Uncharacterized ORF; Ortholog(s) have endoplasmic reticulum localization	3,29	2	2	2	0,40
Afu2g09090	Uncharacterized ORF; Ortholog(s) have role in mitochondrion inheritance, negative regulation of proteolysis, protein folding, replicative cell aging and mitochondrial inner membrane, plasma membrane localization	6,43	2	2	35	0,36
Afu2g13780	Uncharacterized ORF; Ortholog(s) have role in mRNA cis splicing, via spliceosome and U2 snRNP localization	2,42	3	3	23	0,35
Afu6g06750	Uncharacterized ORF; 14-3-3 family protein; predicted gene pair with AFUA_2G03290 (artA	9,56	3	3	4	0,29
Afu5g01970	Verified ORF; Glyceraldehyde-3-phosphate dehydrogenase; predicted gene pair with AFUA_5G01030; protein induced by hydrogen peroxide; reacts with rabbit immunosera exposed to A. fumigatus conidia: induced by L-tyrosine	11,83	4	4	16	0,27
Afu2g11510	Uncharacterized ORF; Ortholog(s) have role in cellular response to drug, rRNA processing, ribosomal large subunit biogenesis, ribosomal subunit export from nucleus and nucleolus, preribosome, large subunit precursor, spindle localization	3,85	2	2	62	0,25
Afu5g02410	Uncharacterized ORF; Putative DEAD/DEAH box helicase; predicted gene pair with AFUA_3G08160 (eukaryotic translation initiation factor eIF4A; ATP-dependent RNA helicase, tifA	5,54	4	4	31	0,18
Afu1g11710	Uncharacterized ORF; Ribosomal protein L1	5,99	2	2	12	0,15
Afu1g13670	Uncharacterized ORF; Protein of unkwown function; abundant in conidia	10,21	2	2	6	0,15
Afu1g04950	Uncharacterized ORF; Ortholog(s) have protein serine/threonine phosphatase activity	5,88	2	2	10	0,09
Afu1g11130	Uncharacterized ORF; 60S ribosomal protein L6	10,00	2	2	4	0,00

Accession	Description	ΣCoverage	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	[1]*pksP*/wt
Afu7g05260	Uncharacterized ORF; Has domain(s) with predicted nucleic acid binding, nucleotide binding activity	6,25	2	2	2	0,00
Afu3g09030	Uncharacterized ORF; Ortholog(s) have role in aerobic respiration, penicillin biosynthetic process and mitochondrial matrix localization	8,06	2	2	9	0,00
Afu5g11320	Verified ORF; Allergen Asp f 29; putative thioredoxin	22,73	2	2	2	0,00
Afu6g05200	Uncharacterized ORF; 60S ribosomal protein L28	11,46	2	2	5	0,00
Afu5g13100	Uncharacterized ORF	17,19	2	2	2	0,00
Afu3g10920	Uncharacterized ORF; Telomere and ribosome associated protein	13,82	4	4	26	0,00
Afu6g07520	Uncharacterized ORF; Putative cell wall integrity signaling protein	6,38	2	2	10	0,00
Afu4g10800	Uncharacterized ORF; 40S ribosomal protein S6	3,80	2	2	2	0,00
Afu1g17370	Uncharacterized ORF; Putative heat shock protein; enriched in dormant conidia	32,58	2	2	11	0,00
Afu7g05660	Uncharacterized ORF; Putative translation elongation factor eEF-3; protein induced by heat shock and hypoxia	2,91	3	3	4	0,00
Afu5g14210	Uncharacterized ORF; Glucose-repressible gene; transcript up-regulated in conidia exposed to neutrophils	56,52	3	3	22	0,00

Table S4: Murine proteins detected in the TMT label-based LC-MS/MS measurement of purified conidia-containing phagolysosomes. [1]Proteins with a *pksP*/wt ratio ≥ 1.5 were considered as enriched on *pksP* mutant conidia (green) and proteins with a *pksP*/wt ≤ 0.67 were considered as enriched on wild-type conidia-containing phagolysosomes (red). [2]Calculated ratios that are based on less than 2 reporter ions (average) are untrustworthy and consequently not considered as differentially regulated. [3] An average variability ≤ 30 % was considered as high confident data (dark colour). Medium confidence data was defined in the range of 30-50 % (light colour)

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
O88342	Wdr1	WD repeat-containing protein 1	11.39	6	6	17	5.01	6.09	2	885.1
D3Z4U0	Zranb2	Zinc finger Ran-binding domain-containing protein 2	8.44	3	3	15	2.62	3.18	2	1.3
P46467	Vps4b	Vacuolar protein sorting-associated protein 4B	17.79	7	7	17	2.52	3.06	2	57.6
Q3TMP1	Gtf3c3	General transcription factor IIIC, polypeptide 3	3.17	3	3	5	2.12	2.58	1	
P06795	Abcb1b	Multidrug resistance protein 1B	8.31	12	10	61	2.09	2.54	1	
Q9D0M0	Exosc7	Exosome complex exonuclease RRP42	10.31	3	3	17	2.08	2.52	2	60.5
Q9EST5	Anp32b	Acidic leucine-rich nuclear phosphoprotein 32 family member B	11.40	5	5	25	1.92	2.33	6	16.3
Q9WVD4	Clcn5	H(+)/Cl(-) exchange transporter 5	2.14	2	2	4	1.81	2.19	1	
Q99K01-3	Pdxdc1	Isoform 3 of Pyridoxal-dependent decarboxylase domain-containing protein 1	3.80	3	3	14	1.74	2.11	2	0.4
Q9JIS8	Slc12a4	Solute carrier family 12 member 4	5.44	7	7	32	1.71	2.07	2	80.8
Q6P9J9	Ano6	Anoctamin-6	4.83	4	4	6	1.70	2.06	1	
Q5SSZ5	Tns3	Tensin-3	1.39	2	2	6	1.66	2.02	1	
Q8K072	Reep4	Receptor expression-enhancing protein 4	11.28	2	2	21	1.63	1.98	4	63.8
Q8VEB4	Pla2g15	Group XV phospholipase A2	6.31	2	2	4	1.61	1.95	2	17.5
Q99LE6	Abcf2	ATP-binding cassette sub-family F member 2	5.10	3	3	9	1.57	1.91	2	54.6
P11370	Fv4	Retrovirus-related Env polyprotein from Fv-4 locus	6.48	5	2	162	1.57	1.90	4	7.1
Q62093	Srsf2	Serine/arginine-rich splicing factor 2	13.57	4	4	67	1.56	1.89	14	13.4
P31938	Map2k1	Dual specificity mitogen-activated protein kinase kinase 1	14.25	6	6	26	1.54	1.88	7	15.5
A2BE93	Set	Protein SET (Fragment)	35.35	6	6	64	1.54	1.87	14	29.3
D3YVV1	Tmem30a	Cell cycle control protein 50A	5.49	2	2	4	1.52	1.85	2	39.5
Q9CPQ1	Cox6c	Cytochrome c oxidase subunit 6C	28.95	3	3	79	1.49	1.81	17	27.2
Q9CQD1	Rab5a	Ras-related protein Rab-5A	24.65	4	2	77	1.48	1.80	3	24.7
P13011	Scd2	Acyl-CoA desaturase 2	3.91	2	2	8	1.48	1.79	4	6.8
P35951	Ldlr	Low-density lipoprotein receptor	3.60	3	3	11	1.47	1.78	2	19.6
Q5SRI3	Dock2	Dedicator of cytokinesis protein 2	3.23	4	4	12	1.46	1.77	2	53.6
Q91VT4	Cbr4	Carbonyl reductase family member 4	10.17	2	2	18	1.46	1.77	1	
Q9EQ32-2	Pik3ap1	Isoform 2 of Phosphoinositide 3-kinase adapter	3.96	2	2	6	1.45	1.77	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		protein 1								
Q8BMS7	Atp2c1	Calcium-transporting ATPase	2.69	2	2	3	1.45	1.76	1	
O08915	Aip	AH receptor-interacting protein	8.48	2	2	4	1.43	1.74	1	
Q9D6T0-2	Nosip	Isoform 2 of Nitric oxide synthase-interacting protein	6.88	2	2	4	1.43	1.74	2	70.2
Q9Z1Z2	Strap	Serine-threonine kinase receptor-associated protein	8.86	3	3	6	1.43	1.74	2	17.0
Q3TWW8	Srsf6	Serine/arginine-rich splicing factor 6	17.40	7	6	84	1.43	1.74	13	15.2
P61750	Arf4	ADP-ribosylation factor 4	40.56	6	2	54	1.42	1.73	10	39.8
O70281	Tpst1	Protein-tyrosine sulfotransferase 1	7.03	2	2	6	1.41	1.72	2	100.8
Q8BI84-3	Mia3	Isoform 3 of Melanoma inhibitory activity protein 3	9.22	9	2	24	1.41	1.71	1	
A0A0G2JDJ5	Fdps	Farnesyl pyrophosphate synthase (Fragment)	30.58	3	3	8	1.40	1.71	2	142.4
Q9WUU7	Ctsz	Cathepsin Z	38.24	9	9	220	1.40	1.70	65	20.9
P62835	Rap1a	Ras-related protein Rap-1A	50.00	9	2	156	1.40	1.70	5	7.0
Q61699-2	Hsph1	Isoform HSP105-beta of Heat shock protein 105 kDa	7.25	5	4	9	1.40	1.70	1	
Q9D8N0	Eef1g	Elongation factor 1-gamma	23.34	14	14	161	1.39	1.69	38	17.1
O70370	Ctss	Cathepsin S	15.29	5	5	32	1.39	1.69	9	12.3
B1AXN9	Rps6ka3	Ribosomal protein S6 kinase alpha-3	4.92	3	3	7	1.39	1.69	1	
P16675	Ctsa	Lysosomal protective protein	16.67	7	7	98	1.38	1.68	29	14.5
P68040	Gnb2l1	Guanine nucleotide-binding protein subunit beta-2-like 1	32.49	12	12	88	1.38	1.67	18	20.7
P28352	Apex1	DNA-(apurinic or apyrimidinic site) lyase	7.57	2	2	13	1.37	1.66	2	8.4
P17751	Tpi1	Triosephosphate isomerase	42.47	10	19	121	1.37	1.66	26	21.8
P50580-2	Pa2g4	Isoform 2 of Proliferation-associated protein 2G4	19.71	7	7	26	1.37	1.66	5	27.6
P67984	Rpl22	60S ribosomal protein L22	35.16	4	4	89	1.37	1.66	26	27.2
Q8C0L0	Tmx4	Thioredoxin-related transmembrane protein 4	5.67	2	2	4	1.36	1.66	3	13.6
Q8VDM4	Psmd2	26S proteasome non-ATPase regulatory subunit 2	5.40	5	5	32	1.35	1.65	3	4.7
Q6PA06-2	Atl2	Isoform 2 of Atlastin-2	9.54	3	3	12	1.35	1.64	2	80.1
P47962	Rpl5	60S ribosomal protein L5	26.94	9	9	161	1.35	1.64	39	16.2
Q93092	Taldo1	Transaldolase	14.84	6	6	26	1.34	1.63	5	22.7
P30355	Alox5ap	Arachidonate 5-lipoxygenase-activating protein	25.47	4	4	44	1.34	1.63	9	15.8
P14152	Mdh1	Malate dehydrogenase, cytoplasmic	13.17	4	4	17	1.34	1.63	4	15.8
Q9DCD0	Pgd	6-phosphogluconate dehydrogenase, decarboxylating	17.60	8	8	55	1.34	1.62	14	13.3
Q61316	Hspa4	Heat shock 70 kDa protein 4	15.22	11	10	40	1.34	1.62	8	4.5

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9JIY5	Htra2	Serine protease HTRA2, mitochondrial	19.87	7	7	37	1.34	1.62	4	36.6
Q8BFR4	Gns	N-acetylglucosamine-6-sulfatase	5.51	3	3	26	1.33	1.62	4	26.7
Q9DCL9	Paics	Multifunctional protein ADE2	20.94	10	9	74	1.33	1.61	12	16.6
Q8BG32	Psmd11	26S proteasome non-ATPase regulatory subunit 11	12.80	5	5	41	1.33	1.61	6	16.3
A0A0J9YUD8	Hmgb1	High mobility group protein B1	22.81	4	4	22	1.33	1.61	6	8.3
P17742	Ppia	Peptidyl-prolyl cis-trans isomerase A	60.98	11	10	130	1.32	1.61	32	13.8
P52633	Stat6	Signal transducer and transcription activator 6	4.66	4	4	15	1.32	1.61	2	2.5
P58252	Eef2	Elongation factor 2	25.52	21	20	294	1.32	1.61	80	20.4
P62960	Ybx1	Nuclease-sensitive element-binding protein 1	33.54	8	4	216	1.32	1.60	49	57.4
F6Q5Z1	Ilk	Integrin-linked protein kinase (Fragment)	11.93	3	3	12	1.32	1.60	1	
P09411	Pgk1	Phosphoglycerate kinase 1	32.61	12	12	143	1.31	1.60	42	20.7
E9QKZ2	Ipo9	Importin-9	1.44	2	2	2	1.31	1.60	1	
Q9DC51	Gnai3	Guanine nucleotide-binding protein G(k) subunit alpha	22.88	8	3	83	1.31	1.59	2	40.1
A2AFS1	Sars	Serine--tRNA ligase, cytoplasmic (Fragment)	17.11	3	3	8	1.31	1.59	2	6.4
Q9Z0N1	Eif2s3x	Eukaryotic translation initiation factor 2 subunit 3, X-linked	10.17	5	5	15	1.31	1.59	2	13.6
P41731	Cd63	CD63 antigen	7.56	2	2	38	1.31	1.59	8	7.2
P50429-2	Arsb	Isoform 2 of Arylsulfatase B	6.26	3	3	15	1.31	1.59	2	6.0
Q9QZE5	Copg1	Coatomer subunit gamma-1	13.04	11	11	70	1.30	1.58	15	21.4
Q8VDW0	Ddx39a	ATP-dependent RNA helicase DDX39A	19.91	10	3	57	1.30	1.58	1	
P48678	Lmna	Prelamin-A/C	75.79	55	52	3878	1.30	1.58	1047	17.6
E9Q5I9	Psmd13	26S proteasome non-ATPase regulatory subunit 13	14.04	6	6	33	1.30	1.58	5	15.5
Q6ZWZ4	Rpl36	60S ribosomal protein L36	40.00	5	4	48	1.30	1.58	11	18.9
P05064	Aldoa	Fructose-bisphosphate aldolase A	43.96	17	17	349	1.30	1.58	67	17.9
Q61029	Tmpo	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	58.41	20	10	646	1.30	1.57	72	13.8
Q8BG13	Rbm3	RNA-binding protein 3	19.48	4	4	7	1.29	1.57	3	6.3
P06745	Gpi	Glucose-6-phosphate isomerase	15.77	8	8	48	1.29	1.57	14	18.6
I7HLV2	Rpl10	60S ribosomal protein L10 (Fragment)	29.35	6	6	85	1.29	1.57	25	31.5
A2A547	Rpl19	Ribosomal protein L19	35.05	8	7	105	1.29	1.57	24	10.5
Q6ZQ38	Cand1	Cullin-associated NEDD8-dissociated protein 1	8.46	9	9	24	1.29	1.57	4	4.5
Q9CR57	Rpl14	60S ribosomal protein L14	31.34	7	7	153	1.29	1.57	44	13.9
Q9DBX5	Pla2g4a	Phospholipase A2	9.73	7	7	65	1.29	1.56	10	28.3
Q62465	Vat1	Synaptic vesicle membrane protein VAT-1 homolog	24.38	8	8	65	1.29	1.56	11	34.5
P17182	Eno1	Alpha-enolase	43.55	15	15	417	1.29	1.56	107	15.1

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9QZL0	Ripk3	Receptor-interacting serine/threonine-protein kinase 3	24.69	9	9	46	1.28	1.56	9	31.4
Q9CWK8	Snx2	Sorting nexin-2	15.80	7	6	28	1.28	1.56	4	24.1
Q5SW88	Rab1a	Protein Rab1a	73.27	14	6	430	1.28	1.56	44	14.9
P14869	Rplp0	60S acidic ribosomal protein P0	42.59	11	11	220	1.28	1.56	54	16.2
Q6NZD2	Snx1	Sorting nexin 1	8.06	4	3	19	1.28	1.55	2	1.6
A0A0G2JDW7	Rps27	40S ribosomal protein S27 (Fragment)	39.02	3	3	99	1.28	1.55	20	11.1
P07901	Hsp90aa1	Heat shock protein HSP 90-alpha	35.33	26	13	412	1.28	1.55	36	19.5
P11499	Hsp90ab1	Heat shock protein HSP 90-beta	42.13	30	25	715	1.27	1.55	85	11.4
P40142	Tkt	Transketolase	24.56	13	13	87	1.27	1.55	22	11.8
P99024	Tubb5	Tubulin beta-5 chain	46.17	16	3	630	1.27	1.54	28	9.5
P18242	Ctsd	Cathepsin D	33.66	12	12	295	1.27	1.54	89	15.4
P62242	Rps8	40S ribosomal protein S8	38.46	8	8	195	1.27	1.54	50	10.6
P60843	Eif4a1	Eukaryotic initiation factor 4A-I	40.15	16	13	255	1.26	1.54	41	16.6
Q5XJY5	Arcn1	Coatomer subunit delta	12.72	6	6	25	1.26	1.54	4	9.5
Q9D3B1	Hacd2	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	16.14	4	4	51	1.26	1.53	14	10.4
E9Q6M7	Pum1	Pumilio homolog 1	2.65	3	2	17	1.26	1.53	1	
O35326	Srsf5	Serine/arginine-rich splicing factor 5	20.82	5	4	46	1.26	1.53	3	14.5
P30681	Hmgb2	High mobility group protein B2	21.43	6	6	51	1.26	1.53	13	29.5
Q8C1E7	Tmem120a	Transmembrane protein 120A	4.96	2	2	6	1.26	1.53	1	
P83882	Rpl36a	60S ribosomal protein L36a	25.47	4	4	112	1.26	1.53	29	9.2
Q9CQW1	Ykt6	Synaptobrevin homolog YKT6	30.81	6	6	36	1.26	1.53	4	6.3
P14733	Lmnb1	Lamin-B1	67.35	45	38	2061	1.26	1.53	444	14.1
A0A0G2JE25	Nras	GTPase NRas (Fragment)	18.00	3	3	8	1.26	1.53	1	
P62267	Rps23	40S ribosomal protein S23	51.75	6	6	134	1.26	1.53	32	13.4
E9Q715	Luc7l2	Putative RNA-binding protein Luc7-like 2	25.74	7	7	119	1.26	1.53	26	12.2
Q9ET30	Tm9sf3	Transmembrane 9 superfamily member 3	9.03	6	6	63	1.26	1.53	15	7.9
Q5XJF6	Rpl10a	Ribosomal protein	45.62	11	11	209	1.26	1.53	54	14.9
Q9D0I9	Rars	Arginine--tRNA ligase, cytoplasmic	3.79	3	3	18	1.26	1.53	1	
O09110-2	Map2k3	Isoform 1 of Dual specificity mitogen-activated protein kinase kinase 3	11.46	4	4	14	1.25	1.52	6	9.1
P68373	Tuba1c	Tubulin alpha-1C chain	48.11	17	2	476	1.25	1.52	5	28.4
Q31125	Slc39a7	Zinc transporter SLC39A7	7.56	3	3	57	1.25	1.52	18	13.8
A0A0R4J079	Acbd3	Acyl-Coenzyme A binding domain containing 3, isoform CRA_b	7.24	3	3	23	1.25	1.52	5	18.8
Q99JX7	Nxf1	Nuclear RNA export factor 1	22.65	11	11	116	1.25	1.52	26	11.8
P13020-2	Gsn	Isoform 2 of Gelsolin	9.44	6	6	33	1.25	1.52	3	5.5
Q9D1G1	Rab1b	Ras-related protein Rab-1B	70.15	13	5	374	1.25	1.52	19	15.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P12265	Gusb	Beta-glucuronidase	29.63	17	17	249	1.25	1.52	67	15.5
Q9Z1G3	Atp6v1c1	V-type proton ATPase subunit C 1	20.16	10	10	80	1.25	1.52	18	7.2
Q99K51	Pls3	Plastin-3	9.37	5	2	70	1.25	1.52	1	
Q922Q9	Chid1	Chitinase domain-containing protein 1	13.74	6	6	21	1.25	1.52	1	
Q8C172	Cers6	Ceramide synthase 6	8.07	4	4	34	1.25	1.52	11	13.2
Q3TXS7	Psmd1	26S proteasome non-ATPase regulatory subunit 1	3.88	4	4	18	1.25	1.52	3	4.7
Q8VDJ3	Hdlbp	Vigilin	10.33	12	12	40	1.25	1.52	5	13.6
F8VQC1	Srp72	Signal recognition particle subunit SRP72	6.86	5	4	22	1.25	1.52	5	3.6
B7FAV1	Flna	Filamin, alpha (Fragment)	14.52	30	30	153	1.25	1.52	22	17.2
Q921V5	Mgat2	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	5.43	2	2	24	1.25	1.51	7	4.9
Q07797	Lgals3bp	Galectin-3-binding protein	12.31	5	5	50	1.25	1.51	8	14.1
P62962	Pfn1	Profilin-1	65.00	7	7	79	1.24	1.51	19	7.8
Q08943	Ssrp1	FACT complex subunit SSRP1	15.68	11	11	72	1.24	1.51	14	23.4
Q9DCH4	Eif3f	Eukaryotic translation initiation factor 3 subunit F	11.91	3	3	12	1.24	1.51	4	8.4
P42932	Cct8	T-complex protein 1 subunit theta	35.95	19	19	258	1.24	1.51	54	10.3
P61255	Rpl26	60S ribosomal protein L26	38.62	8	8	119	1.24	1.51	33	9.0
P27659	Rpl3	60S ribosomal protein L3	33.75	16	16	334	1.24	1.51	77	12.0
P07356	Anxa2	Annexin A2	47.79	18	18	151	1.24	1.51	39	11.1
Q9DCZ4	Apoo	MICOS complex subunit Mic26	13.64	3	3	7	1.24	1.51	2	29.0
P61205	Arf3	ADP-ribosylation factor 3	60.77	9	4	137	1.24	1.51	22	24.2
E9PVC6	Eif4g1	Eukaryotic translation initiation factor 4 gamma 1	16.81	28	25	135	1.24	1.51	26	16.1
Q9D8T2	Gsdmdc1	Gasdermin-D	3.49	2	2	14	1.24	1.50	3	3.9
Q91VR5	Ddx1	ATP-dependent RNA helicase DDX1	12.84	8	8	34	1.24	1.50	8	7.7
P80314	Cct2	T-complex protein 1 subunit beta	31.40	15	15	149	1.24	1.50	28	12.9
P62751	Rpl23a	60S ribosomal protein L23a	51.92	11	11	280	1.24	1.50	68	12.2
P62908	Rps3	40S ribosomal protein S3	80.25	19	19	485	1.23	1.50	122	14.5
B1ARU1	Macf1	Microtubule-actin cross-linking factor 1	6.31	34	2	158	1.23	1.50	1	
Q9CQS8	Sec61b	Protein transport protein Sec61 subunit beta	44.79	4	4	96	1.23	1.50	23	25.2
P62849-2	Rps24	Isoform 2 of 40S ribosomal protein S24	44.62	6	6	102	1.23	1.50	27	7.8
P80316	Cct5	T-complex protein 1 subunit epsilon	12.57	7	7	68	1.23	1.50	13	14.6
Z4YJU8	Golga2	Golgin subfamily A member 2 (Fragment)	2.62	2	2	6	1.23	1.50	2	21.5
Q9Z1B5	Mad2l1	Mitotic spindle assembly checkpoint protein MAD2A	11.71	3	3	17	1.23	1.50	1	
O55142	Rpl35a	60S ribosomal protein L35a	47.27	7	7	124	1.23	1.50	29	9.9
B1AXW5	Prdx1	Peroxiredoxin-1 (Fragment)	48.24	9	7	240	1.23	1.50	30	10.2

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q922Q1	Marc2	Mitochondrial amidoxime reducing component 2	9.76	5	5	39	1.23	1.50	7	7.4
P29351	Ptpn6	Tyrosine-protein phosphatase non-receptor type 6	25.04	13	13	80	1.23	1.49	20	24.8
Q9DB96	Ngdn	Neuroguidin	6.67	2	2	13	1.23	1.49	2	7.5
Q9Z0R9	Fads2	Fatty acid desaturase 2	18.92	8	8	61	1.23	1.49	21	16.8
Q9D8U8	Snx5	Sorting nexin-5	14.60	6	6	23	1.23	1.49	2	16.6
P51863	Atp6v0d1	V-type proton ATPase subunit d 1	29.06	10	10	149	1.23	1.49	41	10.9
Q8R1B4	Eif3c	Eukaryotic translation initiation factor 3 subunit C	10.76	10	10	41	1.23	1.49	7	15.6
Q9CR16	Ppid	Peptidyl-prolyl cis-trans isomerase D	11.35	5	4	27	1.23	1.49	3	7.5
Q6PHN9	Rab35	Ras-related protein Rab-35	31.84	7	4	133	1.23	1.49	7	10.9
E9QAI5	Cad	CAD protein	6.15	13	13	50	1.23	1.49	4	10.4
Q6P9R2	Oxsr1	Serine/threonine-protein kinase R1	4.93	3	2	11	1.23	1.49	3	23.4
Q61753	Phgdh	D-3-phosphoglycerate dehydrogenase	21.20	10	10	90	1.23	1.49	16	15.7
P04184	Tk1	Thymidine kinase, cytosolic	9.01	2	2	9	1.22	1.49	1	
O09167	Rpl21	60S ribosomal protein L21	33.75	7	7	85	1.22	1.49	23	12.2
P54116	Stom	Erythrocyte band 7 integral membrane protein	45.07	11	11	249	1.22	1.49	61	18.9
P60766	Cdc42	Cell division control protein 42 homolog	29.84	5	4	78	1.22	1.49	13	4.0
P12970	Rpl7a	60S ribosomal protein L7a	47.37	16	16	406	1.22	1.49	99	16.5
Q61598-2	Gdi2	Isoform 2 of Rab GDP dissociation inhibitor beta	12.22	5	5	21	1.22	1.48	6	6.9
F8WJ41	Rps15a	40S ribosomal protein S15a (Fragment)	50.00	6	6	166	1.22	1.48	46	12.4
P24547	Impdh2	Inosine-5'-monophosphate dehydrogenase 2	28.21	13	13	124	1.22	1.48	17	14.5
Q01768	Nme2	Nucleoside diphosphate kinase B	55.92	9	9	76	1.22	1.48	14	19.7
P43277	Hist1h1d	Histone H1.3	52.04	18	3	1852	1.22	1.48	43	7.0
Q9CQC6	Bzw1	Basic leucine zipper and W2 domain-containing protein 1	5.73	3	3	7	1.22	1.48	2	13.7
P29391	Ftl1	Ferritin light chain 1	41.53	5	5	42	1.22	1.48	5	23.4
Q921Y0-2	Mob1a	Isoform 2 of MOB kinase activator 1A	26.43	4	4	32	1.22	1.48	8	24.3
Q9D7S7-2	Rpl22l1	Isoform 2 of 60S ribosomal protein L22-like 1	25.62	3	3	89	1.22	1.48	22	8.2
P63276	Rps17	40S ribosomal protein S17	46.67	8	8	77	1.22	1.48	14	27.5
Q99P91	Gpnmb	Transmembrane glycoprotein NMB	2.96	2	2	17	1.22	1.48	6	11.6
Q6ZWZ7	Rpl17	60S ribosomal protein L17	40.22	8	8	239	1.22	1.48	65	11.2
Q9CZD3	Gars	Glycine--tRNA ligase	3.02	3	3	19	1.22	1.48	2	5.9
P39087-2	Grik2	Isoform GluR6-2 of Glutamate receptor ionotropic, kainate 2	2.30	2	1	3	1.22	1.48	1	
P10605	Ctsb	Cathepsin B	35.99	10	10	218	1.21	1.48	52	24.6
Q3U4G3	Xxylt1	Xyloside xylosyltransferase 1	4.59	2	2	3	1.21	1.48	1	
Q8BH07	Arl6ip6	ADP-ribosylation factor-like protein 6-	9.73	2	2	2	1.21	1.47	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		interacting protein 6								
P62192	Psmc1	26S protease regulatory subunit 4	7.27	3	3	20	1.21	1.47	4	7.0
P25444	Rps2	40S ribosomal protein S2	40.96	13	13	471	1.21	1.47	132	15.6
Q6P5F9	Xpo1	Exportin-1	5.23	6	6	38	1.21	1.47	10	26.6
P84096	Rhog	Rho-related GTP-binding protein RhoG	43.46	7	6	88	1.21	1.47	6	12.0
P20152	Vim	Vimentin	79.40	45	42	4661	1.21	1.47	1279	12.3
P50516	Atp6v1a	V-type proton ATPase catalytic subunit A	30.31	18	18	194	1.21	1.47	39	13.8
P11157	Rrm2	Ribonucleoside-diphosphate reductase subunit M2	14.87	5	5	13	1.21	1.47	4	30.0
Q9R1P0	Psma4	Proteasome subunit alpha type-4	16.86	6	6	22	1.21	1.47	1	
P57746	Atp6v1d	V-type proton ATPase subunit D	20.65	5	5	44	1.21	1.47	7	17.1
P35979	Rpl12	60S ribosomal protein L12	63.64	9	9	208	1.21	1.47	42	10.7
D3YX79	Gm8394	Proteasome subunit alpha type	17.01	3	3	45	1.21	1.47	14	28.1
P97351	Rps3a	40S ribosomal protein S3a	56.82	17	17	421	1.21	1.47	116	10.5
Q569Z5	Ddx46	Probable ATP-dependent RNA helicase DDX46	12.60	14	14	77	1.21	1.47	11	11.7
P35293	Rab18	Ras-related protein Rab-18	45.63	8	8	60	1.21	1.47	15	13.2
P11983	Tcp1	T-complex protein 1 subunit alpha	32.01	16	16	168	1.21	1.47	35	17.9
Q3UBX0	Tmem109	Transmembrane protein 109	16.05	5	5	95	1.21	1.47	21	15.2
Q8R480	Nup85	Nuclear pore complex protein Nup85	10.52	8	8	66	1.21	1.47	11	4.8
P62702	Rps4x	40S ribosomal protein S4, X isoform	53.99	15	15	238	1.21	1.46	68	21.3
Q80SZ7	Gng5	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	23.53	2	2	21	1.20	1.46	7	5.7
Q01853	Vcp	Transitional endoplasmic reticulum ATPase	39.33	30	29	307	1.20	1.46	57	15.7
A0A0G2JFP4	Frrs1	Protein Frrs1	4.56	3	3	21	1.20	1.46	5	13.1
Q8CII2	Cdc123	Cell division cycle protein 123 homolog	5.06	2	1	16	1.20	1.46	2	8.0
Q9WV32	Arpc1b	Actin-related protein 2/3 complex subunit 1B	11.56	5	5	15	1.20	1.46	3	8.4
P62814	Atp6v1b2	V-type proton ATPase subunit B, brain isoform	36.79	17	17	202	1.20	1.46	47	15.4
A0A087WP81	Uchl5	Ubiquitin carboxyl-terminal hydrolase isozyme L5 (Fragment)	15.11	4	4	18	1.20	1.46	2	18.5
F6SVV1	Gm9493	Protein Gm9493	39.58	8	8	246	1.20	1.46	56	10.7
P06151	Ldha	L-lactate dehydrogenase A chain	36.45	12	12	190	1.20	1.46	58	13.6
Q8BXQ2	Pigt	GPI transamidase component PIG-T	12.89	8	8	61	1.20	1.45	9	15.5
P47226-2	Tes	Isoform TES1 of Testin	11.96	6	6	20	1.20	1.45	6	16.9
Q8BU14	Sec62	Translocation protein SEC62	13.82	6	6	42	1.20	1.45	11	12.3
Q9D6K8	Fundc2	FUN14 domain-containing protein 2	20.53	5	5	43	1.20	1.45	11	10.1
P34884	Mif	Macrophage migration inhibitory factor	13.91	2	2	12	1.19	1.45	3	5.2
F6YVP7	Gm10260	Protein Gm10260	52.63	12	12	318	1.19	1.45	104	18.2
P55012	Slc12a2	Solute carrier family 12 member 2	2.32	2	1	4	1.19	1.45	1	
Q810D6	Grwd1	Glutamate-rich WD repeat-containing protein 1	5.38	2	2	13	1.19	1.45	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q1MX41	Prkcd	Protein kinase C	4.95	3	3	28	1.19	1.45	6	5.4
Q8CIN4	Pak2	Serine/threonine-protein kinase PAK 2	12.98	6	6	44	1.19	1.45	11	23.4
Q9QUM9	Psma6	Proteasome subunit alpha type-6	22.76	5	5	32	1.19	1.45	9	20.9
Q9R1R8	Rdh11	Retinol dehydrogenase 11	20.67	6	6	51	1.19	1.45	6	7.3
Q3UW53	Fam129a	Protein Niban	3.67	3	3	14	1.19	1.45	2	11.3
A0A0N4SVB8	Arl8b	ADP-ribosylation factor-like protein 8B	52.17	7	3	92	1.19	1.44	12	12.7
Q64324	Stxbp2	Syntaxin-binding protein 2	13.66	7	6	18	1.19	1.44	3	2.2
Q68FL6	Mars	Methionine--tRNA ligase, cytoplasmic	3.99	4	4	10	1.19	1.44	2	5.8
E9PUB7	Msto1	Protein misato homolog 1	12.41	6	6	21	1.19	1.44	3	3.4
Q9DBJ1	Pgam1	Phosphoglycerate mutase 1	33.07	7	7	56	1.19	1.44	6	16.5
P20060	Hexb	Beta-hexosaminidase subunit beta	12.69	7	7	54	1.19	1.44	10	11.0
Q8BK67	Rcc2	Protein RCC2	18.65	8	8	44	1.19	1.44	11	19.7
Q9D1P4	Chordc1	Cysteine and histidine-rich domain-containing protein 1	7.25	2	2	5	1.19	1.44	2	15.4
P62281	Rps11	40S ribosomal protein S11	48.73	9	9	195	1.19	1.44	54	17.1
P62855	Rps26	40S ribosomal protein S26	26.96	3	3	104	1.19	1.44	28	7.6
P14115	Rpl27a	60S ribosomal protein L27a	34.46	5	5	100	1.19	1.44	17	7.4
P63017	Hspa8	Heat shock cognate 71 kDa protein	59.29	38	34	1538	1.18	1.44	299	17.6
P31996	Cd68	Macrosialin	11.04	5	5	307	1.18	1.44	90	11.8
P07724	Alb	Serum albumin	4.44	2	2	4	1.18	1.44	2	13.0
P29416	Hexa	Beta-hexosaminidase subunit alpha	10.80	6	6	59	1.18	1.44	10	9.0
Q921E2	Rab31	Ras-related protein Rab-31	24.74	4	4	39	1.18	1.44	11	8.9
Q9D8E6	Rpl4	60S ribosomal protein L4	42.96	19	19	249	1.18	1.44	61	13.4
Q6ZWN5	Rps9	40S ribosomal protein S9	52.58	14	14	256	1.18	1.43	65	18.8
Q9CZX8	Rps19	40S ribosomal protein S19	52.41	10	10	221	1.18	1.43	57	15.8
O70251	Eef1b	Elongation factor 1-beta	18.67	4	4	13	1.18	1.43	4	12.6
Q9D2N9	Vps33a	Vacuolar protein sorting-associated protein 33A	4.68	2	2	7	1.18	1.43	2	11.7
P23116	Eif3a	Eukaryotic translation initiation factor 3 subunit A	9.52	13	13	41	1.18	1.43	8	5.0
Q99PT1	Arhgdia	Rho GDP-dissociation inhibitor 1	19.12	4	4	34	1.18	1.43	11	10.6
Q9DBZ5	Eif3k	Eukaryotic translation initiation factor 3 subunit K	12.84	2	2	9	1.18	1.43	2	18.1
P62717	Rpl18a	60S ribosomal protein L18a	46.02	9	9	163	1.18	1.43	32	11.8
P62754	Rps6	40S ribosomal protein S6	36.14	10	10	201	1.18	1.43	48	15.1
E9Q3G8	Nup153	Protein Nup153	16.89	23	23	109	1.18	1.43	34	17.7
Q99P88	Nup155	Nuclear pore complex protein Nup155	22.65	29	29	296	1.18	1.43	60	24.0
Q8BHL8	Psmf1	Proteasome inhibitor PI31 subunit	13.28	3	3	29	1.18	1.43	6	8.7
P80315	Cct4	T-complex protein 1 subunit delta	27.27	15	15	133	1.17	1.43	29	20.0
Q8VDD5	Myh9	Myosin-9	51.63	107	107	2020	1.17	1.43	521	12.9

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P14576	Srp54	Signal recognition particle 54 kDa protein	19.05	11	11	59	1.17	1.42	14	20.9
P80313	Cct7	T-complex protein 1 subunit eta	32.72	16	16	105	1.17	1.42	19	16.7
Q8BRF7-3	Scfd1	Isoform 3 of Sec1 family domain-containing protein 1	12.23	6	6	45	1.17	1.42	12	25.7
Q9D1D4	Tmed10	Transmembrane emp24 domain-containing protein 10	43.84	9	9	165	1.17	1.42	47	17.9
Q9CYN2	Spcs2	Signal peptidase complex subunit 2	59.29	14	14	122	1.17	1.42	39	17.6
P10126	Eef1a1	Elongation factor 1-alpha 1	44.59	20	20	755	1.17	1.42	210	19.1
P60229	Eif3e	Eukaryotic translation initiation factor 3 subunit E	8.54	4	4	19	1.17	1.42	3	5.9
Q8R2U0-2	Seh1l	Isoform 2 of Nucleoporin SEH1	17.09	6	6	37	1.17	1.42	6	10.9
Q9Z2U0	Psma7	Proteasome subunit alpha type-7	27.42	6	6	39	1.17	1.42	4	16.1
E9PYI8	Usp14	Ubiquitin carboxyl-terminal hydrolase 14	4.37	2	2	4	1.17	1.42	1	
P68372	Tubb4b	Tubulin beta-4B chain	46.07	16	3	533	1.17	1.42	5	11.4
P61089	Ube2n	Ubiquitin-conjugating enzyme E2 N	29.61	5	5	70	1.17	1.42	21	15.0
Q9Z1Z0	Uso1	General vesicular transport factor p115	7.92	8	8	22	1.17	1.42	3	17.2
Q3T9X3	Dnm2	Dynamin-2	8.49	7	7	30	1.17	1.42	3	29.4
O54984	Asna1	ATPase Asna1	13.51	4	4	21	1.17	1.42	5	19.3
Q61462	Cyba	Cytochrome b-245 light chain	20.31	4	4	91	1.17	1.42	25	8.3
P61027	Rab10	Ras-related protein Rab-10	51.50	10	8	248	1.17	1.42	41	18.7
Q9CWU9	Nup37	Nucleoporin Nup37	17.18	5	5	52	1.17	1.42	12	8.1
P40124	Cap1	Adenylyl cyclase-associated protein 1	25.11	12	12	117	1.17	1.42	33	14.1
Q9QUJ7-2	Acsl4	Isoform Short of Long-chain-fatty-acid--CoA ligase 4	12.39	8	7	42	1.17	1.42	2	3.6
Q9D7N9	Apmap	Adipocyte plasma membrane-associated protein	15.18	6	6	54	1.17	1.42	11	8.8
P48036	Anxa5	Annexin A5	36.05	13	13	114	1.17	1.42	21	13.2
Q99JI6	Rap1b	Ras-related protein Rap-1b	53.80	10	3	165	1.17	1.42	4	6.2
Q8BP67	Rpl24	60S ribosomal protein L24	39.49	8	8	74	1.17	1.42	21	14.7
P26039	Tln1	Talin-1	33.81	77	75	645	1.17	1.42	137	19.8
P19253	Rpl13a	60S ribosomal protein L13a	44.33	13	13	225	1.17	1.42	60	18.4
Q9D0M3-2	Cyc1	Isoform 2 of Cytochrome c1, heme protein, mitochondrial	23.31	5	5	85	1.17	1.42	22	19.3
Q9CPW4	Arpc5	Actin-related protein 2/3 complex subunit 5	26.49	5	5	22	1.17	1.42	4	11.3
P46061	Rangap1	Ran GTPase-activating protein 1	33.11	20	20	202	1.16	1.42	46	15.5
P45376	Akr1b1	Aldose reductase	9.49	3	3	16	1.16	1.41	3	17.9
Q920L1	Fads1	Fatty acid desaturase 1	11.41	5	5	64	1.16	1.41	15	9.6
Q9ERU9	Ranbp2	E3 SUMO-protein ligase RanBP2	23.62	71	70	682	1.16	1.41	166	16.4
O35114	Scarb2	Lysosome membrane protein 2	6.90	4	4	18	1.16	1.41	6	1.1
E9PYL9	Gm10036	Protein Gm10036	28.09	5	5	132	1.16	1.41	34	7.0

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q04899	Cdk18	Cyclin-dependent kinase 18	11.53	5	4	35	1.16	1.41	4	33.5
A2A8U2	Tmem201	Transmembrane protein 201	5.57	4	4	27	1.16	1.41	1	
P47911	Rpl6	60S ribosomal protein L6	41.22	15	15	393	1.16	1.41	105	11.9
Q8BUE4	Aifm2	Apoptosis-inducing factor 2	6.43	3	3	11	1.16	1.41	2	8.6
P14131	Rps16	40S ribosomal protein S16	62.33	12	12	326	1.16	1.41	98	18.3
Q9CXT7-2	Tmem192	Isoform 2 of Transmembrane protein 192	9.95	2	2	9	1.16	1.41	2	16.3
Q8CJF7	Ahctf1	Protein ELYS	10.03	20	20	111	1.16	1.41	24	12.9
P46978	Stt3a	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	19.01	16	14	224	1.16	1.41	52	15.2
O08807	Prdx4	Peroxiredoxin-4	50.36	10	8	225	1.16	1.41	33	26.5
O55143	Atp2a2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	37.16	40	40	675	1.16	1.41	151	12.7
Q9JKX6	Nudt5	ADP-sugar pyrophosphatase	12.84	2	2	19	1.16	1.41	6	10.3
A2A9I0	Gosr2	Golgi SNAP receptor complex member 2	17.58	3	3	23	1.16	1.41	2	3.2
Q80V26	Impad1	Inositol monophosphatase 3	6.46	3	3	14	1.16	1.41	2	3.5
P28656	Nap1l1	Nucleosome assembly protein 1-like 1	6.91	2	2	24	1.16	1.41	4	10.0
Q8VDC0	Lars2	Probable leucine--tRNA ligase, mitochondrial	3.66	3	3	4	1.16	1.41	1	
P11438	Lamp1	Lysosome-associated membrane glycoprotein 1	13.79	5	5	266	1.16	1.41	58	12.3
P54775	Psmc4	26S protease regulatory subunit 6B	11.24	5	5	22	1.16	1.41	4	9.6
G5E829	Atp2b1	Plasma membrane calcium-transporting ATPase 1	11.48	12	12	35	1.16	1.41	13	12.2
Q3U2A8	Vars2	Valine--tRNA ligase, mitochondrial	1.70	2	2	4	1.16	1.41	1	
P52293	Kpna2	Importin subunit alpha-1	25.71	12	12	100	1.16	1.41	24	16.4
Q60692	Psmb6	Proteasome subunit beta type-6	8.40	2	2	11	1.16	1.41	1	
B1AT36	Psmd12	26S proteasome non-ATPase regulatory subunit 12	8.49	5	5	21	1.16	1.41	2	17.1
P61082	Ube2m	NEDD8-conjugating enzyme Ubc12	20.22	4	4	19	1.16	1.40	6	21.8
Q8BXV2	Bri3bp	BRI3-binding protein	19.37	4	4	181	1.16	1.40	46	15.0
O70435	Psma3	Proteasome subunit alpha type-3	14.90	4	4	16	1.16	1.40	3	19.4
Q8BFY9-2	Tnpo1	Isoform 2 of Transportin-1	11.12	9	9	38	1.16	1.40	8	13.1
O88325	Naglu	Alpha-N-acetylglucosaminidase	18.54	12	12	83	1.16	1.40	14	21.3
H3BLG5	Sdcbp	Syntenin-1 (Fragment)	16.47	4	4	13	1.15	1.40	4	14.2
P62830	Rpl23	60S ribosomal protein L23	60.71	8	8	366	1.15	1.40	102	16.4
P35980	Rpl18	60S ribosomal protein L18	28.19	5	5	177	1.15	1.40	53	16.9
P29341	Pabpc1	Polyadenylate-binding protein 1	33.02	22	17	223	1.15	1.40	41	13.8
D6RE33	Edc4	Enhancer of mRNA-decapping protein 4	1.21	2	2	4	1.15	1.40	1	
Q9CQW9	Ifitm3	Interferon-induced transmembrane protein 3	20.44	2	2	6	1.15	1.40	1	
P62918	Rpl8	60S ribosomal protein L8	42.02	10	10	426	1.15	1.40	125	10.4
Q62433	Ndrg1	Protein NDRG1	11.17	3	3	24	1.15	1.40	5	6.5

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
F6RK81	Ergic3	Endoplasmic reticulum-Golgi intermediate compartment protein 3 (Fragment)	11.06	3	3	10	1.15	1.40	1	
Q9EPK2-4	Rp2	Isoform 4 of Protein XRP2	8.06	3	3	7	1.15	1.40	1	
A3KG36	G6pdx	Glucose-6-phosphate 1-dehydrogenase (Fragment)	4.80	2	2	11	1.15	1.40	5	25.3
Q3U9G9	Lbr	Lamin-B receptor	25.08	19	19	322	1.15	1.40	77	18.8
Q9QYJ0	Dnaja2	DnaJ homolog subfamily A member 2	17.23	7	7	32	1.15	1.40	6	5.0
Q5SUC9	Sco1	Protein SCO1 homolog, mitochondrial	5.63	2	2	11	1.15	1.40	3	0.4
O70503	Hsd17b12	Very-long-chain 3-oxoacyl-CoA reductase	35.90	11	11	222	1.15	1.40	60	16.0
P50518	Atp6v1e1	V-type proton ATPase subunit E 1	15.04	4	4	74	1.15	1.40	21	7.0
P21619	Lmnb2	Lamin-B2	52.85	33	26	676	1.15	1.40	78	14.9
B9EJ54	Nup205	MCG21756, isoform CRA_b	15.54	31	31	255	1.15	1.40	57	21.6
Q9CQU3	Rer1	Protein RER1	9.18	2	2	26	1.15	1.40	10	7.8
P00920	Ca2	Carbonic anhydrase 2	22.31	5	5	53	1.15	1.40	15	21.6
Q9CRD2	Emc2	ER membrane protein complex subunit 2	20.54	5	5	33	1.15	1.40	8	4.4
P42125	Eci1	Enoyl-CoA delta isomerase 1, mitochondrial	21.80	6	6	32	1.15	1.40	6	37.5
D3Z2F7	Arpc3	Actin-related protein 2/3 complex subunit 3	12.42	3	3	10	1.15	1.40	3	12.6
Q91WN1	Dnajc9	DnaJ homolog subfamily C member 9	21.24	9	9	46	1.15	1.40	9	14.4
O70310	Nmt1	Glycylpeptide N-tetradecanoyltransferase 1	4.03	2	2	6	1.15	1.40	1	
Q9CYH2	Fam213a	Redox-regulatory protein FAM213A	20.64	4	4	12	1.15	1.40	1	
Q8VDL4-3	Adpgk	Isoform 3 of ADP-dependent glucokinase	18.18	6	6	56	1.15	1.39	10	7.6
A2AEB5	Morf4l2	Mortality factor 4-like protein 2 (Fragment)	10.34	2	2	10	1.15	1.39	3	1.4
E9QKL6	Ifi204	Interferon-activable protein 204	3.88	3	3	18	1.15	1.39	4	14.5
P53994	Rab2a	Ras-related protein Rab-2A	57.08	11	11	174	1.15	1.39	39	11.9
Q7TMF3	Ndufa12	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	38.62	5	5	29	1.15	1.39	9	17.8
E9Q2H8	Hagh	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment)	12.44	3	2	7	1.15	1.39	2	10.3
P80317	Cct6a	T-complex protein 1 subunit zeta	25.24	14	14	161	1.15	1.39	26	11.2
A0A0G2JEY4	3110082I17Rik	Protein 3110082I17Rik	11.24	2	2	4	1.15	1.39	3	10.1
O35134	Polr1a	DNA-directed RNA polymerase I subunit RPA1	1.98	3	3	12	1.15	1.39	1	
P58021	Tm9sf2	Transmembrane 9 superfamily member 2	12.54	8	8	75	1.14	1.39	15	16.0
P62900	Rpl31	60S ribosomal protein L31	52.80	8	8	357	1.14	1.39	97	25.4
P43274	Hist1h1e	Histone H1.4	48.86	16	5	1642	1.14	1.39	110	9.0
O55029	Copb2	Coatomer subunit beta'	11.16	10	10	71	1.14	1.39	15	8.8
P62852	Rps25	40S ribosomal protein S25	38.40	6	6	269	1.14	1.39	83	15.8
Q8BYI6-2	Lpcat2	Isoform 2 of Lysophosphatidylcholine acyltransferase 2	5.75	3	3	17	1.14	1.39	5	3.0
Q80VQ0	Aldh3b1	Aldehyde dehydrogenase family 3 member B1	7.05	3	3	16	1.14	1.39	3	8.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P09581	Csf1r	Macrophage colony-stimulating factor 1 receptor	12.38	12	12	113	1.14	1.39	29	11.1
Q8C605	Pfkp	ATP-dependent 6-phosphofructokinase	9.57	9	9	51	1.14	1.39	9	8.9
Q9D1R9	Rpl34	60S ribosomal protein L34	34.19	5	5	153	1.14	1.39	29	9.7
P68368	Tuba4a	Tubulin alpha-4A chain	44.87	16	3	372	1.14	1.39	8	10.7
Q9D8P4	Mrpl17	39S ribosomal protein L17, mitochondrial	23.86	5	5	16	1.14	1.39	5	35.4
D3YUM1	Ndufv1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	33.19	13	13	99	1.14	1.39	23	14.7
Q9Z1J3-2	Nfs1	Isoform Cytoplasmic of Cysteine desulfurase, mitochondrial	20.91	8	8	31	1.14	1.39	7	23.5
Q9ERE7	Mesdc2	LDLR chaperone MESD	25.45	5	5	46	1.14	1.38	11	8.7
P59999	Arpc4	Actin-related protein 2/3 complex subunit 4	32.14	6	6	33	1.14	1.38	7	20.5
P42208	Sep-02	Septin-2	19.67	5	5	25	1.14	1.38	8	29.6
Q9D0K2	Oxct1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	33.85	13	13	137	1.14	1.38	36	33.7
Q6P6I8	Sirpa	Signal-regulatory protein alpha	14.34	5	5	30	1.14	1.38	10	4.6
Q8BXL7	Arfrp1	ADP-ribosylation factor-related protein 1	12.94	2	2	2	1.14	1.38	1	
Q60737	Csnk2a1	Casein kinase II subunit alpha	7.16	2	2	12	1.14	1.38	1	
Q8C570	Rae1	mRNA export factor	16.58	5	5	113	1.14	1.38	22	11.2
P51829	Adcy7	Adenylate cyclase type 7	2.55	2	2	6	1.14	1.38	1	
Q8BXZ1	Tmx3	Protein disulfide-isomerase TMX3	13.16	8	7	95	1.14	1.38	23	18.9
A0A0G2JEG7	Rpf1	Ribosome production factor 1 (Fragment)	19.05	2	2	5	1.14	1.38	2	11.0
Q8R1V4	Tmed4	Transmembrane emp24 domain-containing protein 4	25.99	7	4	87	1.14	1.38	13	24.1
Q9DC70	Ndufs7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	17.41	4	4	56	1.14	1.38	15	20.9
Q9Z1D1	Eif3g	Eukaryotic translation initiation factor 3 subunit G	24.69	5	5	36	1.14	1.38	7	25.2
Q9EP72	Emc7	ER membrane protein complex subunit 7	19.09	4	4	34	1.14	1.38	8	6.4
Q9CY27	Tecr	Very-long-chain enoyl-CoA reductase	22.73	8	8	126	1.14	1.38	33	7.2
P59110	Senp1	Sentrin-specific protease 1	5.94	3	3	5	1.14	1.38	3	8.1
Q5SU71	Trim25	E3 ubiquitin/ISG15 ligase TRIM25	4.47	3	3	10	1.14	1.38	2	31.0
Q6PFD9	Nup98	Nuclear pore complex protein Nup98-Nup96	22.80	34	33	415	1.14	1.38	99	16.5
A0A0R4J0H7	Ncapd2	Condensin complex subunit 1	3.52	5	5	18	1.14	1.38	1	
Q07813	Bax	Apoptosis regulator BAX	12.50	2	2	10	1.14	1.38	1	
Q8VH51-2	Rbm39	Isoform 2 of RNA-binding protein 39	19.66	9	9	61	1.14	1.38	13	15.1
Q9Z0R6-2	Itsn2	Isoform 2 of Intersectin-2	1.92	2	2	11	1.13	1.38	2	2.1
G3X928	Sec23ip	SEC23-interacting protein	5.21	5	4	29	1.13	1.38	4	7.6
Q60864	Stip1	Stress-induced-phosphoprotein 1	10.31	6	6	18	1.13	1.38	4	9.5

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P35278	Rab5c	Ras-related protein Rab-5C	39.35	7	5	259	1.13	1.38	64	16.8
Q99L04	Dhrs1	Dehydrogenase/reductase SDR family member 1	17.25	6	6	27	1.13	1.38	10	14.0
Q8K0C4	Cyp51a1	Lanosterol 14-alpha demethylase	22.66	11	11	62	1.13	1.38	11	10.4
P62889	Rpl30	60S ribosomal protein L30	55.65	7	7	111	1.13	1.38	26	22.5
Q80W54	Zmpste24	CAAX prenyl protease 1 homolog	12.84	6	6	96	1.13	1.38	17	19.4
Q9WV54	Asah1	Acid ceramidase	14.72	8	8	57	1.13	1.38	9	6.8
P55258	Rab8a	Ras-related protein Rab-8A	38.16	9	4	194	1.13	1.37	8	13.8
Q5SUF2	Luc7l3	Luc7-like protein 3	18.98	8	8	31	1.13	1.37	5	7.8
Q61335	Bcap31	B-cell receptor-associated protein 31	32.24	7	7	228	1.13	1.37	54	11.6
Q3U7R1	Esyt1	Extended synaptotagmin-1	18.50	17	17	106	1.13	1.37	23	22.9
Q9QZI9	Serinc3	Serine incorporator 3	7.42	4	4	39	1.13	1.37	13	10.8
O35704	Sptlc1	Serine palmitoyltransferase 1	9.94	5	5	47	1.13	1.37	9	10.9
Q9D136	Ogfod3	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 3	10.48	3	3	10	1.13	1.37	1	
P51410	Rpl9	60S ribosomal protein L9	35.42	7	7	132	1.13	1.37	38	20.7
Q9Z2G6-2	Sel1l	Isoform 2 of Protein sel-1 homolog 1	12.03	7	7	24	1.13	1.37	7	8.1
Q9CQB5	Cisd2	CDGSH iron-sulfur domain-containing protein 2	55.56	7	7	95	1.13	1.37	19	15.6
D3Z5U3	Dnase2a	Deoxyribonuclease-2-alpha (Fragment)	11.54	2	2	6	1.13	1.37	1	
Q3UB58	Cd72	B-cell differentiation antigen CD72	10.67	3	3	12	1.13	1.37	4	28.8
P41105	Rpl28	60S ribosomal protein L28	43.80	8	8	214	1.13	1.37	47	9.5
P70333	Hnrnph2	Heterogeneous nuclear ribonucleoprotein H2	33.18	12	5	361	1.13	1.37	7	26.7
Q8JZR0	Acsl5	Long-chain-fatty-acid--CoA ligase 5	19.62	14	12	77	1.13	1.37	13	10.4
H3BK44	Ctage5	cTAGE family member 5	9.46	8	8	24	1.13	1.37	5	23.2
O35344	Kpna3	Importin subunit alpha-4	8.64	5	5	50	1.13	1.37	10	7.2
A0A0U1RNT6	Mat2a	S-adenosylmethionine synthase isoform type-2	19.06	7	7	41	1.12	1.37	6	3.4
Q9JLB0-2	Mpp6	Isoform Alpha of MAGUK p55 subfamily member 6	7.05	3	3	12	1.12	1.37	4	17.1
P27046	Man2a1	Alpha-mannosidase 2	6.78	8	8	46	1.12	1.37	4	16.6
P14148	Rpl7	60S ribosomal protein L7	42.59	15	15	329	1.12	1.37	89	23.8
Q8BLF1	Nceh1	Neutral cholesterol ester hydrolase 1	22.55	7	7	84	1.12	1.37	19	12.8
P09405	Ncl	Nucleolin	54.31	43	43	1391	1.12	1.37	377	14.4
Q61171	Prdx2	Peroxiredoxin-2	18.69	4	4	31	1.12	1.37	10	4.1
Q91V04	Tram1	Translocating chain-associated membrane protein 1	8.29	3	3	65	1.12	1.37	14	15.6
Q6ZQI3	Mlec	Malectin	36.43	10	10	136	1.12	1.37	34	13.2
P17918	Pcna	Proliferating cell nuclear antigen	43.30	10	10	196	1.12	1.36	46	9.0
Q8BH24	Tm9sf4	Transmembrane 9 superfamily member 4	11.82	7	7	72	1.12	1.36	19	9.5
Q8BJ71	Nup93	Nuclear pore complex protein Nup93	38.46	32	32	428	1.12	1.36	109	20.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
G3X8Y8	Tlr2	Toll-like receptor	9.31	7	7	29	1.12	1.36	3	11.5
E9Q109	Nip7	60S ribosome subunit biogenesis protein NIP7 homolog	14.29	2	2	17	1.12	1.36	3	0.4
Q9DBG5	Plin3	Perilipin-3	6.86	2	2	6	1.12	1.36	2	1.3
Q6ZWX6	Eif2s1	Eukaryotic translation initiation factor 2 subunit 1	13.97	5	5	29	1.12	1.36	10	20.4
P57780	Actn4	Alpha-actinin-4	21.16	17	17	98	1.12	1.36	18	20.0
Q9DC29	Abcb6	ATP-binding cassette sub-family B member 6, mitochondrial	4.51	3	1	19	1.12	1.36	2	21.8
Q8CIE6	Copa	Coatomer subunit alpha	16.34	18	18	86	1.12	1.36	17	12.9
Q9ESU7	Slc1a5	Amino acid transporter	22.34	11	11	144	1.12	1.36	36	10.4
F8WJG3	Tra2b	Transformer-2 protein homolog beta	21.81	4	4	65	1.12	1.36	11	15.7
D3Z7P3-2	Gls	Isoform 2 of Glutaminase kidney isoform, mitochondrial	20.90	10	1	113	1.12	1.36	2	11.6
P63101	Ywhaz	14-3-3 protein zeta/delta	42.45	10	6	86	1.12	1.36	12	22.9
O35435	Dhodh	Dihydroorotate dehydrogenase (quinone), mitochondrial	16.71	6	6	22	1.12	1.36	2	8.2
Q05144	Rac2	Ras-related C3 botulinum toxin substrate 2	36.98	9	8	254	1.12	1.36	62	18.2
Q6P4S8	Ints1	Integrator complex subunit 1	2.69	7	7	24	1.12	1.36	3	3.7
D3Z0F5	Cops6	COP9 signalosome complex subunit 6	14.48	4	4	15	1.12	1.36	2	26.4
Q921T2	Tor1aip1	Torsin-1A-interacting protein 1	24.03	11	10	201	1.12	1.36	51	20.7
Q8VCB1	Ndc1	Nucleoporin NDC1	12.78	7	7	54	1.12	1.36	15	11.7
P46460	Nsf	Vesicle-fusing ATPase	26.88	19	19	191	1.12	1.36	34	11.8
Q8BWY7-3	Slc39a11	Isoform 3 of Zinc transporter ZIP11	7.46	2	2	9	1.12	1.36	3	2.8
Q921X9	Pdia5	Protein disulfide-isomerase A5	3.29	2	2	9	1.12	1.36	2	51.9
Q91V92	Acly	ATP-citrate synthase	3.67	5	5	24	1.12	1.36	5	17.7
Q9DBG7	Srpr	Signal recognition particle receptor subunit alpha	28.77	17	17	158	1.11	1.35	31	16.8
P62331	Arf6	ADP-ribosylation factor 6	16.00	3	2	17	1.11	1.35	5	39.7
P25911-2	Lyn	Isoform 2 of Tyrosine-protein kinase Lyn	13.85	7	5	47	1.11	1.35	3	15.9
Q8BH74	Nup107	Nuclear pore complex protein Nup107	19.22	18	18	153	1.11	1.35	29	20.4
P62827	Ran	GTP-binding nuclear protein Ran	31.02	8	8	131	1.11	1.35	30	10.9
P58242	Smpdl3b	Acid sphingomyelinase-like phosphodiesterase 3b	11.18	5	5	32	1.11	1.35	9	12.8
E9PUC2	Acsl3	Long-chain-fatty-acid--CoA ligase 3	6.34	3	2	16	1.11	1.35	2	1.1
P61222	Abce1	ATP-binding cassette sub-family E member 1	8.68	5	5	15	1.11	1.35	3	2.7
Q8BH43	Wasf2	Wiskott-Aldrich syndrome protein family member 2	5.23	3	3	8	1.11	1.35	1	
Q9EQ06	Hsd17b11	Estradiol 17-beta-dehydrogenase 11	23.15	7	7	48	1.11	1.35	12	15.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
D3Z1W6	Pbrm1	Protein polybromo-1	3.29	6	6	33	1.11	1.35	3	0.8
P57787	Slc16a3	Monocarboxylate transporter 4	12.13	5	5	73	1.11	1.35	22	22.7
Q9WTX8	Mad1l1	Mitotic spindle assembly checkpoint protein MAD1	11.85	10	10	38	1.11	1.35	14	13.0
P70168	Kpnb1	Importin subunit beta-1	29.68	22	22	232	1.11	1.35	58	14.0
Q9CQV1	Pam16	Mitochondrial import inner membrane translocase subunit TIM16	38.40	6	6	29	1.11	1.35	9	16.5
Q8R1G6	Pdlim2	PDZ and LIM domain protein 2	12.03	4	4	29	1.11	1.35	4	3.4
Q9D2V8	Mfsd10	Major facilitator superfamily domain-containing protein 10	19.30	8	8	66	1.11	1.35	15	10.3
Q6A028	Swap70	Switch-associated protein 70	4.62	3	3	7	1.11	1.35	2	47.0
Q9QXS1-2	Plec	Isoform PLEC-1 of Plectin	62.63	293	289	6500	1.11	1.35	1594	15.1
Q8CFE6	Slc38a2	Sodium-coupled neutral amino acid transporter 2	10.32	4	4	36	1.11	1.35	10	16.7
O35593	Psmd14	26S proteasome non-ATPase regulatory subunit 14	10.97	4	4	18	1.11	1.35	3	4.6
Q7TNV0	Dek	Protein DEK	12.11	5	5	49	1.11	1.35	12	25.2
A0A0U1RNI6	Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	10.65	2	2	16	1.11	1.35	2	7.3
Q9ES52-4	Inpp5d	Isoform 4 of Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	5.53	5	5	16	1.11	1.35	2	3.8
P35279-2	Rab6a	Isoform 2 of Ras-related protein Rab-6A	45.67	9	8	139	1.11	1.35	13	19.3
Q8VCL2	Sco2	Protein SCO2 homolog, mitochondrial	19.22	4	4	30	1.11	1.35	7	15.4
M0QWY0	Emc8	ER membrane protein complex subunit 8 (Fragment)	28.91	3	3	37	1.11	1.35	8	26.4
P58681	Tlr7	Toll-like receptor 7	7.71	8	7	36	1.11	1.35	6	15.1
D3Z4C9	Uqcc2	Ubiquinol-cytochrome-c reductase complex assembly factor 2	18.11	3	3	8	1.11	1.35	2	11.3
P62897	Cycs	Cytochrome c, somatic	39.05	5	5	74	1.11	1.35	16	16.3
P47963	Rpl13	60S ribosomal protein L13	43.13	11	11	413	1.11	1.35	114	11.7
Q9CXS4	Cenpv	Centromere protein V	36.90	7	7	53	1.11	1.35	11	16.8
Q8BHE8	N/A	Uncharacterized protein C2orf47 homolog, mitochondrial	7.22	2	2	14	1.11	1.34	1	
Q8BJS4-3	Sun2	Isoform 3 of SUN domain-containing protein 2	26.75	17	17	123	1.11	1.34	19	11.4
Q9CXE7	Tmed5	Transmembrane emp24 domain-containing protein 5	19.65	5	5	37	1.11	1.34	11	11.3
Q99J27	Slc33a1	Acetyl-coenzyme A transporter 1	6.00	3	3	12	1.11	1.34	3	5.9
F8WHM5	Glg1	Golgi apparatus protein 1 (Fragment)	25.11	29	29	290	1.11	1.34	71	14.5
Q8R0X7	Sgpl1	Sphingosine-1-phosphate lyase 1	19.72	12	12	149	1.11	1.34	42	15.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
O35379	Abcc1	Multidrug resistance-associated protein 1	2.95	4	4	16	1.11	1.34	2	14.8
D3Z6S1	Tmem214	Transmembrane protein 214	10.75	7	7	48	1.11	1.34	9	8.1
Q8BHF7	Pgs1	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, mitochondrial	11.57	5	5	22	1.11	1.34	3	5.1
Q9CWU2	Zdhhc13	Palmitoyltransferase ZDHHC13	9.49	5	5	23	1.11	1.34	8	4.7
Q3UVK0	Ermp1	Endoplasmic reticulum metallopeptidase 1	11.47	10	10	61	1.11	1.34	10	11.2
Q8K3Z9	Pom121	Nuclear envelope pore membrane protein POM 121	7.83	10	10	61	1.11	1.34	15	11.8
Q8R0G9	Nup133	Nuclear pore complex protein Nup133	21.47	23	23	203	1.11	1.34	38	18.6
Q9JKB3-2	Ybx3	Isoform 2 of Y-box-binding protein 3	28.77	7	3	95	1.10	1.34	3	1.0
E9Q855	Scamp3	Secretory carrier-associated membrane protein 3	23.17	5	5	95	1.10	1.34	15	19.0
Q9CPT4	Mydgf	Myeloid-derived growth factor	12.65	3	3	35	1.10	1.34	6	8.5
Q8R332-4	Nup58	Isoform 4 of Nucleoporin p58/p45	14.29	9	9	130	1.10	1.34	38	12.7
Q8R5J9	Arl6ip5	PRA1 family protein 3	27.13	5	5	54	1.10	1.34	14	12.3
F6ZKZ3	Sqrdl	Sulfide:quinone oxidoreductase, mitochondrial	11.00	3	3	9	1.10	1.34	1	
Q61425	Hadh	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	20.38	9	9	53	1.10	1.34	11	12.1
Q4FZF3	Ddx49	Probable ATP-dependent RNA helicase DDX49	5.63	3	3	12	1.10	1.34	1	
Q99JY9	Actr3	Actin-related protein 3	11.24	4	4	20	1.10	1.34	4	14.3
Q8C147	Dock8	Dedicator of cytokinesis protein 8	4.57	9	9	43	1.10	1.34	6	1.6
Q4FZC9-2	Syne3	Isoform 2 of Nesprin-3	17.57	16	16	89	1.10	1.34	18	19.9
Q8QZY1	Eif3l	Eukaryotic translation initiation factor 3 subunit L	4.08	2	2	12	1.10	1.34	4	10.0
P61028	Rab8b	Ras-related protein Rab-8B	38.16	9	4	229	1.10	1.34	8	30.3
P49717	Mcm4	DNA replication licensing factor MCM4	5.45	5	4	18	1.10	1.34	3	1.9
Q9Z2E1	Mbd2	Methyl-CpG-binding domain protein 2	14.25	5	4	35	1.10	1.34	4	8.5
P52480	Pkm	Pyruvate kinase PKM	66.48	35	35	852	1.10	1.34	204	16.9
P26151	Fcgr1	High affinity immunoglobulin gamma Fc receptor I	11.88	5	5	21	1.10	1.34	2	1.5
Q3UW66	Mpst	Sulfurtransferase	25.25	6	6	40	1.10	1.34	10	17.5
Q02053	Uba1	Ubiquitin-like modifier-activating enzyme 1	7.09	7	7	39	1.10	1.34	8	16.4
Q91V55	Rps5	40S ribosomal protein S5	41.18	9	9	216	1.10	1.34	55	12.0
A2AWT6	Ubtf	Nucleolar transcription factor 1	27.51	21	21	191	1.10	1.34	45	16.2
Q8BKE6	Cyp20a1	Cytochrome P450 20A1	24.46	10	10	66	1.10	1.34	11	16.0
P09528	Fth1	Ferritin heavy chain	23.63	4	4	26	1.10	1.34	4	1.9
Q7M739	Tpr	Nuclear pore complex-associated intranuclear coiled-coil protein TPR	35.51	88	87	809	1.10	1.34	194	15.9
A2AR26	Slc2a6	Protein Slc2a6	15.58	5	5	17	1.10	1.34	6	7.5

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P84104-2	Srsf3	Isoform Short of Serine/arginine-rich splicing factor 3	43.55	7	6	81	1.10	1.34	14	21.2
E9Q1V5	Smpd4	Sphingomyelin phosphodiesterase 4	23.86	15	15	67	1.10	1.33	18	14.9
Q9JIZ5	Tfap4	Activator protein 4	5.33	2	2	4	1.10	1.33	1	
A2AL85	Asph	Aspartyl/asparaginyl beta-hydroxylase	36.69	25	25	346	1.10	1.33	95	21.6
P20029	Hspa5	78 kDa glucose-regulated protein	64.43	46	43	2509	1.10	1.33	647	15.3
P35564	Canx	Calnexin	39.59	32	32	1073	1.10	1.33	335	20.6
Q9JHF5	Tcirg1	V-type proton ATPase subunit a	24.82	17	17	152	1.10	1.33	44	21.0
Q3TFD2	Lpcat1	Lysophosphatidylcholine acyltransferase 1	8.24	4	4	45	1.10	1.33	12	17.4
Q9WV55	Vapa	Vesicle-associated membrane protein-associated protein A	38.96	9	8	190	1.10	1.33	49	10.8
Q8K1B8	Fermt3	Fermitin family homolog 3	21.65	12	12	111	1.10	1.33	24	12.7
Q8C7K6	Pcyox1l	Prenylcysteine oxidase-like	9.49	5	5	39	1.10	1.33	5	6.8
Q9Z1N5	Ddx39b	Spliceosome RNA helicase Ddx39b	24.53	12	5	72	1.10	1.33	3	11.9
Q9D1C1	Ube2c	Ubiquitin-conjugating enzyme E2 C	11.17	2	2	6	1.10	1.33	2	0.6
P27773	Pdia3	Protein disulfide-isomerase A3	62.97	41	41	1665	1.10	1.33	492	15.0
O35841	Api5	Apoptosis inhibitor 5	18.06	10	10	51	1.10	1.33	8	4.8
Q9JHZ2	Ankh	Progressive ankylosis protein	4.67	3	3	18	1.09	1.33	4	4.7
Q9EPL8	Ipo7	Importin-7	3.95	3	3	12	1.09	1.33	4	4.9
Q8CEC0-3	Nup88	Isoform 3 of Nuclear pore complex protein Nup88	14.42	12	12	84	1.09	1.33	12	17.1
Q91V41	Rab14	Ras-related protein Rab-14	70.70	12	11	343	1.09	1.33	77	15.8
Q5SS80-2	Dhrs13	Isoform 2 of Dehydrogenase/reductase SDR family member 13	5.61	2	2	8	1.09	1.33	2	9.5
P97855	G3bp1	Ras GTPase-activating protein-binding protein 1	22.80	8	7	124	1.09	1.33	38	23.4
P30993	C5ar1	C5a anaphylatoxin chemotactic receptor 1	9.97	4	4	25	1.09	1.33	4	7.5
P63321	Rala	Ras-related protein Ral-A	11.17	2	2	6	1.09	1.33	1	
Q60817	Naca	Nascent polypeptide-associated complex subunit alpha	22.79	4	4	49	1.09	1.33	10	11.7
P97363	Sptlc2	Serine palmitoyltransferase 2	16.96	8	8	37	1.09	1.33	4	15.0
Q9Z2G9	Htatip2	Oxidoreductase HTATIP2	23.55	6	6	21	1.09	1.33	5	9.1
G5E8R3	Pcx	Pyruvate carboxylase	4.67	5	5	15	1.09	1.33	2	2.4
Q9R1J0	Nsdhl	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	17.68	6	6	80	1.09	1.33	16	10.9
Q9DBR0	Akap8	A-kinase anchor protein 8	9.32	8	8	52	1.09	1.33	10	10.3
A2AP32	Ndufb6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	14.43	2	2	39	1.09	1.33	3	9.3
Q99JZ4	Sar1a	GTP-binding protein SAR1a	22.73	5	2	76	1.09	1.33	10	5.6
D3Z5M2	Gm10110	Polyadenylate-binding protein	16.91	10	5	43	1.09	1.33	4	10.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
F7ACR9	Macf1	Microtubule-actin cross-linking factor 1 (Fragment)	9.41	44	13	176	1.09	1.33	9	10.2
Q3TMX7	Qsox2	Sulfhydryl oxidase 2	9.10	7	7	24	1.09	1.33	9	15.8
Q61210-3	Arhgef1	Isoform 3 of Rho guanine nucleotide exchange factor 1	9.36	7	7	37	1.09	1.33	7	26.5
Q3TYS2	N/A	Uncharacterized protein C17orf62 homolog	16.04	3	3	23	1.09	1.32	2	4.1
Q99N69	Lpxn	Leupaxin	16.84	5	5	27	1.09	1.32	6	7.1
Q3U1U4	Itgam	Integrin alpha-M	12.99	14	12	108	1.09	1.32	18	14.9
H3BJY3	Abr	Active breakpoint cluster region-related protein (Fragment)	22.60	3	3	7	1.09	1.32	1	
Q62167	Ddx3x	ATP-dependent RNA helicase DDX3X	39.73	24	23	234	1.09	1.32	54	13.8
Q9Z1Q9	Vars	Valine--tRNA ligase	14.57	17	17	86	1.09	1.32	15	7.2
Q9CZ13	Uqcrc1	Cytochrome b-c1 complex subunit 1, mitochondrial	33.54	14	13	351	1.09	1.32	77	15.8
A0A0A6YXP3	Mbnl1	Muscleblind-like protein 1 (Fragment)	19.23	4	4	45	1.09	1.32	10	12.3
Q60649	Clpb	Caseinolytic peptidase B protein homolog	13.88	8	8	27	1.09	1.32	8	11.6
Q9WV30-4	Nfat5	Isoform 4 of Nuclear factor of activated T-cells 5	4.00	5	5	12	1.09	1.32	2	32.4
Q62318	Trim28	Transcription intermediary factor 1-beta	32.85	22	22	316	1.09	1.32	85	16.7
P63325	Rps10	40S ribosomal protein S10	56.36	13	12	389	1.09	1.32	103	14.5
O54864-3	Suv39h1	Isoform 3 of Histone-lysine N-methyltransferase SUV39H1	7.69	2	2	8	1.09	1.32	2	23.0
Q6PDM2	Srsf1	Serine/arginine-rich splicing factor 1	44.35	12	12	172	1.09	1.32	47	22.8
Q60952	Cep250	Centrosome-associated protein CEP250	1.12	2	2	4	1.09	1.32	2	7.4
P47758	Srprb	Signal recognition particle receptor subunit beta	45.35	11	11	129	1.09	1.32	35	11.6
Q9WVK4	Ehd1	EH domain-containing protein 1	17.79	8	8	97	1.09	1.32	27	10.8
P63037	Dnaja1	DnaJ homolog subfamily A member 1	23.43	9	9	37	1.09	1.32	10	8.0
P39749	Fen1	Flap endonuclease 1	7.14	3	3	20	1.09	1.32	4	10.8
Q9CPS5	Psmd8	26S proteasome non-ATPase regulatory subunit 8	6.57	2	2	12	1.09	1.32	1	
P55096	Abcd3	ATP-binding cassette sub-family D member 3	12.59	8	8	31	1.09	1.32	9	18.2
Q8VCW4	Unc93b1	Protein unc-93 homolog B1	9.70	4	4	43	1.09	1.32	9	6.8
Q920A5	Scpep1	Retinoid-inducible serine carboxypeptidase	8.19	4	4	26	1.09	1.32	7	7.2
P98083-3	Shc1	Isoform p47Shc of SHC-transforming protein 1	4.48	2	2	14	1.09	1.32	2	2.9
D3Z7B5	C330027C09Rik	Protein C330027C09Rik	3.64	4	4	13	1.09	1.32	1	
Q9DBG6	Rpn2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	34.23	18	18	363	1.09	1.32	104	19.1
P59708	Sf3b6	Splicing factor 3B subunit 6	27.20	3	3	21	1.08	1.32	2	48.1
A0A0A6YWP6	Atp6v1h	V-type proton ATPase subunit H	12.47	4	4	47	1.08	1.32	9	7.9
P62204	Calm1	Calmodulin	22.15	2	3	6	1.08	1.32	3	6.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P10852	Slc3a2	4F2 cell-surface antigen heavy chain	27.00	14	14	183	1.08	1.32	45	19.7
Q8BFZ9	Erlin2	Erlin-2	23.53	9	6	108	1.08	1.32	8	4.6
Q9CZE3	Rab32	Ras-related protein Rab-32	45.29	9	9	85	1.08	1.32	17	8.5
Q80U93	Nup214	Nuclear pore complex protein Nup214	13.14	26	25	222	1.08	1.32	45	21.4
Q99KV1	Dnajb11	DnaJ homolog subfamily B member 11	41.62	16	16	259	1.08	1.32	70	12.5
Q9CXR1	Dhrs7	Dehydrogenase/reductase SDR family member 7	4.73	2	2	3	1.08	1.32	2	0.6
Q9Z0W3	Nup160	Nuclear pore complex protein Nup160	12.84	16	16	134	1.08	1.32	23	19.6
P06797	Ctsl	Cathepsin L1	16.17	4	4	23	1.08	1.32	7	12.6
Q8VI84	Noc3l	Nucleolar complex protein 3 homolog	4.46	4	4	24	1.08	1.32	2	14.8
Q6ZWV7	Rpl35	60S ribosomal protein L35	30.08	6	4	162	1.08	1.32	37	7.9
P43276	Hist1h1b	Histone H1.5	43.95	14	10	1335	1.08	1.32	187	17.8
Q9Z1G4-3	Atp6v0a1	Isoform A1-III of V-type proton ATPase 116 kDa subunit a isoform 1	2.88	3	3	13	1.08	1.32	3	11.3
A0A0M3HEP3	Lias	Lipoyl synthase, mitochondrial	12.46	3	3	10	1.08	1.32	1	
Q9JIF7	Copb1	Coatomer subunit beta	9.34	8	8	44	1.08	1.32	11	43.7
A0A0A6YX02	Lamtor1	Ragulator complex protein LAMTOR1	28.87	3	3	17	1.08	1.32	5	4.7
Q8BKC5	Ipo5	Importin-5	4.28	5	5	27	1.08	1.32	7	17.0
D3YUW8	Pogz	Pogo transposable element with ZNF domain	2.74	3	3	8	1.08	1.32	2	2.6
Q9WUM5	Suclg1	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	22.83	7	6	97	1.08	1.31	25	11.7
H3BJU7	Arhgef2	Rho guanine nucleotide exchange factor 2	13.39	13	13	58	1.08	1.31	12	12.8
P22437	Ptgs1	Prostaglandin G/H synthase 1	11.79	6	6	43	1.08	1.31	15	16.6
Q9QY81	Nup210	Nuclear pore membrane glycoprotein 210	16.76	29	29	228	1.08	1.31	50	16.8
Q8BX70-3	Vps13c	Isoform 3 of Vacuolar protein sorting-associated protein 13C	10.76	33	33	149	1.08	1.31	28	8.3
Q3TQI7	N/A	Uncharacterized protein C9orf78 homolog	6.92	2	2	5	1.08	1.31	2	9.8
F6V9F1	Pcmt1	Protein-L-isoaspartate O-methyltransferase (Fragment)	8.47	2	2	9	1.08	1.31	1	
Q91VI7	Rnh1	Ribonuclease inhibitor	8.77	3	3	16	1.08	1.31	3	1.7
Q9DBH5	Lman2	Vesicular integral-membrane protein VIP36	33.24	10	10	146	1.08	1.31	34	16.6
P52825	Cpt2	Carnitine O-palmitoyltransferase 2, mitochondrial	12.46	8	8	37	1.08	1.31	8	7.3
Q921Y2	Imp3	U3 small nucleolar ribonucleoprotein protein IMP3	46.74	7	7	40	1.08	1.31	8	9.4
Q9ESP1	Sdf2l1	Stromal cell-derived factor 2-like protein 1	12.67	3	3	60	1.08	1.31	19	16.1
Q6ZWQ7	Spcs3	Signal peptidase complex subunit 3	15.56	3	3	69	1.08	1.31	19	13.6
Q8R1F1	Fam129b	Niban-like protein 1	5.87	4	4	13	1.08	1.31	3	0.3
Q8K1M6-3	Dnm1l	Isoform 3 of Dynamin-1-like protein	11.59	8	8	43	1.08	1.31	4	11.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
G3X956	Supt16	FACT complex subunit SPT16	15.66	16	16	115	1.08	1.31	27	18.3
E9QLA5	Inf2	Inverted formin-2	6.37	8	8	49	1.08	1.31	8	5.4
Q62425	Ndufa4	Cytochrome c oxidase subunit NDUFA4	56.10	6	6	111	1.08	1.31	30	17.0
Q8C898	C130026I21Rik	Protein C130026I21Rik	20.96	6	5	17	1.08	1.31	5	1.3
O08579	Emd	Emerin	37.84	10	10	149	1.08	1.31	41	13.8
A2AFJ8	Arhgef6	Rho guanine nucleotide exchange factor 6	4.76	2	2	2	1.08	1.31	2	12.7
P03930	Mtatp8	ATP synthase protein 8	43.28	3	3	34	1.08	1.31	2	0.0
P10923	Spp1	Osteopontin	12.93	3	3	33	1.08	1.31	6	13.3
Q9ES97-3	Rtn3	Isoform 3 of Reticulon-3	11.39	3	2	140	1.08	1.31	16	14.7
E9Q5B5	Hk2	Hexokinase	9.34	8	6	29	1.08	1.31	4	19.0
P61924	Copz1	Coatomer subunit zeta-1	19.21	2	2	4	1.08	1.31	1	
D3Z2J6	Tmx2	Thioredoxin-related transmembrane protein 2	19.46	5	5	32	1.08	1.31	7	10.5
Q68FD5	Cltc	Clathrin heavy chain 1	32.66	46	46	603	1.08	1.31	138	15.5
O70439	Stx7	Syntaxin-7	16.48	4	4	26	1.08	1.31	6	9.7
P37040	Por	NADPH--cytochrome P450 reductase	43.36	27	27	432	1.08	1.31	98	12.6
Q8CGC7	Eprs	Bifunctional glutamate/proline--tRNA ligase	5.29	8	8	28	1.08	1.31	7	1.5
A0A0G2JE08	Tdrkh	Tudor and KH domain-containing protein	12.84	4	4	14	1.08	1.31	7	10.6
E9QAH1	Golgb1	Protein Golgb1	7.57	24	24	89	1.08	1.31	12	9.9
P39098-2	Man1a2	Isoform 2 of Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB	7.82	4	4	25	1.08	1.31	4	2.9
P70280	Vamp7	Vesicle-associated membrane protein 7	10.91	3	3	18	1.08	1.31	5	9.7
Q60611	Satb1	DNA-binding protein SATB1	2.23	2	2	6	1.08	1.31	2	2.1
Q8C7X2-2	Emc1	Isoform 2 of ER membrane protein complex subunit 1	23.24	21	21	160	1.08	1.31	43	12.7
Q9JHU4	Dync1h1	Cytoplasmic dynein 1 heavy chain 1	4.22	21	21	89	1.08	1.31	17	17.2
P62264	Rps14	40S ribosomal protein S14	40.40	7	7	185	1.08	1.31	51	20.0
Q9WUK4	Rfc2	Replication factor C subunit 2	18.91	6	6	26	1.08	1.31	1	
P51150	Rab7a	Ras-related protein Rab-7a	71.01	14	14	281	1.08	1.31	70	17.9
P60867	Rps20	40S ribosomal protein S20	35.29	5	5	146	1.08	1.31	31	8.2
H3BJ02	Stx5a	Syntaxin-5	18.53	4	4	14	1.08	1.31	1	
P20491	Fcer1g	High affinity immunoglobulin epsilon receptor subunit gamma	25.58	3	3	96	1.08	1.31	25	7.7
O70492	Snx3	Sorting nexin-3	35.80	6	6	25	1.08	1.31	4	19.7
Q8CIB6	Tmem230	Transmembrane protein 230	15.00	2	2	14	1.08	1.31	5	23.7
Q9R1T2-2	Sae1	Isoform 2 of SUMO-activating enzyme subunit 1	4.88	2	2	4	1.08	1.31	1	
Q8CI51	Pdlim5	PDZ and LIM domain protein 5	2.71	2	2	9	1.08	1.31	5	5.6
Q99LB4	Capg	Capping protein (Actin filament), gelsolin-like	20.34	6	6	130	1.08	1.31	28	11.0
E9PYT3	Atl3	Atlastin-3	23.51	10	10	120	1.08	1.31	28	12.1
Q8VC65	Nrm	Nurim	13.36	3	3	17	1.08	1.31	3	7.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
D3YUB9	Pabpn1	Polyadenylate-binding protein 2 (Fragment)	23.17	5	5	42	1.07	1.31	10	8.9
Q5SFM8-3	Rbm27	Isoform 3 of RNA-binding protein 27	4.37	4	4	15	1.07	1.31	3	2.7
Q8VBZ0	Dhrsx	Dehydrogenase/reductase SDR family member on chromosome X homolog	18.21	5	5	14	1.07	1.31	3	7.0
P46471	Psmc2	26S protease regulatory subunit 7	17.78	8	8	30	1.07	1.30	2	4.7
A0A0G2JEW4	Prpf38b	Pre-mRNA-splicing factor 38B	11.54	2	2	3	1.07	1.30	1	
P11031	Sub1	Activated RNA polymerase II transcriptional coactivator p15	22.83	3	3	9	1.07	1.30	2	4.1
Q9CRD0	Ociad1	OCIA domain-containing protein 1	19.43	5	5	44	1.07	1.30	13	12.1
Q792F9	Itga4	Alpha-4 integrin	15.31	16	16	226	1.07	1.30	55	14.9
Q922B2	Dars	Aspartate--tRNA ligase, cytoplasmic	18.56	8	8	42	1.07	1.30	9	16.5
Q76MZ3	Ppp2r1a	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	13.07	7	7	29	1.07	1.30	10	5.6
Q9EQH2	Erap1	Endoplasmic reticulum aminopeptidase 1	13.33	12	12	56	1.07	1.30	9	17.9
A0A0N5E9G7	Rfc1	Replication factor C subunit 1	5.40	7	7	22	1.07	1.30	2	17.4
P61514	Rpl37a	60S ribosomal protein L37a	28.26	2	2	31	1.07	1.30	8	10.6
E9Q6Z3	Tmem194	Nuclear envelope integral membrane protein 1	9.28	4	4	10	1.07	1.30	2	4.2
Q9EQP2	Ehd4	EH domain-containing protein 4	16.08	10	10	62	1.07	1.30	14	13.7
P97287	Mcl1	Induced myeloid leukemia cell differentiation protein Mcl-1 homolog	39.88	10	10	94	1.07	1.30	20	12.4
D3YU17	Ncln	Nicalin	16.55	11	11	98	1.07	1.30	13	13.6
Q9WU81	Slc37a2	Sugar phosphate exchanger 2	7.78	3	3	26	1.07	1.30	6	5.9
Q8BWY3	Etf1	Eukaryotic peptide chain release factor subunit 1	13.04	5	5	21	1.07	1.30	5	9.3
O08547	Sec22b	Vesicle-trafficking protein SEC22b	33.49	8	8	229	1.07	1.30	59	11.9
Q8BG07-2	Pld4	Isoform 2 of Phospholipase D4	7.88	4	3	25	1.07	1.30	7	14.0
P70700	Polr1b	DNA-directed RNA polymerase I subunit RPA2	1.50	2	2	6	1.07	1.30	1	
A0A0R4J0D3	Stt3b	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	5.22	6	4	108	1.07	1.30	16	8.8
P11440	Cdk1	Cyclin-dependent kinase 1	30.30	8	7	49	1.07	1.30	10	8.8
Q80VA0	Galnt7	N-acetylgalactosaminyltransferase 7	42.92	29	29	388	1.07	1.30	91	15.5
O55131	Sep-07	Septin-7	10.78	5	4	17	1.07	1.30	4	9.2
Q8BG51	Rhot1	Mitochondrial Rho GTPase 1	6.81	4	3	27	1.07	1.30	2	2.3
P24668	M6pr	Cation-dependent mannose-6-phosphate receptor	34.17	9	9	153	1.07	1.30	48	8.8
Q8C407	Yipf4	Protein YIPF4	8.13	2	2	13	1.07	1.30	4	6.7
Q9CSH3	Dis3	Exosome complex exonuclease RRP44	4.28	4	4	17	1.07	1.30	1	
Q5XG73-2	Acbd5	Isoform 2 of Acyl-CoA-binding domain-containing protein 5	3.39	2	2	12	1.07	1.30	3	13.2

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P59235	Nup43	Nucleoporin Nup43	12.89	4	4	33	1.07	1.30	6	13.7
O70194	Eif3d	Eukaryotic translation initiation factor 3 subunit D	5.47	3	3	30	1.07	1.30	4	15.9
Q8CG29	Myo1f	Myosin IF	7.83	8	5	29	1.07	1.30	2	18.9
P46638	Rab11b	Ras-related protein Rab-11B	52.29	11	11	171	1.07	1.30	41	15.1
Q60855	Ripk1	Receptor-interacting serine/threonine-protein kinase 1	7.32	4	4	23	1.07	1.30	4	6.1
P16332	Mut	Methylmalonyl-CoA mutase, mitochondrial	15.64	11	11	60	1.07	1.30	8	9.0
Q8BH80	Vapb	Vesicle-associated membrane protein, associated protein B and C	39.92	10	9	193	1.07	1.30	52	11.0
Q9CQE8	N/A	UPF0568 protein C14orf166 homolog	9.43	3	3	24	1.07	1.30	3	8.5
Q62186	Ssr4	Translocon-associated protein subunit delta	36.63	5	5	108	1.07	1.30	26	20.3
Q8BHC4	Dcakd	Dephospho-CoA kinase domain-containing protein	26.41	7	7	40	1.07	1.30	3	9.4
P01902	H2-K1	H-2 class I histocompatibility antigen, K-D alpha chain	35.60	11	10	78	1.07	1.30	19	7.1
S4R2J9	Prrc2c	Protein PRRC2C	2.82	7	7	26	1.07	1.30	4	24.6
Q9CWZ7	Napg	Gamma-soluble NSF attachment protein	24.36	8	8	39	1.07	1.30	8	36.3
Q8VBT0	Tmx1	Thioredoxin-related transmembrane protein 1	18.71	6	6	104	1.07	1.30	29	10.2
Q6DVA0	Lemd2	LEM domain-containing protein 2	8.41	4	4	32	1.07	1.30	7	10.8
Q8JZQ9	Eif3b	Eukaryotic translation initiation factor 3 subunit B	6.72	5	5	44	1.07	1.29	8	13.1
Q9EQK5	Mvp	Major vault protein	14.17	10	10	53	1.07	1.29	13	15.5
O35598	Adam10	Disintegrin and metalloproteinase domain-containing protein 10	9.08	6	6	28	1.07	1.29	2	11.9
Q8BU88	Mrpl22	39S ribosomal protein L22, mitochondrial	24.76	5	5	25	1.06	1.29	3	5.3
P97370	Atp1b3	Sodium/potassium-transporting ATPase subunit beta-3	35.61	9	9	169	1.06	1.29	49	17.0
Q8BMK4	Ckap4	Cytoskeleton-associated protein 4	58.43	34	34	478	1.06	1.29	120	10.3
O55242-2	Sigmar1	Isoform 2 of Sigma non-opioid intracellular receptor 1	20.31	4	4	58	1.06	1.29	9	15.8
Q9EQ61	Pes1	Pescadillo homolog	16.44	11	11	126	1.06	1.29	29	11.7
Q9R099	Tbl2	Transducin beta-like protein 2	16.97	6	6	33	1.06	1.29	7	14.5
Q8CCF0-2	Prpf31	Isoform 2 of U4/U6 small nuclear ribonucleoprotein Prp31	16.02	8	8	39	1.06	1.29	10	9.7
Q3U1J4	Ddb1	DNA damage-binding protein 1	13.33	16	16	76	1.06	1.29	11	17.3
Q9WUM4	Coro1c	Coronin-1C	8.44	5	5	16	1.06	1.29	2	23.8
Q9D6K5	Synj2bp	Synaptojanin-2-binding protein	40.00	5	5	40	1.06	1.29	8	7.4
Q9JII5-2	Dazap1	Isoform 2 of DAZ-associated protein 1	16.05	5	5	89	1.06	1.29	17	6.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9JKF1	Iqgap1	Ras GTPase-activating-like protein IQGAP1	27.10	37	37	249	1.06	1.29	51	9.6
Q9QWF0	Chaf1a	Chromatin assembly factor 1 subunit A	3.62	3	3	9	1.06	1.29	1	
Q6ZQM8	Ugt1a7c	UDP-glucuronosyltransferase 1-7C	24.29	12	12	114	1.06	1.29	29	15.3
D3YWT0	Sec11a	Signal peptidase complex catalytic subunit SEC11	24.12	5	5	103	1.06	1.29	24	27.3
F8WIB1	Arl1	ADP-ribosylation factor-like protein 1 (Fragment)	34.78	3	3	24	1.06	1.29	6	19.3
Q3TB92-2	Milr1	Isoform 2 of Allergin-1	12.50	2	2	20	1.06	1.29	1	
P80318	Cct3	T-complex protein 1 subunit gamma	35.60	20	20	162	1.06	1.29	34	13.6
P26369	U2af2	Splicing factor U2AF 65 kDa subunit	24.84	11	11	86	1.06	1.29	22	14.8
D3Z286	Tmppe	Protein Tmppe	6.26	2	2	2	1.06	1.29	1	
Q9DCJ5	Ndufa8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	57.56	9	9	88	1.06	1.29	23	8.3
E9Q986	Ctnnd1	Catenin delta-1	7.23	7	7	37	1.06	1.29	8	17.6
D3YTM0	Cers2	Ceramide synthase 2 (Fragment)	18.64	4	4	99	1.06	1.29	30	17.4
P28798	Grn	Granulins	6.62	3	3	18	1.06	1.29	5	16.8
Q5I012-4	Slc38a10	Isoform 4 of Putative sodium-coupled neutral amino acid transporter 10	2.13	2	2	4	1.06	1.29	1	
Q9R1Q9	Atp6ap1	V-type proton ATPase subunit S1	14.69	6	6	34	1.06	1.29	9	13.1
Q8BTY8-4	Scfd2	Isoform 4 of Sec1 family domain-containing protein 2	7.78	2	2	6	1.06	1.29	2	7.2
Q3UEB3-3	Puf60	Isoform 3 of Poly(U)-binding-splicing factor PUF60	20.44	10	10	80	1.06	1.29	19	18.1
Q8BTS4	Nup54	Nuclear pore complex protein Nup54	32.94	14	13	119	1.06	1.29	29	14.9
Q6GQT9	Nomo1	Nodal modulator 1	21.99	23	23	218	1.06	1.29	50	11.7
Q80X85	Mrps7	28S ribosomal protein S7, mitochondrial	38.43	8	8	64	1.06	1.29	15	15.9
Q9EP69	Sacm1l	Phosphatidylinositide phosphatase SAC1	19.25	11	11	101	1.06	1.29	18	21.0
Q8VBZ3	Clptm1	Cleft lip and palate transmembrane protein 1 homolog	10.09	6	6	42	1.06	1.29	10	10.1
Q9D1C9	Rrp7a	Ribosomal RNA-processing protein 7 homolog A	14.29	3	3	20	1.06	1.29	5	3.7
Q3U0V1	Khsrp	Far upstream element-binding protein 2	44.65	34	29	844	1.06	1.29	179	14.6
E9Q2X6	Smc4	Structural maintenance of chromosomes protein	7.45	9	9	51	1.06	1.29	11	30.7
O09106	Hdac1	Histone deacetylase 1	21.58	11	9	58	1.06	1.29	8	11.9
Q9Z0J0	Npc2	Epididymal secretory protein E1	23.49	3	3	5	1.06	1.29	3	19.7
Q6PCN7	Hltf	Helicase-like transcription factor	3.89	4	3	22	1.06	1.29	3	8.1
P48962	Slc25a4	ADP/ATP translocase 1	60.07	18	9	648	1.06	1.29	37	18.2
P61358	Rpl27	60S ribosomal protein L27	48.53	7	7	213	1.06	1.29	58	14.6
P01897	H2-L	H-2 class I histocompatibility antigen, L-D alpha	23.20	8	5	122	1.06	1.29	10	11.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		chain								
Q8K078-2	Slco4a1	Isoform 2 of Solute carrier organic anion transporter family member 4A1	9.65	7	7	101	1.06	1.28	24	8.8
E9PZ00	Psap	Prosaposin	7.08	4	4	40	1.06	1.28	11	12.1
P14211	Calr	Calreticulin	60.82	25	25	893	1.06	1.28	266	16.3
Q9DB05	Napa	Alpha-soluble NSF attachment protein	39.66	10	10	92	1.06	1.28	23	14.4
P08249	Mdh2	Malate dehydrogenase, mitochondrial	71.30	21	21	835	1.06	1.28	229	19.4
P09103	P4hb	Protein disulfide-isomerase	68.76	37	34	1543	1.06	1.28	436	19.3
Q7M6W1	Rtn1	Reticulon	7.69	2	1	98	1.06	1.28	2	9.9
Q8VI36-2	Pxn	Isoform Alpha of Paxillin	10.05	5	5	38	1.06	1.28	5	1.6
Q8K021	Scamp1	Secretory carrier-associated membrane protein 1	12.43	3	3	13	1.06	1.28	3	19.5
P13864	Dnmt1	DNA (cytosine-5)-methyltransferase 1	29.01	42	42	405	1.06	1.28	90	11.0
Q64433	Hspe1	10 kDa heat shock protein, mitochondrial	67.65	7	7	495	1.06	1.28	138	14.5
P61226	Rap2b	Ras-related protein Rap-2b	16.39	3	3	14	1.06	1.28	3	4.9
Q60862	Orc2	Origin recognition complex subunit 2	9.72	6	6	25	1.06	1.28	4	16.8
Q8BK64	Ahsa1	Activator of 90 kDa heat shock protein ATPase homolog 1	22.78	6	6	65	1.06	1.28	15	8.2
Q99J62	Rfc4	Replication factor C subunit 4	25.00	9	9	64	1.05	1.28	6	11.5
Q8VE80	Thoc3	THO complex subunit 3	7.12	3	3	27	1.05	1.28	2	8.8
P23198	Cbx3	Chromobox protein homolog 3	27.87	6	6	56	1.05	1.28	16	9.6
Q8K2C9	Hacd3	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	12.98	4	4	52	1.05	1.28	12	17.9
Q9CQJ4	Rnf2	E3 ubiquitin-protein ligase RING2	11.90	3	2	10	1.05	1.28	1	
D3YYK0	Abhd11	Abhydrolase domain containing 11, isoform CRA_b	11.45	3	3	13	1.05	1.28	2	0.3
G3X8R0	Reep5	Receptor expression-enhancing protein	16.40	5	5	84	1.05	1.28	18	12.6
Q9JHI5	Ivd	Isovaleryl-CoA dehydrogenase, mitochondrial	8.49	4	4	9	1.05	1.28	2	6.9
Q78IK4	Apool	MICOS complex subunit Mic27	27.92	7	7	31	1.05	1.28	4	1.6
Q9CZ83	Mrpl55	39S ribosomal protein L55, mitochondrial	30.71	4	4	12	1.05	1.28	2	9.4
P10639	Txn	Thioredoxin	20.95	2	2	20	1.05	1.28	4	1.5
G3UX26	Vdac2	Voltage-dependent anion-selective channel protein 2 (Fragment)	74.20	17	16	435	1.05	1.28	119	11.1
O70145	Ncf2	Neutrophil cytosol factor 2	7.62	4	4	15	1.05	1.28	2	4.8
Q8BPU7	Elmo1	Engulfment and cell motility protein 1	11.28	7	7	29	1.05	1.28	7	9.1
Q9CZU3	Skiv2l2	Superkiller viralicidic activity 2-like 2	12.60	14	14	79	1.05	1.28	12	4.7
Q61093	Cybb	Cytochrome b-245 heavy chain	29.82	18	18	179	1.05	1.28	57	12.6
Q922J9	Far1	Fatty acyl-CoA reductase 1	22.14	11	11	123	1.05	1.28	29	13.8
Q80ZW2	Them6	Protein THEM6	43.96	10	10	93	1.05	1.28	17	8.0

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P61161	Actr2	Actin-related protein 2	9.90	4	3	65	1.05	1.28	8	25.2
G3UXL2	Prps1l3	Protein Prps1l3	8.49	3	3	8	1.05	1.28	1	
O89017	Lgmn	Legumain	10.11	4	4	19	1.05	1.28	6	71.8
Q61334	Bcap29	B-cell receptor-associated protein 29	20.00	7	7	124	1.05	1.28	32	13.0
P99029	Prdx5	Peroxiredoxin-5, mitochondrial	46.19	10	10	96	1.05	1.27	25	11.3
Q80UM7	Mogs	Mannosyl-oligosaccharide glucosidase	25.18	18	18	257	1.05	1.27	66	15.0
P62983	Rps27a	Ubiquitin-40S ribosomal protein S27a	53.85	9	9	1065	1.05	1.27	347	15.5
P58742	Aaas	Aladin	18.50	8	8	69	1.05	1.27	19	12.0
Q9DCF9-2	Ssr3	Isoform 2 of Translocon-associated protein subunit gamma	16.20	5	4	34	1.05	1.27	9	4.7
Q921W0	Chmp1a	Charged multivesicular body protein 1a	11.73	3	3	14	1.05	1.27	2	1.1
Q9CPQ8	Atp5l	ATP synthase subunit g, mitochondrial	31.07	3	3	84	1.05	1.27	20	6.8
P03975	Iap	IgE-binding protein	12.93	6	6	41	1.05	1.27	12	15.6
A0A0R4J0R1	Vamp8	Vesicle-associated membrane protein 8	40.59	4	4	60	1.05	1.27	11	8.9
Q6NZL1	Dhx37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	4.26	5	5	19	1.05	1.27	5	11.1
Q9JL26	Fmnl1	Formin-like protein 1	18.46	18	18	107	1.05	1.27	26	12.6
P08113	Hsp90b1	Endoplasmin	46.01	41	39	1853	1.05	1.27	490	14.0
Q9D024	Ccdc47	Coiled-coil domain-containing protein 47	11.39	7	7	71	1.05	1.27	19	6.8
Q62351	Tfrc	Transferrin receptor protein 1	31.98	25	25	461	1.05	1.27	114	14.5
P62715	Ppp2cb	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	6.15	2	2	12	1.05	1.27	2	9.6
Q8K2B3	Sdha	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	37.80	21	21	341	1.05	1.27	83	14.0
O70252	Hmox2	Heme oxygenase 2	32.38	8	8	97	1.05	1.27	25	8.3
Q9CR59	Gadd45gip1	Growth arrest and DNA damage-inducible proteins-interacting protein 1	11.71	3	3	9	1.05	1.27	1	
Q91YQ5	Rpn1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	54.61	37	37	1008	1.05	1.27	260	17.8
Q9DCU6	Mrpl4	39S ribosomal protein L4, mitochondrial	22.79	6	6	44	1.05	1.27	9	23.2
Q9CQ54	Ndufc2	NADH dehydrogenase [ubiquinone] 1 subunit C2	32.50	5	5	22	1.05	1.27	9	17.8
Q9ER88	Dap3	28S ribosomal protein S29, mitochondrial	24.55	9	9	50	1.04	1.27	14	15.9
P10107	Anxa1	Annexin A1	32.66	10	9	61	1.04	1.27	12	19.5
Q6ZQH8	Nup188	Nucleoporin NUP188 homolog	10.29	18	17	68	1.04	1.27	12	13.3
P62315	Snrpd1	Small nuclear ribonucleoprotein Sm D1	36.97	4	4	56	1.04	1.27	13	7.8
Q91XE8	Tmem205	Transmembrane protein 205	17.46	3	3	61	1.04	1.27	14	13.9
Q542I8	Itgb2	Integrin beta	38.31	25	25	275	1.04	1.27	65	23.0
P35282	Rab21	Ras-related protein Rab-21	27.48	5	5	22	1.04	1.27	7	6.4
P57759	Erp29	Endoplasmic reticulum resident protein 29	36.26	8	8	180	1.04	1.27	46	5.7
P48410	Abcd1	ATP-binding cassette sub-family D member 1	11.14	7	7	45	1.04	1.27	5	23.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P51881	Slc25a5	ADP/ATP translocase 2	53.69	17	8	794	1.04	1.27	87	15.5
S4R293	Ncf1	Neutrophil cytosol factor 1	28.38	11		116	1.04	1.27	31	9.0
Q9JKN1	Slc30a7	Zinc transporter 7	9.52	3		57	1.04	1.27	11	10.7
Q9JI13	Utp3	Something about silencing protein 10	10.45	5		54	1.04	1.27	10	7.1
Q8R3K3	Ptcd2	Pentatricopeptide repeat-containing protein 2, mitochondrial	4.72	2		8	1.04	1.27	3	14.6
O54946-2	Dnajb6	Isoform B of DnaJ homolog subfamily B member 6	15.70	4		19	1.04	1.27	8	5.5
Q6NVG1	Lpcat4	Lysophospholipid acyltransferase LPCAT4	7.44	3		14	1.04	1.27	3	29.5
Q99MR3	Slc12a9	Solute carrier family 12 member 9	3.83	4		10	1.04	1.27	5	13.5
P63038	Hspd1	60 kDa heat shock protein, mitochondrial	76.44	37		1563	1.04	1.27	488	25.9
G3UZI2	Syncrip	Heterogeneous nuclear ribonucleoprotein Q	36.81	19		291	1.04	1.27	38	17.3
Q921E6-3	Eed	Isoform 3 of Polycomb protein EED	8.43	3		11	1.04	1.27	3	6.8
Q99LH1	Gnl2	Nucleolar GTP-binding protein 2	7.14	5		26	1.04	1.27	6	6.7
Q3UM18	Lsg1	Large subunit GTPase 1 homolog	9.01	7		38	1.04	1.27	8	12.0
Q9D8V0	Hm13	Minor histocompatibility antigen H13	16.40	6		97	1.04	1.27	33	17.6
Z4YKT6	Dhrs7b	Dehydrogenase/reductase SDR family member 7B	21.43	7		42	1.04	1.27	8	17.8
Q8BYB9	Poglut1	Protein O-glucosyltransferase 1	7.65	3		9	1.04	1.27	1	
E9PZM7	Scaf11	Protein Scaf11	1.51	2		7	1.04	1.27	2	1.5
Q62189	Snrpa	U1 small nuclear ribonucleoprotein A	25.09	7		149	1.04	1.27	32	10.7
E9Q634	Myo1e	Unconventional myosin-Ie	8.94	9		28	1.04	1.26	4	14.0
P00405	Mtco2	Cytochrome c oxidase subunit 2	17.62	4		138	1.04	1.26	43	10.2
Q8BT07	Cep55	Centrosomal protein of 55 kDa	10.82	5		14	1.04	1.26	3	7.1
P62301	Rps13	40S ribosomal protein S13	68.21	13		327	1.04	1.26	80	15.8
Q6P8H8	Alg8	Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	3.23	2		4	1.04	1.26	1	
A0A0G2JEG3	Slc35f6	Solute carrier family 35 member F6	9.09	3		10	1.04	1.26	1	
Q8K4Q8	Colec12	Collectin-12	13.88	12		57	1.04	1.26	12	8.2
Q91WM3	Rrp9	U3 small nucleolar RNA-interacting protein 2	20.00	9		59	1.04	1.26	13	10.8
Q3U8Y1	Mrps11	28S ribosomal protein S11, mitochondrial	13.61	2		17	1.04	1.26	4	12.2
Q6P542	Abcf1	ATP-binding cassette sub-family F member 1	3.58	3		26	1.04	1.26	2	11.5
O54734	Ddost	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	38.32	15		326	1.04	1.26	98	15.9
Q9D0Q7	Mrpl45	39S ribosomal protein L45, mitochondrial	13.73	5		20	1.04	1.26	5	12.8
Q9EQI8	Mrpl46	39S ribosomal protein L46, mitochondrial	10.95	3		17	1.04	1.26	3	32.9
P70404	Idh3g	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	18.58	8		103	1.04	1.26	18	11.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q99MD9-2	Nasp	Isoform 2 of Nuclear autoantigenic sperm protein	5.94	3		24	1.04	1.26	1	
Q8C129	Lnpep	Leucyl-cystinyl aminopeptidase	4.78	5		12	1.04	1.26	2	43.7
Q8BJY1	Psmd5	26S proteasome non-ATPase regulatory subunit 5	5.36	2		9	1.04	1.26	3	45.2
P52875	Tmem165	Transmembrane protein 165	22.60	4		17	1.04	1.26	4	10.5
Q9D1P0	Mrpl13	39S ribosomal protein L13, mitochondrial	41.57	7		60	1.04	1.26	13	6.3
P11152	Lpl	Lipoprotein lipase	20.25	9		58	1.04	1.26	15	10.5
G3X963	Atad2	ATPase family AAA domain-containing protein 2	7.04	8		51	1.04	1.26	6	17.4
Q9WU78	Pdcd6ip	Programmed cell death 6-interacting protein	39.82	34		316	1.04	1.26	83	10.7
P08003	Pdia4	Protein disulfide-isomerase A4	52.82	36		659	1.04	1.26	167	13.4
F6VQH5	Hnrnpdl	Heterogeneous nuclear ribonucleoprotein D-like (Fragment)	27.86	11		167	1.04	1.26	34	12.0
Q9Z2I0	Letm1	LETM1 and EF-hand domain-containing protein 1, mitochondrial	20.46	13		71	1.04	1.26	16	26.6
Q9Z0F8	Adam17	Disintegrin and metalloproteinase domain-containing protein 17	6.65	5		26	1.04	1.26	6	26.7
F6QKD2	Ddx47	Probable ATP-dependent RNA helicase DDX47 (Fragment)	14.44	5		23	1.04	1.26	4	11.5
P84084	Arf5	ADP-ribosylation factor 5	46.11	7		79	1.04	1.26	6	5.6
P61327	Magoh	Protein mago nashi homolog	40.41	6		47	1.04	1.26	12	6.4
Q6PD26	Pigs	GPI transamidase component PIG-S	22.34	11		82	1.04	1.26	17	16.3
Q9D0E1-2	Hnrnpm	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	52.90	41		746	1.04	1.26	196	15.5
O54962	Banf1	Barrier-to-autointegration factor	43.82	3		23	1.04	1.26	5	12.8
Q9WTR1	Trpv2	Transient receptor potential cation channel subfamily V member 2	4.89	3		6	1.04	1.26	2	10.3
E9PVA8	Gcn1l1	Protein Gcn1l1	1.65	5		35	1.04	1.26	7	5.2
P60122	Ruvbl1	RuvB-like 1	35.96	12		68	1.04	1.26	15	25.4
P24369	Ppib	Peptidyl-prolyl cis-trans isomerase B	57.41	15		288	1.03	1.26	75	12.1
Q62086	Pon2	Serum paraoxonase/arylesterase 2	16.38	5		33	1.03	1.26	5	7.2
Q8CI11	Gnl3	Guanine nucleotide-binding protein-like 3	42.57	19		106	1.03	1.26	24	14.1
Q91YT7	Ythdf2	YTH domain-containing family protein 2	15.72	9		74	1.03	1.26	9	19.0
Q9D1Q6	Erp44	Endoplasmic reticulum resident protein 44	31.03	13		115	1.03	1.26	19	14.8
Q8R3N1	Nop14	Nucleolar protein 14	16.05	13		75	1.03	1.26	18	14.7
Q62087	Pon3	Serum paraoxonase/lactonase 3	24.29	7		77	1.03	1.25	15	18.9
Q91ZE0	Tmlhe	Trimethyllysine dioxygenase, mitochondrial	11.16	4		28	1.03	1.25	5	63.3
Q99K23	Ufsp2	Ufm1-specific protease 2	8.89	3		15	1.03	1.25	3	7.5
Q61233	Lcp1	Plastin-2	46.73	25		315	1.03	1.25	63	19.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q60932-2	Vdac1	Isoform Mt-VDAC1 of Voltage-dependent anion-selective channel protein 1	76.68	19		400	1.03	1.25	93	16.0
Q91VZ6	Smap1	Stromal membrane-associated protein 1	7.50	3		34	1.03	1.25	7	12.0
Q8R050-2	Gspt1	Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	4.25	3		10	1.03	1.25	1	
E9QL31	Dab2	Disabled homolog 2	30.34	18		177	1.03	1.25	30	13.8
Q99KI3	Emc3	ER membrane protein complex subunit 3	8.81	2		2	1.03	1.25	1	
Q8BR65	Suds3	Sin3 histone deacetylase corepressor complex component SDS3	7.62	2		6	1.03	1.25	2	3.4
G3X926	Rpf2	MCG1407, isoform CRA_a	22.71	6		54	1.03	1.25	12	10.6
A2AMW0	Capzb	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a	18.85	6		60	1.03	1.25	14	12.2
Q9R1P4	Psma1	Proteasome subunit alpha type-1	36.12	10		67	1.03	1.25	7	19.0
Q61656	Ddx5	Probable ATP-dependent RNA helicase DDX5	44.14	30		893	1.03	1.25	152	10.3
Q6PF96	Etfdh	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	19.96	11		83	1.03	1.25	18	13.0
Q9DBS1	Tmem43	Transmembrane protein 43	38.00	11		113	1.03	1.25	27	18.8
P30412	Ppic	Peptidyl-prolyl cis-trans isomerase C	13.68	3		26	1.03	1.25	2	2.4
P25799-4	Nfkb1	Isoform 4 of Nuclear factor NF-kappa-B p105 subunit	10.39	2		20	1.03	1.25	4	13.7
Q99LR1	Abhd12	Monoacylglycerol lipase ABHD12	11.06	3		9	1.03	1.25	3	17.0
O55234	Psmb5	Proteasome subunit beta type-5	22.35	5		32	1.03	1.25	7	10.8
O88531	Ppt1	Palmitoyl-protein thioesterase 1	26.80	7		40	1.03	1.25	9	12.4
Q9CQF9	Pcyox1	Prenylcysteine oxidase	8.12	3		23	1.03	1.25	4	13.2
O35730-3	Ring1	Isoform 3 of E3 ubiquitin-protein ligase RING1	16.39	2		10	1.03	1.25	1	
Q09200	B4galnt1	Beta-1,4 N-acetylgalactosaminyltransferase 1	21.20	12		108	1.03	1.25	24	14.5
A0A0U1RNJ1	Fasn	Fatty acid synthase	3.32	8		34	1.03	1.25	7	26.9
Q9DCS3	Mecr	Trans-2-enoyl-CoA reductase, mitochondrial	19.57	6		35	1.03	1.25	6	14.6
P11928	Oas1a	2'-5'-oligoadenylate synthase 1A	20.16	6		63	1.03	1.25	14	18.3
Q9Z0M5	Lipa	Lysosomal acid lipase/cholesteryl ester hydrolase	6.55	4		35	1.03	1.25	14	7.5
Q9DBL1	Acadsb	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	11.81	5		14	1.03	1.25	4	5.5
P03966	Mycn	N-myc proto-oncogene protein	6.93	4		18	1.03	1.25	3	3.6
Q61136	Prpf4b	Serine/threonine-protein kinase PRP4 homolog	4.27	4		15	1.03	1.25	1	
P32067	Ssb	Lupus La protein homolog	21.45	10		85	1.03	1.25	12	13.3
Q8R0J2	Mpdu1	Mannose-P-dolichol utilization defect 1	8.10	2		15	1.03	1.25	2	7.0
Q8R3N6	Thoc1	THO complex subunit 1	10.50	7		54	1.03	1.25	15	13.6
A0A0G2JGL8	Dhx30	Putative ATP-dependent RNA helicase DHX30	2.36	2		6	1.03	1.25	2	18.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8VCH6	Dhcr24	Delta(24)-sterol reductase	3.10	2		4	1.03	1.25	1	
Q9D2R8	Mrps33	28S ribosomal protein S33, mitochondrial	28.30	3		20	1.03	1.25	5	41.6
Q9DCN2-2	Cyb5r3	Isoform 2 of NADH-cytochrome b5 reductase 3	46.76	12		191	1.03	1.25	46	17.3
Q8BP92	Rcn2	Reticulocalbin-2	27.19	6		49	1.03	1.25	10	13.5
Q62393-2	Tpd52	Isoform 2 of Tumor protein D52	20.54	4		34	1.03	1.25	5	36.1
Q3UBW1	Spryd7	SPRY domain-containing protein 7	13.50	2		12	1.03	1.25	3	2.5
D3YZZ5	Tmed7	Protein Tmed7	28.13	7		85	1.03	1.25	18	10.4
A2AMV1	Mrto4	RIKEN cDNA 2610012O22, isoform CRA_a	36.13	9		67	1.03	1.25	14	13.2
O35604	Npc1	Niemann-Pick C1 protein	3.76	5		15	1.03	1.25	4	15.3
Q9JIW9	Ralb	Ras-related protein Ral-B	23.79	6		48	1.03	1.25	11	16.6
O08583	Alyref	THO complex subunit 4	34.12	7		164	1.03	1.25	40	15.3
Q8CC88-2	Vwa8	Isoform 2 of von Willebrand factor A domain-containing protein 8	6.26	6		27	1.03	1.25	6	7.6
D3Z568	Ndufb5	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 5, isoform CRA_e	33.61	4		71	1.03	1.25	16	11.0
Q9WTM5	Ruvbl2	RuvB-like 2	34.56	14		135	1.03	1.25	34	11.5
Q08857	Cd36	Platelet glycoprotein 4	4.24	2		15	1.02	1.25	2	2.6
Q9CWX4	Rpusd4	RNA pseudouridylate synthase domain-containing protein 4	7.16	3		15	1.02	1.25	2	22.8
Q9EPJ9	Arfgap1	ADP-ribosylation factor GTPase-activating protein 1	20.53	8		56	1.02	1.25	16	6.8
E9QKE9	Cux1	Homeobox protein cut-like	20.48	26		143	1.02	1.24	1	
Q8BU03	Pwp2	Periodic tryptophan protein 2 homolog	9.68	10		44	1.02	1.24	6	18.6
Q9CY50	Ssr1	Translocon-associated protein subunit alpha	13.99	4		134	1.02	1.24	31	14.2
P35821	Ptpn1	Tyrosine-protein phosphatase non-receptor type 1	12.27	5		27	1.02	1.24	6	18.0
Q8VEH8	Erlec1	Endoplasmic reticulum lectin 1	3.11	2		2	1.02	1.24	2	2.8
P18155	Mthfd2	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	44.29	11		126	1.02	1.24	21	8.7
Q3V3R1	Mthfd1l	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	32.45	31		430	1.02	1.24	103	14.5
P97304	Polr1d	DNA-directed RNA polymerases I and III subunit RPAC2	19.55	2		4	1.02	1.24	1	
Q9EP89	Lactb	Serine beta-lactamase-like protein LACTB, mitochondrial	13.61	6		23	1.02	1.24	4	21.4
Q9JIH2	Nup50	Nuclear pore complex protein Nup50	24.68	10		60	1.02	1.24	14	15.0
P17047-3	Lamp2	Isoform LAMP-2C of Lysosome-associated membrane glycoprotein 2	11.81	6		90	1.02	1.24	16	8.1
G3UVU2	Sf3a2	Splicing factor 3A subunit 2	8.25	4		69	1.02	1.24	21	8.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P15864	Hist1h1c	Histone H1.2	50.94	15		1614	1.02	1.24	83	10.5
Q6A4J8-3	Usp7	Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 7	3.82	3		8	1.02	1.24	2	10.3
Q921H8	Acaa1a	3-ketoacyl-CoA thiolase A, peroxisomal	60.85	20		348	1.02	1.24	95	15.2
Q9CQY5-2	Magt1	Isoform 2 of Magnesium transporter protein 1	14.38	6		91	1.02	1.24	20	12.3
Q64521	Gpd2	Glycerol-3-phosphate dehydrogenase, mitochondrial	27.37	18		118	1.02	1.24	25	17.2
Q5U458	Dnajc11	DnaJ homolog subfamily C member 11	10.20	6		46	1.02	1.24	7	6.7
P62911	Rpl32	60S ribosomal protein L32	25.19	4		99	1.02	1.24	32	13.3
Q9QZM0	Ubqln2	Ubiquilin-2	10.03	5		43	1.02	1.24	2	16.6
Q6P5H2-2	Nes	Isoform 2 of Nestin	1.37	2		4	1.02	1.24	2	14.8
Q9CXU4	Gm10273	MCG11298	16.75	3		32	1.02	1.24	4	5.3
P49718	Mcm5	DNA replication licensing factor MCM5	12.96	8		37	1.02	1.24	7	15.1
Q8VCH8	Ubxn4	UBX domain-containing protein 4	16.60	7		65	1.02	1.24	17	13.2
Q9D7Z3	Nol7	Nucleolar protein 7	11.81	4		16	1.02	1.24	3	2.3
P61620	Sec61a1	Protein transport protein Sec61 subunit alpha isoform 1	14.71	7		264	1.02	1.24	83	15.2
D3Z0V9	Sun1	SUN domain-containing protein 1	6.87	6		44	1.02	1.24	13	16.2
P26516	Psmd7	26S proteasome non-ATPase regulatory subunit 7	5.92	2		14	1.02	1.24	3	0.6
P28033-3	Cebpb	Isoform 2 of CCAAT/enhancer-binding protein beta	16.73	4		27	1.02	1.24	3	3.0
Q64FW2	Retsat	All-trans-retinol 13,14-reductase	14.78	9		65	1.02	1.24	6	19.5
Q91Z49-2	Fyttd1	Isoform 2 of UAP56-interacting factor	17.31	5		27	1.02	1.24	4	18.2
Q8CIE2-2	Zmiz2	Isoform 2 of Zinc finger MIZ domain-containing protein 2	2.03	2		10	1.02	1.24	2	2.8
P30204	Msr1	Macrophage scavenger receptor types I and II	11.79	7		104	1.02	1.24	20	9.2
Q3TBD2-4	Hmha1	Isoform 4 of Minor histocompatibility protein HA-1	5.34	4		10	1.02	1.24	3	12.5
Q99LX0	Park7	Protein deglycase DJ-1	16.40	4		14	1.02	1.24	3	7.0
A2AFJ1	Rbbp7	Histone-binding protein RBBP7	23.56	8		150	1.02	1.24	5	12.7
A0A0N4SV32	Serbp1	Plasminogen activator inhibitor 1 RNA-binding protein	35.36	12		129	1.02	1.24	33	12.4
F8WGB3	Sdhc	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	15.56	2		5	1.02	1.24	1	
O35465	Fkbp8	Peptidyl-prolyl cis-trans isomerase FKBP8	23.63	9		98	1.02	1.24	25	15.0
Q63850	Nup62	Nuclear pore glycoprotein p62	17.30	11		136	1.02	1.24	35	22.2
Q9Z1X4	Ilf3	Interleukin enhancer-binding factor 3	18.82	17		133	1.02	1.24	22	12.3
Q99M28	Rnps1	RNA-binding protein with serine-rich domain 1	13.11	4		39	1.02	1.24	11	13.0

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P70452	Stx4	Syntaxin-4	8.05	3		7	1.02	1.24	1	
Q9CR68	Uqcrfs1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	40.51	12		151	1.02	1.24	37	11.5
Q8C845	Efhd2	EF-hand domain-containing protein D2	50.83	12		182	1.02	1.24	38	18.4
P47738	Aldh2	Aldehyde dehydrogenase, mitochondrial	55.49	23		568	1.02	1.24	157	18.6
Q9WU62-2	Incenp	Isoform 2 of Inner centromere protein	8.56	6		25	1.02	1.24	5	19.0
A2AR02	Ppig	Peptidyl-prolyl cis-trans isomerase G	2.66	2		9	1.02	1.24	1	
Q9D0F3	Lman1	Protein ERGIC-53	27.47	14		184	1.02	1.24	43	11.0
A0A0R4J1Y7	Txndc5	Thioredoxin domain-containing protein 5	40.56	11		108	1.02	1.24	31	20.0
P14685	Psmd3	26S proteasome non-ATPase regulatory subunit 3	7.55	4		16	1.02	1.24	4	12.1
Q8R4R6	Nup35	Nucleoporin NUP53	38.46	9		132	1.02	1.24	39	22.2
Q80YD1	Supv3l1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	4.49	3		11	1.02	1.24	2	12.2
B1B1D8	Mrpl2	39S ribosomal protein L2, mitochondrial	5.92	2		4	1.02	1.24	2	14.4
Q9DAW6	Prpf4	U4/U6 small nuclear ribonucleoprotein Prp4	22.84	10		44	1.02	1.24	8	6.6
P56382	Atp5e	ATP synthase subunit epsilon, mitochondrial	42.31	3		75	1.02	1.24	23	8.0
Q8VE99	Ccdc115	Coiled-coil domain-containing protein 115	43.33	7		69	1.02	1.24	14	21.2
A0A0J9YV01	Zeb2	Zinc finger E-box-binding homeobox 2	3.95	5		12	1.02	1.24	3	7.7
A0A0G2JEC3	Mef2c	Myocyte-specific enhancer factor 2C (Fragment)	8.84	2		12	1.02	1.24	2	9.3
G3UZA4	Csnk2b	Casein kinase II subunit beta (Fragment)	17.89	2		9	1.02	1.24	1	
Q3U4W8	Usp5	Ubiquitin carboxyl-terminal hydrolase 5	2.04	2		9	1.02	1.24	3	27.4
E9Q1T9	Cse1l	Exportin-2	5.36	6		46	1.02	1.23	9	20.5
O08795	Prkcsh	Glucosidase 2 subunit beta	30.13	17		224	1.02	1.23	52	12.3
O35887	Calu	Calumenin	41.90	12		116	1.02	1.23	26	14.3
Q922R8	Pdia6	Protein disulfide-isomerase A6	46.14	15		537	1.02	1.23	157	21.6
Q9Z315	Sart1	U4/U6.U5 tri-snRNP-associated protein 1	19.11	15		93	1.02	1.23	14	30.0
Q922S4	Pde2a	cGMP-dependent 3',5'-cyclic phosphodiesterase	7.42	7		22	1.02	1.23	4	12.2
Q3TAS6-2	Emc10	Isoform 2 of ER membrane protein complex subunit 10	13.39	3		20	1.02	1.23	4	2.6
P23949	Zfp36l2	Zinc finger protein 36, C3H1 type-like 2	7.23	3		12	1.02	1.23	2	10.5
Q8BXN9	Tmem87a	Transmembrane protein 87A	4.68	3		7	1.02	1.23	3	7.0
Q8C0I1	Agps	Alkyldihydroxyacetonephosphate synthase, peroxisomal	26.67	12		75	1.01	1.23	24	15.4
Q9CY57-5	Chtop	Isoform 5 of Chromatin target of PRMT1 protein	23.73	3		12	1.01	1.23	1	
Q9CVB6	Arpc2	Actin-related protein 2/3 complex subunit 2	15.00	5		21	1.01	1.23	2	35.6
O35685	Nudc	Nuclear migration protein nudC	18.07	6		15	1.01	1.23	5	9.2
Q07417	Acads	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	16.75	7		80	1.01	1.23	17	7.8

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q08024-2	Cbfb	Isoform 2 of Core-binding factor subunit beta	9.34	2		3	1.01	1.23	1	
G3UYV7	Rps28	40S ribosomal protein S28 (Fragment)	57.14	3		32	1.01	1.23	9	19.9
Q99KF1	Tmed9	Transmembrane emp24 domain-containing protein 9	36.17	9		165	1.01	1.23	35	17.4
Q00899	Yy1	Transcriptional repressor protein YY1	8.70	4		24	1.01	1.23	3	0.6
Q8BHY2	Noc4l	Nucleolar complex protein 4 homolog	7.75	4		31	1.01	1.23	6	19.1
G3XA10	Gm28062	Heterogeneous nuclear ribonucleoprotein U, isoform CRA_b	25.09	23		727	1.01	1.23	205	14.1
Q99LL5	Pwp1	Periodic tryptophan protein 1 homolog	2.79	2		6	1.01	1.23	1	
P97807-2	Fh	Isoform Cytoplasmic of Fumarate hydratase, mitochondrial	37.26	17		417	1.01	1.23	125	13.3
A0A0R4J1Z3	Tmem33	Transmembrane protein 33	18.70	5		57	1.01	1.23	14	23.9
A6H611	Mipep	Mitochondrial intermediate peptidase	3.23	3		24	1.01	1.23	2	0.1
O88653	Lamtor3	Ragulator complex protein LAMTOR3	14.52	2		8	1.01	1.23	1	
B2RXS4	Plxnb2	Plexin-B2	7.44	13		94	1.01	1.23	20	15.8
Q8VDN2	Atp1a1	Sodium/potassium-transporting ATPase subunit alpha-1	42.33	38		981	1.01	1.23	178	15.0
P08905	Lyz2	Lysozyme C-2	36.49	4		150	1.01	1.23	25	8.4
P19783	Cox4i1	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	43.20	7		170	1.01	1.23	40	10.9
Q9QYE6	Golga5	Golgin subfamily A member 5	10.43	8		25	1.01	1.23	3	10.0
E9Q137	Tex264	Protein Tex264	5.50	2		6	1.01	1.23	1	
Q99M87-3	Dnaja3	Isoform 3 of DnaJ homolog subfamily A member 3, mitochondrial	8.16	3		42	1.01	1.23	11	9.8
Q91VW3	Sh3bgrl3	SH3 domain-binding glutamic acid-rich-like protein 3	18.28	2		10	1.01	1.23	4	12.2
Q9DCW4	Etfb	Electron transfer flavoprotein subunit beta	52.16	14		260	1.01	1.23	59	14.7
O54692	Zw10	Centromere/kinetochore protein zw10 homolog	3.08	2		9	1.01	1.23	2	16.0
E9Q411	Nbas	Protein Nbas	1.32	3		8	1.01	1.23	2	11.5
Q7TN29-2	Smap2	Isoform 2 of Stromal membrane-associated protein 2	20.41	5		37	1.01	1.23	9	12.3
Q64737	Gart	Trifunctional purine biosynthetic protein adenosine-3	5.74	6		12	1.01	1.23	1	
Q9DCA5	Brix1	Ribosome biogenesis protein BRX1 homolog	15.58	7		74	1.01	1.23	19	8.3
A2A6T4	Ict1	Immature colon carcinoma transcript 1, isoform CRA_c	15.59	2		4	1.01	1.23	2	0.4
Q07113	Igf2r	Cation-independent mannose-6-phosphate receptor	7.21	18		103	1.01	1.23	19	14.0
Q922Q8	Lrrc59	Leucine-rich repeat-containing protein 59	46.91	15		429	1.01	1.23	120	18.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN^1	pksP/wt^1	pksP/wt Count^2	pksP/wt Variance [%]^3
Q9CZU6	Cs	Citrate synthase, mitochondrial	27.80	13		400	1.01	1.23	110	14.7
P17095	Hmga1	High mobility group protein HMG-I/HMG-Y	56.07	6		308	1.01	1.23	90	16.3
O35375-5	Nrp2	Isoform B0 of Neuropilin-2	4.44	4		40	1.01	1.23	8	19.3
G3UZA0	Krr1	KRR1 small subunit processome component homolog	23.53	9		72	1.01	1.23	13	8.7
Q9CPP6	Ndufa5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	28.45	4		39	1.01	1.23	8	11.0
E9QAZ2	Gm10020	Ribosomal protein L15	34.80	8		311	1.01	1.23	81	10.6
Q8C6B9	Rps19bp1	Active regulator of SIRT1	46.15	5		27	1.01	1.23	8	19.1
Q9JHI7	Exosc9	Exosome complex component RRP45	4.11	2		9	1.01	1.23	3	9.4
Q8VCF0	Mavs	Mitochondrial antiviral-signaling protein	3.98	2		4	1.01	1.23	2	12.5
Q6P5B0	Rrp12	RRP12-like protein	16.68	25		224	1.01	1.23	55	17.0
P51660	Hsd17b4	Peroxisomal multifunctional enzyme type 2	28.84	18		243	1.01	1.23	51	13.7
P10404	N/A	MLV-related proviral Env polyprotein	13.42	9		467	1.01	1.23	107	8.3
O89053	Coro1a	Coronin-1A	32.97	15		287	1.01	1.23	70	16.6
Q925I1	Atad3	ATPase family AAA domain-containing protein 3	36.89	23		234	1.01	1.23	55	9.9
Q8K2P7	Slc38a1	Sodium-coupled neutral amino acid transporter 1	4.74	3		8	1.01	1.23	3	1.8
Q91UZ1	Plcb4	Phosphoinositide phospholipase C	5.11	6		17	1.01	1.23	2	7.4
O35316	Slc6a6	Sodium- and chloride-dependent taurine transporter	6.28	4		25	1.01	1.23	2	27.0
Q8C2Q8	Atp5c1	ATP synthase subunit gamma	48.91	14		288	1.01	1.23	79	8.4
Q3THE2	Myl12b	Myosin regulatory light chain 12B	49.42	7		68	1.01	1.22	23	10.7
P60335	Pcbp1	Poly(rC)-binding protein 1	40.73	13		487	1.01	1.22	94	12.9
Q9CPQ3	Tomm22	Mitochondrial import receptor subunit TOM22 homolog	54.23	4		15	1.01	1.22	4	13.0
Q9DBD5	Pelp1	Proline-, glutamic acid- and leucine-rich protein 1	4.63	4		27	1.01	1.22	6	18.2
A0A0R4J0E4	Ints7	Integrator complex subunit 7	5.18	4		18	1.01	1.22	5	3.8
Q99KJ8	Dctn2	Dynactin subunit 2	8.46	3		14	1.01	1.22	2	28.1
Q8BH59	Slc25a12	Calcium-binding mitochondrial carrier protein Aralar1	33.38	18		214	1.01	1.22	23	22.7
P62874	Gnb1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	26.47	8		206	1.01	1.22	8	9.5
Q9DB20	Atp5o	ATP synthase subunit O, mitochondrial	52.11	11		194	1.01	1.22	53	14.4
Q8BMS1	Hadha	Trifunctional enzyme subunit alpha, mitochondrial	38.27	28		423	1.01	1.22	110	15.6
Q60780-2	Gas7	Isoform 2 of Growth arrest-specific protein 7	14.41	4		24	1.01	1.22	7	7.3
Q60931	Vdac3	Voltage-dependent anion-selective channel	49.82	13		167	1.01	1.22	31	5.9

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		protein 3								
O70480	Vamp4	Vesicle-associated membrane protein 4	31.91	3		27	1.01	1.22	3	12.2
Q8R2K3	Ssbp1	Single-stranded DNA-binding protein	33.11	4		50	1.01	1.22	14	6.9
G3UVV4	Hk1	Hexokinase	20.17	18		102	1.01	1.22	21	31.7
Q61881	Mcm7	DNA replication licensing factor MCM7	7.79	5		25	1.00	1.22	4	9.1
G3UYZ1	Igsf8	Immunoglobulin superfamily member 8	7.66	4		12	1.00	1.22	4	18.5
Q3UHB1	Nt5dc3	5'-nucleotidase domain-containing protein 3	5.13	3		8	1.00	1.22	1	
Q8CD26	Slc35e1	Solute carrier family 35 member E1	8.07	3		18	1.00	1.22	2	17.8
A2AUE1	Dnajc5	DnaJ homolog subfamily C member 5 (Fragment)	20.57	2		7	1.00	1.22	3	0.1
Q9D8V7	Sec11c	Signal peptidase complex catalytic subunit SEC11C	32.29	6		77	1.00	1.22	23	19.6
E9Q616	Ahnak	Protein Ahnak	43.14	109		1043	1.00	1.22	200	15.2
Q8CGZ0	Cherp	Calcium homeostasis endoplasmic reticulum protein	8.55	8		70	1.00	1.22	16	8.6
Q9CZN7	Shmt2	Serine hydroxymethyltransferase	49.80	24		916	1.00	1.22	255	17.5
Q9DBG3	Ap2b1	AP-2 complex subunit beta	20.28	16		94	1.00	1.22	16	13.3
Q8C9X3	Ikzf1	DNA-binding protein Ikaros	10.61	3		16	1.00	1.22	3	3.6
Q3TE40	Rpa2	Replication protein A 32 kDa subunit	10.37	3		20	1.00	1.22	6	15.7
Q0VBL3	Rbm15	Protein Rbm15	10.91	10		60	1.00	1.22	11	13.1
P67778	Phb	Prohibitin	59.19	16		847	1.00	1.22	247	18.0
E9PWG6	Ncapg	Protein Ncapg	2.09	2		6	1.00	1.22	1	
P15379-2	Cd44	Isoform 13 of CD44 antigen	11.02	4		63	1.00	1.22	18	11.1
Q9ERN0	Scamp2	Secretory carrier-associated membrane protein 2	13.98	4		76	1.00	1.22	21	10.2
Q9JKW0	Arl6ip1	ADP-ribosylation factor-like protein 6-interacting protein 1	8.87	2		37	1.00	1.22	8	5.8
B2M1R6	Hnrnpk	Heterogeneous nuclear ribonucleoprotein K	50.45	20		622	1.00	1.22	151	16.3
O35459	Ech1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	9.79	4		34	1.00	1.22	2	4.7
Q921L3	Tmco1	Transmembrane and coiled-coil domain-containing protein 1	20.21	4		62	1.00	1.22	14	13.2
Q91WS0	Cisd1	CDGSH iron-sulfur domain-containing protein 1	51.85	5		54	1.00	1.22	13	6.9
O55135	Eif6	Eukaryotic translation initiation factor 6	30.20	5		51	1.00	1.22	13	8.0
E9Q2I4	Elmsan1	Protein Elmsan1	2.66	3		19	1.00	1.22	4	0.7
Q3TYR7	Sh3glb1	Endophilin B1 testis variant	5.92	2		4	1.00	1.22	2	6.2
P99028	Uqcrh	Cytochrome b-c1 complex subunit 6, mitochondrial	29.21	2		6	1.00	1.22	2	20.2
Q91WD5	Ndufs2	NADH dehydrogenase [ubiquinone] iron-sulfur	32.18	11		68	1.00	1.22	18	10.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		protein 2, mitochondrial								
P63166	Sumo1	Small ubiquitin-related modifier 1	26.73	3		22	1.00	1.22	4	18.0
E9QN08	Eef1d	Elongation factor 1-delta (Fragment)	18.78	4		20	1.00	1.22	5	4.5
Q6DFW4	Nop58	Nucleolar protein 58	24.25	13		199	1.00	1.22	59	10.4
Q9CQA3	Sdhb	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	35.46	14		166	1.00	1.22	40	8.8
Q9Z110-2	Aldh18a1	Isoform Short of Delta-1-pyrroline-5-carboxylate synthase	32.79	27		394	1.00	1.22	90	22.1
Q8K4P7-3	St7l	Isoform 3 of Suppressor of tumorigenicity 7 protein-like	4.37	2		3	1.00	1.22	2	3.8
Q9CQ06	Mrpl24	39S ribosomal protein L24, mitochondrial	31.48	7		65	1.00	1.22	10	13.9
Q8K1J6	Trnt1	CCA tRNA nucleotidyltransferase 1, mitochondrial	17.05	6		24	1.00	1.21	5	9.1
Q99N93	Mrpl16	39S ribosomal protein L16, mitochondrial	18.33	4		37	1.00	1.21	9	11.4
Q5FWK3	Arhgap1	Rho GTPase-activating protein 1	18.00	8		34	1.00	1.21	3	12.2
Q9QYS9-4	Qki	Isoform 4 of Protein quaking	25.39	6		22	1.00	1.21	7	23.7
Q8CGY8-2	Ogt	Isoform 2 of UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	4.44	5		20	1.00	1.21	4	7.5
Q8BHN3	Ganab	Neutral alpha-glucosidase AB	30.08	29		396	1.00	1.21	109	18.0
Q921N6	Ddx27	Probable ATP-dependent RNA helicase DDX27	30.00	23		160	1.00	1.21	35	8.1
B1AZI6	Thoc2	THO complex subunit 2	7.78	14		79	1.00	1.21	13	8.8
Q8QZT1	Acat1	Acetyl-CoA acetyltransferase, mitochondrial	44.10	16		215	1.00	1.21	50	17.7
Q501J6	Ddx17	Probable ATP-dependent RNA helicase DDX17	28.15	19		365	1.00	1.21	17	11.1
Q99LB2	Dhrs4	Dehydrogenase/reductase SDR family member 4	13.26	4		18	1.00	1.21	2	13.3
P97496-2	Smarcc1	Isoform 2 of SWI/SNF complex subunit SMARCC1	14.98	18		186	1.00	1.21	24	12.6
Q9CZR8	Tsfm	Elongation factor Ts, mitochondrial	24.69	7		76	1.00	1.21	24	30.6
Q9JHJ0	Tmod3	Tropomodulin-3	23.01	8		55	1.00	1.21	10	10.6
E9QPI5	Pds5a	Sister chromatid cohesion protein PDS5 homolog A	12.76	16		60	1.00	1.21	11	14.2
Q3V1V3	Esf1	ESF1 homolog	5.68	5		15	1.00	1.21	4	10.3
Q8K4L0	Ddx54	ATP-dependent RNA helicase DDX54	10.53	9		71	1.00	1.21	15	8.6
O88630	Gosr1	Golgi SNAP receptor complex member 1	14.00	4		20	1.00	1.21	6	8.6
Q9QYL7	Abt1	Activator of basal transcription 1	9.67	3		13	1.00	1.21	3	7.6
E0CXD9	Surf4	Surfeit locus protein 4	31.71	2		30	1.00	1.21	8	13.9
Q8C4Y1	Max	Max protein	11.26	2		4	1.00	1.21	1	
Q6NXL1	Sec24d	Protein Sec24d	2.52	2		6	1.00	1.21	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q921S7	Mrpl37	39S ribosomal protein L37, mitochondrial	24.59	10		56	1.00	1.21	8	22.1
Q922D8	Mthfd1	C-1-tetrahydrofolate synthase, cytoplasmic	8.77	8		24	1.00	1.21	4	20.2
P62196	Psmc5	26S protease regulatory subunit 8	4.93	2		7	1.00	1.21	2	12.6
Q8K2Y7	Mrpl47	39S ribosomal protein L47, mitochondrial	7.14	2		5	1.00	1.21	1	
Q62376	Snrnp70	U1 small nuclear ribonucleoprotein 70 kDa	19.87	13		145	1.00	1.21	33	24.6
B1AT03	Lig3	DNA ligase	3.99	4		21	1.00	1.21	4	18.7
Q6P5E4	Uggt1	UDP-glucose:glycoprotein glucosyltransferase 1	21.34	29		229	1.00	1.21	54	8.9
A0A0R4J119	Cyfip1	Cytoplasmic FMR1-interacting protein 1	1.68	2		4	1.00	1.21	2	4.7
Q60597-2	Ogdh	Isoform 2 of 2-oxoglutarate dehydrogenase, mitochondrial	25.47	22		201	1.00	1.21	46	21.9
O88967	Yme1l1	ATP-dependent zinc metalloprotease YME1L1	21.68	12		88	1.00	1.21	12	17.7
Q9CPR5	Mrpl15	39S ribosomal protein L15, mitochondrial	23.05	7		43	1.00	1.21	6	7.1
Q61033	Tmpo	Lamina-associated polypeptide 2, isoforms alpha/zeta	42.14	25		478	1.00	1.21	25	13.8
Q9D8S4	Rexo2	Oligoribonuclease, mitochondrial	7.59	2		15	1.00	1.21	3	1.6
B9EJ86	Osbpl8	Oxysterol-binding protein	18.90	14		94	1.00	1.21	23	7.5
P05202	Got2	Aspartate aminotransferase, mitochondrial	50.70	24		564	1.00	1.21	156	21.1
P23780	Glb1	Beta-galactosidase	5.10	2		10	1.00	1.21	2	20.2
D3Z198	Mrps17	28S ribosomal protein S17, mitochondrial (Fragment)	20.69	2		14	1.00	1.21	3	3.5
Q9CSU0-3	Rprd1b	Isoform 3 of Regulation of nuclear pre-mRNA domain-containing protein 1B	13.84	2		9	0.99	1.21	1	
Q80WJ7	Mtdh	Protein LYRIC	35.58	19		251	0.99	1.21	65	10.3
Q60715-2	P4ha1	Isoform 2 of Prolyl 4-hydroxylase subunit alpha-1	39.14	22		178	0.99	1.21	5	9.3
Q9CZW5	Tomm70a	Mitochondrial import receptor subunit TOM70	22.59	18		224	0.99	1.21	55	17.9
Q9CQQ7	Atp5f1	ATP synthase F(0) complex subunit B1, mitochondrial	23.83	7		265	0.99	1.21	67	8.7
Q8K2C7-2	Os9	Isoform 2 of Protein -9	12.48	7		39	0.99	1.21	9	11.4
P70460	Vasp	Vasodilator-stimulated phosphoprotein	10.40	4		36	0.99	1.21	4	8.3
P38647	Hspa9	Stress-70 protein, mitochondrial	62.44	45		1652	0.99	1.21	428	12.8
Q9CXF4	Tbc1d15	TBC1 domain family member 15	5.51	4		20	0.99	1.21	3	125.5
Q04750	Top1	DNA topoisomerase 1	27.51	24		221	0.99	1.21	44	12.9
A0A0R4J0V5	Polr2a	DNA-directed RNA polymerase	12.53	22		114	0.99	1.21	23	16.7
J3QMC5	Mdn1	Protein Mdn1	3.99	19		60	0.99	1.21	10	11.1
Q9JIK9	Mrps34	28S ribosomal protein S34, mitochondrial	33.94	6		43	0.99	1.21	9	13.6
Q8BHB4	Wdr3	WD repeat-containing protein 3	15.18	15		131	0.99	1.21	24	3.5
Q9QYI3	Dnajc7	DnaJ homolog subfamily C member 7	17.41	9		58	0.99	1.21	8	8.1
Q8BTI8	Srrm2	Serine/arginine repetitive matrix protein 2	9.77	24		219	0.99	1.21	54	12.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
D3YY98	Stx18	Syntaxin-18 (Fragment)	11.11	3		12	0.99	1.21	3	12.2
Q9CPX7	Mrps16	28S ribosomal protein S16, mitochondrial	30.37	4		54	0.99	1.21	14	14.2
Q61009	Scarb1	Scavenger receptor class B member 1	7.47	5		10	0.99	1.21	2	13.9
P62320	Snrpd3	Small nuclear ribonucleoprotein Sm D3	31.75	3		75	0.99	1.21	20	14.7
E9Q421	Pigk	GPI-anchor transamidase	8.29	3		14	0.99	1.21	1	
A0A0R4J1N9	Tfam	Transcription factor A, mitochondrial	33.67	8		68	0.99	1.21	17	12.0
Q9D903	Ebna1bp2	Probable rRNA-processing protein EBP2	45.75	16		169	0.99	1.21	39	19.2
P56480	Atp5b	ATP synthase subunit beta, mitochondrial	60.30	24		914	0.99	1.21	266	29.7
Q9EPU0-2	Upf1	Isoform 2 of Regulator of nonsense transcripts 1	6.83	6		34	0.99	1.20	7	15.7
Q9CRB9	Chchd3	MICOS complex subunit Mic19	57.27	15		222	0.99	1.20	55	15.0
Q9D051	Pdhb	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	30.08	9		98	0.99	1.20	26	10.7
E9Q7H6	Tars2	Threonine--tRNA ligase, mitochondrial	19.78	13		66	0.99	1.20	13	17.4
Q8CCJ3	Ufl1	E3 UFM1-protein ligase 1	22.57	18		101	0.99	1.20	24	8.9
Q3ULG5	Mcm6	DNA helicase	5.29	5		29	0.99	1.20	5	18.4
Q3UL36	Arglu1	Arginine and glutamate-rich protein 1	16.61	7		29	0.99	1.20	7	3.8
Q99ME9	Gtpbp4	Nucleolar GTP-binding protein 1	30.91	21		197	0.99	1.20	43	9.9
Q9QXX4	Slc25a13	Calcium-binding mitochondrial carrier protein Aralar2	22.63	15		227	0.99	1.20	21	12.3
E9Q3Q6	Alcam	CD166 antigen	19.12	9		63	0.99	1.20	17	11.2
Q91W59-2	Rbms1	Isoform 2 of RNA-binding motif, single-stranded-interacting protein 1	9.73	3		16	0.99	1.20	3	12.6
Q5XG71	Utp20	Small subunit processome component 20 homolog	13.45	38		210	0.99	1.20	39	9.8
Q99JY0	Hadhb	Trifunctional enzyme subunit beta, mitochondrial	31.16	15		232	0.99	1.20	51	16.5
Q7TSS2	Ube2q1	Ubiquitin-conjugating enzyme E2 Q1	5.69	2		4	0.99	1.20	1	
Q8VEE4	Rpa1	Replication protein A 70 kDa DNA-binding subunit	20.55	12		68	0.99	1.20	15	13.3
Q9CZT6	Cmss1	Protein CMSS1	14.86	4		22	0.99	1.20	7	2.3
Q9JJA4	Wdr12	Ribosome biogenesis protein WDR12	22.46	9		83	0.99	1.20	14	15.0
P61982	Ywhag	14-3-3 protein gamma	32.79	8		84	0.99	1.20	3	42.3
Q64511	Top2b	DNA topoisomerase 2-beta	28.04	43		448	0.99	1.20	46	14.6
Q9Z0S9	Rabac1	Prenylated Rab acceptor protein 1	20.00	3		13	0.99	1.20	2	10.6
P62071	Rras2	Ras-related protein R-Ras2	8.82	2		12	0.99	1.20	3	2.8
P26443	Glud1	Glutamate dehydrogenase 1, mitochondrial	50.54	26		589	0.99	1.20	158	12.8
Q9CQN1	Trap1	Heat shock protein 75 kDa, mitochondrial	33.71	21		428	0.99	1.20	97	14.5
Q9WTI7-3	Myo1c	Isoform 3 of Unconventional myosin-Ic	18.10	17		71	0.99	1.20	11	9.0
Q03265	Atp5a1	ATP synthase subunit alpha, mitochondrial	56.78	31		1267	0.99	1.20	342	16.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8CGC6	Rbm28	RNA-binding protein 28	25.20	18		145	0.99	1.20	24	6.8
Q60648	Gm2a	Ganglioside GM2 activator	21.24	5		14	0.99	1.20	2	14.7
Q3UPL0-2	Sec31a	Isoform 2 of Protein transport protein Sec31A	5.37	5		20	0.99	1.20	5	5.2
E9QPX3	Ndufs4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	19.43	3		64	0.99	1.20	17	12.1
P26041	Msn	Moesin	33.45	24		248	0.99	1.20	45	15.8
Q9D7A8	Armc1	Armadillo repeat-containing protein 1	6.38	2		4	0.99	1.20	2	5.3
P21460	Cst3	Cystatin-C	29.29	4		28	0.99	1.20	5	6.6
Q9D125	Mrps25	28S ribosomal protein S25, mitochondrial	29.24	6		27	0.99	1.20	5	5.1
P28667	Marcksl1	MARCKS-related protein	11.00	2		13	0.99	1.20	1	
Q9CQX4	Paf	PCNA-associated factor	21.82	3		12	0.99	1.20	2	5.9
O88569	Hnrnpa2b1	Heterogeneous nuclear ribonucleoproteins A2/B1	64.87	23		1505	0.99	1.20	393	14.8
Q9CQU0	Txndc12	Thioredoxin domain-containing protein 12	22.94	3		21	0.99	1.20	6	7.5
Q8VHE0	Sec63	Translocation protein SEC63 homolog	14.87	10		111	0.99	1.20	32	13.0
Q9DBE9	Ftsj3	pre-rRNA processing protein FTSJ3	25.54	18		145	0.99	1.20	29	13.4
Q9JIG8	Praf2	PRA1 family protein 2	12.36	2		18	0.99	1.20	3	9.0
P61804	Dad1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	35.40	4		16	0.99	1.20	5	7.6
O35130	Emg1	Ribosomal RNA small subunit methyltransferase NEP1	30.33	6		52	0.99	1.20	12	12.0
F6QTS1	Cops4	COP9 signalosome complex subunit 4 (Fragment)	9.49	2		14	0.99	1.20	2	11.3
Q61035	Hars	Histidine--tRNA ligase, cytoplasmic	6.29	3		8	0.99	1.20	1	
Q91YK2	Rrp1b	Ribosomal RNA processing protein 1 homolog B	13.54	9		52	0.99	1.20	10	8.9
Q8BK72	Mrps27	28S ribosomal protein S27, mitochondrial	20.96	8		37	0.99	1.20	6	6.0
O09159	Man2b1	Lysosomal alpha-mannosidase	4.94	5		21	0.99	1.20	5	8.3
O70152	Dpm1	Dolichol-phosphate mannosyltransferase subunit 1	14.23	3		21	0.99	1.20	6	18.2
Q8BKZ9	Pdhx	Pyruvate dehydrogenase protein X component, mitochondrial	11.18	6		72	0.99	1.20	12	8.7
Q8BH86-2	N/A	Isoform 2 of UPF0317 protein C14orf159 homolog, mitochondrial	10.70	6		35	0.99	1.20	8	25.3
Q8R2N2	Cirh1a	Cirhin	12.10	10		49	0.99	1.20	12	12.5
Q8JZN2	Csde1	Cold shock domain-containing protein E1	11.34	9		51	0.99	1.20	8	32.8
Q91YP2	Nln	Neurolysin, mitochondrial	4.40	3		16	0.99	1.20	1	
P62137	Ppp1ca	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	26.97	8		106	0.99	1.20	29	16.7
P63024	Vamp3	Vesicle-associated membrane protein 3	23.30	2		8	0.99	1.20	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q99KI0	Aco2	Aconitate hydratase, mitochondrial	48.21	34		734	0.98	1.20	156	17.7
P54823	Ddx6	Probable ATP-dependent RNA helicase DDX6	18.63	8		45	0.98	1.20	10	26.3
Q99LC3	Ndufa10	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	14.08	6		39	0.98	1.20	10	16.1
Q8BGH2	Samm50	Sorting and assembly machinery component 50 homolog	33.26	14		108	0.98	1.20	19	16.1
P97300-3	Nptn	Isoform 3 of Neuroplastin	19.49	5		36	0.98	1.20	7	2.9
P24270	Cat	Catalase	37.38	18		240	0.98	1.20	62	17.0
P62880	Gnb2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	26.47	8		236	0.98	1.20	18	19.0
Q9R233-2	Tapbp	Isoform Short of Tapasin	14.02	6		73	0.98	1.20	14	27.8
Q8R164	Bphl	Valacyclovir hydrolase	15.46	4		13	0.98	1.20	3	31.6
Q9QXK7	Cpsf3	Cleavage and polyadenylation specificity factor subunit 3	13.01	8		31	0.98	1.20	4	5.6
E9QPQ8	Mrpl48	39S ribosomal protein L48, mitochondrial	9.00	2		13	0.98	1.20	2	0.7
Q99PL5	Rrbp1	Ribosome-binding protein 1	65.61	79		774	0.98	1.20	192	20.9
Q8R2Q8	Bst2	Bone marrow stromal antigen 2	16.86	3		14	0.98	1.19	3	12.9
P17426-2	Ap2a1	Isoform B of AP-2 complex subunit alpha-1	12.77	13		96	0.98	1.19	3	10.1
Q61768	Kif5b	Kinesin-1 heavy chain	3.95	3		12	0.98	1.19	2	10.3
Q922E6	Fastkd2	FAST kinase domain-containing protein 2	2.61	2		4	0.98	1.19	2	12.2
P70295	Aup1	Ancient ubiquitous protein 1	29.27	13		115	0.98	1.19	25	21.2
P16045	Lgals1	Galectin-1	37.78	5		27	0.98	1.19	5	5.3
P17809	Slc2a1	Solute carrier family 2, facilitated glucose transporter member 1	8.13	4		26	0.98	1.19	5	6.6
Q99JF8	Psip1	PC4 and SFRS1-interacting protein	25.00	16		142	0.98	1.19	39	14.6
Q91YR7	Prpf6	Pre-mRNA-processing factor 6	16.47	16		144	0.98	1.19	33	9.0
P61290	Psme3	Proteasome activator complex subunit 3	24.80	6		20	0.98	1.19	2	1.0
Q9CQ56	Use1	Vesicle transport protein USE1	24.81	8		33	0.98	1.19	4	2.8
P09055	Itgb1	Integrin beta-1	8.65	6		35	0.98	1.19	9	9.4
Q8CHT3	Ints5	Integrator complex subunit 5	3.24	3		33	0.98	1.19	4	23.0
Q8K3J1	Ndufs8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	21.23	4		15	0.98	1.19	2	12.2
Q8R2T8-2	Gtf3c5	Isoform 2 of General transcription factor 3C polypeptide 5	4.67	2		4	0.98	1.19	2	13.6
Q99MR6-3	Srrt	Isoform C of Serrate RNA effector molecule homolog	16.09	13		80	0.98	1.19	16	15.1
Q60605	Myl6	Myosin light polypeptide 6	29.80	4		48	0.98	1.19	10	15.8
Q921W2	Tial1	Nucleolysin TIAR	28.53	9		161	0.98	1.19	29	15.5
Q99N92	Mrpl27	39S ribosomal protein L27, mitochondrial	12.84	2		3	0.98	1.19	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q61263	Soat1	Sterol O-acyltransferase 1	18.70	10		131	0.98	1.19	51	17.3
Q9D1M7	Fkbp11	Peptidyl-prolyl cis-trans isomerase FKBP11	14.43	4		52	0.98	1.19	11	15.8
O70318	Epb41l2	Band 4.1-like protein 2	10.02	9		53	0.98	1.19	9	14.7
P97452	Bop1	Ribosome biogenesis protein BOP1	22.27	13		132	0.98	1.19	33	17.6
Q91YZ2	Ctbp2	C-terminal binding protein 2, isoform CRA_b	7.14	4		17	0.98	1.19	3	27.0
P38060	Hmgcl	Hydroxymethylglutaryl-CoA lyase, mitochondrial	27.69	8		80	0.98	1.19	19	9.9
P52912	Tia1	Nucleolysin TIA-1	19.69	7		94	0.98	1.19	4	2.6
P37913	Lig1	DNA ligase 1	5.68	5		22	0.98	1.19	5	10.4
P14901	Hmox1	Heme oxygenase 1	26.64	6		53	0.98	1.19	16	13.6
Q78PY7	Snd1	Staphylococcal nuclease domain-containing protein 1	35.49	27		298	0.98	1.19	65	18.3
Q8BP40	Acp6	Lysophosphatidic acid phosphatase type 6	17.22	7		54	0.98	1.19	10	9.2
Q5SUT0	Ewsr1	RNA-binding protein EWS	8.09	5		59	0.98	1.19	12	5.6
Q810A7-2	Ddx42	Isoform 2 of ATP-dependent RNA helicase DDX42	8.02	6		14	0.98	1.19	1	
Q8VBT6	Apobr	Apolipoprotein B receptor	8.49	7		30	0.98	1.19	5	11.8
D3Z074	Diaph1	Protein diaphanous homolog 1	5.00	5		11	0.98	1.19	5	24.2
Q5RL20	Mrpl43	39S ribosomal protein L43, mitochondrial	33.33	6		39	0.98	1.19	7	15.7
O88986	Gcat	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	12.26	4		38	0.98	1.19	18	22.6
Q9JIK5	Ddx21	Nucleolar RNA helicase 2	60.52	48		1258	0.98	1.19	276	11.8
P70388-2	Rad50	Isoform 2 of DNA repair protein RAD50	3.68	4		20	0.98	1.19	4	10.6
E9PVX6	Mki67	Protein Mki67	33.62	94		967	0.98	1.19	233	16.7
P56183-2	Rrp1	Isoform 2 of Ribosomal RNA processing protein 1 homolog A	18.96	8		91	0.98	1.19	19	16.5
E9PWK1	Ephx1	Epoxide hydrolase 1	22.90	10		85	0.98	1.19	14	10.7
Q91YW3	Dnajc3	DnaJ homolog subfamily C member 3	28.57	15		126	0.98	1.19	30	6.0
Q8C5N3-2	Cwc22	Isoform 2 of Pre-mRNA-splicing factor CWC22 homolog	5.10	5		21	0.98	1.19	3	4.8
P53986	Slc16a1	Monocarboxylate transporter 1	4.46	2		23	0.98	1.19	2	18.3
P17427	Ap2a2	AP-2 complex subunit alpha-2	13.22	12		100	0.98	1.19	5	6.3
Q99L28	Rsl24d1	Probable ribosome biogenesis protein RLP24	11.66	2		27	0.98	1.19	8	3.9
Q6ZQL4	Wdr43	WD repeat-containing protein 43	26.14	18		119	0.98	1.19	29	9.7
P33174	Kif4	Chromosome-associated kinesin KIF4	9.10	10		38	0.98	1.19	6	8.5
Q9CQR4	Acot13	Acyl-coenzyme A thioesterase 13	21.43	3		11	0.98	1.19	2	20.0
Q6P5D8	Smchd1	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	9.37	15		66	0.98	1.19	18	15.2
Q3UUQ7	Pgap1	GPI inositol-deacylase	3.04	3		15	0.98	1.19	6	12.5
Q8BL97-3	Srsf7	Isoform 3 of Serine/arginine-rich splicing factor	42.04	8		112	0.98	1.19	13	13.5

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		7								
Q8CCM6-2	Timm21	Isoform 2 of Mitochondrial import inner membrane translocase subunit Tim21	9.02	2		18	0.98	1.19	4	16.1
Q6PE01	Snrnp40	U5 small nuclear ribonucleoprotein 40 kDa protein	27.65	7		104	0.98	1.19	26	17.0
A0A0R4J0I9	Lrp1	Low density lipoprotein receptor-related protein 1	13.86	56		510	0.98	1.19	114	14.7
P62806	Hist1h4a	Histone H4	64.08	12		3267	0.98	1.19	943	25.3
O08602	Raet1a	Retinoic acid early-inducible protein 1-alpha	13.04	3		19	0.98	1.19	7	22.9
Q8BUI3	LRWD1	Leucine-rich repeat and WD repeat-containing protein 1	18.83	8		26	0.98	1.18	6	15.8
P32020	Scp2	Non-specific lipid-transfer protein	9.87	7		107	0.98	1.18	24	7.5
Q8JZN5	Acad9	Acyl-CoA dehydrogenase family member 9, mitochondrial	18.08	12		97	0.98	1.18	18	9.9
D3Z1Z0	Timm17a	Mitochondrial import inner membrane translocase subunit Tim17-A (Fragment)	39.18	3		18	0.97	1.18	4	5.8
D3Z041	Acsl1	Long-chain-fatty-acid--CoA ligase 1	12.88	7		36	0.97	1.18	7	6.0
Q61578	Fdxr	NADPH:adrenodoxin oxidoreductase, mitochondrial	17.81	8		53	0.97	1.18	10	15.7
Q8R5K4-2	Nol6	Isoform 2 of Nucleolar protein 6	13.52	12		76	0.97	1.18	13	15.0
Q9JHS9	Cwc15	Spliceosome-associated protein CWC15 homolog	11.35	3		16	0.97	1.18	3	7.0
G3X9I1	Fam3c	DNA segment, Chr 6, Wayne State University 176, expressed, isoform CRA_a	8.12	2		5	0.97	1.18	2	0.2
Q91YU8	Ppan	Suppressor of SWI4 1 homolog	24.68	12		94	0.97	1.18	23	12.0
Q8BWT1	Acaa2	3-ketoacyl-CoA thiolase, mitochondrial	34.76	11		93	0.97	1.18	20	11.3
Q6PB66	Lrpprc	Leucine-rich PPR motif-containing protein, mitochondrial	38.15	54		509	0.97	1.18	115	14.0
D3Z0M9	Ddx23	MCG18410, isoform CRA_a	17.83	16		94	0.97	1.18	20	11.2
K3W4Q8	Bsg	Basigin	38.53	7		229	0.97	1.18	54	18.5
Q8K366	Exosc10	Exosc10 protein	9.16	7		28	0.97	1.18	4	5.2
Q8BK35	Gltscr2	MCG2065, isoform CRA_c	15.29	8		64	0.97	1.18	10	10.0
P35550	Fbl	rRNA 2'-O-methyltransferase fibrillarin	48.93	15		404	0.97	1.18	104	11.1
Q91YE7-2	Rbm5	Isoform 2 of RNA-binding protein 5	8.35	7		46	0.97	1.18	2	16.3
Q78IS1	Tmed3	Transmembrane emp24 domain-containing protein 3	15.84	4		27	0.97	1.18	4	6.7
Q8BH95	Echs1	Enoyl-CoA hydratase, mitochondrial	29.66	8		72	0.97	1.18	22	20.4
Q9D883	U2af1	Splicing factor U2AF 35 kDa subunit	16.74	5		65	0.97	1.18	18	10.1
A1L314	Mpeg1	Macrophage-expressed gene 1 protein	12.76	8		75	0.97	1.18	13	21.1

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q99N96	Mrpl1	39S ribosomal protein L1, mitochondrial	21.73	7		86	0.97	1.18	21	21.3
P63168	Dynll1	Dynein light chain 1, cytoplasmic	20.22	2		40	0.97	1.18	7	7.2
Q8CFI7	Polr2b	DNA-directed RNA polymerase II subunit RPB2	12.01	14		62	0.97	1.18	18	12.8
Q8BMD8	Slc25a24	Calcium-binding mitochondrial carrier protein SCaMC-1	17.89	8		78	0.97	1.18	16	15.1
Q9ERS2	Ndufa13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	29.86	5		38	0.97	1.18	8	12.5
P14206	Rpsa	40S ribosomal protein SA	39.66	11		183	0.97	1.18	38	15.7
D3Z3F4	Mtx1	Metaxin-1 (Fragment)	25.83	11		175	0.97	1.18	48	18.1
Q5SUH7	Clint1	Clathrin interactor 1	21.51	14		84	0.97	1.18	24	11.0
Q80XI3-2	Eif4g3	Isoform 2 of Eukaryotic translation initiation factor 4 gamma 3	1.92	4		13	0.97	1.18	1	
Q8BYK6	Ythdf3	YTH domain-containing family protein 3	19.15	10		74	0.97	1.18	8	13.4
Q03963	Eif2ak2	Interferon-induced, double-stranded RNA-activated protein kinase	4.08	2		4	0.97	1.18	1	
Q8R3C6	Rbm19	Probable RNA-binding protein 19	14.50	11		86	0.97	1.18	14	9.3
E9Q9A5	Pnkp	Bifunctional polynucleotide phosphatase/kinase	10.49	5		16	0.97	1.18	5	5.2
Q9D338	Mrpl19	39S ribosomal protein L19, mitochondrial	20.55	6		31	0.97	1.18	8	9.2
Q69ZQ2	Isy1	Pre-mRNA-splicing factor ISY1 homolog	24.91	6		29	0.97	1.18	4	4.8
Q8CG48	Smc2	Structural maintenance of chromosomes protein 2	11.42	13		54	0.97	1.18	12	12.2
A0A0U1RNK7	Dock7	Dedicator of cytokinesis protein 7	1.67	3		8	0.97	1.18	2	10.1
D3YVN7	Gm9755	Elongation factor Tu	56.19	24		597	0.97	1.18	157	14.9
Q91VA7	Idh3b	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	33.07	12		136	0.97	1.18	33	10.2
Q9DC16	Ergic1	Endoplasmic reticulum-Golgi intermediate compartment protein 1	29.31	7		68	0.97	1.18	11	15.8
O89001	Cpd	Carboxypeptidase D	1.45	2		9	0.97	1.18	3	4.0
Q9CQ69	Uqcrq	Cytochrome b-c1 complex subunit 8	42.68	4		34	0.97	1.18	7	18.2
Q8BMF4	Dlat	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	22.59	12		166	0.97	1.18	36	16.1
P08752	Gnai2	Guanine nucleotide-binding protein G(i) subunit alpha-2	39.72	12		182	0.97	1.18	23	14.9
Q9CR62	Slc25a11	Mitochondrial 2-oxoglutarate/malate carrier protein	34.39	9		158	0.97	1.18	39	11.1
Q9JKR6	Hyou1	Hypoxia up-regulated protein 1	37.14	35		693	0.97	1.18	185	15.9
P27601	Gna13	Guanine nucleotide-binding protein subunit alpha-13	12.20	5		59	0.97	1.18	7	9.0

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
O88983	Stx8	Syntaxin-8	7.63	2		13	0.97	1.18	1	
O70126	Aurkb	Aurora kinase B	25.22	6		37	0.97	1.18	8	13.4
A2ASL8	Lnp	Limb and neural patterns, isoform CRA_c	8.51	3		16	0.97	1.18	2	4.1
Q80X82	Sympk	Symplekin	7.32	9		45	0.97	1.18	7	10.3
Q9WTP7	Ak3	GTP:AMP phosphotransferase AK3, mitochondrial	37.44	7		25	0.97	1.18	8	21.7
V9GX42	Meaf6	Chromatin modification-related protein MEAF6	24.86	3		11	0.97	1.18	4	6.2
Q8CAQ8-3	Immt	Isoform 3 of MICOS complex subunit Mic60	52.61	39		756	0.97	1.18	3	7.9
E9PU93	Ash2l	Set1/Ash2 histone methyltransferase complex subunit ASH2	6.74	4		21	0.97	1.18	4	2.2
G3X972	Sec24c	Protein Sec24c	11.04	12		76	0.97	1.18	19	18.3
Q3UDR8	Yipf3	Protein YIPF3	6.92	3		12	0.97	1.18	1	
Q8K363	Ddx18	ATP-dependent RNA helicase DDX18	19.24	13		182	0.97	1.18	46	13.6
Q60865	Caprin1	Caprin-1	9.05	8		50	0.97	1.18	8	12.1
Q91VE6-2	Nifk	Isoform 2 of MKI67 FHA domain-interacting nucleolar phosphoprotein	41.26	11		181	0.97	1.18	41	8.7
Q8BIQ5	Cstf2	Cleavage stimulation factor subunit 2	19.48	11		85	0.97	1.18	4	17.2
O35691	Pnn	Pinin	24.41	20		315	0.97	1.18	74	7.0
Q6PGF5	Bms1	BMS1 homolog, ribosome assembly protein (Yeast)	10.75	16		76	0.97	1.18	19	13.2
Q3TFP0	Srsf10	Serine/arginine-rich-splicing factor 10	35.16	7		92	0.97	1.18	19	12.5
B1AU25	Aifm1	Apoptosis-inducing factor 1, mitochondrial	32.40	18		230	0.97	1.18	61	14.6
P54071	Idh2	Isocitrate dehydrogenase [NADP], mitochondrial	41.59	20		374	0.97	1.18	82	13.2
P07742	Rrm1	Ribonucleoside-diphosphate reductase large subunit	2.65	2		2	0.97	1.18	1	
A0A087WS29	Ktn1	Kinectin	22.23	25		130	0.97	1.18	25	15.5
Q3URQ0	Tex10	Testis-expressed sequence 10 protein	10.13	9		45	0.97	1.18	8	18.3
Q9CY16	Mrps28	28S ribosomal protein S28, mitochondrial	28.49	5		31	0.97	1.18	3	13.9
Q922Q4	Pycr2	Pyrroline-5-carboxylate reductase 2	35.31	10		117	0.97	1.17	32	21.4
Q9D5T0	Atad1	ATPase family AAA domain-containing protein 1	23.27	7		44	0.97	1.17	10	12.8
Q9CPY3	Cdca5	Sororin	8.33	2		4	0.97	1.17	4	13.5
Q9JJZ4	Ube2j1	Ubiquitin-conjugating enzyme E2 J1	11.95	3		30	0.97	1.17	6	16.4
F6YJB6	Gm28036	Protein Gm28036 (Fragment)	4.74	3		16	0.97	1.17	1	
Q9CQU1	Mfap1	Microfibrillar-associated protein 1	15.03	7		36	0.97	1.17	5	7.4
Q9D0R4	Ddx56	Probable ATP-dependent RNA helicase DDX56	20.88	11		106	0.97	1.17	18	13.7
Q9CQ75	Ndufa2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	47.47	5		50	0.97	1.17	14	29.8
Q99K28	Arfgap2	ADP-ribosylation factor GTPase-activating protein 2	21.35	11		71	0.97	1.17	17	16.0

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8K297	Colgalt1	Procollagen galactosyltransferase 1	18.80	11		90	0.97	1.17	24	14.6
Q4VBE8	Wdr18	WD repeat-containing protein 18	14.85	6		47	0.97	1.17	9	15.9
Q9JJT0	Rcl1	RNA 3'-terminal phosphate cyclase-like protein	11.26	5		31	0.97	1.17	4	20.4
Q99LM2	Cdk5rap3	CDK5 regulatory subunit-associated protein 3	17.69	10		45	0.96	1.17	10	7.1
Q3UFM5	Nom1	Nucleolar MIF4G domain-containing protein 1	11.24	9		23	0.96	1.17	6	20.5
Q8BVK9	Sp110	Sp110 nuclear body protein	13.48	6		39	0.96	1.17	11	5.6
P59017	Bcl2l13	Bcl-2-like protein 13	9.68	4		19	0.96	1.17	6	17.0
Q9CYN9	Atp6ap2	Renin receptor	22.57	7		43	0.96	1.17	10	14.2
A8Y5J3	Cpsf3l	Integrator complex subunit 11	4.84	3		11	0.96	1.17	2	21.3
Q08288	Lyar	Cell growth-regulating nucleolar protein	19.07	8		63	0.96	1.17	15	15.4
Q9JJF9	Sppl2a	Signal peptide peptidase-like 2A	2.10	2		12	0.96	1.17	2	7.8
Q9CPT5	Nop16	Nucleolar protein 16	22.47	5		28	0.96	1.17	1	
P58281	Opa1	Dynamin-like 120 kDa protein, mitochondrial	17.08	14		59	0.96	1.17	11	11.0
F7BUB8	Epb41	Protein 4.1 (Fragment)	14.40	3		10	0.96	1.17	1	
Q99LI2	Clcc1	Chloride channel CLIC-like protein 1	9.83	6		68	0.96	1.17	11	19.6
Q91X78	Erlin1	Erlin-1	18.21	7		95	0.96	1.17	7	4.8
Q9QX47-3	Son	Isoform 3 of Protein SON	9.73	21		172	0.96	1.17	40	12.5
Q9D2G2	Dlst	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	29.30	12		249	0.96	1.17	59	11.7
Q8CHI8-5	Ep400	Isoform 5 of E1A-binding protein p400	0.83	2		4	0.96	1.17	1	
Q9QZD8	Slc25a10	Mitochondrial dicarboxylate carrier	27.87	6		72	0.96	1.17	15	16.0
Q99N84	Mrps18b	28S ribosomal protein S18b, mitochondrial	9.06	3		15	0.96	1.17	5	5.3
Q9CXT8	Pmpcb	Mitochondrial-processing peptidase subunit beta	20.65	9		152	0.96	1.17	12	13.7
Q9DB77	Uqcrc2	Cytochrome b-c1 complex subunit 2, mitochondrial	41.94	17		500	0.96	1.17	134	14.9
P62488	Polr2g	DNA-directed RNA polymerase II subunit RPB7	13.37	2		4	0.96	1.17	1	
Q9CR47	Nsa2	Ribosome biogenesis protein NSA2 homolog	19.23	5		45	0.96	1.17	12	2.9
Q3UFY8	Trmt10c	Mitochondrial ribonuclease P protein 1	4.83	2		8	0.96	1.17	1	
A2AQA7	Aqr	Intron-binding protein aquarius	10.00	12		74	0.96	1.17	13	9.0
Q8VDQ9	Kri1	Protein KRI1 homolog	8.24	7		17	0.96	1.17	5	6.4
Q922P9	Glyr1	Putative oxidoreductase GLYR1	14.65	8		32	0.96	1.17	7	19.7
A0A087WNV1	Agfg1	Arf-GAP domain and FG repeat-containing protein 1	19.39	9		77	0.96	1.17	20	26.1
Q8CH25-2	Sltm	Isoform 2 of SAFB-like transcription modulator	9.87	10		62	0.96	1.17	12	26.8
E9QN31	Nop2	Probable 28S rRNA (cytosine-C(5))-methyltransferase	24.94	19		274	0.96	1.17	65	21.3
Q91ZA3	Pcca	Propionyl-CoA carboxylase alpha chain,	11.60	7		70	0.96	1.17	15	31.5

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		mitochondrial								
Q9Z1Q5	Clic1	Chloride intracellular channel protein 1	14.52	4		5	0.96	1.17	4	4.8
Q9JKX4	Aatf	Protein AATF	17.49	8		55	0.96	1.17	14	16.1
Q6PDG5-2	Smarcc2	Isoform 2 of SWI/SNF complex subunit SMARCC2	14.29	15		119	0.96	1.17	8	26.0
Q9ESV0	Ddx24	ATP-dependent RNA helicase DDX24	28.00	22		176	0.96	1.17	43	11.5
O54825	Bysl	Bystin	19.27	8		67	0.96	1.17	15	18.8
Q8BFV2	Pcid2	PCI domain-containing protein 2	9.02	3		11	0.96	1.17	2	0.1
Q6P4T2	Snrnp200	U5 small nuclear ribonucleoprotein 200 kDa helicase	28.51	56		551	0.96	1.17	127	12.7
O35857	Timm44	Mitochondrial import inner membrane translocase subunit TIM44	29.87	13		108	0.96	1.17	19	7.4
P45878	Fkbp2	Peptidyl-prolyl cis-trans isomerase FKBP2	34.29	4		32	0.96	1.17	9	12.8
Q9DCD2	Xab2	Pre-mRNA-splicing factor SYF1	13.22	10		64	0.96	1.17	6	24.2
E9PUF4	Rbm26	RNA-binding protein 26	3.26	3		8	0.96	1.17	1	
E9QJS0	Mrps10	28S ribosomal protein S10, mitochondrial	22.50	3		31	0.96	1.17	6	8.2
Q8BYL4	Yars2	Tyrosine--tRNA ligase, mitochondrial	17.80	8		55	0.96	1.17	9	12.6
D3Z3S1	Preb	Prolactin regulatory element binding, isoform CRA_b	24.57	7		47	0.96	1.17	5	9.9
Q9CQI7	Snrpb2	U2 small nuclear ribonucleoprotein B''	25.33	6		110	0.96	1.17	24	7.6
E9Q066	Larp4	La-related protein 4	4.60	3		21	0.96	1.17	4	4.4
Q9D0D4	Dimt1	Probable dimethyladenosine transferase	12.78	4		18	0.96	1.17	6	14.7
Q9CZJ1	Utp11l	Probable U3 small nucleolar RNA-associated protein 11	21.74	6		46	0.96	1.17	12	7.2
P10922	H1f0	Histone H1.0	27.32	5		112	0.96	1.17	35	5.9
Q9D270	Zdhhc21	Probable palmitoyltransferase ZDHHC21	10.94	3		14	0.96	1.17	3	15.4
O35286	Dhx15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	31.45	25		329	0.96	1.17	64	13.9
Q9Z2I8-2	Suclg2	Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	38.28	14		192	0.96	1.17	43	11.5
G3X9B1	Heatr1	HEAT repeat containing 1	17.69	41		362	0.96	1.16	73	13.0
Q6NXK9	Man1c1	alpha-1,2-Mannosidase	6.40	4		17	0.96	1.16	3	8.1
P26043	Rdx	Radixin	12.18	8		68	0.96	1.16	4	10.2
Q8CGK3	Lonp1	Lon protease homolog, mitochondrial	31.40	27		228	0.96	1.16	63	19.4
Q60902-3	Eps15l1	Isoform 3 of Epidermal growth factor receptor substrate 15-like 1	4.95	4		8	0.96	1.16	2	3.3
Q8BLN5	Lss	Lanosterol synthase	21.69	13		61	0.96	1.16	16	14.5
Q99LC5	Etfa	Electron transfer flavoprotein subunit alpha, mitochondrial	56.16	16		257	0.96	1.16	75	17.3

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P47791-2	Gsr	Isoform Cytoplasmic of Glutathione reductase, mitochondrial	17.93	6		38	0.96	1.16	10	7.4
O35129	Phb2	Prohibitin-2	68.90	21		938	0.96	1.16	275	17.5
Q80SW1	Ahcyl1	Putative adenosylhomocysteinase 2	6.04	3		17	0.96	1.16	1	
D3Z494	Akr1b10	MCG142264, isoform CRA_a	5.56	2		8	0.96	1.16	1	
P10810	Cd14	Monocyte differentiation antigen CD14	39.07	13		180	0.96	1.16	41	12.7
A2AQ17	Ndufaf1	Complex I intermediate-associated protein 30, mitochondrial	5.18	2		2	0.96	1.16	1	
Q6PR54-2	Rif1	Isoform 2 of Telomere-associated protein RIF1	6.10	14		61	0.96	1.16	13	15.1
Q05D44	Eif5b	Eukaryotic translation initiation factor 5B	1.89	2		6	0.96	1.16	1	
P50544	Acadvl	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	27.13	14		98	0.96	1.16	18	11.7
Q8C4J7	Tbl3	Transducin beta-like protein 3	26.22	15		110	0.96	1.16	28	16.5
Q99N15	Hsd17b10	17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase	53.64	9		152	0.96	1.16	43	18.9
Q64516-1	Gk	Isoform 1 of Glycerol kinase	8.59	6		31	0.96	1.16	5	11.3
Q8VD58	Evi2b	Protein EVI2B	4.05	2		15	0.96	1.16	2	7.7
P61965	Wdr5	WD repeat-containing protein 5	10.78	3		9	0.96	1.16	2	8.3
Q9D8M4	Rpl7l1	60S ribosomal protein L7-like 1	40.24	11		64	0.96	1.16	18	15.6
D3YZ62	Myo5a	Unconventional myosin-Va	3.56	7		35	0.96	1.16	4	12.1
Q99JW4	Lims1	LIM and senescent cell antigen-like-containing domain protein 1	6.15	2		6	0.96	1.16	1	
Q61187	Tsg101	Tumor susceptibility gene 101 protein	17.14	5		38	0.96	1.16	9	6.4
Q8BIP0	Dars2	Aspartate--tRNA ligase, mitochondrial	9.65	6		30	0.96	1.16	5	14.0
Q80YR5	Safb2	Scaffold attachment factor B2	15.34	13		74	0.96	1.16	3	10.9
E9Q1S3	Sec23a	Protein transport protein Sec23A	10.87	6		30	0.96	1.16	5	6.2
O08734	Bak1	Bcl-2 homologous antagonist/killer	17.70	5		46	0.96	1.16	5	9.9
Q9QUI0	Rhoa	Transforming protein RhoA	26.94	5		31	0.96	1.16	1	
Q8VEA8	Rab7b	Ras-related protein Rab-7b	14.57	2		15	0.96	1.16	4	10.8
Q8BTY2	Slc4a7	Sodium bicarbonate cotransporter 3	8.12	9		42	0.96	1.16	4	4.6
P63154	Crnkl1	Crooked neck-like protein 1	15.36	10		41	0.96	1.16	10	12.4
Q569Z6	Thrap3	Thyroid hormone receptor-associated protein 3	18.19	19		160	0.96	1.16	46	11.3
Q8C7V8-2	Ccdc134	Isoform 2 of Coiled-coil domain-containing protein 134	10.42	2		10	0.95	1.16	1	
Q9CYV5	Tmem135	Transmembrane protein 135	4.59	2		4	0.95	1.16	1	
Q9ESW4	Agk	Acylglycerol kinase, mitochondrial	8.31	3		15	0.95	1.16	4	1.9
G5E8G0	Hnrnpd	Heterogeneous nuclear ribonucleoprotein D, isoform CRA_b	29.62	9		200	0.95	1.16	50	11.5

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9D554	Sf3a3	Splicing factor 3A subunit 3	30.74	14		135	0.95	1.16	32	8.8
D3Z5R0	Mb21d1	Cyclic GMP-AMP synthase	27.16	9		38	0.95	1.16	7	12.7
Q3TUE1	Fubp1	Far upstream element-binding protein 1	38.32	25		578	0.95	1.16	109	20.7
Q8BVE8	Whsc1	Histone-lysine N-methyltransferase NSD2	3.44	4		12	0.95	1.16	3	15.4
G5E866	Sf3b1	Splicing factor 3B subunit 1	27.22	30		337	0.95	1.16	81	10.9
Q8VDF2	Uhrf1	E3 ubiquitin-protein ligase UHRF1	31.97	25		270	0.95	1.16	57	15.6
P61021	Rab5b	Ras-related protein Rab-5B	24.65	4		64	0.95	1.16	2	0.8
P97742	Cpt1a	Carnitine O-palmitoyltransferase 1, liver isoform	8.15	6		17	0.95	1.16	2	14.0
F7CBP1	Eif4g2	Eukaryotic translation initiation factor 4 gamma 2	10.48	8		38	0.95	1.16	8	9.3
P97765	Wbp2	WW domain-binding protein 2	13.79	4		21	0.95	1.16	8	17.4
P70279	Surf6	Surfeit locus protein 6	35.77	14		146	0.95	1.16	36	10.7
E9Q390	Myof	Myoferlin	18.75	35		217	0.95	1.16	35	11.3
Q9Z277	Baz1b	Tyrosine-protein kinase BAZ1B	21.10	32		215	0.95	1.16	46	11.2
Q3TWV4	Ap2m1	AP-2 complex subunit mu	23.56	12		112	0.95	1.16	25	16.2
Q9WVL3	Slc12a7	Solute carrier family 12 member 7	5.08	5		21	0.95	1.16	3	12.8
Q8BHX3	Cdca8	Borealin	13.84	4		14	0.95	1.16	4	18.4
Q8C5H8-3	Nadk2	Isoform 3 of NAD kinase 2, mitochondrial	10.93	4		15	0.95	1.16	1	
Q9D6Z1	Nop56	Nucleolar protein 56	40.69	24		425	0.95	1.16	102	15.8
Q924T2	Mrps2	28S ribosomal protein S2, mitochondrial	25.77	5		25	0.95	1.16	5	8.0
Q9D0L7-2	Armc10	Isoform 2 of Armadillo repeat-containing protein 10	22.26	5		25	0.95	1.16	5	28.1
Q921K2	Parp1	Poly [ADP-ribose] polymerase	35.60	35		405	0.95	1.16	101	18.0
P62305	Snrpe	Small nuclear ribonucleoprotein E	25.00	2		54	0.95	1.16	13	8.8
Q8VEM8	Slc25a3	Phosphate carrier protein, mitochondrial	24.65	10		489	0.95	1.16	127	17.7
Q9CR61	Ndufb7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	25.55	3		18	0.95	1.16	6	18.1
Q8K2M0-2	Mrpl38	Isoform 2 of 39S ribosomal protein L38, mitochondrial	5.20	2		40	0.95	1.16	8	20.5
Q9QZK7	Dok3	Docking protein 3	6.53	3		5	0.95	1.15	1	
Q91V01	Lpcat3	Lysophospholipid acyltransferase 5	4.52	2		19	0.95	1.15	3	14.1
Q80Y44	Ddx10	Probable ATP-dependent RNA helicase DDX10	11.66	10		61	0.95	1.15	16	6.0
Q9D1N9	Mrpl21	39S ribosomal protein L21, mitochondrial	12.92	3		27	0.95	1.15	4	7.3
Q9CQT2	Rbm7	RNA-binding protein 7	6.79	2		6	0.95	1.15	2	14.1
P58064	Mrps6	28S ribosomal protein S6, mitochondrial	35.20	5		58	0.95	1.15	12	15.6
Q8R0S2	Iqsec1	IQ motif and SEC7 domain-containing protein 1	2.60	2		2	0.95	1.15	1	
Q8BN21-2	Vrk2	Isoform 2 of Serine/threonine-protein kinase VRK2	6.61	2		8	0.95	1.15	1	
O88796	Rpp30	Ribonuclease P protein subunit p30	12.69	3		11	0.95	1.15	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8BGJ5	Ptbp1	MCG13402, isoform CRA_a	31.38	15		412	0.95	1.15	63	13.8
P29758	Oat	Ornithine aminotransferase, mitochondrial	43.74	15		266	0.95	1.15	64	13.3
P35486	Pdha1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	21.03	11		102	0.95	1.15	22	10.3
P97821	Ctsc	Dipeptidyl peptidase 1	6.71	2		12	0.95	1.15	3	12.4
Q8VHM5	Hnrnpr	Heterogeneous nuclear ribonucleoprotein R	31.49	21		315	0.95	1.15	38	18.9
Q9CPY7-2	Lap3	Isoform 2 of Cytosol aminopeptidase	23.36	11		84	0.95	1.15	16	13.1
Q9CQC7	Ndufb4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	36.43	4		60	0.95	1.15	12	24.5
Q61112	Sdf4	45 kDa calcium-binding protein	15.24	5		46	0.95	1.15	6	10.5
Q91VD9	Ndufs1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	40.58	27		376	0.95	1.15	89	13.5
Q6NS46	Pdcd11	Protein RRP5 homolog	25.03	43		338	0.95	1.15	76	16.4
Q9CQL5	Mrpl18	39S ribosomal protein L18, mitochondrial	10.56	2		8	0.95	1.15	3	22.6
Q8VHZ7	Imp4	U3 small nucleolar ribonucleoprotein protein IMP4	21.31	7		42	0.95	1.15	10	20.8
Q00PI9	Hnrnpul2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	17.32	16		97	0.95	1.15	20	14.4
Q9Z2N8	Actl6a	Actin-like protein 6A	5.59	2		6	0.95	1.15	1	
A0A0R4J2B0	Celf2	CUGBP Elav-like family member 2	13.18	7		83	0.95	1.15	24	16.9
D6RJ50	Parl	Rhomboid-like protein	18.13	2		6	0.95	1.15	2	3.9
D3YXK1	Samd1	Atherin	3.66	2		4	0.95	1.15	2	18.2
Q9JIX8-4	Acin1	Isoform 4 of Apoptotic chromatin condensation inducer in the nucleus	23.81	31		276	0.95	1.15	61	16.5
E9QL43	Nupl2	Nucleoporin-like protein 2	6.67	3		12	0.95	1.15	1	
Q91ZW3	Smarca5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	32.25	36		369	0.95	1.15	72	11.5
Q921F2	Tardbp	TAR DNA-binding protein 43	35.27	12		202	0.95	1.15	54	14.7
Q9JKF6	Pvrl1	Nectin-1	5.05	2		10	0.95	1.15	3	1.8
Q01320	Top2a	DNA topoisomerase 2-alpha	30.76	49		812	0.95	1.15	149	12.2
Q9CX34	Sugt1	Protein SGT1 homolog	23.51	7		35	0.95	1.15	8	5.7
Q99KG3-2	Rbm10	Isoform 2 of RNA-binding protein 10	14.77	12		76	0.95	1.15	9	3.4
Q6NV83-3	U2surp	Isoform 3 of U2 snRNP-associated SURP motif-containing protein	19.80	18		164	0.95	1.15	34	13.3
Q8R3Y8-2	Irf2bp1	Isoform 2 of Interferon regulatory factor 2-binding protein 1	4.96	3		15	0.95	1.15	2	9.0
Q9D6M3	Slc25a22	Mitochondrial glutamate carrier 1	16.72	6		40	0.95	1.15	8	8.8
Q9Z1Q2	Abhd16a	Abhydrolase domain-containing protein 16A	10.39	6		28	0.95	1.15	6	7.2

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
O88811	Stam2	Signal transducing adapter molecule 2	9.18	5		18	0.95	1.15	2	14.1
Q62383	Supt6h	Transcription elongation factor SPT6	3.19	5		29	0.95	1.15	6	31.9
B1ATZ0	Hgs	Hepatocyte growth factor-regulated tyrosine kinase substrate	7.83	7		36	0.95	1.15	7	13.2
Q9DAU1	Cnpy3	Protein canopy homolog 3	19.93	5		36	0.95	1.15	6	9.2
A0A0G2JFW6	Rprd2	Regulation of nuclear pre-mRNA domain-containing protein 2 (Fragment)	6.42	7		24	0.95	1.15	3	4.0
Q8CGF7-3	Tcerg1	Isoform 3 of Transcription elongation regulator 1	5.61	6		24	0.95	1.15	5	7.2
O08784	Tcof1	Treacle protein	14.55	21		106	0.94	1.15	21	18.6
P97384	Anxa11	Annexin A11	31.41	17		192	0.94	1.15	45	13.8
Q61941	Nnt	NAD(P) transhydrogenase, mitochondrial	11.60	12		82	0.94	1.15	8	25.0
B2RWS6	Ep300	Histone acetyltransferase p300	1.37	3		14	0.94	1.15	2	2.4
Q7M6Y3-2	Picalm	Isoform 2 of Phosphatidylinositol-binding clathrin assembly protein	23.28	11		127	0.94	1.15	30	11.3
F6V6T4	Tmed2	Transmembrane emp24 domain-containing protein 2 (Fragment)	39.20	7		249	0.94	1.15	68	14.9
Q9Z210	Pex11b	Peroxisomal membrane protein 11B	14.67	4		33	0.94	1.15	7	14.1
Q99L45	Eif2s2	Eukaryotic translation initiation factor 2 subunit 2	6.04	2		6	0.94	1.15	1	
Q8C2Q3	Rbm14	RNA-binding protein 14	32.59	21		411	0.94	1.15	93	16.7
Q8CFQ9	Fus	Fusion, derived from t(1216) malignant liposarcoma (Human)	8.90	6		85	0.94	1.15	30	11.0
Q80TY0-5	Fnbp1	Isoform 5 of Formin-binding protein 1	5.62	2		4	0.94	1.15	1	
Q8VIJ6	Sfpq	Splicing factor, proline- and glutamine-rich	35.48	27		657	0.94	1.15	154	16.7
Q80ZP8	Manf	Armet protein	35.15	7		96	0.94	1.15	25	17.5
Q8BGS0-2	Mak16	Isoform 2 of Protein MAK16 homolog	13.79	4		10	0.94	1.15	4	6.3
P13597-2	Icam1	Isoform 2 of Intercellular adhesion molecule 1	13.94	7		29	0.94	1.15	5	12.1
Q9QZQ8	H2afy	Core histone macro-H2A.1	48.12	16		344	0.94	1.14	80	20.3
Q9DCM0	Ethe1	Persulfide dioxygenase ETHE1, mitochondrial	12.20	2		3	0.94	1.14	2	18.4
Q3TDN2	Faf2	FAS-associated factor 2	17.75	5		27	0.94	1.14	6	27.9
Q9CYH6	Rrs1	Ribosome biogenesis regulatory protein homolog	30.41	13		239	0.94	1.14	47	10.8
Q9DCC8	Tomm20	Mitochondrial import receptor subunit TOM20 homolog	31.03	4		83	0.94	1.14	17	16.6
P21107-2	Tpm3	Isoform 2 of Tropomyosin alpha-3 chain	51.61	16		170	0.94	1.14	29	15.0
H3BKL8	Dusp3	Dual-specificity protein phosphatase 3	28.97	3		13	0.94	1.14	2	46.1
O54790	Mafg	Transcription factor MafG	36.42	7		38	0.94	1.14	5	14.3
Q8VDM6	Hnrnpul1	Heterogeneous nuclear ribonucleoprotein U-like	23.98	18		168	0.94	1.14	31	17.7

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		protein 1								
Q80X50	Ubap2l	Ubiquitin-associated protein 2-like	23.58	20		344	0.94	1.14	13	6.9
P36371	Tap2	Antigen peptide transporter 2	8.26	5		28	0.94	1.14	6	37.4
Q8VE37	Rcc1	Regulator of chromosome condensation	32.54	11		160	0.94	1.14	41	17.4
Q9R0A0	Pex14	Peroxisomal membrane protein PEX14	23.14	8		58	0.94	1.14	15	20.7
A0A0G2JFX7	Rbm8a	RNA-binding protein 8A	32.16	5		79	0.94	1.14	4	5.3
Q9CQB4	Uqcrb	Cytochrome b-c1 complex subunit 7	55.86	7		177	0.94	1.14	40	8.7
Q8K4Z5	Sf3a1	Splicing factor 3A subunit 1	31.23	26		315	0.94	1.14	81	12.6
O08749	Dld	Dihydrolipoyl dehydrogenase, mitochondrial	37.13	14		281	0.94	1.14	64	14.8
Q60960	Kpna1	Importin subunit alpha-5	9.29	5		23	0.94	1.14	5	8.2
Q3UKJ7	Smu1	WD40 repeat-containing protein SMU1	19.10	8		63	0.94	1.14	13	9.8
Q9QYA2	Tomm40	Mitochondrial import receptor subunit TOM40 homolog	24.65	7		85	0.94	1.14	21	17.0
Q8BY02	Nkrf	NF-kappa-B-repressing factor	2.75	2		4	0.94	1.14	1	
Q9R1C7-2	Prpf40a	Isoform 2 of Pre-mRNA-processing factor 40 homolog A	18.66	16		100	0.94	1.14	22	13.7
Q99KC8	Vwa5a	von Willebrand factor A domain-containing protein 5A	8.07	5		15	0.94	1.14	5	7.9
P25206	Mcm3	DNA replication licensing factor MCM3	10.34	8		27	0.94	1.14	3	31.6
Q8BGA9	Oxa1l	Mitochondrial inner membrane protein OXA1L	3.93	2		22	0.94	1.14	8	14.8
Q8BYU6	Tor1aip2	Torsin-1A-interacting protein 2	6.18	3		24	0.94	1.14	2	34.8
O88508	Dnmt3a	DNA (cytosine-5)-methyltransferase 3A	4.63	5		32	0.94	1.14	7	9.2
Q8JZQ2	Afg3l2	AFG3-like protein 2	13.47	12		48	0.94	1.14	8	7.2
Q64133	Maoa	Amine oxidase [flavin-containing] A	15.97	8		48	0.94	1.14	8	6.3
Q8BHD7-2	Ptbp3	Isoform 2 of Polypyrimidine tract-binding protein 3	13.08	8		235	0.94	1.14	7	5.1
Q3TA68	Wdr36	Protein Wdr36	22.31	16		128	0.94	1.14	28	12.3
Q8CAQ8-2	Immt	Isoform 2 of MICOS complex subunit Mic60	51.34	40		748	0.94	1.14	1	
P04441-2	Cd74	Isoform Short of H-2 class II histocompatibility antigen gamma chain	39.07	7		72	0.94	1.14	19	17.7
Q99P72	Rtn4	Reticulon-4	23.92	19		386	0.94	1.14	97	22.9
Q8R326-2	Pspc1	Isoform 2 of Paraspeckle component 1	22.96	13		133	0.94	1.14	14	15.6
P57784	Snrpa1	U2 small nuclear ribonucleoprotein A'	53.33	11		137	0.94	1.14	38	17.2
Q8BGD9	Eif4b	Eukaryotic translation initiation factor 4B	9.49	5		16	0.94	1.14	3	2.5
Q8K301	Ddx52	Probable ATP-dependent RNA helicase DDX52	14.38	8		56	0.94	1.14	9	16.1
Q9DB73-2	Cyb5r1	Isoform 2 of NADH-cytochrome b5 reductase 1	17.11	3		25	0.94	1.14	8	10.3
Q99JR1	Sfxn1	Sideroflexin-1	29.19	9		98	0.94	1.14	22	19.4
E0CX19	Hibch	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	12.22	4		22	0.94	1.14	4	27.3

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
F8WHY8	Mta1	Metastasis-associated protein MTA1	15.76	11		65	0.94	1.14	9	7.5
Q99PV0	Prpf8	Pre-mRNA-processing-splicing factor 8	25.01	61		641	0.94	1.14	135	13.3
Q923G2	Polr2h	DNA-directed RNA polymerases I, II, and III subunit RPABC3	24.00	3		13	0.94	1.14	5	29.7
Q60759	Gcdh	Glutaryl-CoA dehydrogenase, mitochondrial	3.42	2		2	0.94	1.14	1	
Q9DB34	Chmp2a	Charged multivesicular body protein 2a	15.32	3		13	0.94	1.14	4	27.8
Q91XA2	Golm1	Golgi membrane protein 1	19.85	7		40	0.94	1.14	11	8.9
Q8BH04	Pck2	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	20.47	11		140	0.94	1.14	39	16.8
Q640M1	Utp14a	U3 small nucleolar RNA-associated protein 14 homolog A	31.42	22		104	0.94	1.14	29	16.4
Q3UYV9	Ncbp1	Nuclear cap-binding protein subunit 1	7.47	6		24	0.94	1.14	2	1.4
A2A8V8	Srrm1	Serine/arginine repetitive matrix protein 1	4.18	3		17	0.94	1.14	6	15.7
Q9CY73	Mrpl44	39S ribosomal protein L44, mitochondrial	14.11	6		50	0.94	1.14	8	19.4
Q9DC71	Mrps15	28S ribosomal protein S15, mitochondrial	25.58	7		36	0.94	1.14	7	4.5
F8WHU8	Slirp	SRA stem-loop-interacting RNA-binding protein, mitochondrial (Fragment)	18.63	2		35	0.94	1.14	13	23.0
Q8BIJ6	Iars2	Isoleucine--tRNA ligase, mitochondrial	11.46	9		70	0.94	1.14	14	17.2
Q8BUY5	Timmdc1	Complex I assembly factor TIMMDC1, mitochondrial	7.72	2		4	0.94	1.14	2	3.7
Q91YM4-2	Tbrg4	Isoform 2 of Protein TBRG4	4.17	3		20	0.93	1.14	2	5.7
Q9R1Q7	Plp2	Proteolipid protein 2	17.76	2		135	0.93	1.13	39	15.6
P63254	Crip1	Cysteine-rich protein 1	24.68	2		10	0.93	1.13	2	6.2
Q9WTK3	Gpaa1	Glycosylphosphatidylinositol anchor attachment 1 protein	7.09	5		37	0.93	1.13	10	7.8
Q59J78	Ndufaf2	Mimitin, mitochondrial	26.79	4		14	0.93	1.13	3	17.4
Q9ESY9	Ifi30	Gamma-interferon-inducible lysosomal thiol reductase	9.68	2		9	0.93	1.13	2	4.2
Q8BVY0	Rsl1d1	Ribosomal L1 domain-containing protein 1	35.18	16		315	0.93	1.13	69	12.5
P09671	Sod2	Superoxide dismutase [Mn], mitochondrial	27.03	7		130	0.93	1.13	33	17.6
Q8K310	Matr3	Matrin-3	33.45	30		519	0.93	1.13	142	16.6
Q80ZX0	Sec24b	Protein Sec24b	1.92	2		6	0.93	1.13	3	0.6
Q3UHX9-2	D2Wsu81e	Isoform 2 of Putative methyltransferase C9orf114 homolog	23.19	8		55	0.93	1.13	13	5.4
Q9JLJ2	Aldh9a1	4-trimethylaminobutyraldehyde dehydrogenase	12.96	7		37	0.93	1.13	7	5.4
Q9QXE7	Tbl1x	F-box-like/WD repeat-containing protein TBL1X	9.49	4		43	0.93	1.13	8	8.3
Q9DB25	Alg5	Dolichyl-phosphate beta-glucosyltransferase	10.49	3		26	0.93	1.13	4	8.6
Q9CW03	Smc3	Structural maintenance of chromosomes protein 3	37.30	44		321	0.93	1.13	64	17.9

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9WUU9	Mcm3ap	Germinal-center associated nuclear protein	1.47	3		13	0.93	1.13	1	
Q3TKT4	Smarca4	Transcription activator BRG1	12.90	19		130	0.93	1.13	27	12.6
Q9CU62	Smc1a	Structural maintenance of chromosomes protein 1A	25.14	33		276	0.93	1.13	61	19.4
A2AER8	Pqbp1	Polyglutamine-binding protein 1 (Fragment)	8.90	2		10	0.93	1.13	1	
A2AJ72	Fubp3	MCG130458	35.50	21		288	0.93	1.13	43	19.5
Q99LI7	Cstf3	Cleavage stimulation factor subunit 3	12.97	9		66	0.93	1.13	10	17.7
Q99MU3-3	Adar	Isoform 3 of Double-stranded RNA-specific adenosine deaminase	6.62	4		15	0.93	1.13	4	9.0
E9Q784	Zc3h13	Protein Zc3h13	1.74	3		10	0.93	1.13	2	0.8
Q9CWJ9	Atic	Bifunctional purine biosynthesis protein PURH	10.98	4		13	0.93	1.13	3	18.5
Q9Z0H1	Wdr46	WD repeat-containing protein 46	24.44	14		173	0.93	1.13	43	14.6
P54728	Rad23b	UV excision repair protein RAD23 homolog B	8.65	4		13	0.93	1.13	2	7.6
Q6ZQ58	Larp1	La-related protein 1	1.87	2		4	0.93	1.13	1	
Q6NVF9	Cpsf6	Cleavage and polyadenylation specificity factor subunit 6	17.97	8		115	0.93	1.13	31	15.5
Q9CQF0	Mrpl11	39S ribosomal protein L11, mitochondrial	42.19	8		46	0.93	1.13	7	7.3
E9QNN1	Dhx9	ATP-dependent RNA helicase A	29.05	37		671	0.93	1.13	163	17.5
E9QP59	Lemd3	Inner nuclear membrane protein Man1	7.95	6		32	0.93	1.13	9	12.1
Q8K4P0	Wdr33	pre-mRNA 3' end processing protein WDR33	7.82	9		32	0.93	1.13	9	4.1
Q60749	Khdrbs1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	28.44	11		180	0.93	1.13	46	13.8
D3Z7C0	Mrpl40	39S ribosomal protein L40, mitochondrial	43.83	6		49	0.93	1.13	12	21.7
P22892	Ap1g1	AP-1 complex subunit gamma-1	4.01	4		17	0.93	1.13	4	13.5
O88665	Brd7	Bromodomain-containing protein 7	3.53	3		7	0.93	1.13	2	16.8
Q3TBA3	Tap1	Antigen peptide transporter 1	3.88	3		12	0.93	1.13	1	
Q9CXC3	Mgme1	Mitochondrial genome maintenance exonuclease 1	5.03	2		8	0.93	1.13	3	7.7
Q921J2	Rheb	GTP-binding protein Rheb	16.85	4		28	0.93	1.13	8	14.9
D3Z132	Thoc6	THO complex subunit 6 homolog	19.29	6		28	0.93	1.13	5	15.7
Q921M3	Sf3b3	Splicing factor 3B subunit 3	26.62	32		382	0.93	1.12	91	18.0
Q99KE1	Me2	NAD-dependent malic enzyme, mitochondrial	23.94	11		132	0.93	1.12	33	7.8
Q9D823	Rpl37	60S ribosomal protein L37	38.14	5		62	0.93	1.12	18	15.3
O88455	Dhcr7	7-dehydrocholesterol reductase	9.34	4		58	0.93	1.12	15	9.4
P21279	Gnaq	Guanine nucleotide-binding protein G(q) subunit alpha	10.58	4		15	0.93	1.12	4	4.6
A0A0A0MQB0	BC003331	Protein BC003331	11.21	4		10	0.92	1.12	2	24.7
E0CX20	Bud31	Protein BUD31 homolog	14.58	2		8	0.92	1.12	2	9.0
P70362	Ufd1l	Ubiquitin fusion degradation protein 1 homolog	12.70	4		16	0.92	1.12	5	7.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q14C51	Ptcd3	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	20.15	12		74	0.92	1.12	18	16.1
Q9Z0V7	Timm17b	Mitochondrial import inner membrane translocase subunit Tim17-B	16.86	3		16	0.92	1.12	7	11.2
Q9WV70	Noc2l	Nucleolar complex protein 2 homolog	15.13	12		117	0.92	1.12	33	17.9
Q9Z2D8-2	Mbd3	Isoform 2 of Methyl-CpG-binding domain protein 3	11.46	3		23	0.92	1.12	2	14.4
Q9DC23	Dnajc10	DnaJ homolog subfamily C member 10	8.45	6		19	0.92	1.12	2	21.7
P62309	Snrpg	Small nuclear ribonucleoprotein G	18.42	2		62	0.92	1.12	19	8.5
P01942	Hba	Hemoglobin subunit alpha	15.49	2		81	0.92	1.12	24	9.6
Q8K215	Lyrm4	LYR motif-containing protein 4	48.35	4		19	0.92	1.12	3	6.1
Q7TPV4	Mybbp1a	Myb-binding protein 1A	33.41	43		1127	0.92	1.12	303	12.8
G3X9U9	Fis1	Fission 1 (Mitochondrial outer membrane) homolog (Yeast), isoform CRA_c	17.93	2		5	0.92	1.12	2	13.8
Q8BHS3	Rbm22	Pre-mRNA-splicing factor RBM22	15.48	6		46	0.92	1.12	11	13.9
Q791V5	Mtch2	Mitochondrial carrier homolog 2	29.70	7		56	0.92	1.12	15	9.0
Q9D287	Bcas2	Pre-mRNA-splicing factor SPF27	26.22	7		58	0.92	1.12	8	21.7
Q9CRA8	Exosc5	Exosome complex component RRP46	22.98	4		11	0.92	1.12	4	31.8
Q9D0W5	Ppil1	Peptidyl-prolyl cis-trans isomerase-like 1	29.52	5		34	0.92	1.12	11	13.9
B0QZF8	Usp36	Ubiquitin carboxyl-terminal hydrolase 36 (Fragment)	8.99	7		22	0.92	1.12	2	0.4
Q9DC61	Pmpca	Mitochondrial-processing peptidase subunit alpha	19.08	12		69	0.92	1.12	13	15.3
Q9D0S9	Hint2	Histidine triad nucleotide-binding protein 2, mitochondrial	25.77	3		23	0.92	1.12	8	9.4
Q9ESX5	Dkc1	H/ACA ribonucleoprotein complex subunit 4	33.20	15		197	0.92	1.12	50	9.6
Q9EPE9	Atp13a1	Manganese-transporting ATPase 13A1	11.50	12		120	0.92	1.12	20	19.1
Q9Z1P6	Ndufa7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	38.94	5		25	0.92	1.12	5	3.1
A0A0R4J027	Irg1	Cis-aconitate decarboxylase	9.22	4		28	0.92	1.12	2	10.8
O35892-2	Sp100	Isoform 2 of Nuclear autoantigen Sp-100	4.96	3		9	0.92	1.12	2	18.6
Q6A068	Cdc5l	Cell division cycle 5-like protein	29.30	20		191	0.92	1.12	52	12.9
P49710	Hcls1	Hematopoietic lineage cell-specific protein	12.96	7		28	0.92	1.12	6	11.1
Q9QZA0	Ca5b	Carbonic anhydrase 5B, mitochondrial	6.94	2		6	0.92	1.12	1	
Q91VC9	Ghitm	Growth hormone-inducible transmembrane protein	8.67	3		14	0.92	1.12	1	
A0A0U1RPD8	Gtf3c1	General transcription factor 3C polypeptide 1	4.24	8		31	0.92	1.12	7	33.2
A0A087WNZ7	Trip12	E3 ubiquitin-protein ligase TRIP12	2.61	5		17	0.92	1.12	4	19.6
Q9Z1N2	Orc1	Origin recognition complex subunit 1	10.60	9		28	0.92	1.12	6	20.0

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q3U4F0	Sfxn3	Sideroflexin-3	19.22	5		29	0.92	1.12	8	9.8
Q61733	Mrps31	28S ribosomal protein S31, mitochondrial	14.84	6		52	0.92	1.12	6	10.7
Q8K411-2	Pitrm1	Isoform 2 of Presequence protease, mitochondrial	18.84	18		112	0.92	1.12	21	11.4
Q9CQS4	Slc25a46	Solute carrier family 25 member 46	7.66	3		15	0.92	1.12	1	
A0A0R4J083	Acadl	Long-chain-specific acyl-CoA dehydrogenase, mitochondrial	30.00	14		125	0.92	1.12	33	14.3
Q3TEA8-2	Hp1bp3	Isoform 2 of Heterochromatin protein 1-binding protein 3	26.25	15		239	0.92	1.12	51	13.2
P70227	Itpr3	Inositol 1,4,5-trisphosphate receptor type 3	5.06	14		66	0.92	1.12	7	9.4
Q99020	Hnrnpab	Heterogeneous nuclear ribonucleoprotein A/B	42.11	12		524	0.92	1.12	131	10.3
Q9CZ91	Srfbp1	Serum response factor-binding protein 1	10.88	5		20	0.92	1.12	3	0.4
Q6KCD5-2	Nipbl	Isoform 2 of Nipped-B-like protein	2.79	6		25	0.92	1.12	6	4.7
Q61687	Atrx	Transcriptional regulator ATRX	4.77	11		44	0.92	1.12	10	28.9
Q9D1M0	Sec13	Protein SEC13 homolog	13.98	4		92	0.92	1.12	30	38.6
Q791T5-2	Mtch1	Isoform 2 of Mitochondrial carrier homolog 1	6.72	3		17	0.92	1.12	1	
A0A0R4J098	Zfp326	DBIRD complex subunit ZNF326	6.72	4		15	0.92	1.12	3	4.7
Q9ERA6	Tfip11	Tuftelin-interacting protein 11	4.53	4		21	0.92	1.12	1	
Q8R2M2	Dnttip2	Deoxynucleotidyltransferase terminal-interacting protein 2	22.56	16		133	0.92	1.12	27	9.6
Q8K224	Nat10	N-acetyltransferase 10	30.76	29		332	0.92	1.11	74	17.9
P20108	Prdx3	Thioredoxin-dependent peroxide reductase, mitochondrial	24.12	6		170	0.92	1.11	34	20.2
Q9JJ89	Ccdc86	Coiled-coil domain-containing protein 86	20.89	8		39	0.92	1.11	8	7.2
Q6PCP5-4	Mff	Isoform 4 of Mitochondrial fission factor	21.10	3		9	0.92	1.11	2	12.6
Q8JZX4	Rbm17	Splicing factor 45	28.89	12		89	0.92	1.11	22	14.8
Q9CX86	Hnrnpa0	Heterogeneous nuclear ribonucleoprotein A0	46.56	13		270	0.92	1.11	53	10.8
E9Q5C9	Nolc1	Protein Nolc1	30.34	25		326	0.92	1.11	71	15.0
Q61599	Arhgdib	Rho GDP-dissociation inhibitor 2	22.00	3		13	0.92	1.11	2	11.3
E9Q6A7	Bptf	Protein Bptf	0.79	3		6	0.92	1.11	1	
F8VQ93	Phip	PH-interacting protein	2.58	4		18	0.92	1.11	4	8.7
Q9Z2I9	Sucla2	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	30.45	15		145	0.92	1.11	33	15.6
Q571H0	Urb1	Nucleolar pre-ribosomal-associated protein 1	1.19	3		6	0.92	1.11	1	
Q6IRU2	Tpm4	Tropomyosin alpha-4 chain	16.94	5		16	0.92	1.11	1	
G5E897	Kdelc2	KDEL (Lys-Asp-Glu-Leu) containing 2, isoform CRA_b	8.35	4		13	0.92	1.11	3	12.4
Q80YW0	Cyth4	Cytohesin-4	9.92	4		13	0.92	1.11	3	9.6
P52503	Ndufs6	NADH dehydrogenase [ubiquinone] iron-sulfur	43.10	3		37	0.92	1.11	6	10.3

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN^{1}	pksP/wt^{1}	pksP/wt Count^{2}	pksP/wt Variance [%]^{3}
		protein 6, mitochondrial								
Q8K1R3	Pnpt1	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	11.75	10		83	0.92	1.11	15	11.1
E9Q7L1	Urb2	Protein Urb2	2.69	4		23	0.92	1.11	5	14.4
D3Z792	Rtn4ip1	Reticulon-4-interacting protein 1, mitochondrial	11.63	2		7	0.92	1.11	1	
Q9R0E1	Plod3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	16.19	12		126	0.91	1.11	35	17.6
A0A087WR08	Taf9	Transcription initiation factor TFIID subunit 9 (Fragment)	12.26	2		4	0.91	1.11	1	
Q8VDP4	Ccar2	Cell cycle and apoptosis regulator protein 2	12.15	13		80	0.91	1.11	14	8.9
Q91VC3	Eif4a3	Eukaryotic initiation factor 4A-III	38.44	18		273	0.91	1.11	59	15.2
B2RY56	Rbm25	RNA-binding protein 25	17.30	14		167	0.91	1.11	34	15.4
P62313	Lsm6	U6 snRNA-associated Sm-like protein LSm6	35.00	4		8	0.91	1.11	2	6.5
P47740	Aldh3a2	Fatty aldehyde dehydrogenase	11.36	5		40	0.91	1.11	7	3.9
Q9DB85	Rrp8	Ribosomal RNA-processing protein 8	14.88	7		34	0.91	1.11	7	21.4
G3X9L6	Gm10250	MCG55033	71.25	10		143	0.91	1.11	43	13.9
Q9R0M6	Rab9a	Ras-related protein Rab-9A	8.96	2		4	0.91	1.11	2	11.2
Q9D3D9	Atp5d	ATP synthase subunit delta, mitochondrial	13.69	2		178	0.91	1.11	54	8.0
P97379	G3bp2	Ras GTPase-activating protein-binding protein 2	16.18	8		66	0.91	1.11	16	22.1
Q8BJ48	Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	13.93	6		50	0.91	1.11	9	16.3
Q9DAV9	Tmem38b	Trimeric intracellular cation channel type B	27.74	8		132	0.91	1.11	34	20.8
Q61191	Hcfc1	Host cell factor 1	5.43	9		45	0.91	1.11	9	16.8
Q6PAC3	Dcaf13	DDB1- and CUL4-associated factor 13	12.58	6		71	0.91	1.11	10	7.2
Q9CQC9	Sar1b	GTP-binding protein SAR1b	21.21	4		28	0.91	1.11	3	1.7
Q9DBY8	Nvl	Nuclear valosin-containing protein-like	9.94	7		25	0.91	1.11	5	4.9
Q6NZF1	Zc3h11a	Zinc finger CCCH domain-containing protein 11A	7.32	5		14	0.91	1.11	2	10.5
E9QAE3	Btaf1	Protein Btaf1	5.84	11		28	0.91	1.11	8	14.4
Q64092-3	Tfe3	Isoform 3 of Transcription factor E3	12.96	7		48	0.91	1.11	10	10.4
A2AMC3	Pofut1	GDP-fucose protein O-fucosyltransferase 1	8.52	2		25	0.91	1.11	4	11.8
Q8CD10	Micu2	Calcium uptake protein 2, mitochondrial	5.79	2		6	0.91	1.11	1	
Q8BU11	Tox4	TOX high mobility group box family member 4	4.52	3		21	0.91	1.11	2	1.8
Q61081	Cdc37	Hsp90 co-chaperone Cdc37	10.55	4		16	0.91	1.11	5	23.9
Q9DC33	Hmg20a	High mobility group protein 20A	9.25	2		13	0.91	1.11	4	6.4
F6QL70	Gm17669	Protein Gm17669	16.88	3		93	0.91	1.11	16	17.6
G3UWD2	Runx1	Runt related transcription factor 1, isoform CRA_c	16.63	7		33	0.91	1.11	7	18.5
Q91W52	Tmem19	Transmembrane protein 19	5.95	2		2	0.91	1.11	1	
P81269	Atf1	Cyclic AMP-dependent transcription factor ATF-	11.52	4		17	0.91	1.11	3	9.5

Accession	**Gene**	**Protein Description**	**Coverage [%]**	**Peptides**	**Unique Peptides**	**PSMs**	**pksP/wt MN[1]**	**pksP/wt[1]**	**pksP/wt Count[2]**	**pksP/wt Variance [%][3]**
		1								
Q9CXW2	Mrps22	28S ribosomal protein S22, mitochondrial	20.33	8		58	0.91	1.11	13	17.8
Q9DCT2	Ndufs3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	33.08	8		79	0.91	1.10	21	15.4
P27048	Snrpb	Small nuclear ribonucleoprotein-associated protein B	16.02	4		58	0.91	1.10	13	17.5
Q5RJG1	Nol10	Nucleolar protein 10	11.94	10		46	0.91	1.10	9	8.3
Q99JY4	Trabd	TraB domain-containing protein	5.05	2		12	0.91	1.10	2	4.8
Q9D1Q4	Dpm3	Dolichol-phosphate mannosyltransferase subunit 3	23.91	2		21	0.91	1.10	7	10.6
Q99K48	Nono	Non-POU domain-containing octamer-binding protein	35.94	22		441	0.91	1.10	78	20.7
G5E8P1	Brd1	MCG7283	1.89	2		10	0.91	1.10	3	5.4
Q61686	Cbx5	Chromobox protein homolog 5	31.94	6		29	0.91	1.10	9	9.2
Q9CQF3	Nudt21	Cleavage and polyadenylation specificity factor subunit 5	30.40	7		52	0.91	1.10	15	13.0
Q9CQF8	Mrpl57	Ribosomal protein 63, mitochondrial	19.61	2		17	0.91	1.10	4	7.0
D3YXK2	Safb	Scaffold attachment factor B1	17.29	17		162	0.91	1.10	28	9.4
P10853	Hist1h2bf	Histone H2B type 1-F/J/L	68.25	13		2777	0.91	1.10	33	9.7
Q9D6R2	Idh3a	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	37.98	14		311	0.91	1.10	68	17.5
Q922U1	Prpf3	U4/U6 small nuclear ribonucleoprotein Prp3	22.25	16		95	0.91	1.10	22	18.8
Q3V009	Tmed1	Transmembrane emp24 domain-containing protein 1	11.45	2		17	0.91	1.10	2	2.2
Q8BP47	Nars	Asparagine--tRNA ligase, cytoplasmic	3.76	3		7	0.91	1.10	1	
Q9Z0H3-2	Smarcb1	Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	14.63	3		26	0.91	1.10	4	3.2
Q5SSI6	Utp18	U3 small nucleolar RNA-associated protein 18 homolog	11.41	6		103	0.90	1.10	26	25.2
Q80UJ7	Rab3gap1	Rab3 GTPase-activating protein catalytic subunit	4.08	4		15	0.90	1.10	1	
P12815	Pdcd6	Programmed cell death protein 6	14.66	3		6	0.90	1.10	1	
F8WHU7	Stag1	Cohesin subunit SA-1	5.81	9		53	0.90	1.10	3	7.2
B1ARW4	Ndufs5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 (Fragment)	27.47	2		20	0.90	1.10	6	10.4
Q3U6F1	Rbpj	Recombining-binding protein suppressor of hairless	12.04	5		58	0.90	1.10	11	10.7
O55013	Trappc3	Trafficking protein particle complex subunit 3	8.89	2		6	0.90	1.10	1	
Q61584-2	Fxr1	Isoform A of Fragile X mental retardation	10.20	5		33	0.90	1.10	4	19.8

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		syndrome-related protein 1								
A0A0A6YXW7	Uck2	Uridine-cytidine kinase 2 (Fragment)	30.48	4		30	0.90	1.10	7	4.8
P0C0S6	H2afz	Histone H2A.Z	31.25	4		887	0.90	1.10	49	19.9
E9Q5Q0	Atxn2l	Ataxin-2-like protein (Fragment)	10.78	10		42	0.90	1.10	9	31.6
A0A0R3P9C8	Ndufa9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	30.56	12		155	0.90	1.10	34	15.7
P19536	Cox5b	Cytochrome c oxidase subunit 5B, mitochondrial	31.25	5		60	0.90	1.10	13	15.5
Q8C7V3	Utp15	U3 small nucleolar RNA-associated protein 15 homolog	36.74	19		100	0.90	1.10	23	12.3
P68254-2	Ywhaq	Isoform 2 of 14-3-3 protein theta	23.05	6		55	0.90	1.10	1	
Q9CW46	Raver1	Ribonucleoprotein PTB-binding 1	21.12	13		91	0.90	1.10	20	21.1
P45952	Acadm	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	25.89	10		112	0.90	1.10	19	12.3
Q8BGS7	Cept1	Choline/ethanolaminephosphotransferase 1	6.73	3		14	0.90	1.10	1	
Q9CZX9	Emc4	ER membrane protein complex subunit 4	22.40	3		46	0.90	1.10	13	4.2
Q91WK2	Eif3h	Eukaryotic translation initiation factor 3 subunit H	7.95	2		6	0.90	1.10	2	13.7
O88952	Lin7c	Protein lin-7 homolog C	6.60	2		10	0.90	1.10	1	
Q9D0T1	Nhp2l1	NHP2-like protein 1	40.63	7		160	0.90	1.10	39	20.8
A2ALB2	Rexo4	RNA exonuclease 4	24.94	10		64	0.90	1.09	13	21.5
P18760	Cfl1	Cofilin-1	52.41	9		153	0.90	1.09	46	34.9
D3Z4V1	Plrg1	Pleiotropic regulator 1	20.83	8		57	0.90	1.09	11	5.9
Q9CPS7	Pno1	RNA-binding protein PNO1	28.63	7		48	0.90	1.09	11	16.3
Q9D2R6	Coa3	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	17.59	2		26	0.90	1.09	6	7.2
P63085	Mapk1	Mitogen-activated protein kinase 1	9.78	3		7	0.90	1.09	1	
Q8R323	Rfc3	Replication factor C subunit 3	25.84	7		40	0.90	1.09	6	15.1
Q9CXY6	Ilf2	Interleukin enhancer-binding factor 2	32.56	12		113	0.90	1.09	32	20.2
Q9JKK7-3	Tmod2	Isoform 3 of Tropomodulin-2	9.38	2		36	0.90	1.09	11	8.4
Q810V0	Mphosph10	U3 small nucleolar ribonucleoprotein protein MPP10	18.36	12		66	0.90	1.09	18	10.3
Q8BJW5-2	Nol11	Isoform 2 of Nucleolar protein 11	13.94	13		72	0.90	1.09	16	5.5
Q9EQC8	Prcc	Papillary renal cell carcinoma (Translocation-associated)	9.78	4		36	0.90	1.09	9	93.2
O35405	Pld3	Phospholipase D3	5.12	3		4	0.90	1.09	1	
H3BJ37	Comtd1	Catechol O-methyltransferase domain-containing protein 1	11.00	3		41	0.90	1.09	11	17.2
A0A087WRN1	Bclaf1	Bcl-2-associated transcription factor 1 (Fragment)	18.70	12		84	0.90	1.09	24	15.8

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q3UPF5-2	Zc3hav1	Isoform 2 of Zinc finger CCCH-type antiviral protein 1	8.62	6		22	0.90	1.09	4	20.0
Q0P678	Zc3h18	Zinc finger CCCH domain-containing protein 18	8.33	8		54	0.90	1.09	12	16.5
O88736	Hsd17b7	3-keto-steroid reductase	7.19	2		12	0.90	1.09	1	
Q6P8N8	Clpx	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	14.52	9		50	0.90	1.09	12	7.1
Q9DC48	Cdc40	Pre-mRNA-processing factor 17	13.30	6		25	0.90	1.09	3	1.4
P70372	Elavl1	ELAV-like protein 1	34.97	10		216	0.90	1.09	53	11.2
Q3UMR5	Mcu	Calcium uniporter protein, mitochondrial	10.00	3		24	0.90	1.09	4	27.0
O55128	Sap18	Histone deacetylase complex subunit SAP18	52.94	8		107	0.90	1.09	30	9.6
Q8VHK9	Dhx36	ATP-dependent RNA helicase DHX36	2.40	2		12	0.90	1.09	3	4.3
Q61102	Abcb7	ATP-binding cassette sub-family B member 7, mitochondrial	15.03	11		73	0.90	1.09	16	10.9
Q922H2	Pdk3	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	20.24	7		35	0.90	1.09	4	11.7
Q3UJB0	Sf3b2	Protein Sf3b2	29.38	24		270	0.90	1.09	79	24.7
Q80T69	Rsbn1	Round spermatid basic protein 1	1.76	2		2	0.90	1.09	1	
Q8R0H9	Gga1	ADP-ribosylation factor-binding protein GGA1	4.57	3		15	0.90	1.09	1	
Q6Y685-2	Tacc1	Isoform 2 of Transforming acidic coiled-coil-containing protein 1	4.08	2		3	0.90	1.09	2	20.8
A2AMY5	Ubap2	Ubiquitin-associated protein 2	8.05	9		68	0.90	1.09	20	12.8
Q8BGC4	Zadh2	Zinc-binding alcohol dehydrogenase domain-containing protein 2	19.10	6		42	0.90	1.09	7	4.2
Q80UW8	Polr2e	DNA-directed RNA polymerases I, II, and III subunit RPABC1	23.33	5		56	0.90	1.09	9	14.5
Q9R190	Mta2	Metastasis-associated protein MTA2	29.94	22		179	0.90	1.09	47	17.3
F6WLY0	Lrmp	Lymphoid-restricted membrane protein (Fragment)	7.34	4		18	0.90	1.09	4	7.8
E9Q7G0	Numa1	Protein Numa1	14.18	28		137	0.89	1.09	31	11.8
Q9D824-3	Fip1l1	Isoform 3 of Pre-mRNA 3'-end-processing factor FIP1	15.11	6		121	0.89	1.09	40	33.6
Q8CH18-3	Ccar1	Isoform 3 of Cell division cycle and apoptosis regulator protein 1	10.98	12		77	0.89	1.09	12	24.6
Q9D1H8	Mrpl53	39S ribosomal protein L53, mitochondrial	16.95	2		6	0.89	1.09	1	
Q8BW10	Nob1	RNA-binding protein NOB1	12.66	5		18	0.89	1.09	6	115.7
E9Q4Q2	Sf1	Splicing factor 1	16.06	7		53	0.89	1.09	16	13.1
P49312	Hnrnpa1	Heterogeneous nuclear ribonucleoprotein A1	51.56	18		793	0.89	1.09	145	14.2
Q80W00-2	Ppp1r10	Isoform 2 of Serine/threonine-protein phosphatase 1 regulatory subunit 10	5.72	5		18	0.89	1.09	3	10.1

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9D964	Gatm	Glycine amidinotransferase, mitochondrial	22.46	11		88	0.89	1.08	17	16.3
A2AUR7	Rsu1	Ras suppressor protein 1	15.77	4		16	0.89	1.08	2	11.4
A0A0B4J1E2	Snw1	SNW domain-containing protein 1	21.64	12		103	0.89	1.08	19	8.8
P53395	Dbt	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	13.49	6		49	0.89	1.08	6	9.9
Q9DCE5	Pak1ip1	p21-activated protein kinase-interacting protein 1	12.57	5		51	0.89	1.08	17	14.8
Q62192	Cd180	CD180 antigen	11.80	5		27	0.89	1.08	6	20.5
Q8BK08	Tmem11	Transmembrane protein 11, mitochondrial	25.26	5		26	0.89	1.08	4	5.7
Q9JI44-2	Dmap1	Isoform 2 of DNA methyltransferase 1-associated protein 1	5.26	2		11	0.89	1.08	3	1.9
Q80YQ2	Med23	Mediator of RNA polymerase II transcription subunit 23	3.51	4		11	0.89	1.08	4	3.3
Q9D7N3	Mrps9	28S ribosomal protein S9, mitochondrial	25.13	9		52	0.89	1.08	12	5.4
Q8R2Y8	Ptrh2	Peptidyl-tRNA hydrolase 2, mitochondrial	48.62	6		54	0.89	1.08	18	14.7
Q99KP6	Prpf19	Pre-mRNA-processing factor 19	29.96	14		247	0.89	1.08	61	10.7
Q3UDD3	Poldip3	Polymerase delta-interacting protein 3	8.44	3		13	0.89	1.08	4	3.8
Q60972	Rbbp4	Histone-binding protein RBBP4	22.59	9		190	0.89	1.08	12	15.5
B1AQD3	Rab34	Ras-related protein Rab-34	5.58	2		10	0.89	1.08	3	10.4
Q9D0G0	Mrps30	28S ribosomal protein S30, mitochondrial	20.59	8		74	0.89	1.08	9	6.0
Q8JZN7	Rhot2	Mitochondrial Rho GTPase 2	4.19	3		13	0.89	1.08	2	8.4
Q8BKT7	Thoc5	THO complex subunit 5 homolog	8.64	7		43	0.89	1.08	11	6.1
Q3UJU9	Rmdn3	Regulator of microtubule dynamics protein 3	7.87	4		29	0.89	1.08	5	10.1
A2BE28-2	Las1l	Isoform 2 of Ribosomal biogenesis protein LAS1L	9.35	6		37	0.89	1.08	5	18.9
Q9D6U8	Fam162a	Protein FAM162A	18.06	2		16	0.89	1.08	4	7.9
Q9D1H6	Ndufaf4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	36.42	6		14	0.89	1.08	5	17.2
G5E8C4	Tmtc3	MCG142017, isoform CRA_a	5.11	4		14	0.89	1.08	2	31.5
P57716	Ncstn	Nicastrin	12.43	9		55	0.89	1.08	9	8.5
Q9D662	Sec23b	Protein transport protein Sec23B	17.99	12		94	0.89	1.08	24	11.9
Q9QZ23	Nfu1	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	13.33	3		22	0.89	1.08	2	10.0
O35737	Hnrnph1	Heterogeneous nuclear ribonucleoprotein H	38.75	13		462	0.89	1.08	26	18.8
Q7TMY4	Thoc7	THO complex subunit 7 homolog	14.71	3		11	0.89	1.08	3	10.6
O88696	Clpp	ATP-dependent Clp protease proteolytic subunit, mitochondrial	20.22	4		91	0.89	1.08	28	34.2
Q8BJ05-2	Zc3h14	Isoform 2 of Zinc finger CCCH domain-	4.49	2		6	0.89	1.08	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN^{1}	pksP/wt^{1}	pksP/wt Count^{2}	pksP/wt Variance [%]^{3}
		containing protein 14								
Q9D8S9	Bola1	BolA-like protein 1	10.95	2		10	0.89	1.08	4	15.2
Q6P9R1	Ddx51	ATP-dependent RNA helicase DDX51	14.24	7		20	0.89	1.08	4	16.9
Q91W39	Ncoa5	Nuclear receptor coactivator 5	5.18	3		25	0.89	1.08	5	8.5
Q9CQN7	Mrpl41	39S ribosomal protein L41, mitochondrial	37.04	5		30	0.89	1.08	9	20.1
D3YZ09	Gar1	H/ACA ribonucleoprotein complex subunit 1 (Fragment)	25.25	5		89	0.89	1.08	23	8.5
A0A0G2JFF9	Hax1	HCLS1-associated protein X-1	14.57	3		19	0.89	1.08	6	33.4
Q8VCY6	Utp6	U3 small nucleolar RNA-associated protein 6 homolog	13.23	9		39	0.89	1.08	6	16.2
P60710	Actb	Actin, cytoplasmic 1	61.60	20		1998	0.89	1.08	566	15.8
D3YUK4	Ndufb10	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 (Fragment)	58.39	8		69	0.89	1.08	25	12.1
Q60520	Sin3a	Paired amphipathic helix protein Sin3a	6.75	8		34	0.89	1.08	5	4.7
Q9D880	Timm50	Mitochondrial import inner membrane translocase subunit TIM50	32.29	10		100	0.88	1.08	30	16.9
P08030	Aprt	Adenine phosphoribosyltransferase	17.22	3		8	0.88	1.07	1	
Q9QYR9	Acot2	Acyl-coenzyme A thioesterase 2, mitochondrial	8.17	4		28	0.88	1.07	3	7.3
Q8R5L1	C1qbp	Complement component 1 Q subcomponent-binding protein, mitochondrial	41.22	7		93	0.88	1.07	28	9.8
A0A0R4J0R3	Isg20l2	Interferon-stimulated 20 kDa exonuclease-like 2	10.87	4		27	0.88	1.07	5	10.6
Q4VA53	Pds5b	Sister chromatid cohesion protein PDS5 homolog B	13.00	18		95	0.88	1.07	14	8.4
P83870	Phf5a	PHD finger-like domain-containing protein 5A	27.27	4		24	0.88	1.07	6	1.8
P47754	Capza2	F-actin-capping protein subunit alpha-2	25.87	6		42	0.88	1.07	4	16.7
Q9D172	D10Jhu81e	ES1 protein homolog, mitochondrial	17.67	5		71	0.88	1.07	17	4.9
O88374	Bcat2	Branched-chain-amino-acid aminotransferase	5.95	2		18	0.88	1.07	5	11.7
S4R1M0	Ptprc	Receptor-type tyrosine-protein phosphatase C	12.39	15		69	0.88	1.07	15	15.2
Q8K0D5	Gfm1	Elongation factor G, mitochondrial	20.51	15		82	0.88	1.07	17	17.8
F8WIX8	Hist1h2al	Histone H2A	44.80	10		1364	0.88	1.07	19	18.6
Q8BKS9	Kiaa0020	Pumilio domain-containing protein KIAA0020	29.52	18		220	0.88	1.07	43	12.6
Q8CI61	Bag4	BAG family molecular chaperone regulator 4	3.06	2		6	0.88	1.07	1	
D3YZN4	Spg7	Paraplegin	2.66	2		8	0.88	1.07	1	
Q9JK30-2	Orc3	Isoform 2 of Origin recognition complex subunit 3	5.18	4		18	0.88	1.07	3	26.3
P55302	Lrpap1	Alpha-2-macroglobulin receptor-associated protein	24.44	10		111	0.88	1.07	13	19.0
Q61937	Npm1	Nucleophosmin	49.32	16		732	0.88	1.07	246	15.4
Q91ZN5-2	Slc35b2	Isoform 2 of Adenosine 3'-phospho 5'-	7.07	3		15	0.88	1.07	4	22.8

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		phosphosulfate transporter 1								
Q8JZU2	Slc25a1	Tricarboxylate transport protein, mitochondrial	21.22	7		114	0.88	1.07	25	16.7
O54941	Smarce1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	14.84	7		61	0.88	1.07	16	7.8
Q9QWT9-3	Kifc1	Isoform 3 of Kinesin-like protein KIFC1	9.17	5		17	0.88	1.07	1	
Q9JJF3	No66	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	18.91	10		86	0.88	1.07	15	19.1
P43275	Hist1h1a	Histone H1.1	30.05	9		926	0.88	1.07	113	19.6
Q9R0E2	Plod1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	11.13	8		27	0.88	1.07	3	5.6
Q99J56	Derl1	Derlin-1	7.17	2		14	0.88	1.07	4	10.9
A0A0G2JG95	Pgam5	Serine/threonine-protein phosphatase PGAM5, mitochondrial (Fragment)	31.84	7		83	0.88	1.07	23	7.8
A0A0R4J0L6	Mrps35	28S ribosomal protein S35, mitochondrial	15.63	5		22	0.88	1.07	6	19.2
Q9Z1M8	Ik	Protein Red	11.67	7		37	0.88	1.07	9	5.0
Q9D0D3	Mtpap	Poly(A) RNA polymerase, mitochondrial	3.93	2		4	0.88	1.06	1	
Q9R059	Fhl3	Four and a half LIM domains protein 3	26.30	6		28	0.88	1.06	13	19.6
Q6NZQ2	Ddx31	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31	3.78	3		8	0.88	1.06	2	23.9
A2ATP5	Myef2	Myelin expression factor 2	24.91	14		104	0.88	1.06	27	21.1
O88307	Sorl1	Sortilin-related receptor	2.57	5		24	0.88	1.06	3	8.3
D3YYD5	Vps29	Vacuolar protein sorting-associated protein 29 (Fragment)	14.52	2		5	0.88	1.06	3	11.4
Q99MN9	Pccb	Propionyl-CoA carboxylase beta chain, mitochondrial	17.19	7		29	0.88	1.06	6	15.1
G5E924	Hnrnpl	Heterogeneous nuclear ribonucleoprotein L (Fragment)	40.33	20		530	0.87	1.06	156	9.9
P61164	Actr1a	Alpha-centractin	9.57	3		25	0.87	1.06	1	
Q80U72	Scrib	Protein scribble homolog	1.99	2		4	0.87	1.06	2	4.2
Q60715	P4ha1	Prolyl 4-hydroxylase subunit alpha-1	39.14	21		162	0.87	1.06	3	10.2
Q99JI4	Psmd6	26S proteasome non-ATPase regulatory subunit 6	12.08	5		18	0.87	1.06	4	58.9
Q921I9	Exosc4	Exosome complex component RRP41	15.10	3		24	0.87	1.06	3	10.6
Q99JB2	Stoml2	Stomatin-like protein 2, mitochondrial	34.28	11		171	0.87	1.06	43	19.6
Q9Z2X1-2	Hnrnpf	Isoform 2 of Heterogeneous nuclear ribonucleoprotein F	40.25	13		591	0.87	1.06	132	12.1
Q6P3Y5-2	Znf280c	Isoform 2 of Zinc finger protein 280C	4.04	3		7	0.87	1.06	3	3.4
Q8R105	Vps37c	Vacuolar protein sorting-associated protein 37C	9.09	2		6	0.87	1.06	2	29.9

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9WVG6-2	Carm1	Isoform 2 of Histone-arginine methyltransferase CARM1	4.62	3		9	0.87	1.06	2	19.7
Q9JJI8	Rpl38	60S ribosomal protein L38	31.43	3		102	0.87	1.06	22	13.0
Q8C5L7	Rbm34	RNA-binding protein 34	7.20	3		8	0.87	1.06	1	
Q8CAG6	Plek	Pleckstrin	6.42	2		9	0.87	1.06	1	
E9QQ99	Syvn1	E3 ubiquitin-protein ligase synoviolin	4.10	3		19	0.87	1.06	3	6.7
Q80ZS3	Mrps26	28S ribosomal protein S26, mitochondrial	25.00	4		51	0.87	1.06	9	13.7
Q8BFP9	Pdk1	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	14.29	5		28	0.87	1.06	9	6.8
Q60596	Xrcc1	DNA repair protein XRCC1	9.35	5		21	0.87	1.06	4	11.8
Q8BZR4	Acot8	Acyl-coenzyme A thioesterase 8	13.43	4		31	0.87	1.06	4	19.0
A0A0R4J0B4	Cmas	Cytidine monophospho-N-acetylneuraminic acid synthetase	15.28	7		42	0.87	1.06	6	14.0
Q9JKF7	Mrpl39	39S ribosomal protein L39, mitochondrial	13.39	4		36	0.87	1.06	8	27.3
Q9JIQ3	Diablo	Diablo homolog, mitochondrial	8.86	3		17	0.87	1.06	4	14.9
Q8BTW3	Exosc6	Exosome complex component MTR3	12.45	3		4	0.87	1.06	4	26.8
Q9CQR2	Rps21	40S ribosomal protein S21	48.19	4		55	0.87	1.06	10	14.5
O55201-2	Supt5h	Isoform 2 of Transcription elongation factor SPT5	6.98	7		37	0.87	1.06	4	13.5
Q8K1Z0	Coq9	Ubiquinone biosynthesis protein COQ9, mitochondrial	8.63	3		32	0.87	1.06	5	27.1
Q64012-2	Raly	Isoform 1 of RNA-binding protein Raly	46.62	15		502	0.87	1.05	128	14.8
P05213	Tuba1b	Tubulin alpha-1B chain	53.66	18		499	0.87	1.05	4	8.2
P97868-2	Rbbp6	Isoform 2 of E3 ubiquitin-protein ligase RBBP6	1.77	3		5	0.87	1.05	2	4.0
Q3UN00	P2rx7	P2X purinoceptor	3.94	2		4	0.87	1.05	2	25.6
Q8K4Z3	Apoa1bp	NAD(P)H-hydrate epimerase	9.22	2		24	0.87	1.05	8	13.5
O88532	Zfr	Zinc finger RNA-binding protein	7.82	8		33	0.87	1.05	7	8.0
G3UWZ0	Baz1a	Bromodomain adjacent to zinc finger domain protein 1A	8.76	14		56	0.87	1.05	15	21.7
Q8R180	Ero1l	ERO1-like protein alpha	29.09	15		216	0.87	1.05	49	21.8
Q8BJ03-2	Cox15	Isoform 2 of Cytochrome c oxidase assembly protein COX15 homolog	5.56	2		27	0.87	1.05	6	14.1
Q9QWH1-2	Phc2	Isoform 2 of Polyhomeotic-like protein 2	8.98	3		7	0.87	1.05	1	
A2AL12	Hnrnpa3	Heterogeneous nuclear ribonucleoprotein A3	49.06	21		812	0.86	1.05	211	15.0
B7ZCL8	Mpp1	55 kDa erythrocyte membrane protein	3.81	2		6	0.86	1.05	2	6.2
Q9CWZ3-2	Rbm8a	Isoform 2 of RNA-binding protein 8A	31.21	5		91	0.86	1.05	6	4.8
Q61164	Ctcf	Transcriptional repressor CTCF	5.30	4		53	0.86	1.05	10	10.9
P09450	Junb	Transcription factor jun-B	11.34	4		19	0.86	1.05	5	8.0
Q9D1B9	Mrpl28	39S ribosomal protein L28, mitochondrial	19.07	5		21	0.86	1.05	3	20.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8CB77	Tceb3	Transcription elongation factor B polypeptide 3	4.27	3		8	0.86	1.05	1	
A2BFF8	Dync1i2	Cytoplasmic dynein 1 intermediate chain 2	3.44	2		11	0.86	1.05	3	10.2
Q9WUR9	Ak4	Adenylate kinase 4, mitochondrial	22.42	5		60	0.86	1.05	12	25.4
Q9D0N7	Chaf1b	Chromatin assembly factor 1 subunit B	3.32	2		5	0.86	1.05	6	22.3
P62869	Tceb2	Transcription elongation factor B polypeptide 2	19.49	3		12	0.86	1.05	1	
E9PZA7	Trrap	Transformation/transcription domain-associated protein	1.46	6		22	0.86	1.05	3	14.1
Q9WVA3	Bub3	Mitotic checkpoint protein BUB3	25.15	8		90	0.86	1.05	26	7.8
P27661	H2afx	Histone H2AX	67.13	11		1653	0.86	1.05	160	9.9
F7ARZ1	Mrps23	28S ribosomal protein S23, mitochondrial (Fragment)	39.17	5		81	0.86	1.05	24	16.7
P84089	Erh	Enhancer of rudimentary homolog	24.04	3		73	0.86	1.04	16	8.7
Q6R0H7-4	Gnas	Isoform XLas-4 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	3.22	4		46	0.86	1.04	1	
Q9D7P6	Iscu	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	23.81	5		24	0.86	1.04	5	5.8
P53564	Cux1	Homeobox protein cut-like 1	19.27	26		144	0.86	1.04	1	
Q3TAW3	Acox3	Acyl-coenzyme A oxidase	3.12	2		2	0.86	1.04	2	7.2
A1L3S7	Gatad2b	Gatad2b protein	10.21	5		29	0.86	1.04	5	30.2
Q80WW9	Ddrgk1	DDRGK domain-containing protein 1	26.98	8		63	0.86	1.04	14	13.5
Q8BFY6	Pef1	Peflin	4.00	2		9	0.86	1.04	2	18.2
Q9EPU4	Cpsf1	Cleavage and polyadenylation specificity factor subunit 1	9.23	14		75	0.86	1.04	12	16.0
D3Z4B0	Srsf11	Protein Srsf11 (Fragment)	13.02	2		12	0.85	1.04	2	39.2
Q9CQ40	Mrpl49	39S ribosomal protein L49, mitochondrial	13.86	2		10	0.85	1.04	3	12.9
Q99MR8	Mccc1	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	5.30	3		17	0.85	1.04	1	
Q3ULD5	Mccc2	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	3.91	2		2	0.85	1.04	1	
P62317	Snrpd2	Small nuclear ribonucleoprotein Sm D2	55.08	7		179	0.85	1.04	49	13.4
Q99MN1	Kars	Lysine--tRNA ligase	7.90	4		23	0.85	1.04	2	37.0
F8WGD9	Agpat5	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	16.84	5		23	0.85	1.04	3	9.3
Q8BMC4	Nop9	Nucleolar protein 9	3.77	2		10	0.85	1.03	1	
Q9WTP6-2	Ak2	Isoform 2 of Adenylate kinase 2, mitochondrial	59.05	12		160	0.85	1.03	42	13.1
Q5SUA5	Myo1g	Unconventional myosin-Ig	5.86	5		42	0.85	1.03	2	8.7
A0A0N4SW94	Myadm	Myeloid-associated differentiation marker (Fragment)	33.33	2		58	0.85	1.03	19	18.5
Q80X50-2	Ubap2l	Isoform 2 of Ubiquitin-associated protein 2-like	24.95	20		312	0.85	1.03	1	

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9DBR1-2	Xrn2	Isoform 2 of 5'-3' exoribonuclease 2	10.35	9		33	0.85	1.03	8	6.8
A0A0R4J008	Hdac2	Histone deacetylase	6.76	4		62	0.85	1.03	12	29.4
E9QAS4	Chd4	Chromodomain-helicase-DNA-binding protein 4	14.72	30		235	0.85	1.03	73	27.7
P68433	Hist1h3a	Histone H3.1	41.18	10		1401	0.85	1.03	520	14.6
O88874	Ccnk	Cyclin-K	2.53	2		7	0.85	1.03	2	0.0
Q8C5Q4	Grsf1	G-rich sequence factor 1	12.32	4		10	0.85	1.03	3	21.3
F7BGR7	Gm21992	Protein Gm21992	18.66	9		52	0.85	1.03	2	10.8
Q3U186	Rars2	Probable arginine--tRNA ligase, mitochondrial	12.80	7		58	0.85	1.03	14	13.2
Q8R2E9	Ero1b	ERO1-like protein beta	8.57	4		40	0.85	1.03	1	
Q9Z204-2	Hnrnpc	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	56.33	20		799	0.85	1.03	234	13.4
Q9CYX7	Rrp15	RRP15-like protein	16.73	6		31	0.85	1.03	8	6.1
O88441	Mtx2	Metaxin-2	9.13	2		23	0.85	1.03	4	6.4
D3YWX2	Ylpm1	YLP motif-containing protein 1	5.56	9		39	0.85	1.03	12	12.0
E9Q4M4	Chchd6	MICOS complex subunit	14.69	3		13	0.85	1.03	2	5.0
Q4FK66	Prpf38a	Pre-mRNA-splicing factor 38A	8.97	3		19	0.85	1.03	4	7.8
O88384	Vti1b	Vesicle transport through interaction with t-SNAREs homolog 1B	14.22	3		16	0.85	1.03	7	17.9
E9Q166	Atad2b	Protein Atad2b	4.52	6		29	0.84	1.03	1	
Q8BG15-6	Ctdspl2	Isoform 6 of CTD small phosphatase-like protein 2	9.90	4		17	0.84	1.03	4	17.8
Q9WVA4	Tagln2	Transgelin-2	47.24	8		32	0.84	1.03	8	14.1
A0A0A0MQM0	Eif5a	Eukaryotic translation initiation factor 5A (Fragment)	21.48	4		51	0.84	1.02	12	12.5
Q61249	Igbp1	Immunoglobulin-binding protein 1	12.06	4		9	0.84	1.02	2	6.1
Q80Y14	Glrx5	Glutaredoxin-related protein 5, mitochondrial	29.61	3		15	0.84	1.02	4	23.3
Q99N87	Mrps5	28S ribosomal protein S5, mitochondrial	13.19	6		43	0.84	1.02	5	8.1
Q8R0S1	Atf7	Cyclic AMP-dependent transcription factor ATF-7	3.87	2		7	0.84	1.02	2	15.6
Q9D4G5	Pop1	Blood vessel epicardial substance	2.27	2		4	0.84	1.02	1	
Q07076	Anxa7	Annexin A7	38.23	18		471	0.84	1.02	125	14.6
Q8QZY9	Sf3b4	Splicing factor 3B subunit 4	6.60	3		4	0.84	1.02	2	34.6
Q8BUV8	Gpr107	Protein GPR107	4.36	3		7	0.84	1.02	4	2.6
Q9JJG9	Noa1	Nitric oxide-associated protein 1	3.61	2		12	0.84	1.02	1	
Q8VHI3	Pofut2	GDP-fucose protein O-fucosyltransferase 2	8.39	4		16	0.84	1.02	2	8.8
P52927	Hmga2	High mobility group protein HMGI-C	64.81	6		165	0.84	1.02	51	16.4
P17433	Spi1	Transcription factor PU.1	9.56	3		14	0.84	1.02	3	10.7
Q9D6K9	Cers5	Ceramide synthase 5	3.62	2		21	0.84	1.02	3	3.3
A2BH40	Arid1a	AT-rich interactive domain-containing protein	3.11	7		27	0.84	1.02	5	7.8

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		1A								
Q80UU9	Pgrmc2	Membrane-associated progesterone receptor component 2	34.56	6		42	0.84	1.02	6	27.4
O35218	Cpsf2	Cleavage and polyadenylation specificity factor subunit 2	2.17	2		14	0.84	1.01	1	
Q3TIX9	Usp39	U4/U6.U5 tri-snRNP-associated protein 2	13.65	7		27	0.83	1.01	4	12.5
Q9JIX0	Eny2	Transcription and mRNA export factor ENY2	25.74	2		2	0.83	1.01	1	
Q8BIZ6	Snip1	Smad nuclear-interacting protein 1	8.09	2		6	0.83	1.01	2	25.0
Q3TZX8-2	Nol9	Isoform 2 of Polynucleotide 5'-hydroxyl-kinase NOL9	6.11	4		20	0.83	1.01	2	25.7
Q5SYD0	Myo1d	Unconventional myosin-Id	14.41	15		70	0.83	1.01	12	11.3
P62075	Timm13	Mitochondrial import inner membrane translocase subunit Tim13	26.32	2		8	0.83	1.01	1	
Q91YN9	Bag2	BAG family molecular chaperone regulator 2	35.71	7		31	0.83	1.01	7	7.7
Q91VA6	Poldip2	Polymerase delta-interacting protein 2	25.00	8		45	0.83	1.01	13	39.0
Q8CEC6	Ppwd1	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	5.26	3		26	0.83	1.01	7	18.7
J3JS24	Mgat1	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (Fragment)	14.50	2		6	0.83	1.01	1	
A0A0G2JGD2	S100a4	Protein S100-A4 (Fragment)	21.79	3		32	0.83	1.01	4	5.5
Q91VM5	Rbmxl1	RNA binding motif protein, X-linked-like-1	50.52	23		822	0.83	1.01	29	11.8
Q99JR8-2	Smarcd2	Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	20.04	8		67	0.83	1.01	14	17.0
Q91XV3	Basp1	Brain acid soluble protein 1	9.29	2		2	0.83	1.01	1	
D3YWT1	Hnrnph3	MCG11326, isoform CRA_b	23.26	8		95	0.83	1.00	17	14.5
Q9CQX2	Cyb5b	Cytochrome b5 type B	50.68	4		37	0.83	1.00	12	14.8
Q8R4N0	Clybl	Citrate lyase subunit beta-like protein, mitochondrial	3.85	2		3	0.83	1.00	1	
P01900	H2-D1	H-2 class I histocompatibility antigen, D-D alpha chain	23.84	8		122	0.83	1.00	9	14.7
Q61990-2	Pcbp2	Isoform 2 of Poly(rC)-binding protein 2	37.46	11		461	0.82	1.00	84	29.0
Q9D0B0	Srsf9	Serine/arginine-rich splicing factor 9	25.23	5		61	0.82	1.00	12	16.5
Q78HU3	Mvb12a	Multivesicular body subunit 12A	7.01	2		2	0.82	1.00	1	
Q9D1L0	Chchd2	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	24.18	2		17	0.82	1.00	5	8.5
Q3UHX0	Nol8	Nucleolar protein 8	2.88	3		8	0.82	1.00	2	7.7
Q9D6J6	Ndufv2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	29.84	6		63	0.82	1.00	17	12.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8CHT0	Aldh4a1	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	4.98	4		21	0.82	1.00	5	21.4
G3UYD0	Gtf2i	General transcription factor II-I	3.18	3		15	0.82	1.00	3	28.0
O09005	Degs1	Sphingolipid delta(4)-desaturase DES1	7.43	3		13	0.82	1.00	3	12.4
Q9D0F6	Rfc5	Replication factor C subunit 5	12.98	4		8	0.82	1.00	2	40.5
Q6PIC6	Atp1a3	Sodium/potassium-transporting ATPase subunit alpha-3	22.41	18		380	0.82	0.99	3	7.2
Q64152-2	Btf3	Isoform 2 of Transcription factor BTF3	24.07	3		10	0.82	0.99	2	37.9
G3X959	Pphln1	Periphilin 1, isoform CRA_a	9.97	5		15	0.82	0.99	2	12.3
Q9D7J9	Echdc3	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	9.33	3		13	0.82	0.99	2	7.4
P62743	Ap2s1	AP-2 complex subunit sigma	10.56	2		5	0.82	0.99	2	5.6
P16110	Lgals3	Galectin-3	43.94	12		836	0.82	0.99	244	13.6
D3Z6B9	Aldh1l2	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	7.04	6		30	0.82	0.99	7	16.3
Q9WV02	Rbmx	RNA-binding motif protein, X chromosome	50.13	23		747	0.82	0.99	5	10.5
P42128	Foxk1	Forkhead box protein K1	5.01	2		11	0.82	0.99	3	5.2
P17665	Cox7c	Cytochrome c oxidase subunit 7C, mitochondrial	28.57	2		30	0.82	0.99	7	25.8
P47753	Capza1	F-actin-capping protein subunit alpha-1	26.57	6		57	0.81	0.99	8	10.4
G5E850	Cyb5a	Cytochrome b-5, isoform CRA_a	56.12	4		104	0.81	0.99	22	8.0
Q99N95	Mrpl3	39S ribosomal protein L3, mitochondrial	18.10	6		35	0.81	0.99	6	12.1
F8WJK8	St13	Hsc70-interacting protein	16.57	7		70	0.81	0.99	19	15.1
Q64692	St8sia4	CMP-N-acetylneuraminate-poly-alpha-2,8-sialyltransferase	5.01	2		6	0.81	0.99	1	
Q6ZWZ6	Rps12	40S ribosomal protein S12	25.00	3		72	0.81	0.99	12	15.2
F7CK55	Col4a5	Protein Col4a5 (Fragment)	4.50	3		12	0.81	0.99	3	11.4
Q9CQT5	Pomp	Proteasome maturation protein	14.89	2		4	0.81	0.99	2	16.6
P53702	Hccs	Cytochrome c-type heme lyase	13.60	4		36	0.81	0.99	8	8.2
Q9QYI4	Dnajb12	DnaJ homolog subfamily B member 12	6.12	2		15	0.81	0.99	3	12.0
Q8BXA1	Golim4	Golgi integral membrane protein 4	17.56	10		48	0.81	0.98	10	26.8
P97760	Polr2c	DNA-directed RNA polymerase II subunit RPB3	6.55	2		14	0.81	0.98	2	3.7
Q9CZX5	Pinx1	PIN2/TERF1-interacting telomerase inhibitor 1	9.94	2		5	0.81	0.98	4	15.2
P17439	Gba	Glucosylceramidase	10.49	5		25	0.81	0.98	4	72.8
P97930	Dtymk	Thymidylate kinase	27.83	7		28	0.81	0.98	4	14.7
Q99MJ9	Ddx50	ATP-dependent RNA helicase DDX50	3.54	3		137	0.81	0.98	2	19.7
Q6PCM2-2	Ints6	Isoform 2 of Integrator complex subunit 6	2.63	2		3	0.81	0.98	2	17.4
D3Z6W5	Tmem9b	TMEM9 domain family, member B, isoform CRA_a	11.29	2		3	0.81	0.98	3	13.8
Q9R0X4	Acot9	Acyl-coenzyme A thioesterase 9, mitochondrial	13.90	5		22	0.81	0.98	4	20.4

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q9CQ49	Ncbp2	Nuclear cap-binding protein subunit 2	24.36	4		17	0.81	0.98	6	19.5
B0R091	Chp1	Calcineurin B homologous protein 1	28.27	5		30	0.81	0.98	6	10.8
Q923D5	Wbp11	WW domain-binding protein 11	8.27	5		25	0.80	0.98	5	8.8
D3Z7R0	Bckdk	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial (Fragment)	16.82	3		11	0.80	0.97	2	37.6
Q6DFZ2	Syne2	Nesprin-2 (Fragment)	0.84	2		5	0.80	0.97	2	1.6
G5E8J8	Wiz	MCG14253, isoform CRA_a	5.97	4		16	0.80	0.97	6	17.2
Q99N94	Mrpl9	39S ribosomal protein L9, mitochondrial	35.09	9		97	0.80	0.97	25	21.2
Q61792	Lasp1	LIM and SH3 domain protein 1	36.50	10		99	0.80	0.97	24	15.9
Q06185	Atp5i	ATP synthase subunit e, mitochondrial	49.30	4		98	0.80	0.97	36	22.3
P62334	Psmc6	26S protease regulatory subunit 10B	13.11	5		23	0.80	0.97	4	48.5
Q9D1K2	Atp6v1f	V-type proton ATPase subunit F	41.18	5		30	0.80	0.97	5	4.3
Q9QZH3	Ppie	Peptidyl-prolyl cis-trans isomerase E	15.61	4		14	0.80	0.97	1	
Q9CQF7	Pfdn1	Prefoldin 1	20.49	3		27	0.80	0.97	2	3.8
Q9JMD0-4	Znf207	Isoform 4 of BUB3-interacting and GLEBS motif-containing protein ZNF207	4.35	2		8	0.80	0.97	2	69.4
Q3U821	Wdr75	Protein Wdr75	8.92	8		50	0.80	0.97	8	4.7
Q9WUK2	Eif4h	Eukaryotic translation initiation factor 4H	20.16	6		29	0.79	0.97	6	13.3
A2AEK1	Cstf2	AlphaCstF-64 variant 4	18.23	10		61	0.79	0.96	3	20.2
Q3UPH1	Prrc1	Protein PRRC1	7.90	3		12	0.79	0.96	2	59.7
Q99JX3	Gorasp2	Golgi reassembly-stacking protein 2	15.96	6		34	0.79	0.96	4	5.2
Q3TYA6	Mphosph8	M-phase phosphoprotein 8	3.61	3		7	0.79	0.96	2	7.7
Q8R404	Mic13	MICOS complex subunit MIC13	24.37	2		9	0.79	0.96	1	
Q9ERB0	Snap29	Synaptosomal-associated protein 29	36.92	9		55	0.79	0.96	15	25.5
P30416	Fkbp4	Peptidyl-prolyl cis-trans isomerase FKBP4	6.11	3		21	0.79	0.96	5	6.2
B1AWE0	Clta	Clathrin light chain A	13.43	4		28	0.79	0.96	4	6.5
Q9ER00	Stx12	Syntaxin-12	22.63	5		25	0.79	0.96	2	26.6
Q6P069-2	Sri	Isoform 2 of Sorcin	18.03	3		14	0.79	0.96	2	2.4
D6RGM8	Tm9sf1	Transmembrane 9 superfamily member 1	8.15	3		17	0.79	0.96	3	26.2
P81117	Nucb2	Nucleobindin-2	16.67	5		26	0.78	0.95	6	19.0
Q9CRB2	Nhp2	H/ACA ribonucleoprotein complex subunit 2	37.91	5		47	0.78	0.95	11	15.8
G5E8J9	Scyl2	SCY1-like protein 2	3.23	3		9	0.78	0.95	2	3.9
Q99LC2	Cstf1	Cleavage stimulation factor subunit 1	10.21	4		33	0.78	0.95	9	7.8
Q99LP6	Grpel1	GrpE protein homolog 1, mitochondrial	32.72	8		154	0.78	0.95	32	17.0
P14069	S100a6	Protein S100-A6	24.72	3		36	0.78	0.95	3	1.7
G3UYG6	Gigyf2	PERQ amino acid-rich with GYF domain-containing protein 2	5.60	9		33	0.78	0.95	9	9.8
Q9CQQ8	Lsm7	U6 snRNA-associated Sm-like protein LSm7	22.33	3		28	0.78	0.95	6	18.5
Q8CGP7	Hist1h2ak	Histone H2A type 1-K	65.38	11		1321	0.78	0.95	10	12.1

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
G3UYQ2	Bag6	Large proline-rich protein BAG6	4.99	5		19	0.78	0.95	2	73.7
Q5SXC4	Vezf1	Protein Vezf1	2.70	2		10	0.78	0.95	2	17.6
P53996-2	Cnbp	Isoform 2 of Cellular nucleic acid-binding protein	45.88	8		237	0.78	0.94	68	15.8
Q8BRG8-3	Tmem209	Isoform 3 of Transmembrane protein 209	18.26	6		24	0.78	0.94	4	46.2
Q1HFZ0-2	Nsun2	Isoform 2 of tRNA (cytosine(34)-C(5))-methyltransferase	7.53	5		17	0.77	0.94	3	5.6
P48771	Cox7a2	Cytochrome c oxidase subunit 7A2, mitochondrial	27.71	2		33	0.77	0.94	8	7.2
Q8R317-2	Ubqln1	Isoform 2 of Ubiquilin-1	12.09	5		61	0.77	0.94	7	10.2
Q61550	Rad21	Double-strand-break repair protein rad21 homolog	17.95	9		56	0.77	0.94	15	8.7
Q9D819	Ppa1	Inorganic pyrophosphatase	16.61	5		10	0.77	0.94	1	
Q8K0Z7	Taco1	Translational activator of cytochrome c oxidase 1	8.84	2		9	0.77	0.93	2	49.3
Q9Z103	Adnp	Activity-dependent neuroprotector homeobox protein	4.60	4		15	0.77	0.93	4	21.1
Q9JIG7	Ccdc22	Coiled-coil domain-containing protein 22	7.02	3		9	0.77	0.93	1	
O70591	Pfdn2	Prefoldin subunit 2	22.73	3		9	0.77	0.93	2	6.5
Q05186	Rcn1	Reticulocalbin-1	5.85	2		2	0.77	0.93	1	
Q9Z148-2	Ehmt2	Isoform 2 of Histone-lysine N-methyltransferase EHMT2	4.18	5		19	0.76	0.93	4	54.5
G8JL40	Kdm1a	Lysine-specific histone demethylase 1A (Fragment)	9.81	5		17	0.76	0.92	3	14.6
G3UYP1	Rragb	Ras-related GTP-binding protein B (Fragment)	19.83	2		9	0.76	0.92	1	
E9Q467	Abcc4	Protein Abcc4	1.60	2		6	0.76	0.92	1	
A0A0R4J045	Rrp36	Ribosomal RNA-processing protein 36 homolog	9.73	2		7	0.76	0.92	2	15.3
P53569	Cebpz	CCAAT/enhancer-binding protein zeta	11.41	11		48	0.75	0.91	6	35.4
Q8VDT9	Mrpl50	39S ribosomal protein L50, mitochondrial	14.47	2		3	0.75	0.91	2	59.6
S4R1Y2	Rbpms	RNA-binding protein with multiple-splicing (Fragment)	44.65	6		31	0.75	0.91	8	7.0
P56391	Cox6b1	Cytochrome c oxidase subunit 6B1	56.98	5		74	0.75	0.91	27	8.9
P51670	Ccl9	C-C motif chemokine 9	12.30	2		2	0.75	0.91	2	27.3
E9QJV4	Prpf39	Pre-mRNA-processing factor 39	7.52	4		25	0.74	0.90	6	9.4
Q3TCX3-3	Kiaa0907	Isoform 3 of UPF0469 protein KIAA0907	7.67	3		11	0.74	0.90	4	26.6
O35638	Stag2	Cohesin subunit SA-2	4.87	7		44	0.74	0.90	2	4.7
Q3UH06-4	Rreb1	Isoform 4 of Ras-responsive element-binding protein 1	2.48	2		3	0.74	0.90	1	
P50171	Hsd17b8	Estradiol 17-beta-dehydrogenase 8	18.92	4		23	0.73	0.89	4	32.9

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
P47955	Rplp1	60S acidic ribosomal protein P1	57.02	3		7	0.73	0.89	3	69.3
Q8C052	Map1s	Microtubule-associated protein 1S	2.26	2		6	0.73	0.89	2	3.8
A0A087WP63	Srcap	Protein Gm42715 (Fragment)	0.74	2		4	0.73	0.88	1	
Q920A7	Afg3l1	AFG3-like protein 1	8.24	7		64	0.73	0.88	13	25.6
A0A0R4J1R7	Pcbd2	Pterin-4-alpha-carbinolamine dehydratase 2	21.36	3		5	0.72	0.88	1	
Q8CH02	Sugp1	SURP and G-patch domain-containing protein 1	4.20	2		4	0.72	0.88	1	
Q03958	Pfdn6	Prefoldin subunit 6	23.62	3		22	0.72	0.87	5	9.4
F7C134	Ncor1	Nuclear receptor corepressor 1 (Fragment)	1.22	2		4	0.72	0.87	1	
P13439	Umps	Uridine 5'-monophosphate synthase	6.44	3		18	0.72	0.87	3	252.0
Q9DB15	Mrpl12	39S ribosomal protein L12, mitochondrial	29.35	6		113	0.71	0.87	15	17.5
P62307	Snrpf	Small nuclear ribonucleoprotein F	24.42	2		36	0.71	0.86	15	4.8
Q91XD7	Creld1	Cysteine-rich with EGF-like domain protein 1	8.81	4		23	0.70	0.86	6	7.8
A0A0A0MQG2	Sptbn1	Spectrin beta chain, non-erythrocytic 1 (Fragment)	0.96	2		2	0.70	0.85	1	
Q924L1-3	Letmd1	Isoform 3 of LETM1 domain-containing protein 1	12.32	2		6	0.70	0.85	1	
Q9D0R2	Tars	Threonine--tRNA ligase, cytoplasmic	2.91	2		2	0.70	0.85	1	
Q8BIH0-2	Sap130	Isoform 2 of Histone deacetylase complex subunit SAP130	2.73	2		6	0.70	0.84	1	
Q7TPD0-2	Ints3	Isoform 2 of Integrator complex subunit 3	15.45	4		24	0.69	0.84	2	15.0
H3BKY1	Glmp	Glycosylated lysosomal membrane protein	8.78	2		61	0.69	0.84	15	37.5
P62073	Timm10	Mitochondrial import inner membrane translocase subunit Tim10	17.78	2		3	0.69	0.84	4	10.2
Q99LF4	Rtcb	tRNA-splicing ligase RtcB homolog	7.92	4		29	0.69	0.84	4	30.3
Q9WVM1	Racgap1	Rac GTPase-activating protein 1	3.98	3		10	0.69	0.84	1	
Q02819	Nucb1	Nucleobindin-1	30.07	13		101	0.69	0.84	24	19.3
Q8QZV7	Asun	Protein asunder homolog	2.19	2		4	0.69	0.84	1	
Q9D8Y1	Tmem126a	Transmembrane protein 126A	14.80	3		11	0.69	0.83	1	
Q8K202-3	Polr1e	Isoform 3 of DNA-directed RNA polymerase I subunit RPA49	7.63	3		13	0.69	0.83	2	34.5
Q4VBD2	Tapt1	Transmembrane anterior posterior transformation protein 1	6.74	4		14	0.68	0.83	1	
Q9D1I6	Mrpl14	39S ribosomal protein L14, mitochondrial	11.72	2		13	0.68	0.83	1	
P62259	Ywhae	14-3-3 protein epsilon	30.98	9		101	0.68	0.83	19	26.2
P35922-9	Fmr1	Isoform ISO9 of Fragile X mental retardation protein 1 homolog	5.28	4		16	0.68	0.82	2	31.1
Q8CFX1	H6pd	GDH/6PGL endoplasmic bifunctional protein	2.79	3		9	0.67	0.82	1	
Q8C9B9	Dido1	Death-inducer obliterator 1	0.66	2		5	0.67	0.82	3	0.7
Q7TSH6	Scaf4	Protein Scaf4	3.30	4		11	0.67	0.81	3	4.6

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8K199	Cmc2	COX assembly mitochondrial protein 2 homolog	25.32	2		9	0.66	0.81	2	18.4
P12787	Cox5a	Cytochrome c oxidase subunit 5A, mitochondrial	26.03	5		56	0.66	0.81	12	12.4
F8WJI3	Ccdc58	Coiled-coil domain-containing protein 58	18.66	2		12	0.66	0.80	1	
P99027	Rplp2	60S acidic ribosomal protein P2	60.00	5		102	0.66	0.80	23	17.4
Q9JHS3	Lamtor2	Ragulator complex protein LAMTOR2	33.60	3		7	0.65	0.79	1	
B7ZWL1	Cnot1	CCR4-NOT transcription complex subunit 1	2.28	5		10	0.64	0.78	1	
A2A9C8	Med8	Mediator of RNA polymerase II transcription subunit 8	25.58	3		14	0.63	0.77	4	10.7
Q9Z1A1	Tfg	Protein Tfg	23.68	8		148	0.62	0.76	34	15.5
P16858	Gapdh	Glyceraldehyde-3-phosphate dehydrogenase	55.86	17		839	0.61	0.75	243	19.5
Q8JZM0	Tfb1m	Dimethyladenosine transferase 1, mitochondrial	9.57	3		13	0.61	0.74	2	24.0
E9PV44	Atpif1	ATPase inhibitor, mitochondrial	22.97	3		81	0.60	0.73	24	8.5
Q9D0R8	Lsm12	Protein LSM12 homolog	11.28	2		9	0.59	0.71	1	
Q9CR60	Golt1b	Vesicle transport protein GOT1B	15.94	2		6	0.57	0.69	2	61.2
P08207	S100a10	Protein S100-A10	27.84	3		14	0.57	0.69	3	4.8
D3Z7P3	Gls	Glutaminase kidney isoform, mitochondrial	23.29	13		125	0.56	0.69	1	
A0A0J9YVG0	Ppm1g	Protein phosphatase 1G	3.68	2		6	0.55	0.67	1	
A0A0R4J1D9	Fgd3	FYVE, RhoGEF and PH domain-containing protein 3	4.14	2		7	0.54	0.65	1	
P17897	Lyz1	Lysozyme C-1	36.49	4		67	0.53	0.64	2	39.3
Q6ZWM4	Lsm8	U6 snRNA-associated Sm-like protein LSm8	61.46	4		24	0.50	0.61	3	21.1
A0A0A6YWB3	Gpatch4	G patch domain-containing protein 4 (Fragment)	8.79	2		6	0.49	0.59	1	
Q9QYJ3	Dnajb1	DnaJ homolog subfamily B member 1	11.76	4		11	0.48	0.58	1	
Q8BU33-3	Ilvbl	Isoform 3 of Acetolactate synthase-like protein	7.48	2		4	0.46	0.56	1	
Q9D8B3	Chmp4b	Charged multivesicular body protein 4b	7.59	2		11	0.44	0.53	2	268.9
Q5PSV9	Mdc1	Mediator of DNA damage checkpoint protein 1	3.57	4		7	0.43	0.53	1	
Q3TZZ7	Esyt2	Extended synaptotagmin-2	5.21	4		17	0.42	0.51	1	
A2APB8	Tpx2	Targeting protein for Xklp2	8.99	6		19	0.39	0.47	1	
Q9R1P1	Psmb3	Proteasome subunit beta type-3	11.22	2		2	0.38	0.47	1	
Q8BWM0	Ptges2	Prostaglandin E synthase 2	8.59	2		9	0.35	0.43	1	
A0A087WQH8	Slc35a4	Probable UDP-sugar transporter protein SLC35A4	31.07	2		6	0.01	0.02	1	
Q60872	Eif1a	Eukaryotic translation initiation factor 1A	17.36	3		12				
Q9DBC7	Prkar1a	cAMP-dependent protein kinase type I-alpha regulatory subunit	9.45	3		14				
Q8R092	N/A	Uncharacterized protein C1orf43 homolog	7.51	2		6				
Q64674	Srm	Spermidine synthase	7.62	2		6				
Q62313	Tgoln1	Trans-Golgi network integral membrane protein 1	5.10	2		5				

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN^{1}	pksP/wt^{1}	pksP/wt Count^{2}	pksP/wt Variance [%]^{3}
O09061	Psmb1	Proteasome subunit beta type-1	6.67	2		3				
O70469	Dok2	Docking protein 2	5.34	2		9				
Q9CX00	Ist1	IST1 homolog	6.63	3		15				
Q9QXA5	Lsm4	U6 snRNA-associated Sm-like protein LSm4	13.87	2		14				
P35585	Ap1m1	AP-1 complex subunit mu-1	6.38	3		8				
Q8BVU5	Nudt9	ADP-ribose pyrophosphatase, mitochondrial	4.86	2		4				
Q9CQI6	Cotl1	Coactosin-like protein	11.27	2		10				
Q8R4H9	Slc30a5	Zinc transporter 5	3.55	3		9				
P54729	Nub1	NEDD8 ultimate buster 1	2.93	2		4				
O54782	Man2b2	Epididymis-specific alpha-mannosidase	2.46	2		6				
O88708	Orc4	Origin recognition complex subunit 4	3.46	2		3				
Q91V35	Ptpra	Receptor-type tyrosine-protein phosphatase	4.67	4		15				
O55022	Pgrmc1	Membrane-associated progesterone receptor component 1	16.41	5		36				
O89023	Tpp1	Tripeptidyl-peptidase 1	2.14	2		3				
P42232	Stat5b	Signal transducer and activator of transcription 5B	2.29	2		2				
Q8CIM8-3	Ints4	Isoform 3 of Integrator complex subunit 4	9.42	2		6				
Q91X21	Kiaa2013	Uncharacterized protein KIAA2013	4.26	3		9				
Q9DCE9	Igtp	Protein Igtp	5.91	2		8				
Q9Z2Q2-3	Knop1	Isoform 3 of Lysine-rich nucleolar protein 1	9.49	2		4				
Q14B01	Rnf113a2	Protein Rnf113a2	4.75	2		6				
Q9JJL8	Sars2	Serine--tRNA ligase, mitochondrial	5.02	2		6				
Q9CR89-2	Ergic2	Isoform 2 of Endoplasmic reticulum-Golgi intermediate compartment protein 2	6.29	2		2				
Q8R2Y0-2	Abhd6	Isoform 2 of Monoacylglycerol lipase ABHD6	7.27	2		12				
O35639	Anxa3	Annexin A3	7.43	3		19				
Q9JI10-2	Stk3	Isoform 2 of Serine/threonine-protein kinase 3	4.92	2		7				
Q6P8X1	Snx6	Sorting nexin-6	4.43	2		9				
A0A0R4J2B5	2310022A10Rik	Protein 2310022A10Rik	5.37	2		3				
Q505D7	Opa3	Optic atrophy 3 protein homolog	10.61	2		6				
Q9CQ43	Dut	Deoxyuridine triphosphatase	14.20	2		8				
Q91WG3	Trub2	Probable tRNA pseudouridine synthase 2	8.76	2		6				
Q91WC9	Daglb	Sn1-specific diacylglycerol lipase beta	4.33	3		17				
Q8BIJ7	Rufy1	RUN and FYVE domain-containing protein 1	4.78	3		6				
Q9CQV5	Mrps24	28S ribosomal protein S24, mitochondrial	10.18	2		8				
Q3URS9-2	Ccdc51	Isoform 2 of Coiled-coil domain-containing protein 51	4.27	2		6				
Q8C3X2	Ccdc90b	Coiled-coil domain-containing protein 90B,	7.03	2		4				

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		mitochondrial								
Q3TRM4-2	Pnpla6	Isoform 2 of Neuropathy target esterase	2.49	3		8				
Q14CH7	Aars2	Alanine--tRNA ligase, mitochondrial	3.16	2		6				
Q9D9V3-2	Echdc1	Isoform 2 of Ethylmalonyl-CoA decarboxylase	5.35	2		6				
Q9Z329-3	Itpr2	Isoform 3 of Inositol 1,4,5-trisphosphate receptor type 2	1.50	5		32				
Q8CFE3	Rcor1	REST corepressor 1	5.66	3		3				
Q5EG47	Prkaa1	5'-AMP-activated protein kinase catalytic subunit alpha-1	4.83	2		6				
Q6ZPY7	Kdm3b	Lysine-specific demethylase 3B	1.09	2		4				
A2AI91	Phka1	Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	0.68	2		3				
A2RSQ0	Dennd5b	DENN domain-containing protein 5B	1.02	2		3				
Q8VD46	Asz1	Ankyrin repeat, SAM and basic leucine zipper domain-containing protein 1	3.16	2		2				
Q8VD75	Hip1	Huntingtin-interacting protein 1	2.33	2		11				
P12815-2	Pdcd6	Isoform 2 of Programmed cell death protein 6	13.76	3		6				
O88559-2	Men1	Isoform 2 of Menin	3.06	2		4				
Q9ESU6	Brd4	Bromodomain-containing protein 4	1.57	2		4				
E9Q2A6	Ptk2b	Protein-tyrosine kinase 2-beta	4.76	5		12				
O35226-5	Psmd4	Isoform Rpn10E of 26S proteasome non-ATPase regulatory subunit 4	5.38	2		4				
Q9WV03	Fam50a	Protein FAM50A	7.96	2		4				
P51569	Gla	Alpha-galactosidase A	3.82	2		2				
Q9JIF0-3	Prmt1	Isoform 3 of Protein arginine N-methyltransferase 1	5.83	2		4				
Q3TIR3	Ric8a	Synembryn-A	3.02	2		7				
Q8K2F8	Lsm14a	Protein LSM14 homolog A	3.03	2		8				
Q9Z1F9	Uba2	SUMO-activating enzyme subunit 2	4.23	3		6				
Q3TCN2	Plbd2	Putative phospholipase B-like 2	2.69	2		6				
Q99LB0	Dnttip1	Deoxynucleotidyltransferase terminal-interacting protein 1	5.18	2		12				
Q62159	Rhoc	Rho-related GTP-binding protein RhoC	27.98	5		33				
Q9DBT5	Ampd2	AMP deaminase 2	2.51	2		6				
O08599	Stxbp1	Syntaxin-binding protein 1	5.72	3		4				
Q9D023	Mpc2	Mitochondrial pyruvate carrier 2	11.81	2		8				
Q8K409	Polb	DNA polymerase beta	4.78	2		3				
Q9JI11	Stk4	Serine/threonine-protein kinase 4	5.34	2		5				
O54833	Csnk2a2	Casein kinase II subunit alpha'	6.57	2		6				

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8BHN5	Rbm45	RNA-binding protein 45	5.46	3		9				
P00158	Mt-Cyb	Cytochrome b	3.94	2		2				
P22315	Fech	Ferrochelatase, mitochondrial	9.05	3		8				
O08810	Eftud2	116 kDa U5 small nuclear ribonucleoprotein component	33.57	28		307				
Q9CQM9	Glrx3	Glutaredoxin-3	6.53	2		9				
A0A0R4J114	Diexf	Digestive organ expansion factor homolog	2.47	2		2				
A0A0R4J1N8	Rdh13	Retinol dehydrogenase 13	13.71	2		6				
Q9QZD9	Eif3i	Eukaryotic translation initiation factor 3 subunit I	5.85	2		2				
Q9CXJ4	Abcb8	ATP-binding cassette sub-family B member 8, mitochondrial	2.37	2		2				
Q8VCG3	Wdr74	WD repeat-containing protein 74	7.03	2		3				
Q6P5E6	Gga2	ADP-ribosylation factor-binding protein GGA2	4.15	2		7				
Q8CGP2	Hist1h2bp	Histone H2B type 1-P	68.25	13		2737				
Q9Z2Z6	Slc25a20	Mitochondrial carnitine/acylcarnitine carrier protein	10.63	4		21				
Q91VM9	Ppa2	Inorganic pyrophosphatase 2, mitochondrial	11.21	4		19				
Q61166	Mapre1	Microtubule-associated protein RP/EB family member 1	6.34	2		4				
Q8BMQ2-2	Gtf3c4	Isoform 2 of General transcription factor 3C polypeptide 4	2.83	2		3				
Q7TSY8	Sgol2	Shugoshin-like 2	1.03	2		2				
Q8BMJ2	Lars	Leucine--tRNA ligase, cytoplasmic	2.63	3		5				
Q8BL74	Gtf3c2	General transcription factor 3C polypeptide 2	1.65	2		4				
Q6A099	Gbf1	MKIAA0248 protein (Fragment)	1.39	3		5				
P11680	Cfp	Properdin	6.03	3		16				
O54950	Prkag1	5'-AMP-activated protein kinase subunit gamma-1	5.76	2		4				
Q810B6	Ankfy1	Rabankyrin-5	1.63	2		2				
Q91VN6	Ddx41	Probable ATP-dependent RNA helicase DDX41	7.88	4		10				
Q3TL44	Nlrx1	NLR family member X1	2.56	2		6				
Q3TSR0	Extl2	Exostosin-like 2	4.43	2		2				
P47811-4	Mapk14	Isoform 4 of Mitogen-activated protein kinase 14	13.78	4		7				
Q2TBE6	Pi4k2a	Phosphatidylinositol 4-kinase type 2-alpha	8.56	2		4				
P48377	Rfx1	MHC class II regulatory factor RFX1	2.60	2		4				
Q6P9P6	Kif11	Kinesin-like protein KIF11	1.52	2		2				
E9PWW9	Rsf1	Protein Rsf1	1.04	2		4				

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
A2A6J4	Lsp1	Lymphocyte-specific protein 1	5.28	2		12				
Q7TPM0	Cbx1	Cbx1 protein	17.39	2		2				
Q8BN82-2	Slc17a5	Isoform 2 of Sialin	3.62	2		4				
Q6PGG2-2	Gmip	Isoform 2 of GEM-interacting protein	2.26	2		2				
Q8CHY6	Gatad2a	Transcriptional repressor p66 alpha	4.61	3		12				
A0A0G2JFY0	Spata5	Spermatogenesis-associated protein 5	3.56	2		21				
P53566-4	Cebpa	Isoform 3 of CCAAT/enhancer-binding protein alpha	9.92	2		8				
A2A6U3	Sep-09	Septin-9	3.01	2		2				
J3QN06	Carkd	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	12.13	3		22				
A2AGT5-2	Ckap5	Isoform 2 of Cytoskeleton-associated protein 5	1.83	4		8				
O88587-2	Comt	Isoform Soluble of Catechol O-methyltransferase	12.61	3		16				
A2AWL7-2	Mga	Isoform 2 of MAX gene-associated protein	0.83	2		10				
Q80U63-2	Mfn2	Isoform 2 of Mitofusin-2	4.13	2		6				
P16546-2	Sptan1	Isoform 2 of Spectrin alpha chain, non-erythrocytic 1	1.10	2		4				
Q6ZWR6-4	Syne1	Isoform 4 of Nesprin-1	0.16	2		5				
Q920Q4-2	Vps16	Isoform 2 of Vacuolar protein sorting-associated protein 16 homolog	9.55	3		9				
E9QA74	Myo18a	Unconventional myosin-XVIIIa	1.10	2		6				
G3UZ34	Eftud2	116 kDa U5 small nuclear ribonucleoprotein component	32.85	28		308				
A0A0A0MQG1	Obsl1	Obscurin-like protein 1 (Fragment)	1.29	2		10				
J3KMH5	Mia3	Melanoma inhibitory activity protein 3	8.83	8		24				
D3YZS3	Ube2l3	Ubiquitin-conjugating enzyme E2 L3	20.17	2		6				
F6VQ81	Tpd52l2	Tumor protein D54 (Fragment)	26.09	3		9				
A0A0J9YTY0	Sep-11	Septin-11	5.88	3		4				
A8XU21	Ncf4	Neutrophil cytosol factor 4 (Fragment)	7.31	2		6				
D3YXD3	Prkrip1	PRKR-interacting protein 1 (Fragment)	8.48	2		6				
A0A087WS03	Pign	GPI ethanolamine phosphate transferase 1	2.13	2		6				
D3Z0X3	Orc5	Origin recognition complex subunit 5 (Fragment)	8.01	3		10				
A2A481	Zmynd8	Protein Zmynd8	2.75	2		5				
G3UXX5	Polr1c	DNA-directed RNA polymerases I and III subunit RPAC1 (Fragment)	15.88	2		11				
B1ATP7	Elac2	Zinc phosphodiesterase ELAC protein 2	2.31	2		4				
F6ZL86	Dnajc1	DnaJ homolog subfamily C member 1	4.48	2		6				

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
		(Fragment)								
A0A0A6YXW4	Mrpl30	39S ribosomal protein L30, mitochondrial (Fragment)	10.94	2		2				
E9PYC6	Eci2	Enoyl-CoA delta isomerase 2, mitochondrial (Fragment)	19.41	3		13				
F7AC58	Piezo1	Piezo-type mechanosensitive ion channel component (Fragment)	0.95	2		9				
F6QKK2	Arl8a	ADP-ribosylation factor-like protein 8A (Fragment)	36.97	5		53				
D3Z158	Qars	Protein Qars	4.03	3		11				
D3YTP0	Steap3	Metalloreductase STEAP3 (Fragment)	4.77	2		6				
A0A0U1RPC6	Txnrd2	Thioredoxin reductase 2, mitochondrial (Fragment)	10.30	2		9				
Q8K2C8	Gpat4	Glycerol-3-phosphate acyltransferase 4	4.39	2		6				
Q8CGA3	Slc43a2	Large neutral amino acids transporter small subunit 4	2.99	2		4				
Q80VY9	Dhx33	Putative ATP-dependent RNA helicase DHX33	4.73	3		12				
Q62419	Sh3gl1	Endophilin-A2	4.35	2		2				
A2AIV2	Kiaa1429	Protein virilizer homolog	1.05	2		4				
Q9CYW4	Hdhd3	Haloacid dehalogenase-like hydrolase domain-containing protein 3	8.37	2		8				
Q6QD59	Bnip1	Vesicle transport protein SEC20	13.16	3		8				
Q8BZR9	Ncbp3	Nuclear cap-binding protein subunit 3	5.53	4		8				
Q9JHP7-3	Kdelc1	Isoform 3 of KDEL motif-containing protein 1	7.09	2		4				
Q8K2Q9-2	Shtn1	Isoform 2 of Shootin-1	4.17	2		8				
Q9ERG0-2	Lima1	Isoform Alpha of LIM domain and actin-binding protein 1	5.23	2		4				
Q8VE88-2	Fam114a2	Isoform 2 of Protein FAM114A2	4.49	2		4				
Q8BU30	Iars	Isoleucine--tRNA ligase, cytoplasmic	2.77	3		6				
E9PYL2	Prr12	Proline-rich protein 12	1.13	2		2				
A2ABV5	Med14	Mediator of RNA polymerase II transcription subunit 14	1.92	2		4				
A2ANX3	Atp8b4	Phospholipid-transporting ATPase	1.42	2		2				
E9QAT4	Sec16a	Protein Sec16a	0.72	2		4				
O35144-2	Terf2	Isoform 2 of Telomeric repeat-binding factor 2	4.47	2		4				
Q8K327	Champ1	Chromosome alignment-maintaining phosphoprotein 1	3.49	3		6				
Q8BY89-2	Slc44a2	Isoform 2 of Choline transporter-like protein 2	2.13	2		2				
O35295	Purb	Transcriptional activator protein Pur-beta	8.95	2		2				

Accession	Gene	Protein Description	Coverage [%]	Peptides	Unique Peptides	PSMs	pksP/wt MN[1]	pksP/wt[1]	pksP/wt Count[2]	pksP/wt Variance [%][3]
Q8VI93	Oas3	2'-5'-oligoadenylate synthase 3	2.90	2		5				
P32233	Drg1	Developmentally-regulated GTP-binding protein 1	6.54	2		2				
P28658	Atxn10	Ataxin-10	5.05	2		4				
Q9JMG1	Edf1	Endothelial differentiation-related factor 1	10.14	2		4				
Q924S8	Spred1	Sprouty-related, EVH1 domain-containing protein 1	9.68	3		10				
Q8VCW8	Acsf2	Acyl-CoA synthetase family member 2, mitochondrial	3.90	2		8				
Q8BT14-2	Cnot4	Isoform 2 of CCR4-NOT transcription complex subunit 4	2.80	2		4				
P68181-2	Prkacb	Isoform 2 of cAMP-dependent protein kinase catalytic subunit beta	5.33	2		4				
Q8R2S9	Actr8	Actin-related protein 8	2.72	2		4				
Q99MS7-4	Ehbp1l1	Isoform 4 of EH domain-binding protein 1-like protein 1	2.77	2		2				
A0A0N4SVC2	Tra2a	Transformer-2 protein homolog alpha	7.50	2		2				
E9Q0X9	Mettl17	Methyltransferase-like protein 17, mitochondrial	8.05	2		2				
F6ZE40	Coq6	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial (Fragment)	5.00	2		8				
A0A0N4SV38	Zfp638	Protein Zfp638	1.86	2		4				
M0QWI3	Mtf2	Metal-response element-binding transcription factor 2 (Fragment)	17.83	2		6				
D3Z3Z8	Polr2i	DNA-directed RNA polymerase II subunit RPB9 (Fragment)	21.69	2		4				
F7DD52	Mroh3	Protein Mroh3 (Fragment)	0.00	2		3				
A2AAN2	Srp68	Signal recognition particle subunit SRP68	3.07	2		11				
A0A0A6YVR9	Surf1	Surfeit locus protein 1 (Fragment)	15.83	2		4				
A3KGL3	Dhdds	Dehydrodolichyl diphosphate syntase complex subunit Dhdds (Fragment)	8.91	2		4				
A2A4N9	Dhx8	ATP-dependent RNA helicase DHX8 (Fragment)	1.62	2		3				
B0V2Q9	Lclat1	Lysocardiolipin acyltransferase 1 (Fragment)	11.60	2		9				

Table S5: ***A. fumigatus*** **proteins detected in the TMT label-based LC-MS/MS measurement of purified conidia-containing phagolysosomes.** [1]Proteins with a *pksP/*wt ratio ≥ 1.5 were considered as enriched on *pksP* mutant conidia (green) and proteins with a *pksP/*wt ≤ 0.67 were considered as enriched on wild-type conidia-containing phagolysosomes (red). [2]Calculated ratios that are based on less than 2 reporter ions (average) are untrustworthy and consequently not considered as differentially regulated. [3] An average variability ≤ 30 % was considered as high confident data (dark colour). Medium confidence data was defined in the range of 30-50 % (light colour)

Accession	Protein Description	Cover-age [%]	Unique Peptides	Peptides	PSMs	*pksP*/wt MN[1]	*pksP*/wt[1]	*pksP*/wt Count[2]	*pksP*/wt Variance [%][3]
Afu3g13755	Protein of unknown function	18.35	2	2	2	2.55	3.22	1	
Afu1g11710	Ribosomal protein L1	5.99	2	2	37	1.26	1.59	12	20.1
Afu2g15570	Ortholog(s) have GTP binding activity, role in cellular response to osmotic stress, hyphal growth, intracellular protein transport, retrograde transport, endosome to Golgi and Golgi membrane, cytosol, nucleus, spitzenkorper localization	10.63	1	2	58	1.22	1.54	3	14.3
Afu1g02550	Tubulin alpha-1 subunit; gene pair with AFUA_2G14990 (tubulin alpha-2 subunit)	4.69	3	3	20	1.21	1.52	12	6.9
Afu4g08040	Ortholog(s) have GTP binding activity	10.09	2	2	46	1.16	1.47	13	6.7
Afu5g04320	Ortholog(s) have GTPase activity and role in ER to Golgi vesicle-mediated transport, Golgi organization, cellular response to drug, cellular response to nitrogen starvation, negative regulation of G0 to G1 transition, protein secretion	39.80	6	7	153	1.16	1.46	35	21.3
Afu4g07660	ATP-dependent RNA helicase	4.60	2	3	9	1.15	1.45	1	
Afu2g10750	Putative RNA helicase; transcript induced by exposure to human airway epithelial cells	3.46	1	2	19	1.10	1.39	3	0.5
Afu2g03380	Ortholog(s) have cytosol, mitochondrion, nucleus localization	18.11	2	2	34	1.10	1.39	12	23.0
Afu6g12990	Putative cytosolic large ribosomal subunit protein L7A	6.08	2	2	18	1.10	1.38	6	5.9
Afu3g06970	40S ribosomal protein S9; transcript induced by exposure to human airway epithelial cells	8.81	2	2	22	1.09	1.38	7	7.2
Afu5g12130	Rab small monomeric GTPase	23.98	4	4	74	1.08	1.36	21	13.8
Afu6g13300	GTP-Binding nuclear protein Ran	22.79	5	5	71	1.07	1.35	18	9.8
Afu5g11230	Ras family GTPase protein	8.45	2	2	7	1.06	1.34	6	9.6
Afu1g15020	40S ribosomal protein S5; reacts with rabbit immunosera exposed to A. fumigatus conidia	8.84	3	3	106	1.05	1.33	33	7.4
Afu4g10350	Polyubiquitin; calcium induced	60.51	6	6	715	1.04	1.31	277	13.6
Afu1g13780	Has domain(s) with predicted DNA binding, protein heterodimerization activity, role in DNA-dependent transcription, initiation, nucleosome assembly and nucleosome, nucleus localization	28.16	3	3	1426	1.04	1.31	470	18.7
Afu7g01000	Putative alcohol dehydrogenase involved in ethanol metabolism; predicted gene pair with AFUA_6G11430 (aldA); increased	4.67	3	3	36	1.04	1.31	20	25.1

Accession	Protein Description	Cover-age [%]	Unique Peptides	Peptides	PSMs	*pksP*/wt MN[1]	*pksP*/wt[1]	*pksP*/wt Count[2]	*pksP*/wt Variance [%][3]
	expression in biofilm; induced by L-tyrosine; induced in neutrophil-exposed conidia; repressed by gliotoxin exposure								
Afu5g10550	ATP synthase F1, beta subunit; reacts with rabbit immunosera exposed to A. fumigatus conidia; hypoxia induced protein	7.71	3	3	114	1.03	1.30	34	29.2
Afu5g04170	Heat shock protein; allergen Asp f 12; likely essential; required for conidiation and cell wall integrity; transcript induced by growth on hydrogen peroxide; enters the nucleus in response to heat shock	3.97	3	3	152	1.01	1.28	44	6.9
Afu1g02190	Ras GTPase; hypoxia repressed protein	19.05	4	4	53	1.01	1.28	16	11.0
Afu2g04620	Hsp70 chaperone; protein enriched in dormant conidia	8.78	4	6	387	1.00	1.27	89	15.0
Afu1g14680	Ortholog(s) have DNA binding activity and cytosol, nucleus localization	0.97	2	2	3	1.00	1.26	2	7.3
Afu1g10910	Beta-tubulin; predicted gene pair with AFUA_7G00250 (tubulin beta-2 subunit); protein induced by hydrogen peroxide	5.36	2	2	13	1.00	1.26	4	17.6
Afu1g05630	40S ribosomal protein S3	9.02	3	3	12	1.00	1.26	5	10.7
Afu1g07440	Molecular chaperone; conidia-enriched protein	10.34	6	8	172	0.98	1.24	52	13.2
Afu3g05360	Has domain(s) with predicted DNA binding, protein heterodimerization activity, role in nucleosome assembly and nucleosome, nucleus localization	5.28	3	3	690	0.97	1.23	305	9.2
Afu3g12080	Ortholog(s) have mRNA binding activity	11.96	2	2	12	0.96	1.21	4	36.4
Afu2g11510	Ortholog(s) have role in cellular response to drug, rRNA processing, ribosomal large subunit biogenesis, ribosomal subunit export from nucleus and nucleolus, preribosome, large subunit precursor, spindle localization	3.85	2	2	13	0.94	1.19	3	14.4
Afu1g11730	Ortholog(s) have GTPase activity, role in ER to Golgi veside-mediated transport, Golgi to plasma membrane transport, cellular response to drug, macroautophagy and Golgi apparatus, glyoxysome localization	27.32	3	3	22	0.90	1.13	3	11.9
Afu8g05320	Putative mitochondrial F1 ATPase subunit alpha; hypoxia induced protein	6.29	4	4	125	0.89	1.13	38	19.4
Afu5g02410	Putative DEAD/DEAH box helicase; predicted gene pair with AFUA_3G08160 (eukaryotic translation initiation factor eIF4A; ATP-dependent RNA helicase, tifA)	3.56	3	3	36	0.89	1.12	11	14.7
Afu2g03030	Putative pre-mRNA splicing factor; intein-containing protein, inteins are protein intervening sequences that can self-excise through protein splicing	2.08	8	8	58	0.89	1.12	12	16.3
Afu2g03290	14-3-3 family protein; predicted gene pair with AFUA_6G06750; conidia-enriched protein; protein induced by hydrogen peroxide; reacts with rabbit immunosera exposed to A. fumigatus conidia; hypoxia repressed protein	6.90	2	2	18	0.88	1.11	4	34.3

Accession	**Protein Description**	**Cover-age [%]**	**Unique Peptides**	**Peptides**	**PSMs**	***pksP*/wt MN[1]**	***pksP*/wt[1]**	***pksP*/wt Count[2]**	***pksP*/wt Variance [%][3]**
Afu3g05350	Histone H2B	12.14	2	2	551	0.87	1.10	219	12.1
Afu2g13780	Ortholog(s) have role in mRNA cis splicing, via spliceosome and U2 snRNP localization	3.34	4	4	32	0.87	1.09	7	5.0
Afu6g12930	Mitochondrial aconitate hydratase; citric acid cycle enzyme; protein abundant in conidia; transcript induced in conidia exposed to neutrophils; reacts with rabbit immunosera exposed to A. fumigatus conidia; hypoxia induced	2.03	2	2	55	0.86	1.09	9	8.3
Afu1g06220	Ortholog(s) have cytosol, nucleus localization	4.24	2	2	9	0.86	1.08	1	
Afu4g04520	Ortholog(s) have mitochondrion localization	4.05	2	2	8	0.86	1.08	3	8.2
Afu6g04740	Actin	21.37	8	8	742	0.84	1.06	263	12.7
Afu3g08660	Putative isocitrate dehydrogenase; protein induced by heat shock	3.79	2	2	23	0.82	1.03	7	9.0
Afu2g09090	Ortholog(s) have role in mitochondrion inheritance, negative regulation of proteolysis, protein folding, replicative cell aging and mitochondrial inner membrane, plasma membrane localization	6.43	2	2	157	0.80	1.00	54	9.4
Afu1g13790	Histone H3	22.06	5	5	387	0.76	0.96	181	7.8
Afu2g09290	Putative antigenic mitochondrial protein; reacts with rabbit immunosera exposed to A. fumigatus conidia; hypoxia induced protein	1.53	2	2	24	0.67	0.85	13	6.6
Afu1g04950	Ortholog(s) have protein serine/threonine phosphatase activity	7.43	2	2	9	0.52	0.66	3	24.3

Table S6: Murine proteins detected in the label-free LC-MS/MS measurement of whole cell lysate. Protein quantities were calculated with the 'Top Three' method. [1]Proteins with a *pksP/*wt ratio ≥ 2 were considered as enriched on *pksP* mutant conidia (green) and proteins with a *pksP*/wt ≤ 0.5 were considered as enriched on wild-type conidia-containing phagolysosomes (red). n.a.- not available; protein values only detected in one condition.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q8BFZ3	Actbl2	Beta-actin-like protein 2	24	7	2197	1	n.a.
P63330	Ppp2ca	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	13	4	27	1	n.a.
Q99PG2-2	Ogfr	Isoform 2 of Opioid growth factor receptor	9	2	17	2	n.a.
A0A0U1RP81	Immt	MICOS complex subunit MIC60	39	21	505	1	n.a.
E9Q827	Arpp19	cAMP-regulated phosphoprotein 19	13	2	20	2	n.a.
J3QPW1	Pitpna	Phosphatidylinositol transfer protein alpha isoform	6	2	37	1	n.a.
Q8QZY9	Sf3b4	Splicing factor 3B subunit 4	5	2	26	2	n.a.
P43277	Hist1h1d	Histone H1.3	41	14	947	2	n.a.
Q01405	Sec23a	Protein transport protein Sec23A	7	5	104	4	n.a.
A0A0A6YXB7	Ssr2	Translocon-associated protein subunit beta	4	2	20	2	n.a.
Q9WV02	Rbmx	RNA-binding motif protein, X chromosome	27	12	509	1	n.a.
Q59J78	Ndufaf2	Mimitin, mitochondrial	19	3	24	3	n.a.
P50543	S100a11	Protein S100-A11	10	2	9	2	n.a.
Q9D824	Fip1l1	Pre-mRNA 3'-end-processing factor FIP1	6	3	30	3	n.a.
V9GXM1	Arfgap1	ADP-ribosylation factor GTPase-activating protein 1	9	5	58	5	n.a.
Q80Y14	Glrx5	Glutaredoxin-related protein 5, mitochondrial	16	2	33	2	n.a.
Q9D0J8	Ptms	Parathymosin	22	2	30	2	n.a.
Q9CQF7	Pfdn1	Prefoldin 1	14	2	14	1	n.a.
P52479-2	Usp10	Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10	2	2	18	2	n.a.
Q9D7S9	Chmp5	Charged multivesicular body protein 5	6	2	13	2	n.a.
Q9EQU5-2	Set	Isoform 2 of Protein SET	25	7	145	1	n.a.
P62715	Ppp2cb	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	13	4	36	1	n.a.
Q5SSL4-2	Abr	Isoform 2 of Active breakpoint cluster region-related protein	4	4	31	4	n.a.
P18608	Hmgn1	Non-histone chromosomal protein HMG-14	17	2	18	2	n.a.
P17879	Hspa1b	Heat shock 70 kDa protein 1B	15	9	657	2	n.a.
G3X977	Itih2	Inter-alpha trypsin inhibitor, heavy chain 2	2	3	25	3	n.a.
P19973	Lsp1	Lymphocyte-specific protein 1	14	3	28	3	n.a.
Q8BYI6	Lpcat2	Lysophosphatidylcholine acyltransferase 2	4	3	25	3	n.a.
O88543	Cops3	COP9 signalosome complex subunit 3	8	3	29	3	n.a.
Q8CG29	Myo1f	Myosin IF	5	5	52	3	n.a.
Q8BJF9	Chmp2b	Charged multivesicular body protein 2b	29	7	71	7	n.a.
Q6PDG5	Smarcc2	SWI/SNF complex subunit SMARCC2	3	5	36	3	n.a.
Q6P4T3	Eya3	Eyes absent homolog	3	2	45	2	n.a.
Q8VDD8	Wash1	WAS protein family homolog 1	3	2	12	2	n.a.
Q8K2Q7	Brox	BRO1 domain-containing protein BROX	5	2	6	2	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
A2A4P4	Gm27029	Protein Gm27029	5	3	22	3	n.a.
Q9JI10	Stk3	Serine/threonine-protein kinase 3	3	2	18	2	n.a.
Q3U422	Ndufv3	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	5	3	26	3	n.a.
P54276	Msh6	DNA mismatch repair protein Msh6	1	2	18	2	n.a.
Q9WV30-2	Nfat5	Isoform 2 of Nuclear factor of activated T-cells 5	1	2	12	2	n.a.
A6H619	Phrf1	PHD and RING finger domain-containing protein 1	1	2	8	2	n.a.
Q9JJ78	Pbk	Lymphokine-activated killer T-cell-originated protein kinase	4	2	9	2	n.a.
Q6GSS7	Hist2h2aa1	Histone H2A type 2-A	46	7	650	2	n.a.
Q9Z2D6-2	Mecp2	Isoform B of Methyl-CpG-binding protein 2	3	2	11	2	n.a.
Q9QZK7	Dok3	Docking protein 3	6	3	20	3	n.a.
Q924N4	Slc12a6	Solute carrier family 12 member 6	1	2	34	2	n.a.
Q8VCE0	Atp1a3	Sodium/potassium-transporting ATPase subunit alpha	14	11	375	2	n.a.
P36371	Tap2	Antigen peptide transporter 2	2	2	23	2	n.a.
Q6NXL1	Sec24d	Protein Sec24d	1	2	38	2	n.a.
Q923D4	Sf3b5	Splicing factor 3B subunit 5	30	2	15	2	n.a.
O88845	Akap10	A-kinase anchor protein 10, mitochondrial	3	2	29	2	n.a.
G3X961	Klhdc4	Kelch domain containing 4, isoform CRA_a	3	2	20	2	n.a.
E9Q2M9	Wdfy4	Protein Wdfy4	1	3	29	3	n.a.
Q6P549	Inppl1	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	2	3	58	1	n.a.
F8WJ93	Eml4	Echinoderm microtubule-associated protein-like 4	2	2	25	2	n.a.
Q7TT50	Cdc42bpb	Serine/threonine-protein kinase MRCK beta	2	3	16	2	n.a.
P01027	C3	Complement C3	1	2	9	2	n.a.
A0A0R4J0U8	Trmt1l	RIKEN cDNA 1190005F20, isoform CRA_a	2	2	9	2	n.a.
Q6P5B5	Fxr2	Fragile X mental retardation syndrome-related protein 2	6	4	66	2	n.a.
Q8VEJ4	Nle1	Notchless protein homolog 1	7	3	19	3	n.a.
Q9ERB0	Snap29	Synaptosomal-associated protein 29	20	5	41	5	n.a.
Q6NXN1	Szrd1	SUZ domain-containing protein 1	10	2	9	2	n.a.
Q99L13	Hibadh	3-hydroxyisobutyrate dehydrogenase, mitochondrial	8	2	24	2	n.a.
O55222	Ilk	Integrin-linked protein kinase	3	2	18	2	n.a.
O35382	Exoc4	Exocyst complex component 4	2	2	22	2	n.a.
Q8BI72	Cdkn2aip	CDKN2A-interacting protein	6	3	23	3	n.a.
Q9Z2K1	Krt16	Keratin, type I cytoskeletal 16	13	6	192	3	n.a.
D6RFQ2	Gm42957	Protein Gm42957	5	2	9	2	n.a.
F7BGR7	Gm21992	Protein Gm21992	10	5	110	5	n.a.
Q91WG2	Rabep2	Rab GTPase-binding effector protein 2	3	2	12	2	n.a.
Q8BWZ3	Naa25	N-alpha-acetyltransferase 25, NatB auxiliary subunit	1	2	8	2	n.a.
Q9JLB0	Mpp6	MAGUK p55 subfamily member 6	3	2	19	2	n.a.
P48722	Hspa4l	Heat shock 70 kDa protein 4L	6	6	32	5	n.a.
P11152	Lpl	Lipoprotein lipase	7	3	43	3	n.a.
Q9QYE6	Golga5	Golgin subfamily A member 5	3	3	18	3	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q8BFS6	Cpped1	Serine/threonine-protein phosphatase CPPED1	5	2	15	2	n.a.
P68433	Hist1h3a	Histone H3.1	31	7	1557	2	n.a.
Q8CI08-2	Slain2	Isoform 2 of SLAIN motif-containing protein 2	3	2	9	2	n.a.
Q3UMU9-3	Hdgfrp2	Isoform 3 of Hepatoma-derived growth factor-related protein 2	5	4	21	3	n.a.
Q9Z0H8	Clip2	CAP-Gly domain-containing linker protein 2	1	2	17	1	n.a.
Q9Z2M7	Pmm2	Phosphomannomutase 2	9	2	15	2	n.a.
Q9ERU3	Znf22	Zinc finger protein 22	8	2	9	2	n.a.
Q64133	Maoa	Amine oxidase [flavin-containing] A	3	2	8	2	n.a.
Q91XA2	Golm1	Golgi membrane protein 1	4	2	14	2	n.a.
A2BFF9	Dync1i2	Cytoplasmic dynein 1 intermediate chain 2	6	3	50	3	n.a.
F8WIA1	Clip1	CAP-Gly domain-containing linker protein 1	2	4	33	3	n.a.
Q3U821	Wdr75	WD repeat-containing protein 75	2	3	22	3	n.a.
Q9JKX4	Aatf	Protein AATF	4	2	21	2	n.a.
Q922E4	Pcyt2	Ethanolamine-phosphate cytidylyltransferase	5	2	9	2	n.a.
P70297	Stam	Signal transducing adapter molecule 1	3	2	18	1	n.a.
P97449	Anpep	Aminopeptidase N	3	3	12	3	n.a.
Q9D3E6	Stag1	Cohesin subunit SA-1	1	2	9	1	n.a.
Q60605	Myl6	Myosin light polypeptide 6	24	4	17	4	n.a.
Q9CYI4	Luc7l	Putative RNA-binding protein Luc7-like 1	16	5	105	2	n.a.
Q8BHJ9	Slu7	Pre-mRNA-splicing factor SLU7	6	4	25	4	n.a.
A0A140LJJ5	Akap13	A-kinase anchor protein 13	1	2	15	2	n.a.
Q8R0K9	E2f4	Transcription factor E2F4	4	2	14	2	n.a.
Q8BIQ5	Cstf2	Cleavage stimulation factor subunit 2	5	3	28	3	n.a.
E9Q5G3	Kif23	Kinesin-like protein KIF23	2	2	8	2	n.a.
Q6NSP9	Hmga2	High mobility group protein HMGI-C	23	2	43	2	n.a.
D3Z041	Acsl1	Long-chain-fatty-acid--CoA ligase 1	2	2	24	1	n.a.
Q6P9Q6-2	Fkbp15	Isoform B of FK506-binding protein 15	2	3	18	3	n.a.
Q9JHS4	Clpx	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	4	2	18	2	n.a.
M0QWX4	Senp1	Sentrin-specific protease 1	3	2	15	2	n.a.
O88271	Cfdp1	Craniofacial development protein 1	6	2	9	2	n.a.
P58058	Nadk	NAD kinase	4	2	25	2	n.a.
P24527	Lta4h	Leukotriene A-4 hydrolase	4	2	16	2	n.a.
Q6NZN0	Rbm26	RNA-binding protein 26	3	3	22	3	n.a.
Q9CZA6	Nde1	Nuclear distribution protein nudE homolog 1	7	3	20	3	n.a.
Q61624	Znf148	Zinc finger protein 148	2	2	17	2	n.a.
Q3UDC3	Tom1	Target of Myb protein 1	4	2	14	2	n.a.
Q9R0L6-2	Pcm1	Isoform 2 of Pericentriolar material 1 protein	1	2	14	2	n.a.
F7DEU6	Impdh1	Inosine-5'-monophosphate dehydrogenase	3	2	76	1	n.a.
E9QAX2	Myo18a	Unconventional myosin-XVIIIa	1	3	22	3	n.a.
Q14B01	Rnf113a2	Protein Rnf113a2	10	3	18	3	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
O88983	Stx8	Syntaxin-8	8	2	13	2	n.a.
Q922S8	Kif2c	Kinesin-like protein KIF2C	4	3	18	2	n.a.
Q9JM52-3	Mink1	Isoform 3 of Misshapen-like kinase 1	1	2	13	1	n.a.
P50171-2	Hsd17b8	Isoform Long of Estradiol 17-beta-dehydrogenase 8	9	2	9	2	n.a.
Q99KK9	Hars2	Probable histidine--tRNA ligase, mitochondrial	5	3	60	1	n.a.
Q60838	Dvl2	Segment polarity protein dishevelled homolog DVL-2	5	3	23	3	n.a.
A0A0R4J135	Selenbp2	Selenium-binding protein 2	6	3	18	3	n.a.
Q99K95	Rtfdc1	Protein RTF2 homolog	7	2	14	2	n.a.
A3KGJ7	Cep250	Centrosome-associated protein CEP250	1	2	15	2	n.a.
P61202-2	Cops2	Isoform 2 of COP9 signalosome complex subunit 2	3	2	14	2	n.a.
Q8CFE4	Scyl2	SCY1-like protein 2	2	3	14	3	n.a.
P63154	Crnkl1	Crooked neck-like protein 1	5	4	55	4	n.a.
P47857-3	Pfkm	Isoform 3 of ATP-dependent 6-phosphofructokinase, muscle type	2	3	54	1	n.a.
P35290	Rab24	Ras-related protein Rab-24	9	2	8	2	n.a.
A0A0R4J0G9	Mtrr	Methionine synthase reductase	3	2	18	2	n.a.
Q9ERG0	Lima1	LIM domain and actin-binding protein 1	3	2	17	2	n.a.
E9QKG8	Hjurp	Holliday junction recognition protein	3	2	16	2	n.a.
E9Q7L1	Urb2	Protein Urb2	1	2	23	2	n.a.
Q6NZH9	Rasgrp3	Protein Rasgrp3	2	2	14	2	n.a.
F8VPV0	Pcnt	Pericentrin	1	2	9	2	n.a.
Q9QYR9	Acot2	Acyl-coenzyme A thioesterase 2, mitochondrial	4	2	8	2	n.a.
P06801	Me1	NADP-dependent malic enzyme	3	2	8	2	n.a.
Q64261	Cdk6	Cyclin-dependent kinase 6	5	2	27	1	n.a.
Q08509	Eps8	Epidermal growth factor receptor kinase substrate 8	5	3	21	3	n.a.
Q8VI33	Taf9	Transcription initiation factor TFIID subunit 9	7	2	17	2	n.a.
A0A087WQT6	Casp8	Caspase-8	5	3	15	3	n.a.
Q6NZQ2	Ddx31	Probable ATP-dependent RNA helicase DDX31	2	2	6	2	n.a.
P97765	Wbp2	WW domain-binding protein 2	9	2	85	2	n.a.
Q99N96	Mrpl1	39S ribosomal protein L1, mitochondrial	7	2	5	2	n.a.
Q91ZR1	Rab4b	Ras-related protein Rab-4B	9	2	74	1	n.a.
O70469	Dok2	Docking protein 2	5	2	19	2	n.a.
Q9CPN8	Igf2bp3	Insulin-like growth factor 2 mRNA-binding protein 3	3	2	9	2	n.a.
Q8K1N4	Spats2	Spermatogenesis-associated serine-rich protein 2	4	2	15	2	n.a.
Q4WJ30	AFUA_1G07440	Molecular chaperone Hsp70	15	12	619	2	n.a.
E9PVN6	Gm20498	Protein Gm20498	14	3	15	3	n.a.
O35144	Terf2	Telomeric repeat-binding factor 2	4	2	8	2	n.a.
P04627	Araf	Serine/threonine-protein kinase A-Raf	3	2	20	2	n.a.
P58681	Tlr7	Toll-like receptor 7	1	2	17	2	n.a.
E9Q9Q2	R3hdm1	Protein R3hdm1	2	2	6	2	n.a.
Q6DFZ1	Gbf1	Golgi-specific brefeldin A-resistance factor 1	2	2	9	2	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9CQD1	Rab5a	Ras-related protein Rab-5A	15	3	41	1	n.a.
P70227	Itpr3	Inositol 1,4,5-trisphosphate receptor type 3	1	5	29	4	n.a.
Q9DAV9	Tmem38b	Trimeric intracellular cation channel type B	13	4	30	4	n.a.
P97477-2	Aurka	Isoform 2 of Aurora kinase A	4	2	6	1	n.a.
P30355	Alox5ap	Arachidonate 5-lipoxygenase-activating protein	11	2	40	2	170.00
Q3V4D5	Naa10	N-acetyltransferase ARD1 homolog (S. cerevisiae), isoform CRA_b	16	3	38	1	106.14
Q9QUR6	Prep	Prolyl endopeptidase	24	13	130	13	42.85
G3X9Q0	Mbnl1	Muscleblind-like 1 (Drosophila), isoform CRA_a	16	4	44	4	13.35
P36536	Sar1a	GTP-binding protein SAR1a	26	4	36	2	10.86
Q80YW0	Cyth4	Cytohesin-4	7	3	20	3	10.83
Q61029	Tmpo	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	38	14	557	2	9.73
F8WHQ1	Tpd52	Tumor protein D52	26	4	51	4	9.35
P47915	Rpl29	60S ribosomal protein L29	24	4	165	4	9.28
Q8C166	Cpne1	Copine-1	6	4	39	3	8.99
Q99KV1	Dnajb11	DnaJ homolog subfamily B member 11	23	6	118	6	8.56
Q922H2	Pdk3	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	14	5	35	5	8.47
P14901	Hmox1	Heme oxygenase 1	10	2	13	2	8.47
Q8CBB6	Hist1h2br	Histone H2B	61	10	1613	2	7.98
Q91VM5	Rbmxl1	RNA binding motif protein, X-linked-like-1	37	17	598	6	7.86
J3QN31	Adssl1	Adenylosuccinate synthetase isozyme 1	10	5	77	5	7.31
Q9DB15	Mrpl12	39S ribosomal protein L12, mitochondrial	33	4	55	4	7.13
Q6ZQ08-4	Cnot1	Isoform 4 of CCR4-NOT transcription complex subunit 1	1	4	15	4	6.92
E0CXZ9	Kcnab2	Voltage-gated potassium channel subunit beta-2	11	3	26	3	6.73
Q8K1M6	Dnm1l	Dynamin-1-like protein	12	8	70	8	6.46
Q8BQ30-2	Ppp1r18	Isoform 2 of Phostensin	5	3	29	3	6.31
Q8R4R6	Nup35	Nucleoporin NUP53	20	5	106	5	5.94
O35459	Ech1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	10	3	22	3	5.86
P28474	Adh5	Alcohol dehydrogenase class-3	12	4	45	4	5.74
O35345	Kpna6	Importin subunit alpha-7	2	2	26	1	5.73
Q8BTS4	Nup54	Nuclear pore complex protein Nup54	12	5	44	5	5.39
Q9Z0U1	Tjp2	Tight junction protein ZO-2	2	3	17	3	5.38
Q9R0N0	Galk1	Galactokinase	14	6	107	6	5.14
Q9CRB2	Nhp2	H/ACA ribonucleoprotein complex subunit 2	16	2	38	2	5.12
Q6PGL7	Fam21	WASH complex subunit FAM21	2	3	10	3	5.00
P14069	S100a6	Protein S100-A6	16	2	106	2	4.88
Q8C5H8	Nadk2	NAD kinase 2, mitochondrial	5	2	9	2	4.85
Q9D2E2	Toe1	Target of EGR1 protein 1	5	3	20	3	4.73
F8WIV2	Serpinb6a	Serpin B6	6	3	72	3	4.72
P25799	Nfkb1	Nuclear factor NF-kappa-B p105 subunit	2	2	24	2	4.67
Q9JL62	Gltp	Glycolipid transfer protein	12	3	12	3	4.60

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
P99029	Prdx5	Peroxiredoxin-5, mitochondrial	21	4	55	4	4.54
Q61249	Igbp1	Immunoglobulin-binding protein 1	17	5	40	5	4.54
Q61205	Pafah1b3	Platelet-activating factor acetylhydrolase IB subunit gamma	6	2	21	2	4.42
P35278	Rab5c	Ras-related protein Rab-5C	38	6	141	4	4.42
Q9DCJ5	Ndufa8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	21	3	46	3	4.33
Q99KP3	Cryl1	Lambda-crystallin homolog	5	2	14	2	4.29
P61164	Actr1a	Alpha-centractin	10	3	39	3	4.29
P84102	Serf2	Small EDRK-rich factor 2	32	4	59	4	4.29
P22752	Hist1h2ab	Histone H2A type 1	46	7	642	2	4.27
Q920E5	Fdps	Farnesyl pyrophosphate synthase	20	7	99	7	4.24
Q8K2T1	Nmral1	NmrA-like family domain-containing protein 1	8	3	30	3	4.11
Q8R480	Nup85	Nuclear pore complex protein Nup85	5	4	85	4	4.08
Q91WC0	Setd3	Histone-lysine N-methyltransferase setd3	5	3	26	3	4.03
Q99KJ8	Dctn2	Dynactin subunit 2	22	8	55	8	3.95
P70335	Rock1	Rho-associated protein kinase 1	3	4	26	2	3.79
P61759	Vbp1	Prefoldin subunit 3	20	4	27	4	3.79
O35295	Purb	Transcriptional activator protein Pur-beta	17	4	59	4	3.75
Q3UBX0	Tmem109	Transmembrane protein 109	8	2	47	2	3.72
Q8CHP8	Pgp	Glycerol-3-phosphate phosphatase	8	3	15	3	3.67
P15864	Hist1h1c	Histone H1.2	45	15	985	5	3.65
P16110	Lgals3	Galectin-3	36	9	176	9	3.58
Q8BFV2	Pcid2	PCI domain-containing protein 2	4	2	19	2	3.57
Q99J95	Cdk9	Cyclin-dependent kinase 9	11	4	61	3	3.50
Q9WU62	Incenp	Inner centromere protein	5	4	35	4	3.48
P62717	Rpl18a	60S ribosomal protein L18a	23	5	188	5	3.47
P23492	Pnp	Purine nucleoside phosphorylase	24	5	42	5	3.39
Q9DB34	Chmp2a	Charged multivesicular body protein 2a	23	5	71	5	3.39
O54988	Slk	STE20-like serine/threonine-protein kinase	8	11	117	10	3.38
Q8VE22	Mrps23	28S ribosomal protein S23, mitochondrial	22	3	12	3	3.36
Q9R0Q4	Morf4l2	Mortality factor 4-like protein 2	14	4	77	4	3.32
P47856	Gfpt1	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	7	5	26	5	3.27
Q07113	Igf2r	Cation-independent mannose-6-phosphate receptor	1	3	26	3	3.23
Q99LM2	Cdk5rap3	CDK5 regulatory subunit-associated protein 3	6	3	31	3	3.17
B9EJ86	Osbpl8	Oxysterol-binding protein-related protein 8	3	2	15	2	3.15
Q3U2G2	Hspa4	Heat shock 70 kDa protein 4	38	30	535	28	3.14
E9Q0V4	Mpc1	Mitochondrial pyruvate carrier 1	9	2	12	2	3.09
Q64674	Srm	Spermidine synthase	16	5	84	5	3.07
Q921M7	Fam49b	Protein FAM49B	28	8	60	8	3.06
P26151	Fcgr1	High affinity immunoglobulin gamma Fc receptor I	2	2	11	2	3.04
Q00651	Itga4	Integrin alpha-4	5	7	122	7	3.04

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q8R010	Aimp2	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	9	3	65	3	3.02
Q9CQE5	Rgs10	Regulator of G-protein signaling 10	28	3	39	3	2.95
P13020-2	Gsn	Isoform 2 of Gelsolin	24	19	312	19	2.94
Q80X90	Flnb	Filamin-B	12	30	423	26	2.93
Q9DCE5	Pak1ip1	p21-activated protein kinase-interacting protein 1	8	3	30	3	2.93
P28063	Psmb8	Proteasome subunit beta type-8	9	3	69	3	2.89
Q99J77	Nans	N-acetylneuraminic acid synthase (Sialic acid synthase)	12	4	41	4	2.85
Q9DAU1	Cnpy3	Protein canopy homolog 3	15	4	33	4	2.85
Q8R0A0	Gtf2f2	General transcription factor IIF subunit 2	10	3	15	3	2.83
P26350	Ptma	Prothymosin alpha	23	6	363	6	2.79
P35979	Rpl12	60S ribosomal protein L12	43	8	177	8	2.78
B1AX58	Pls3	Plastin-3	12	8	323	5	2.78
G3X8X7	Vps16	Vacuolar protein sorting 16 (Yeast)	3	3	25	3	2.76
A0A0A6YVS2	Tmco1	Transmembrane and coiled-coil domain-containing protein 1 (Fragment)	13	4	63	4	2.72
Q9CQQ7	Atp5f1	ATP synthase F(0) complex subunit B1, mitochondrial	16	5	103	5	2.71
J3QNK8	Abi1	Abl interactor 1	5	3	26	3	2.66
Q8VDW0	Ddx39a	ATP-dependent RNA helicase DDX39A	22	8	109	3	2.66
Q9D2R8	Mrps33	28S ribosomal protein S33, mitochondrial	21	2	8	2	2.65
O35344	Kpna3	Importin subunit alpha-4	11	5	51	3	2.65
Q6PB44	Ptpn23	Tyrosine-protein phosphatase non-receptor type 23	1	2	9	2	2.65
P56546-2	Ctbp2	Isoform 2 of C-terminal-binding protein 2	5	6	129	4	2.61
P62911	Rpl32	60S ribosomal protein L32	34	6	79	6	2.61
Q9CQE8	N/A	UPF0568 protein C14orf166 homolog	11	3	24	3	2.59
Q05CL8	Larp7	La-related protein 7	7	4	30	4	2.58
A0A0R4J254	Xpo4	Exportin-4	2	3	17	3	2.58
Q8K363	Ddx18	ATP-dependent RNA helicase DDX18	11	5	48	5	2.53
Q99M31-2	Hspa14	Isoform 2 of Heat shock 70 kDa protein 14	12	6	48	6	2.51
P45376	Akr1b1	Aldose reductase	15	5	171	4	2.49
Q66JS6	Eif3j2	Eukaryotic translation initiation factor 3 subunit J-B	14	5	39	5	2.48
Q6R891	Ppp1r9b	Neurabin-2	5	4	28	4	2.47
P97300	Nptn	Neuroplastin	5	3	36	3	2.46
P58281-2	Opa1	Isoform 2 of Dynamin-like 120 kDa protein, mitochondrial	8	8	66	8	2.46
E9PY58	Clpb	Caseinolytic peptidase B protein homolog	5	4	30	4	2.45
Q93092	Taldo1	Transaldolase	34	14	234	14	2.45
Q8K2Q9	Shtn1	Shootin-1	7	5	40	5	2.43
O55013	Trappc3	Trafficking protein particle complex subunit 3	12	3	34	3	2.38
E9Q512	Trip11	Protein Trip11	2	5	42	5	2.36
P52480	Pkm	Pyruvate kinase PKM	50	28	2404	2	2.36
G5E829	Atp2b1	Plasma membrane calcium-transporting ATPase 1	3	3	14	3	2.35
Q9DCL8	Ppp1r2	Protein phosphatase inhibitor 2	5	2	18	2	2.34

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
O08553	Dpysl2	Dihydropyrimidinase-related protein 2	9	5	70	5	2.34
Q9ER72	Cars	Cysteine--tRNA ligase, cytoplasmic	9	8	123	8	2.34
Q9D8L3	Ssr4	Signal sequence receptor, delta	19	3	96	3	2.32
P09055	Itgb1	Integrin beta-1	4	3	41	3	2.31
Q8K1A5	Tmem41b	Transmembrane protein 41B	7	2	9	2	2.29
P27601	Gna13	Guanine nucleotide-binding protein subunit alpha-13	7	3	49	1	2.28
P05201	Got1	Aspartate aminotransferase, cytoplasmic	22	9	118	9	2.27
Q9EQP2	Ehd4	EH domain-containing protein 4	17	9	93	8	2.27
P70398	Usp9x	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	1	2	11	2	2.27
P32921	Wars	Tryptophan--tRNA ligase, cytoplasmic	9	6	48	6	2.26
Q8K3W3	Casc3	Protein CASC3	3	2	23	2	2.26
Q9DCL9	Paics	Multifunctional protein ADE2	30	11	200	11	2.25
Q9DBC7	Prkar1a	cAMP-dependent protein kinase type I-alpha regulatory subunit	6	2	19	2	2.24
Q6IRU2	Tpm4	Tropomyosin alpha-4 chain	24	7	89	6	2.23
P63005	Pafah1b1	Platelet-activating factor acetylhydrolase IB subunit alpha	9	5	22	5	2.22
P60840	Ensa	Alpha-endosulfine	19	2	11	2	2.22
Q8BT60	Cpne3	Copine-3	5	3	42	2	2.21
P07091	S100a4	Protein S100-A4	17	3	136	3	2.21
P53994	Rab2a	Ras-related protein Rab-2A	25	5	52	5	2.20
Q9Z1S0	Bub1b	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	3	4	36	4	2.18
P00405	Mtco2	Cytochrome c oxidase subunit 2	10	3	127	3	2.18
G3X8Y8	Tlr2	Toll-like receptor	3	3	15	3	2.17
Q99LR1	Abhd12	Monoacylglycerol lipase ABHD12	15	5	62	5	2.13
Q8BMS9	Rassf2	Ras association domain-containing protein 2	6	2	21	2	2.12
O35639	Anxa3	Annexin A3	20	6	75	6	2.11
P10107	Anxa1	Annexin A1	39	13	246	13	2.10
P97429	Anxa4	Annexin A4	25	7	110	7	2.10
H3BJN3	Cux1	Protein CASP	16	12	119	3	2.10
Q3TRM8	Hk3	Hexokinase-3	5	5	43	5	2.09
Q810D6	Grwd1	Glutamate-rich WD repeat-containing protein 1	4	2	15	2	2.08
Q9D0G0	Mrps30	28S ribosomal protein S30, mitochondrial	13	5	54	5	2.06
Q8VD65	Pik3r4	Phosphoinositide 3-kinase regulatory subunit 4	1	2	21	2	2.06
Q9CY58	Serbp1	Plasminogen activator inhibitor 1 RNA-binding protein	40	20	651	20	2.05
Q9CY73	Mrpl44	39S ribosomal protein L44, mitochondrial	5	2	19	2	2.05
Q8BRF7	Scfd1	Sec1 family domain-containing protein 1	5	4	55	4	2.05
Q62419	Sh3gl1	Endophilin-A2	9	4	41	4	2.04
G5E8E3	2310022A10Rik	Protein 2310022A10Rik	11	5	48	5	2.04
Q9QZM0	Ubqln2	Ubiquilin-2	6	3	100	2	2.03
P20108	Prdx3	Thioredoxin-dependent peroxide reductase, mitochondrial	12	3	50	3	2.03
Q01730	Rsu1	Ras suppressor protein 1	8	3	18	3	2.02

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q61699	Hsph1	Heat shock protein 105 kDa	20	16	314	14	2.02
P84104	Srsf3	Serine/arginine-rich splicing factor 3	23	4	95	3	2.02
Q9CZX8	Rps19	40S ribosomal protein S19	55	11	494	11	1.99
Q8CD92	Ttc27	Tetratricopeptide repeat protein 27	3	3	12	3	1.99
G3UXA6	Ptbp3	Polypyrimidine tract-binding protein 3	11	7	241	4	1.99
Q9WUM5	Suclg1	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	12	4	67	4	1.98
Q80Y81	Elac2	Zinc phosphodiesterase ELAC protein 2	2	2	29	2	1.98
G3X972	Sec24c	Protein Sec24c	10	10	129	10	1.98
Q9D902	Gtf2e2	General transcription factor IIE subunit 2	15	5	24	5	1.97
P54227	Stmn1	Stathmin	57	10	141	10	1.97
Q60715-2	P4ha1	Isoform 2 of Prolyl 4-hydroxylase subunit alpha-1	17	9	131	9	1.97
P35831	Ptpn12	Tyrosine-protein phosphatase non-receptor type 12	2	2	15	2	1.96
B9EKS2	Kdm3b	Jumonji domain containing 1B	2	4	35	4	1.96
O35226-2	Psmd4	Isoform Rpn10B of 26S proteasome non-ATPase regulatory subunit 4	9	3	21	3	1.94
O88307	Sorl1	Sortilin-related receptor	1	3	19	3	1.92
P47226	Tes	Testin	12	6	104	6	1.92
Q62313	Tgoln1	Trans-Golgi network integral membrane protein 1	12	4	21	4	1.89
Q3UKW2	Calm1	Calmodulin	29	6	289	6	1.89
O70591	Pfdn2	Prefoldin subunit 2	30	4	69	4	1.89
E9QPQ8	Mrpl48	39S ribosomal protein L48, mitochondrial	9	2	11	2	1.88
Q9D6U8	Fam162a	Protein FAM162A	9	2	25	2	1.88
Q8BHG9	Cggbp1	CGG triplet repeat-binding protein 1	11	3	15	3	1.87
Q9CXS4	Cenpv	Centromere protein V	11	3	61	3	1.85
O08582	Gtpbp1	GTP-binding protein 1	4	3	22	3	1.85
P01900	H2-D1	H-2 class I histocompatibility antigen, D-D alpha chain	18	7	129	4	1.85
P06745	Gpi	Glucose-6-phosphate isomerase	20	11	376	11	1.85
Q810A7	Ddx42	ATP-dependent RNA helicase DDX42	6	6	60	6	1.84
Q8BGH2	Samm50	Sorting and assembly machinery component 50 homolog	5	3	88	3	1.84
Q8CE96	Trmt6	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	7	5	33	5	1.83
Q9D0R4	Ddx56	Probable ATP-dependent RNA helicase DDX56	7	4	58	4	1.83
Q9QYA2	Tomm40	Mitochondrial import receptor subunit TOM40 homolog	18	5	75	5	1.82
Q91UZ1	Plcb4	Phosphoinositide phospholipase C	2	4	29	4	1.80
Q9CZJ1	Utp11	Probable U3 small nucleolar RNA-associated protein 11	12	3	52	3	1.79
O35280	Chek1	Serine/threonine-protein kinase Chk1	7	3	21	3	1.79
O35130	Emg1	Ribosomal RNA small subunit methyltransferase NEP1	9	2	36	2	1.77
Q9Z0R6	Itsn2	Intersectin-2	3	5	49	5	1.76
P08030	Aprt	Adenine phosphoribosyltransferase	33	6	112	6	1.76
Q69Z38	Peak1	Pseudopodium-enriched atypical kinase 1	1	3	15	3	1.76
P61226	Rap2b	Ras-related protein Rap-2b	11	2	23	2	1.75
E9QPX3	Ndufs4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	16	3	48	3	1.74

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
P54923	Adprh	[Protein ADP-ribosylarginine] hydrolase	10	3	21	3	1.74
O70378	Emc8	ER membrane protein complex subunit 8	10	3	60	3	1.74
P63073	Eif4e	Eukaryotic translation initiation factor 4E	18	4	59	4	1.73
Q8K1M3	Prkar2a	Protein kinase, cAMP dependent regulatory, type II alpha	9	4	41	4	1.73
Q9CQT1	Mri1	Methylthioribose-1-phosphate isomerase	9	4	48	4	1.73
P17751	Tpi1	Triosephosphate isomerase	37	9	398	9	1.72
Q9CQA1	Trappc5	Trafficking protein particle complex subunit 5	11	2	6	2	1.72
O70439	Stx7	Syntaxin-7	26	6	62	6	1.72
H3BJQ9	Cux1	Homeobox protein cut-like	11	16	169	7	1.71
P70429	Evl	Ena/VASP-like protein	11	4	48	4	1.70
Q91YE6	Ipo9	Importin-9	3	3	15	3	1.69
P80314	Cct2	T-complex protein 1 subunit beta	45	19	576	19	1.69
Q9D554	Sf3a3	Splicing factor 3A subunit 3	15	8	125	8	1.68
Q99P72	Rtn4	Reticulon-4	19	16	223	16	1.68
Q9WUM4	Coro1c	Coronin-1C	12	9	147	9	1.67
Q8CI11	Gnl3	Guanine nucleotide-binding protein-like 3	22	10	93	10	1.65
P07356	Anxa2	Annexin A2	49	18	556	18	1.64
Q9CQJ6	Denr	Density-regulated protein	16	3	27	3	1.64
Q8R2P8	Kars	Lysine--tRNA ligase	10	8	99	8	1.64
P21550	Eno3	Beta-enolase	8	3	122	2	1.64
Q3THS6	Mat2a	S-adenosylmethionine synthase isoform type-2	13	5	65	5	1.63
P20152	Vim	Vimentin	75	38	2267	36	1.63
Q9CQ60	Pgls	6-phosphogluconolactonase	26	4	56	4	1.62
A0A0R4J138	Arsb	Arylsulfatase B	7	4	106	4	1.61
Q3UIA2	Arhgap17	Rho GTPase-activating protein 17	3	3	38	3	1.61
P14824	Anxa6	Annexin A6	8	6	63	6	1.60
P70315	Was	Wiskott-Aldrich syndrome protein homolog	9	4	43	4	1.60
Q99PU8-3	Dhx30	Isoform 3 of Putative ATP-dependent RNA helicase DHX30	2	3	11	3	1.60
A0A0A0MQA5	Tuba4a	Tubulin alpha chain (Fragment)	33	14	525	3	1.59
O35375	Nrp2	Neuropilin-2	3	3	31	3	1.58
F2Z456	Cyb5r3	NADH-cytochrome b5 reductase	25	8	113	8	1.58
P50518	Atp6v1e1	V-type proton ATPase subunit E 1	24	6	117	6	1.57
Q9D8S5	Srsf5	MCG7614, isoform CRA_c	19	5	78	4	1.57
P21956	Mfge8	Lactadherin	4	2	19	2	1.57
Q9JMD0	Znf207	BUB3-interacting and GLEBS motif-containing protein ZNF207	5	2	11	2	1.57
Q9WUP7	Uchl5	Ubiquitin carboxyl-terminal hydrolase isozyme L5	5	2	33	2	1.55
Q6PAQ4	Rexo4	RNA exonuclease 4	13	5	28	5	1.55
Q9EQ80	Nif3l1	NIF3-like protein 1	8	3	27	3	1.55
A2AUD5	Tpd52l2	Tumor protein D54	12	4	61	4	1.55
P54822	Adsl	Adenylosuccinate lyase	6	3	20	3	1.55

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
O70251	Eef1b	Elongation factor 1-beta	22	5	137	5	1.54
P70268-2	Pkn1	Isoform 2 of Serine/threonine-protein kinase N1	2	2	14	2	1.54
Q9CQU5	Zwint	ZW10 interactor	5	2	16	2	1.53
Q9Z2Q5	Mrpl40	39S ribosomal protein L40, mitochondrial	14	2	24	2	1.53
G3X9Q3	Hmha1	Histocompatibility (Minor) HA-1, isoform CRA_a	10	9	125	9	1.52
P26043	Rdx	Radixin	26	18	348	10	1.51
Q9JHJ0	Tmod3	Tropomodulin-3	15	5	74	5	1.50
P47930	Fosl2	Fos-related antigen 2	10	2	34	2	1.50
Q60597-3	Ogdh	Isoform 3 of 2-oxoglutarate dehydrogenase, mitochondrial	16	15	152	15	1.50
P16045	Lgals1	Galectin-1	32	5	61	5	1.50
P11157	Rrm2	Ribonucleoside-diphosphate reductase subunit M2	8	3	36	3	1.50
Q9D735	N/A	Uncharacterized protein C19orf43 homolog	12	2	33	2	1.49
Q06180	Ptpn2	Tyrosine-protein phosphatase non-receptor type 2	4	2	5	2	1.49
A2BDX3	Mocs3	Adenylyltransferase and sulfurtransferase MOCS3	4	2	114	2	1.49
Q91VW3	Sh3bgrl3	SH3 domain-binding glutamic acid-rich-like protein 3	47	4	79	4	1.48
Q9D0S9	Hint2	Histidine triad nucleotide-binding protein 2, mitochondrial	17	4	26	4	1.47
Q9D7B2	Lims1	LIM and senescent cell antigen-like domains 1, isoform CRA_c	5	2	28	2	1.47
Q91YM4	Tbrg4	Protein TBRG4	10	7	50	7	1.46
Q6P5D8	Smchd1	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	2	5	60	5	1.46
Q3U3M5	Ccnk	Cyclin-K	4	2	30	2	1.46
Q3TE40	Rpa2	Replication protein A 32 kDa subunit	7	2	32	2	1.46
Q61655	Ddx19a	ATP-dependent RNA helicase DDX19A	10	5	115	5	1.45
Q9D1E6	Tbcb	Tubulin-folding cofactor B	18	5	96	5	1.45
Q9WU78	Pdcd6ip	Programmed cell death 6-interacting protein	27	20	384	20	1.44
Q80VJ3	Dnph1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	12	2	18	2	1.44
Q9D8T7	Slirp	SRA stem-loop-interacting RNA-binding protein, mitochondrial	29	3	36	3	1.44
Q8K3X4	Irf2bpl	Interferon regulatory factor 2-binding protein-like	3	2	18	2	1.43
A0A0R4J064	Adpgk	ADP-dependent glucokinase	13	5	58	5	1.43
Q9D0F3	Lman1	Protein ERGIC-53	19	7	58	7	1.43
P36552	Cpox	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	4	2	12	2	1.43
P47791	Gsr	Glutathione reductase, mitochondrial	9	3	32	3	1.43
P35293	Rab18	Ras-related protein Rab-18	26	5	44	5	1.43
P17182	Eno1	Alpha-enolase	52	21	1460	20	1.43
Q91Z53	Grhpr	Glyoxylate reductase/hydroxypyruvate reductase	8	3	28	3	1.43
A0A0G2JGQ4	Nub1	NEDD8 ultimate buster 1	4	3	24	3	1.42
O55029	Copb2	Coatomer subunit beta'	7	7	80	7	1.42
Q3UHX2	Pdap1	28 kDa heat- and acid-stable phosphoprotein	29	8	97	8	1.42
Q64516	Gk	Glycerol kinase	6	4	45	4	1.42
Q921Y2	Imp3	U3 small nucleolar ribonucleoprotein protein IMP3	13	2	18	2	1.41
Q91ZJ5	Ugp2	UTP--glucose-1-phosphate uridylyltransferase	7	5	35	5	1.41

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q99NH0	Ankrd17	Ankyrin repeat domain-containing protein 17	1	3	12	3	1.41
Q60865	Caprin1	Caprin-1	18	12	218	12	1.41
O88712	Ctbp1	C-terminal-binding protein 1	7	4	109	2	1.41
Q80VJ2	Sra1	Steroid receptor RNA activator 1	16	3	26	3	1.40
P32020	Scp2	Non-specific lipid-transfer protein	10	7	105	7	1.38
Q8K3J1	Ndufs8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	11	3	33	3	1.37
Q60749	Khdrbs1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	19	5	96	5	1.37
Q8R326	Pspc1	Paraspeckle component 1	9	6	105	5	1.36
Q91VX2	Ubap2	Ubiquitin-associated protein 2	9	8	173	8	1.36
Q8C605	Pfkp	ATP-dependent 6-phosphofructokinase	11	10	156	8	1.36
Q9CR16	Ppid	Peptidyl-prolyl cis-trans isomerase D	15	8	103	8	1.35
A0A0R4J104	Dab2	Disabled homolog 2	16	12	242	12	1.35
P56399	Usp5	Ubiquitin carboxyl-terminal hydrolase 5	14	11	148	11	1.35
A0A0N4SW28	Gng12	Guanine nucleotide-binding protein subunit gamma	21	2	65	2	1.34
Q811D0-3	Dlg1	Isoform 3 of Disks large homolog 1	3	3	18	3	1.34
Q64727	Vcl	Vinculin	15	16	137	16	1.34
D3Z0M9	Ddx23	MCG18410, isoform CRA_a	6	5	76	5	1.34
Q3U1U4	Itgam	Integrin alpha-M	4	7	113	7	1.34
Q9D8M4	Rpl7l1	60S ribosomal protein L7-like 1	12	3	23	3	1.33
Q3TW96	Uap1l1	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	12	7	94	7	1.33
Q60930	Vdac2	Voltage-dependent anion-selective channel protein 2	17	5	180	5	1.33
Q99LH1	Gnl2	Nucleolar GTP-binding protein 2	5	4	47	4	1.33
Q920A5	Scpep1	Retinoid-inducible serine carboxypeptidase	5	3	64	3	1.31
Q8C7V3	Utp15	U3 small nucleolar RNA-associated protein 15 homolog	7	5	45	5	1.31
O35643	Ap1b1	AP-1 complex subunit beta-1	13	10	79	3	1.31
Q6PAM1	Txlna	Alpha-taxilin	18	9	60	9	1.31
P09411	Pgk1	Phosphoglycerate kinase 1	47	21	1166	21	1.31
A2A4P0	Dhx8	ATP-dependent RNA helicase DHX8	1	2	14	2	1.31
P10404	N/A	MLV-related proviral Env polyprotein	5	5	218	5	1.31
P61290	Psme3	Proteasome activator complex subunit 3	16	4	37	4	1.30
P26883	Fkbp1a	Peptidyl-prolyl cis-trans isomerase FKBP1A	25	2	62	2	1.29
P97355	Sms	Spermine synthase	7	3	35	3	1.29
P97351	Rps3a	40S ribosomal protein S3a	53	19	863	19	1.29
Q922Q1	Marc2	Mitochondrial amidoxime reducing component 2	12	5	61	5	1.29
P63101	Ywhaz	14-3-3 protein zeta/delta	44	12	543	8	1.29
Q9DBC3	Cmtr1	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	4	3	29	3	1.29
Q9Z1M8	Ik	Protein Red	15	10	96	10	1.29
P27612	Plaa	Phospholipase A-2-activating protein	9	8	100	8	1.28
D3Z5I1	Zc3hav1	Zinc finger CCCH-type antiviral protein 1	3	3	39	3	1.28
Q8C0D0	Trub1	Probable tRNA pseudouridine synthase 1	5	2	11	2	1.28

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
P01902	H2-K1	H-2 class I histocompatibility antigen, K-D alpha chain	17	7	83	7	1.28
A0A0B4J1E2	Snw1	SNW domain-containing protein 1	19	10	132	10	1.28
Q9CQ73	Pkp2	Plakophilin 2	2	2	14	2	1.27
Q8K327	Champ1	Chromosome alignment-maintaining phosphoprotein 1	4	4	43	4	1.27
A0A0R4IZY0	Thop1	Thimet oligopeptidase	8	6	45	6	1.26
P58468	Fam207a	Protein FAM207A	16	3	15	3	1.26
Q78RX3	Smim12	Small integral membrane protein 12	21	2	29	2	1.26
E9Q496	Use1	Vesicle transport protein USE1	10	3	21	3	1.26
Q9D0F9	Pgm1	Phosphoglucomutase-1	19	9	81	9	1.26
Q922Y1	Ubxn1	UBX domain-containing protein 1	20	5	48	5	1.25
P12265	Gusb	Beta-glucuronidase	16	8	110	8	1.25
P62334	Psmc6	26S protease regulatory subunit 10B	21	8	52	8	1.25
G5E896	Edc4	Enhancer of mRNA decapping 4, isoform CRA_b	3	5	20	5	1.25
Q6A068	Cdc5l	Cell division cycle 5-like protein	11	9	77	9	1.25
Q60972	Rbbp4	Histone-binding protein RBBP4	14	6	107	2	1.24
A2A9M4	Dock7	Dedicator of cytokinesis protein 7	1	3	26	3	1.24
E9QKR0	Gnb2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	11	5	140	5	1.24
P47199	Cryz	Quinone oxidoreductase	6	3	29	3	1.24
Q9QUJ7	Acsl4	Long-chain-fatty-acid--CoA ligase 4	6	5	84	4	1.24
Q9D819	Ppa1	Inorganic pyrophosphatase	19	6	50	6	1.23
P49452	Cenpc	Centromere protein C	4	4	23	4	1.23
Q91YT7	Ythdf2	YTH domain-containing family protein 2	15	8	234	5	1.23
P29595	Nedd8	NEDD8	28	2	57	2	1.23
P28667	Marcksl1	MARCKS-related protein	14	2	51	2	1.23
P62754	Rps6	40S ribosomal protein S6	26	7	279	7	1.23
P51863	Atp6v0d1	V-type proton ATPase subunit d 1	18	5	78	5	1.23
Q921G6	Lrch4	Leucine-rich repeat and calponin homology domain-containing protein 4	9	4	22	4	1.22
P97461	Rps5	40S ribosomal protein S5	28	7	332	7	1.22
Q9CVB6	Arpc2	Actin-related protein 2/3 complex subunit 2	30	9	94	9	1.22
Q9CT10	Ranbp3	Ran-binding protein 3	15	6	42	6	1.22
G3X9G4	Dnm2	Dynamin-2	7	6	24	6	1.22
P62196	Psmc5	26S protease regulatory subunit 8	18	8	241	6	1.21
Q91YN9	Bag2	BAG family molecular chaperone regulator 2	17	4	48	4	1.21
Q9D1C1	Ube2c	Ubiquitin-conjugating enzyme E2 C	10	2	65	2	1.20
Q9Z0P5	Twf2	Twinfilin-2	26	8	46	8	1.20
Q8R1F1	Fam129b	Niban-like protein 1	7	7	58	7	1.20
Q9WVJ2	Psmd13	26S proteasome non-ATPase regulatory subunit 13	23	9	165	9	1.20
F8VQC1	Srp72	Signal recognition particle subunit SRP72	16	11	82	11	1.19
Q9D6T0	Nosip	Nitric oxide synthase-interacting protein	11	3	32	3	1.19
Q8JZQ2	Afg3l2	AFG3-like protein 2	12	10	85	8	1.19

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
O08529	Capn2	Calpain-2 catalytic subunit	7	6	54	6	1.19
P54728	Rad23b	UV excision repair protein RAD23 homolog B	13	7	141	5	1.19
Q8VBT0	Tmx1	Thioredoxin-related transmembrane protein 1	10	3	74	3	1.19
Q99JB2	Stoml2	Stomatin-like protein 2, mitochondrial	25	8	147	8	1.19
Q8VDM6	Hnrnpul1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	13	9	206	9	1.18
O55135	Eif6	Eukaryotic translation initiation factor 6	26	4	30	4	1.18
P63028	Tpt1	Translationally-controlled tumor protein	52	6	133	6	1.18
Q9CQ65	Mtap	S-methyl-5'-thioadenosine phosphorylase	15	4	50	4	1.18
P55258	Rab8a	Ras-related protein Rab-8A	49	12	326	7	1.17
Q5U458	Dnajc11	DnaJ homolog subfamily C member 11	5	4	43	4	1.17
Q05816	Fabp5	Fatty acid-binding protein, epidermal	7	2	90	2	1.17
Q0VBL3	Rbm15	Protein Rbm15	12	10	81	10	1.17
A2AWN8	Ythdf1	YTH domain family 1, isoform CRA_a	14	8	228	3	1.17
Q8K0V4	Cnot3	CCR4-NOT transcription complex subunit 3	3	3	27	3	1.17
Q8BGD9	Eif4b	Eukaryotic translation initiation factor 4B	32	18	322	18	1.17
P60122	Ruvbl1	RuvB-like 1	24	8	128	8	1.16
Q62093	Srsf2	Serine/arginine-rich splicing factor 2	26	6	184	6	1.16
Q5SUR0	Pfas	Phosphoribosylformylglycinamidine synthase	8	9	67	9	1.16
Q8BYL4	Yars2	Tyrosine--tRNA ligase, mitochondrial	8	4	37	4	1.16
P51125	Cast	Calpastatin	5	3	43	3	1.16
Q91XD6	Vps36	Vacuolar protein-sorting-associated protein 36	4	2	17	2	1.16
Q6PE01	Snrnp40	U5 small nuclear ribonucleoprotein 40 kDa protein	11	2	14	2	1.16
Q6P9R2	Oxsr1	Serine/threonine-protein kinase R1	8	4	32	4	1.15
Q80WW9	Ddrgk1	DDRGK domain-containing protein 1	13	3	71	3	1.15
P09528	Fth1	Ferritin heavy chain	12	2	14	2	1.15
P05063	Aldoc	Fructose-bisphosphate aldolase C	19	8	138	5	1.15
S4R1M2	Safb	Scaffold attachment factor B1	7	7	68	6	1.15
Q9JKN1	Slc30a7	Zinc transporter 7	5	2	39	2	1.15
Q9Z1G3	Atp6v1c1	V-type proton ATPase subunit C 1	13	7	111	7	1.14
Q80X81	Acat3	Acetyl-Coenzyme A acetyltransferase 3	4	2	21	2	1.14
P46471	Psmc2	26S protease regulatory subunit 7	27	10	150	10	1.14
E9PUQ5	Golga2	Golgin subfamily A member 2	7	7	60	7	1.14
Q8BLF1	Nceh1	Neutral cholesterol ester hydrolase 1	13	3	18	3	1.14
A0A023T778	Magohb	Mago nashi protein	35	6	43	6	1.14
G3X956	Supt16	FACT complex subunit SPT16	11	12	226	12	1.14
O89023	Tpp1	Tripeptidyl-peptidase 1	4	2	30	2	1.14
Q9CW03	Smc3	Structural maintenance of chromosomes protein 3	14	16	180	16	1.14
P58021	Tm9sf2	Transmembrane 9 superfamily member 2	3	2	25	2	1.13
Q9CQ54	Ndufc2	NADH dehydrogenase [ubiquinone] 1 subunit C2	15	2	27	2	1.13
Q9CRB9	Chchd3	MICOS complex subunit Mic19	29	7	193	7	1.13

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9R1J0	Nsdhl	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	7	3	24	3	1.13
A2AFQ2	Hsd17b10	3-hydroxyacyl-CoA dehydrogenase type-2	30	5	50	5	1.13
P99026	Psmb4	Proteasome subunit beta type-4	21	4	82	4	1.13
Q9Z1T1	Ap3b1	AP-3 complex subunit beta-1	3	5	19	5	1.13
Q60676	Ppp5c	Serine/threonine-protein phosphatase 5	5	3	60	3	1.12
P68040	Rack1	Receptor of activated protein C kinase 1	27	11	325	11	1.12
Q6PDL0	Dync1li2	Cytoplasmic dynein 1 light intermediate chain 2	6	3	30	3	1.12
Q07076	Anxa7	Annexin A7	25	11	613	11	1.11
Q91YU8	Ppan	Suppressor of SWI4 1 homolog	11	6	116	6	1.11
Q6PGH2	Hn1l	Hematological and neurological expressed 1-like protein	18	3	47	3	1.11
A0A0R4J170	Smarca4	Transcription activator BRG1	8	13	107	13	1.11
D3YVW2	Golim4	Golgi integral membrane protein 4	7	4	42	4	1.10
Q925I1	Atad3	ATPase family AAA domain-containing protein 3	19	12	90	12	1.10
Q8BVI4	Qdpr	Dihydropteridine reductase	7	2	15	2	1.10
B1AU75	Nasp	Nuclear autoantigenic sperm protein	5	5	59	5	1.10
Q9CWX9	Ddx47	Probable ATP-dependent RNA helicase DDX47	5	2	14	2	1.10
Q3ULJ0	Gpd1l	Glycerol-3-phosphate dehydrogenase 1-like protein	4	2	31	2	1.10
Q9DC61	Pmpca	Mitochondrial-processing peptidase subunit alpha	12	7	63	7	1.10
O35841	Api5	Apoptosis inhibitor 5	19	10	91	10	1.10
P10639	Txn	Thioredoxin	22	3	116	3	1.10
P14685	Psmd3	26S proteasome non-ATPase regulatory subunit 3	28	16	168	16	1.09
P55302	Lrpap1	Alpha-2-macroglobulin receptor-associated protein	31	13	101	13	1.09
Q5SWN2	Rpa1	Replication protein A 70 kDa DNA-binding subunit	7	5	100	5	1.09
E9QPB3	Wdhd1	WD repeat and HMG-box DNA-binding protein 1	4	4	44	4	1.09
Q4WW28	AFUA_5G14210	Glucose repressible protein Grg1, putative	28	2	24	2	1.09
B1AZI6	Thoc2	THO complex subunit 2	5	9	60	9	1.08
E9QK89	Mdc1	Mediator of DNA damage checkpoint protein 1	1	2	43	2	1.08
Z4YJY0	Fam175b	BRISC complex subunit Abro1	4	2	30	2	1.08
E9Q616	Ahnak	Protein Ahnak	41	103	1905	103	1.08
P28352	Apex1	DNA-(apurinic or apyrimidinic site) lyase	16	6	146	6	1.08
P53702	Hccs	Cytochrome c-type heme lyase	6	2	14	2	1.08
A0A0R4J0Q5	Lmnb2	Lamin-B2	37	25	555	20	1.08
P49138	Mapkapk2	MAP kinase-activated protein kinase 2	9	5	46	5	1.07
O54692	Zw10	Centromere/kinetochore protein zw10 homolog	2	2	9	2	1.07
P56391	Cox6b1	Cytochrome c oxidase subunit 6B1	29	4	81	4	1.07
Q80SZ7	Gng5	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	23	2	42	2	1.07
P00493	Hprt1	Hypoxanthine-guanine phosphoribosyltransferase	16	3	40	3	1.06
Q91XH5	Spr	Sepiapterin reductase	17	4	26	4	1.06
Q3UXS0	Scamp3	Secretory carrier-associated membrane protein 3	12	4	46	4	1.06
P45377	Akr1b8	Aldose reductase-related protein 2	7	3	68	2	1.06

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q64521	Gpd2	Glycerol-3-phosphate dehydrogenase, mitochondrial	12	9	116	9	1.05
Q9WV80	Snx1	Sorting nexin-1	5	3	24	2	1.05
P42128	Foxk1	Forkhead box protein K1	3	3	15	3	1.05
P61982	Ywhag	14-3-3 protein gamma	42	11	577	6	1.05
Q7TSI3	Ppp6r1	Serine/threonine-protein phosphatase 6 regulatory subunit 1	4	3	54	3	1.04
P48036	Anxa5	Annexin A5	53	15	508	15	1.04
Q9CPQ3	Tomm22	Mitochondrial import receptor subunit TOM22 homolog	42	3	53	3	1.04
Q9QZ88-2	Vps29	Isoform 2 of Vacuolar protein sorting-associated protein 29	14	3	43	3	1.04
E9QLA5	Inf2	Inverted formin-2	6	7	59	7	1.04
P46664	Adss	Adenylosuccinate synthetase isozyme 2	15	6	64	6	1.04
Q9JZ25	Arpc1b	Actin-related protein 2/3 complex subunit 1B	16	6	107	6	1.04
Q9QUI0	Rhoa	Transforming protein RhoA	34	7	260	7	1.03
Q8VD04	Gripap1	GRIP1-associated protein 1	7	5	60	5	1.03
P14234	Fgr	Tyrosine-protein kinase Fgr	6	4	45	2	1.03
Q08288	Lyar	Cell growth-regulating nucleolar protein	17	6	93	6	1.03
F6WMJ3	Arhgef6	Rho guanine nucleotide exchange factor 6	3	3	18	2	1.03
Q9ER00	Stx12	Syntaxin-12	9	3	50	3	1.03
Q9D7S7	Rpl22l1	60S ribosomal protein L22-like 1	25	3	82	3	1.03
Q9R1P0	Psma4	Proteasome subunit alpha type-4	12	4	73	4	1.02
Q9CS42	Prps2	Ribose-phosphate pyrophosphokinase 2	7	4	29	1	1.02
Q8BGQ7	Aars	Alanine--tRNA ligase, cytoplasmic	16	15	216	15	1.02
H7BX59	Pus1	tRNA pseudouridine synthase	6	3	12	3	1.02
P97370	Atp1b3	Sodium/potassium-transporting ATPase subunit beta-3	8	3	80	3	1.02
Q9DCX2	Atp5h	ATP synthase subunit d, mitochondrial	44	6	137	6	1.01
Q3TMX5	Manf	Arginine-rich, mutated in early stage tumors, isoform CRA_b	27	5	48	5	1.01
Q6NZB0	Dnajc8	DnaJ homolog subfamily C member 8	17	6	176	6	1.01
Q61024	Asns	Asparagine synthetase [glutamine-hydrolyzing]	10	6	133	6	1.01
Q8CDN6	Txnl1	Thioredoxin-like protein 1	22	4	51	4	1.01
P10854	Hist1h2bm	Histone H2B type 1-M	65	10	1591	1	1.00
P02301	H3f3c	Histone H3.3C	30	6	1489	1	1.00
Q9WVA4	Tagln2	Transgelin-2	59	11	330	11	1.00
Q8BYK6-3	Ythdf3	Isoform 3 of YTH domain-containing family protein 3	15	8	222	4	1.00
P70333	Hnrnph2	Heterogeneous nuclear ribonucleoprotein H2	22	6	166	2	1.00
P03995	Gfap	Glial fibrillary acidic protein	6	3	132	1	1.00
P70318	Tial1	Nucleolysin TIAR	7	3	123	2	1.00
Q9DCH4	Eif3f	Eukaryotic translation initiation factor 3 subunit F	22	7	97	7	1.00
Q60929	Mef2a	Myocyte-specific enhancer factor 2A	11	4	94	2	1.00
Q8BQ46	Taf15	Protein Taf15	17	6	87	4	1.00
P52912	Tia1	Nucleolysin TIA-1	6	3	85	2	1.00
A0A0H2UH28	Mef2c	Myocyte-specific enhancer factor 2C	10	5	82	3	1.00

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q6IFX2	Krt42	Keratin, type I cytoskeletal 42	12	5	76	2	1.00
Q8CI61	Bag4	BAG family molecular chaperone regulator 4	13	5	53	5	1.00
Q6R0H7	Gnas	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	2	2	51	1	1.00
Q9D3B1	Hacd2	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	8	2	48	2	1.00
Q3TCX3	Kiaa0907	UPF0469 protein KIAA0907	4	2	44	2	1.00
Q9CX00	Ist1	IST1 homolog	4	2	42	2	1.00
P97377	Cdk2	Cyclin-dependent kinase 2	12	4	41	2	1.00
Q64518	Atp2a3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	2	3	39	1	1.00
Q80U58	Pum2	Pumilio homolog 2	4	5	38	2	1.00
Q04736	Yes1	Tyrosine-protein kinase Yes	6	4	34	2	1.00
Q3THK3	Gtf2f1	General transcription factor IIF subunit 1	12	5	31	5	1.00
Q3TB24	Dnajb2	DnaJ homolog subfamily B member 2	6	2	26	1	1.00
Q9QXB9	Drg2	Developmentally-regulated GTP-binding protein 2	4	2	25	1	1.00
Q91X58	Zfand2b	AN1-type zinc finger protein 2B	9	2	24	2	1.00
B2RRI2	Sbno1	Protein strawberry notch homolog 1	1	2	24	2	1.00
Q8VCF0	Mavs	Mitochondrial antiviral-signaling protein	7	3	23	3	1.00
O88811	Stam2	Signal transducing adapter molecule 2	5	3	21	2	1.00
P0C0A3	Chmp6	Charged multivesicular body protein 6	10	2	18	2	1.00
Q8BFY6	Pef1	Peflin	4	2	17	2	1.00
Q3TVI8	Pbxip1	Pre-B-cell leukemia transcription factor-interacting protein 1	4	3	16	3	1.00
D3Z1Z1	Spg7	Paraplegin	1	2	16	2	1.00
Q80VY9	Dhx33	Putative ATP-dependent RNA helicase DHX33	3	2	15	2	1.00
Q8K4B0	Mta1	Metastasis-associated protein MTA1	3	2	15	1	1.00
G5E8V9	Arfip1	MCG18094	10	3	15	1	1.00
Q9D0F6	Rfc5	Replication factor C subunit 5	4	2	15	2	1.00
Q71FD5	Znrf2	E3 ubiquitin-protein ligase ZNRF2	14	2	15	2	1.00
Q60902	Eps15l1	Epidermal growth factor receptor substrate 15-like 1	4	3	15	3	1.00
K4DI61	Phf10	PHD finger protein 10	5	3	14	3	1.00
Q8BUL6	Plekha1	Pleckstrin homology domain-containing family A member 1	6	2	13	2	1.00
Q91Z96	Bmp2k	BMP-2-inducible protein kinase	1	2	12	2	1.00
Q8BMC4	Nop9	Nucleolar protein 9	3	2	12	2	1.00
Q99M04	Lias	Lipoyl synthase, mitochondrial	6	2	12	2	1.00
Q8BGB5	Limd2	LIM domain-containing protein 2	15	2	12	2	1.00
P29452	Casp1	Caspase-1	4	2	12	2	1.00
P26323	Fli1	Friend leukemia integration 1 transcription factor	5	2	12	2	1.00
Q8R570	Snap47	Synaptosomal-associated protein 47	6	2	12	2	1.00
Q80WT5	Aftph	Aftiphilin	1	2	12	2	1.00
Q99KI3	Emc3	ER membrane protein complex subunit 3	5	2	12	2	1.00
Q9WTV7	Rlim	E3 ubiquitin-protein ligase RLIM	5	2	12	2	1.00
Q3UJD6	Usp19	Ubiquitin carboxyl-terminal hydrolase 19	2	2	11	2	1.00

Accession	**Gene**	**Description**	**Coverage**	**Peptides**	**Unique Peptides**	**PSMs**	**[1]*pksP*/wt**
Q5RIM6	Ncor1	Nuclear receptor co-repressor 1, isoform CRA_a	1	2	11	2	1.00
F8VQ29	Iqgap3	Protein Iqgap3	1	2	11	1	1.00
Q02257	Jup	Junction plakoglobin	2	2	10	2	1.00
A0A0R4IZZ6	Fnbp4	Formin binding protein 4	2	2	10	2	1.00
Q9EPQ8	Tcf20	Transcription factor 20	1	3	10	3	1.00
B2C3G8	Stat5a	Signal transducer and activator of transcription	2	2	10	1	1.00
Q8CIM8	Ints4	Integrator complex subunit 4	2	2	9	2	1.00
Q5I1X5	Ppp1r13l	RelA-associated inhibitor	2	2	9	2	1.00
Q3UFM6	Dgcr14	Expressed sequence 2 embryonic lethal, isoform CRA_a	4	2	9	2	1.00
Q8R1K1	Ubac2	Ubiquitin-associated domain-containing protein 2	6	2	9	2	1.00
A2CG76	Ehmt2	Histone-lysine N-methyltransferase EHMT2	1	2	9	2	1.00
Q80W00	Ppp1r10	Serine/threonine-protein phosphatase 1 regulatory subunit 10	2	2	9	2	1.00
Q9QXD8	Limd1	LIM domain-containing protein 1	2	2	9	2	1.00
A2AUY4	Baz2b	Protein Baz2b	1	2	9	2	1.00
A2A6A1	Gpatch8	G patch domain-containing protein 8	1	2	9	2	1.00
E9PWE2	Tcf3	Transcription factor E2-alpha	3	2	9	2	1.00
O54864-2	Suv39h1	Isoform 2 of Histone-lysine N-methyltransferase SUV39H1	5	2	8	2	1.00
Q9D773	Mrpl2	39S ribosomal protein L2, mitochondrial	7	2	8	2	1.00
Q8C142	Ldlrap1	Low density lipoprotein receptor adapter protein 1	7	2	8	2	1.00
A2A7Q5	P3h1	Prolyl 3-hydroxylase 1	3	2	8	2	1.00
Q9CZT6	Cmss1	Protein CMSS1	7	2	7	2	1.00
Q8R105	Vps37c	Vacuolar protein sorting-associated protein 37C	5	2	7	2	1.00
Q14CH7	Aars2	Alanine--tRNA ligase, mitochondrial	2	2	6	2	1.00
P57746	Atp6v1d	V-type proton ATPase subunit D	6	2	6	2	1.00
O70472	Tmem131	Transmembrane protein 131	1	2	6	2	1.00
B1AQJ2	Usp36	Ubiquitin carboxyl-terminal hydrolase 36	2	2	6	2	1.00
E9Q557	Dsp	Desmoplakin	1	2	6	2	1.00
Q3TC33	Ccdc127	Coiled-coil domain-containing protein 127	6	2	6	2	1.00
Q62431	Arid3a	AT-rich interactive domain-containing protein 3A	4	2	6	2	1.00
Q9Z1N2	Orc1	Origin recognition complex subunit 1	2	2	6	2	1.00
Q8VC04	Tmem106a	Transmembrane protein 106A	6	2	6	2	1.00
Q61712	Dnajc1	DnaJ homolog subfamily C member 1	4	2	6	2	1.00
A2AQ19	Rtf1	RNA polymerase-associated protein RTF1 homolog	2	2	6	2	1.00
K4DI77	Wdr81	WD repeat-containing protein 81 (Fragment)	1	2	6	2	1.00
A0A0R4J0U5	Abcd2	ATP-binding cassette sub-family D member 2	2	2	6	2	1.00
Q8R4N0	Clybl	Citrate lyase subunit beta-like protein, mitochondrial	5	2	6	2	1.00
G3UWD2	Runx1	Runt related transcription factor 1, isoform CRA_c	6	2	6	2	1.00
Q921V5	Mgat2	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	4	2	21	2	1.00
Q6P542	Abcf1	ATP-binding cassette sub-family F member 1	6	5	81	4	1.00
Q9CQH7	Btf3l4	Transcription factor BTF3 homolog 4	9	2	24	1	0.99

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9R0P5	Dstn	Destrin	10	2	176	1	0.99
Q9R1T2	Sae1	SUMO-activating enzyme subunit 1	29	8	101	8	0.99
Q62465	Vat1	Synaptic vesicle membrane protein VAT-1 homolog	21	6	82	6	0.99
Q9EQH3	Vps35	Vacuolar protein sorting-associated protein 35	10	7	62	7	0.99
Q9CZ91	Srfbp1	Serum response factor-binding protein 1	10	3	62	3	0.98
O55236	Rngtt	mRNA-capping enzyme	3	2	12	2	0.98
Q78IK2	Usmg5	Up-regulated during skeletal muscle growth protein 5	43	2	21	2	0.98
Q9QYI3	Dnajc7	DnaJ homolog subfamily C member 7	23	13	185	13	0.97
Q6NZL1	Dhx37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	3	4	24	4	0.97
Q9CQB4	Uqcrb	Cytochrome b-c1 complex subunit 7	17	2	33	2	0.97
A2AE27	Ampd2	AMP deaminase 2	12	12	136	12	0.97
P70122	Sbds	Ribosome maturation protein SBDS	11	3	38	3	0.97
Q9CZD3	Gars	Glycine--tRNA ligase	14	10	201	10	0.96
O89086	Rbm3	RNA-binding protein 3	22	3	108	3	0.96
P46467	Vps4b	Vacuolar protein sorting-associated protein 4B	9	4	38	4	0.96
Q6ZWV7	Rpl35	60S ribosomal protein L35	21	3	116	3	0.96
P09671	Sod2	Superoxide dismutase [Mn], mitochondrial	16	3	45	3	0.96
Q9CPV4	Glod4	Glyoxalase domain-containing protein 4	20	5	27	5	0.96
Q99KK7	Dpp3	Dipeptidyl peptidase 3	6	6	63	6	0.96
A2AFQ0	Huwe1	E3 ubiquitin-protein ligase HUWE1	2	8	74	8	0.96
Q8K1I7	Wipf1	WAS/WASL-interacting protein family member 1	12	6	67	6	0.96
Q9D7P6	Iscu	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	14	3	55	3	0.96
Q60780	Gas7	Growth arrest-specific protein 7	13	6	108	6	0.96
Q61599	Arhgdib	Rho GDP-dissociation inhibitor 2	42	7	139	7	0.95
D3YZP9	Ccdc6	Coiled-coil domain-containing protein 6	3	2	24	2	0.95
P41241	Csk	Tyrosine-protein kinase CSK	7	4	24	4	0.95
P48428	Tbca	Tubulin-specific chaperone A	26	4	69	4	0.95
A0A0R4J1E2	Eef1d	Elongation factor 1-delta	15	9	190	9	0.95
Q8VHM5	Hnrnpr	Heterogeneous nuclear ribonucleoprotein R	9	6	112	4	0.95
Q3U4X8	Lig1	DNA ligase	10	9	93	9	0.95
Q9WUK4	Rfc2	Replication factor C subunit 2	14	5	45	5	0.95
P61514	Rpl37a	60S ribosomal protein L37a	36	4	127	4	0.94
Q58A65	Spag9	C-Jun-amino-terminal kinase-interacting protein 4	1	2	24	2	0.94
P56812	Pdcd5	Programmed cell death protein 5	38	4	30	4	0.94
Q9D1A2	Cndp2	Cytosolic non-specific dipeptidase	14	6	114	6	0.94
P62962	Pfn1	Profilin-1	60	7	340	7	0.94
Q9DBD5	Pelp1	Proline-, glutamic acid- and leucine-rich protein 1	2	2	28	2	0.94
Q9ESU7	Slc1a5	Amino acid transporter	14	6	75	6	0.94
Q14AX6	Cdk12	Cyclin-dependent kinase 12	3	4	37	3	0.94
P57716	Ncstn	Nicastrin	10	6	51	6	0.94

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q80ZX0	Sec24b	Protein Sec24b	3	3	42	3	0.94
O08709	Prdx6	Peroxiredoxin-6	37	6	103	6	0.93
Q62348	Tsn	Translin	14	4	37	4	0.93
G3UXW9	Gps1	COP9 signalosome complex subunit 1	9	5	60	5	0.93
Q8VBZ3	Clptm1	Cleft lip and palate transmembrane protein 1 homolog	7	5	116	5	0.93
O35601	Fyb	FYN-binding protein	3	2	17	2	0.93
Q61687	Atrx	Transcriptional regulator ATRX	2	7	68	7	0.93
Q9JLQ0	Cd2ap	CD2-associated protein	4	3	35	3	0.93
Q9JKF1	Iqgap1	Ras GTPase-activating-like protein IQGAP1	20	28	369	27	0.92
P50580	Pa2g4	Proliferation-associated protein 2G4	18	8	174	8	0.92
Q8JZU2	Slc25a1	Tricarboxylate transport protein, mitochondrial	6	2	54	2	0.92
Q7TND5	Rpf1	Ribosome production factor 1	5	2	12	2	0.92
G5E8N7	Pnkp	Bifunctional polynucleotide phosphatase/kinase	4	2	9	2	0.92
Q60520-1	Sin3a	Isoform 2 of Paired amphipathic helix protein Sin3a	2	4	29	4	0.92
P68510	Ywhah	14-3-3 protein eta	42	10	479	6	0.92
Q9D8P4	Mrpl17	39S ribosomal protein L17, mitochondrial	8	2	19	2	0.92
P26040	Ezr	Ezrin	12	11	218	4	0.92
Q8BSY0	Asph	Aspartyl/asparaginyl beta-hydroxylase	15	8	137	8	0.92
Q99JF8	Psip1	PC4 and SFRS1-interacting protein	25	12	163	11	0.91
Q8R016	Blmh	Bleomycin hydrolase	14	6	57	6	0.91
Q9CQW9	Ifitm3	Interferon-induced transmembrane protein 3	32	3	57	3	0.91
Q60875	Arhgef2	Rho guanine nucleotide exchange factor 2	12	13	165	13	0.91
Q9EPL8	Ipo7	Importin-7	3	4	48	4	0.91
Q8CCF0	Prpf31	U4/U6 small nuclear ribonucleoprotein Prp31	10	6	93	6	0.91
Q8BZH4	Pogz	Pogo transposable element with ZNF domain	1	2	15	2	0.91
Q3TXV4	Rab31	Rab22B	21	4	53	4	0.91
Q8VHR5	Gatad2b	Transcriptional repressor p66-beta	7	4	25	4	0.91
Q9WTL7	Lypla2	Acyl-protein thioesterase 2	6	2	36	2	0.90
Q8CHW4	Eif2b5	Translation initiation factor eIF-2B subunit epsilon	3	2	27	2	0.90
P62821	Rab1A	Ras-related protein Rab-1A	43	10	491	4	0.90
Q9JJ28	Flii	Protein flightless-1 homolog	2	2	39	2	0.90
Q9D9K3	Aven	Cell death regulator Aven	3	2	20	2	0.90
Q61543	Glg1	Golgi apparatus protein 1	7	10	87	10	0.89
P26039	Tln1	Talin-1	37	81	1552	81	0.89
Q9JIX8	Acin1	Apoptotic chromatin condensation inducer in the nucleus	9	16	239	16	0.89
P27661	H2afx	Histone H2AX	38	6	552	3	0.89
Q9Z1Q5	Clic1	Chloride intracellular channel protein 1	35	6	98	6	0.89
Q99LB4	Capg	Capping protein (Actin filament), gelsolin-like	35	8	584	8	0.89
Q6ZWZ7	Rpl17	60S ribosomal protein L17	31	6	138	6	0.89
Q99LJ0	Cttnbp2nl	CTTNBP2 N-terminal-like protein	8	4	21	4	0.89

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
Q9QZD9	Eif3i	Eukaryotic translation initiation factor 3 subunit I	20	6	89	6	0.89
Q9QXS1	Plec	Plectin	28	131	2375	129	0.89
O35685	Nudc	Nuclear migration protein nudC	44	16	322	16	0.89
Q9QXK3	Copg2	Coatomer subunit gamma-2	5	5	54	3	0.88
O54946	Dnajb6	DnaJ homolog subfamily B member 6	11	4	51	3	0.88
Q8R1N4	Nudcd3	NudC domain-containing protein 3	9	4	28	4	0.88
Q9D0I9	Rars	Arginine--tRNA ligase, cytoplasmic	19	14	157	14	0.88
Q9DBJ1	Pgam1	Phosphoglycerate mutase 1	50	9	741	9	0.88
E9PZM7	Scaf11	Protein Scaf11	3	4	20	4	0.88
Q9D4H8	Cul2	Cullin-2	4	4	31	4	0.88
E9Q5K9	Ythdc1	YTH domain-containing protein 1	6	5	27	5	0.88
P48678	Lmna	Prelamin-A/C	64	44	2111	42	0.88
E9QNP0	Kxd1	KxDL motif-containing protein 1	20	5	1161	5	0.88
P59017	Bcl2l13	Bcl-2-like protein 13	5	2	44	2	0.87
P68181-4	Prkacb	Isoform 4 of cAMP-dependent protein kinase catalytic subunit beta	3	2	52	2	0.87
P62908	Rps3	40S ribosomal protein S3	64	14	663	14	0.87
Q91VH2	Snx9	Sorting nexin-9	6	4	67	4	0.87
O70126	Aurkb	Aurora kinase B	8	3	15	2	0.87
Q99KH8	Stk24	Serine/threonine-protein kinase 24	4	2	15	2	0.87
Q91VI7	Rnh1	Ribonuclease inhibitor	16	6	77	6	0.87
P41105	Rpl28	60S ribosomal protein L28	40	8	261	8	0.87
Q6ZWQ7	Spcs3	Signal peptidase complex subunit 3	15	3	88	3	0.86
P53986	Slc16a1	Monocarboxylate transporter 1	11	5	106	5	0.86
Q5SUH7	Clint1	Clathrin interactor 1	13	7	116	7	0.86
Q9CPW4	Arpc5	Actin-related protein 2/3 complex subunit 5	43	6	91	6	0.86
Q8BMA6	Srp68	Signal recognition particle subunit SRP68	16	10	120	10	0.86
Q8BVF2	Pdcl3	Phosducin-like protein 3	10	3	50	3	0.86
A0A0R4J0I9	Lrp1	Low density lipoprotein receptor-related protein 1	8	35	441	35	0.86
F8WH69	Ncf1	Neutrophil cytosol factor 1	31	11	175	11	0.86
O70435	Psma3	Proteasome subunit alpha type-3	20	7	105	7	0.86
Q6ZWM4	Lsm8	U6 snRNA-associated Sm-like protein LSm8	27	3	55	3	0.85
Q3UPH1	Prrc1	Protein PRRC1	8	4	45	4	0.85
Q8BMD8	Slc25a24	Calcium-binding mitochondrial carrier protein SCaMC-1	10	7	92	7	0.85
Q9CR57	Rpl14	60S ribosomal protein L14	20	4	104	4	0.85
Q9CR68	Uqcrfs1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	26	8	203	8	0.85
Q8CHP5	Pym1	Partner of Y14 and mago	9	2	33	2	0.85
Q8BGT7	Smndc1	Survival of motor neuron-related-splicing factor 30	10	2	19	2	0.85
P06795	Abcb1b	Multidrug resistance protein 1B	2	4	31	4	0.84
O88342	Wdr1	WD repeat-containing protein 1	10	8	196	8	0.84
P63325	Rps10	40S ribosomal protein S10	39	8	339	7	0.84

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
P26443	Glud1	Glutamate dehydrogenase 1, mitochondrial	30	16	359	16	0.84
Q9CXR1	Dhrs7	Dehydrogenase/reductase SDR family member 7	5	2	8	2	0.84
P70349	Hint1	Histidine triad nucleotide-binding protein 1	16	2	35	2	0.84
Q91V41	Rab14	Ras-related protein Rab-14	26	6	285	5	0.84
Q64152-2	Btf3	Isoform 2 of Transcription factor BTF3	45	7	152	6	0.84
Q60692	Psmb6	Proteasome subunit beta type-6	13	3	130	3	0.84
Q61166	Mapre1	Microtubule-associated protein RP/EB family member 1	31	7	107	7	0.84
Q9CYR6	Pgm3	Phosphoacetylglucosamine mutase	4	2	18	2	0.84
P54726	Rad23a	UV excision repair protein RAD23 homolog A	7	3	69	1	0.84
A0JNY3	Gphn	Gephyrin	4	3	19	3	0.84
Q3UZ39	Lrrfip1	Leucine-rich repeat flightless-interacting protein 1	4	3	59	3	0.83
Q52KC3	Mcm5	DNA helicase	17	13	178	13	0.83
Q9CQW2	Arl8b	ADP-ribosylation factor-like protein 8B	14	3	117	1	0.83
P13439	Umps	Uridine 5'-monophosphate synthase	12	8	64	8	0.83
P08249	Mdh2	Malate dehydrogenase, mitochondrial	33	10	625	10	0.83
Q9R0X4	Acot9	Acyl-coenzyme A thioesterase 9, mitochondrial	6	3	25	3	0.83
Q9ESZ8	Gtf2i	General transcription factor II-I	6	6	50	6	0.83
Q99LF4	Rtcb	tRNA-splicing ligase RtcB homolog	12	6	80	6	0.83
P26041	Msn	Moesin	40	35	1038	27	0.82
Q3UJB0	Sf3b2	Protein Sf3b2	25	20	344	20	0.82
Q9JJY4	Ddx20	Probable ATP-dependent RNA helicase DDX20	3	2	18	2	0.82
E9Q9C3	Mllt4	Afadin	2	4	36	4	0.82
Q9WTX6	Cul1	Cullin-1	4	4	23	4	0.82
Q99JR1	Sfxn1	Sideroflexin-1	22	5	55	4	0.82
P25976	Ubtf	Nucleolar transcription factor 1	13	10	79	10	0.82
Q9JK23	Psmg1	Proteasome assembly chaperone 1	5	2	54	2	0.82
Q78PY7	Snd1	Staphylococcal nuclease domain-containing protein 1	23	19	300	19	0.82
Q9CZ44-3	Nsfl1c	Isoform 3 of NSFL1 cofactor p47	36	12	104	12	0.82
Q8K1J6	Trnt1	CCA tRNA nucleotidyltransferase 1, mitochondrial	5	3	28	3	0.81
D3Z7B5	C330027C09Rik	Protein C330027C09Rik	5	5	32	5	0.81
Q9D8U8	Snx5	Sorting nexin-5	16	6	89	5	0.81
A0A0R4J069	Scly	Selenocysteine lyase	4	2	27	2	0.81
P97311	Mcm6	DNA replication licensing factor MCM6	21	18	222	18	0.81
Q61768	Kif5b	Kinesin-1 heavy chain	13	13	115	13	0.81
Q8VCG1	Dut	Deoxyuridine triphosphatase, isoform CRA_b	15	3	96	3	0.81
P00375	Dhfr	Dihydrofolate reductase	14	3	67	3	0.81
Q62446	Fkbp3	Peptidyl-prolyl cis-trans isomerase FKBP3	21	5	81	5	0.80
P09103	P4hb	Protein disulfide-isomerase	55	25	1237	25	0.80
P20491	Fcer1g	High affinity immunoglobulin epsilon receptor subunit gamma	25	3	137	3	0.80
P32067	Ssb	Lupus La protein homolog	22	13	234	13	0.80

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
D3Z5F7	Gm20521	Protein Gm20521	8	3	41	3	0.80
Q8BJS4	Sun2	SUN domain-containing protein 2	12	9	114	9	0.80
Q9EST5-2	Anp32b	Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B	11	5	83	2	0.80
Q8CIH5	Plcg2	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	4	6	48	6	0.80
Q7TPR4	Actn1	Alpha-actinin-1	14	13	179	7	0.80
Q3UPL0	Sec31a	Protein transport protein Sec31A	10	13	132	13	0.80
P62960	Ybx1	Nuclease-sensitive element-binding protein 1	39	11	385	8	0.80
Q99L45	Eif2s2	Eukaryotic translation initiation factor 2 subunit 2	19	6	129	6	0.80
P61222	Abce1	ATP-binding cassette sub-family E member 1	15	9	154	9	0.79
O54734	Ddost	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	12	6	140	6	0.79
Q8VBV3	Exosc2	Exosome complex component RRP4	10	3	34	3	0.79
Q62087	Pon3	Serum paraoxonase/lactonase 3	10	3	48	3	0.79
Q91VK1	Bzw2	Basic leucine zipper and W2 domain-containing protein 2	15	7	44	7	0.79
Q9WVE8	Pacsin2	Protein kinase C and casein kinase substrate in neurons protein 2	4	2	53	2	0.79
Q99PT1	Arhgdia	Rho GDP-dissociation inhibitor 1	40	8	257	8	0.79
Q9QXX4	Slc25a13	Calcium-binding mitochondrial carrier protein Aralar2	14	8	69	6	0.79
A0A140T8T4	Rpl9-ps6	Protein Rpl9-ps6	29	3	48	3	0.79
E9QPI5	Pds5a	Sister chromatid cohesion protein PDS5 homolog A	6	8	69	8	0.79
P10922	H1f0	Histone H1.0	27	5	181	5	0.78
P11031	Sub1	Activated RNA polymerase II transcriptional coactivator p15	16	3	64	3	0.78
Q8VHN8	Nudt16l1	Protein syndesmos	8	2	15	2	0.78
Q99KQ4	Nampt	Nicotinamide phosphoribosyltransferase	5	3	36	3	0.78
Q91W39	Ncoa5	Nuclear receptor coactivator 5	15	9	55	9	0.77
A2BE28	Las1l	Ribosomal biogenesis protein LAS1L	7	5	55	5	0.77
Q61598	Gdi2	Rab GDP dissociation inhibitor beta	12	5	107	5	0.77
O08759	Ube3a	Ubiquitin-protein ligase E3A	5	5	27	5	0.77
Q9Z0X1	Aifm1	Apoptosis-inducing factor 1, mitochondrial	18	10	214	10	0.77
B1ARU1	Macf1	Microtubule-actin cross-linking factor 1	6	39	279	4	0.77
P83882	Rpl36a	60S ribosomal protein L36a	17	4	86	4	0.77
Q99MK8	Adrbk1	Beta-adrenergic receptor kinase 1	5	4	48	4	0.77
Q9D0R2	Tars	Threonine--tRNA ligase, cytoplasmic	23	17	242	17	0.77
Q91W90	Txndc5	Thioredoxin domain-containing protein 5	10	4	33	4	0.77
Q9D892	Itpa	Inosine triphosphate pyrophosphatase	17	3	35	3	0.76
O08807	Prdx4	Peroxiredoxin-4	20	6	181	4	0.76
Q60932	Vdac1	Voltage-dependent anion-selective channel protein 1	45	8	115	8	0.76
O88384	Vti1b	Vesicle transport through interaction with t-SNAREs homolog 1B	18	4	66	4	0.76
P42932	Cct8	T-complex protein 1 subunit theta	43	23	654	23	0.76
Q60787	Lcp2	Lymphocyte cytosolic protein 2	10	7	107	7	0.76
P35550	Fbl	rRNA 2'-O-methyltransferase fibrillarin	32	10	172	10	0.76
A0A023T672	RBM8	RNA-binding protein 8A	15	2	25	2	0.76

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9DBR0	Akap8	A-kinase anchor protein 8	10	5	90	5	0.76
Q9R1P4	Psma1	Proteasome subunit alpha type-1	38	11	299	11	0.76
Q9CY64	Blvra	Biliverdin reductase A	27	8	116	8	0.75
E9QKE4	Rab3gap2	Rab3 GTPase-activating protein non-catalytic subunit	3	5	42	5	0.75
P46638	Rab11b	Ras-related protein Rab-11B	29	7	247	7	0.75
Q9JHR7	Ide	Insulin-degrading enzyme	4	5	41	5	0.75
Q9CQV1	Pam16	Mitochondrial import inner membrane translocase subunit TIM16	26	3	38	3	0.75
P04441-2	Cd74	Isoform Short of H-2 class II histocompatibility antigen gamma chain	28	5	30	5	0.75
Q6A0A2	Larp4b	La-related protein 4B	8	7	66	7	0.75
Q61081	Cdc37	Hsp90 co-chaperone Cdc37	32	12	103	12	0.75
P62889	Rpl30	60S ribosomal protein L30	25	4	120	4	0.75
P62192	Psmc1	26S protease regulatory subunit 4	29	15	246	13	0.74
P35486	Pdha1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	10	5	56	5	0.74
A0A0R4J0F6	Gak	Cyclin-G-associated kinase	2	4	44	4	0.74
Q922B2	Dars	Aspartate--tRNA ligase, cytoplasmic	23	11	178	11	0.74
Q91XV3	Basp1	Brain acid soluble protein 1	11	2	32	2	0.74
Q6A028	Swap70	Switch-associated protein 70	14	11	152	11	0.74
A0A0R4J1Y3	Osgep	Probable tRNA N6-adenosine threonylcarbamoyltransferase	5	2	12	2	0.74
Q99LX0	Park7	Protein deglycase DJ-1	25	5	127	5	0.74
A0A0A6YVU8	Gm9774	MCG119397	6	2	101	2	0.74
Q4VBE8	Wdr18	WD repeat-containing protein 18	10	4	42	4	0.74
P0C0S6	H2afz	Histone H2A.Z	31	4	498	2	0.74
Q8JZQ9	Eif3b	Eukaryotic translation initiation factor 3 subunit B	18	14	144	14	0.74
E9Q390	Myof	Myoferlin	6	11	101	11	0.74
Q7TNC4	Luc7l2	Putative RNA-binding protein Luc7-like 2	25	10	206	7	0.73
P05064	Aldoa	Fructose-bisphosphate aldolase A	54	22	1188	19	0.73
Q3UL36	Arglu1	Arginine and glutamate-rich protein 1	8	3	31	3	0.73
Q922V4	Plrg1	Pleiotropic regulator 1	7	5	72	5	0.73
Q8BQM4	Heatr3	HEAT repeat-containing protein 3	2	2	7	2	0.73
Q9WVK4	Ehd1	EH domain-containing protein 1	7	4	32	3	0.73
Q9CX34	Sugt1	Protein SGT1 homolog	20	7	156	7	0.73
Q9EQC8	Prcc	Papillary renal cell carcinoma (Translocation-associated)	11	4	70	4	0.73
P31266	Rbpj	Recombining binding protein suppressor of hairless	8	4	62	4	0.73
Q7TMB8	Cyfip1	Cytoplasmic FMR1-interacting protein 1	6	8	75	8	0.73
P58389	Ppp2r4	Serine/threonine-protein phosphatase 2A activator	5	2	27	2	0.73
Q3UYV9	Ncbp1	Nuclear cap-binding protein subunit 1	2	2	15	2	0.73
P63242	Eif5a	Eukaryotic translation initiation factor 5A-1	31	5	281	5	0.73
Q91WK2	Eif3h	Eukaryotic translation initiation factor 3 subunit H	19	7	225	7	0.73
Q91YI0	Asl	Argininosuccinate lyase	3	2	13	2	0.73
Q61334	Bcap29	B-cell receptor-associated protein 29	17	7	90	7	0.73

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
G3UXL2	Prps1l3	Protein Prps1l3	13	6	50	3	0.72
A2AJI0	Map7d1	MAP7 domain-containing protein 1	5	4	27	4	0.72
Q4PJX1	Odr4	Protein odr-4 homolog	6	3	14	3	0.72
Q99KP6-2	Prpf19	Isoform 2 of Pre-mRNA-processing factor 19	25	9	158	9	0.72
P18052	Ptpra	Receptor-type tyrosine-protein phosphatase alpha	2	2	32	2	0.72
H3BL37	Tcof1	Treacle protein	17	21	313	21	0.72
O70310	Nmt1	Glycylpeptide N-tetradecanoyltransferase 1	12	7	77	7	0.72
P29391	Ftl1	Ferritin light chain 1	41	6	77	6	0.72
Q6XLQ8	Calu	Calumenin	29	9	125	9	0.72
B1AWD9	Clta	Clathrin light chain A	14	5	67	5	0.72
Q6ZWX6	Eif2s1	Eukaryotic translation initiation factor 2 subunit 1	39	10	118	10	0.72
O35593	Psmd14	26S proteasome non-ATPase regulatory subunit 14	17	3	23	3	0.71
Q80W54	Zmpste24	CAAX prenyl protease 1 homolog	7	3	61	3	0.71
Q8CBC8	Bcat1	Branched-chain-amino-acid aminotransferase, cytosolic	3	2	34	2	0.71
Q6ZWU9	Rps27	40S ribosomal protein S27	29	3	59	3	0.71
Q62384	Zpr1	Zinc finger protein ZPR1	7	4	31	4	0.71
P84084	Arf5	ADP-ribosylation factor 5	31	5	186	3	0.71
Q9D1R9	Rpl34	60S ribosomal protein L34	21	4	172	4	0.71
Q9JK48	Sh3glb1	Endophilin-B1	6	3	52	2	0.71
Q8BU30	Iars	Isoleucine--tRNA ligase, cytoplasmic	10	14	131	14	0.71
A0A0X1KG62	Nelfb	Negative elongation factor B	4	3	41	3	0.71
Q8C845	Efhd2	EF-hand domain-containing protein D2	40	9	204	9	0.71
G3X9Q6	Larp4	La-related protein 4	6	5	63	5	0.71
A0A087WQS2	Bzw1	Basic leucine zipper and W2 domain-containing protein 1	21	11	195	11	0.70
A2AHK0	Dgkz	Diacylglycerol kinase	1	2	29	2	0.70
O88544	Cops4	COP9 signalosome complex subunit 4	10	5	73	5	0.70
Q9CQ75	Ndufa2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	30	3	58	3	0.70
Q61937	Npm1	Nucleophosmin	62	18	1579	18	0.70
Q61171	Prdx2	Peroxiredoxin-2	26	5	174	5	0.70
Q91WM3	Rrp9	U3 small nucleolar RNA-interacting protein 2	15	6	90	6	0.70
E9QB02	Mars	Methionine--tRNA ligase, cytoplasmic	17	14	147	14	0.70
Q52KI8	Srrm1	Serine/arginine repetitive matrix protein 1	3	3	94	3	0.70
Q9CQU0	Txndc12	Thioredoxin domain-containing protein 12	12	2	30	2	0.70
Q8BMK4	Ckap4	Cytoskeleton-associated protein 4	29	17	219	17	0.70
Q64514	Tpp2	Tripeptidyl-peptidase 2	8	13	118	13	0.70
E9PYD5	Tcea1	Transcription elongation factor A protein 1	16	4	51	4	0.70
Q9DC23	Dnajc10	DnaJ homolog subfamily C member 10	2	3	11	3	0.70
Q00PI9	Hnrnpul2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	7	6	111	6	0.70
Q9Z1D1	Eif3g	Eukaryotic translation initiation factor 3 subunit G	19	7	66	7	0.70
Q9CYN9	Atp6ap2	Renin receptor	8	3	27	3	0.70

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
E9PYL9	Gm10036	Protein Gm10036	21	4	244	4	0.70
G5E902	Slc25a3	MCG10343, isoform CRA_b	21	10	451	10	0.70
Q3TWW8	Srsf6	Serine/arginine-rich splicing factor 6	16	7	180	4	0.70
Q60864	Stip1	Stress-induced-phosphoprotein 1	40	27	451	27	0.70
O54984	Asna1	ATPase Asna1	4	2	43	2	0.70
P48410	Abcd1	ATP-binding cassette sub-family D member 1	3	3	21	3	0.69
P61957	Sumo2	Small ubiquitin-related modifier 2	23	2	103	1	0.69
B7ZNL2	Nap1l4	Nap1l4 protein	9	3	43	2	0.69
P97363	Sptlc2	Serine palmitoyltransferase 2	8	4	27	4	0.69
Q9JIF7	Copb1	Coatomer subunit beta	8	9	148	9	0.69
Q8BK64	Ahsa1	Activator of 90 kDa heat shock protein ATPase homolog 1	14	5	96	5	0.69
Q3UZG4	Aimp1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	18	5	59	5	0.69
E9PWB2	Csnk1a1	Casein kinase I isoform alpha	7	2	56	2	0.69
Q4QRL3	Ccdc88b	Coiled-coil domain-containing protein 88B	5	7	57	7	0.69
Q8K2F8	Lsm14a	Protein LSM14 homolog A	5	3	14	3	0.69
Q9D8T2	Gsdmdc1	Gasdermin-D	11	6	62	6	0.69
Q8BTM8	Flna	Filamin-A	25	51	948	47	0.69
P70372	Elavl1	ELAV-like protein 1	17	6	182	6	0.69
Q8R0J7	Vps37b	Vacuolar protein sorting-associated protein 37B	11	3	37	3	0.69
O09167	Rpl21	60S ribosomal protein L21	21	3	72	3	0.69
Q99JI4	Psmd6	26S proteasome non-ATPase regulatory subunit 6	11	5	72	5	0.69
Q6ZPZ3	Zc3h4	Zinc finger CCCH domain-containing protein 4	6	6	77	6	0.68
P62301	Rps13	40S ribosomal protein S13	29	5	149	5	0.68
P12382	Pfkl	ATP-dependent 6-phosphofructokinase, liver type	15	11	185	8	0.68
Q9D338	Mrpl19	39S ribosomal protein L19, mitochondrial	11	3	56	3	0.68
Q9CR62	Slc25a11	Mitochondrial 2-oxoglutarate/malate carrier protein	15	4	53	4	0.68
O88967	Yme1l1	ATP-dependent zinc metalloprotease YME1L1	5	4	33	4	0.68
P47911	Rpl6	60S ribosomal protein L6	39	16	708	16	0.68
Q8BP40	Acp6	Lysophosphatidic acid phosphatase type 6	8	4	67	4	0.68
Q5SYH2	Tmem199	Transmembrane protein 199	8	2	27	2	0.68
Q6ZQ58	Larp1	La-related protein 1	11	13	169	13	0.68
Q6ZQ38	Cand1	Cullin-associated NEDD8-dissociated protein 1	12	15	181	15	0.68
Q9WTX8	Mad1l1	Mitotic spindle assembly checkpoint protein MAD1	10	7	97	7	0.68
Q7TQ95	Lnp	Protein lunapark	12	4	50	4	0.68
Q921F4	Hnrnpll	Heterogeneous nuclear ribonucleoprotein L-like	8	4	53	4	0.67
Q9JKB3-2	Ybx3	Isoform 2 of Y-box-binding protein 3	29	7	187	4	0.67
H3BKH6	Esd	S-formylglutathione hydrolase	19	5	60	5	0.67
Q4VAA2	Cdv3	Protein CDV3	26	4	22	4	0.67
A2AH25	Arhgap1	Rho GTPase-activating protein 1	13	7	77	7	0.67
P61979-2	Hnrnpk	Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	35	15	1155	15	0.67

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
O08749	Dld	Dihydrolipoyl dehydrogenase, mitochondrial	11	6	266	6	0.67
Q9CPS7	Pno1	RNA-binding protein PNO1	13	3	50	3	0.67
P11440	Cdk1	Cyclin-dependent kinase 1	24	7	121	5	0.67
Q8R2K3	Ssbp1	Single-stranded DNA-binding protein	39	5	118	5	0.67
Q80TY0	Fnbp1	Formin-binding protein 1	9	6	59	6	0.67
P17918	Pcna	Proliferating cell nuclear antigen	36	8	319	8	0.67
Q9EPU4	Cpsf1	Cleavage and polyadenylation specificity factor subunit 1	3	4	28	4	0.67
Q3UW53	Fam129a	Protein Niban	3	4	39	4	0.67
P53395	Dbt	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	11	6	110	6	0.67
Q80WQ2	Vac14	Protein VAC14 homolog	3	3	41	3	0.67
Q8C0C7	Farsa	Phenylalanine--tRNA ligase alpha subunit	6	4	77	4	0.67
Q8BGC0	Htatsf1	HIV Tat-specific factor 1 homolog	2	2	8	2	0.67
Q91Z38	Ttc1	Tetratricopeptide repeat protein 1	7	2	6	2	0.67
P16254	Srp14	Signal recognition particle 14 kDa protein	20	3	31	3	0.66
Q08024-2	Cbfb	Isoform 2 of Core-binding factor subunit beta	18	3	29	3	0.66
Q9Z0J0	Npc2	Epididymal secretory protein E1	12	3	35	3	0.66
P47713	Pla2g4a	Cytosolic phospholipase A2	12	8	92	8	0.66
Q8BJY1	Psmd5	26S proteasome non-ATPase regulatory subunit 5	13	5	45	5	0.66
P47962	Rpl5	60S ribosomal protein L5	24	9	335	9	0.66
A0A0J9YUL3	Sep-11	Septin 11, isoform CRA_b	7	3	40	3	0.66
A0A0G2JH17	Ints1	Integrator complex subunit 1	2	5	33	5	0.66
Q9CQ69	Uqcrq	Cytochrome b-c1 complex subunit 8	31	5	90	5	0.66
Q3TCU5	Tapbp	Tapasin	4	2	17	2	0.66
Q4FZF3	Ddx49	Probable ATP-dependent RNA helicase DDX49	8	4	49	4	0.66
Q9JHZ2	Ankh	Progressive ankylosis protein	4	2	38	2	0.66
Q8K0C9	Gmds	GDP-mannose 4,6 dehydratase	9	4	33	4	0.66
P51150	Rab7a	Ras-related protein Rab-7a	53	10	165	10	0.66
O55234	Psmb5	Proteasome subunit beta type-5	28	7	135	7	0.66
P54775	Psmc4	26S protease regulatory subunit 6B	22	10	181	9	0.66
Q9Z0N1	Eif2s3x	Eukaryotic translation initiation factor 2 subunit 3, X-linked	14	6	68	6	0.66
Q9D8X2	Ccdc124	Coiled-coil domain-containing protein 124	16	4	56	4	0.66
P63158	Hmgb1	High mobility group protein B1	49	8	313	8	0.65
Q9EQU5	Set	Protein SET	25	8	226	2	0.65
E9Q1G8	Sep-07	Septin-7	17	9	89	9	0.65
P57780	Actn4	Alpha-actinin-4	39	30	354	24	0.65
Q8VDJ3	Hdlbp	Vigilin	14	21	215	21	0.65
Q91W50	Csde1	Cold shock domain-containing protein E1	16	13	204	13	0.65
Q61074	Ppm1g	Protein phosphatase 1G	5	4	41	4	0.65
Q9ES28	Arhgef7	Rho guanine nucleotide exchange factor 7	9	8	65	7	0.65

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
A0A0R4J0Z1	Pdia4	Protein disulfide-isomerase A4	40	27	781	27	0.65
A0A0A0MQF6	Gapdh	Glyceraldehyde-3-phosphate dehydrogenase	37	13	1080	13	0.65
F8VQC7	Ktn1	Kinectin	9	14	231	14	0.65
Q8BG32	Psmd11	26S proteasome non-ATPase regulatory subunit 11	17	7	115	7	0.65
Q921W0	Chmp1a	Charged multivesicular body protein 1a	12	3	40	3	0.65
Q9Z2I8	Suclg2	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial	21	10	74	10	0.65
A0A0R4J1C8	Cd68	Macrosialin	5	2	107	2	0.65
Q91Z50	Fen1	Flap endonuclease 1	16	6	78	6	0.65
G5E8N5	Ldha	L-lactate dehydrogenase	31	10	443	10	0.64
A2RSX9	Arfip1	Arfip1 protein	10	3	26	1	0.64
Q80U93	Nup214	Nuclear pore complex protein Nup214	9	16	247	16	0.64
A2AFF6	Stag2	Cohesin subunit SA-2	2	3	12	2	0.64
Q9CPY7	Lap3	Cytosol aminopeptidase	16	8	117	8	0.64
Q9CQE7-2	Ergic3	Isoform 2 of Endoplasmic reticulum-Golgi intermediate compartment protein 3	3	2	27	2	0.64
Q9CQW1	Ykt6	Synaptobrevin homolog YKT6	24	5	128	5	0.64
P01942	Hba	Hemoglobin subunit alpha	15	2	138	2	0.64
P09581	Csf1r	Macrophage colony-stimulating factor 1 receptor	2	3	18	3	0.64
P56183	Rrp1	Ribosomal RNA processing protein 1 homolog A	10	5	89	5	0.64
Q922Q8	Lrrc59	Leucine-rich repeat-containing protein 59	22	6	72	6	0.64
O55201	Supt5h	Transcription elongation factor SPT5	7	8	64	8	0.64
P62317	Snrpd2	Small nuclear ribonucleoprotein Sm D2	37	4	115	4	0.64
Q3U367	Aldh9a1	4-trimethylaminobutyraldehyde dehydrogenase	19	10	162	10	0.64
Q9Z2L7	Crlf3	Cytokine receptor-like factor 3	7	4	48	4	0.63
Q9Z277	Baz1b	Tyrosine-protein kinase BAZ1B	7	13	115	13	0.63
O88844	Idh1	Isocitrate dehydrogenase [NADP] cytoplasmic	21	8	139	8	0.63
E9PXC0	Srp54b	Protein Srp54b	13	7	116	7	0.63
Q6A0A9	FAM120A	Constitutive coactivator of PPAR-gamma-like protein 1	8	9	54	9	0.63
P21126	Ubl4a	Ubiquitin-like protein 4A	11	2	12	2	0.63
B7ZCF1	Psmc3	26S protease regulatory subunit 6A	15	7	106	7	0.63
Q91VN4	Chchd6	MICOS complex subunit Mic25	13	3	52	3	0.63
Q8C3J5	Dock2	Dedicator of cytokinesis protein 2	4	9	89	9	0.63
Q9CYX7	Rrp15	RRP15-like protein	8	3	45	3	0.63
Q9QUM9	Psma6	Proteasome subunit alpha type-6	28	7	93	7	0.63
Q61490	Alcam	CD166 antigen	7	4	45	4	0.63
P14115	Rpl27a	60S ribosomal protein L27a	19	3	105	3	0.63
P60867	Rps20	40S ribosomal protein S20	22	3	169	3	0.63
P62082	Rps7	40S ribosomal protein S7	24	7	235	7	0.63
Q3TIV5	Zc3h15	Zinc finger CCCH domain-containing protein 15	11	4	18	4	0.63
Q64433	Hspe1	10 kDa heat shock protein, mitochondrial	67	7	512	7	0.63
Q8VBW6	Nae1	NEDD8-activating enzyme E1 regulatory subunit	3	2	18	2	0.63

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q99MR6	Srrt	Serrate RNA effector molecule homolog	12	12	215	12	0.62
Q99KE1	Me2	NAD-dependent malic enzyme, mitochondrial	14	8	138	8	0.62
D3YVN7	Gm9755	Elongation factor Tu	39	15	344	15	0.62
A2ADH1	Magt1	Magnesium transporter protein 1	6	3	80	3	0.62
Q9QYB1	Clic4	Chloride intracellular channel protein 4	13	3	68	3	0.62
P25911-2	Lyn	Isoform 2 of Tyrosine-protein kinase Lyn	21	9	87	8	0.62
E9QN37	Mpeg1	Macrophage-expressed gene 1 protein	10	6	68	6	0.62
Q8BK67	Rcc2	Protein RCC2	14	8	123	8	0.62
Q8K411	Pitrm1	Presequence protease, mitochondrial	10	11	85	11	0.62
P10810	Cd14	Monocyte differentiation antigen CD14	15	4	51	4	0.62
E0CZ72	Kif2a	Kinesin-like protein	2	2	21	1	0.62
Q9ES00	Ube4b	Ubiquitin conjugation factor E4 B	1	2	9	2	0.62
O09061	Psmb1	Proteasome subunit beta type-1	27	6	70	6	0.62
Q9DBL7	Coasy	Bifunctional coenzyme A synthase	5	3	28	3	0.62
P10126	Eef1a1	Elongation factor 1-alpha 1	34	16	1289	16	0.62
P20060	Hexb	Beta-hexosaminidase subunit beta	9	5	39	5	0.62
Q9ES52	Inpp5d	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	12	15	144	13	0.62
Q9D937	N/A	Uncharacterized protein C11orf98 homolog	26	3	65	3	0.62
P25206	Mcm3	DNA replication licensing factor MCM3	15	11	124	11	0.62
Q8VE70	Pdcd10	Programmed cell death protein 10	8	2	15	2	0.61
O08599-2	Stxbp1	Isoform 2 of Syntaxin-binding protein 1	5	3	44	3	0.61
Q6PHN9	Rab35	Ras-related protein Rab-35	21	5	143	3	0.61
Q80VD1	Fam98b	Protein FAM98B	5	2	42	2	0.61
Q8K4L0	Ddx54	ATP-dependent RNA helicase DDX54	14	9	57	9	0.61
Q6ZQM8	Ugt1a7c	UDP-glucuronosyltransferase 1-7C	13	6	48	6	0.61
P34022	Ranbp1	Ran-specific GTPase-activating protein	13	3	74	3	0.61
Q99JX7	Nxf1	Nuclear RNA export factor 1	9	5	59	5	0.61
Q8C3I8	Hgh1	Protein HGH1 homolog	7	2	12	2	0.61
Q922J9-4	Far1	Isoform 4 of Fatty acyl-CoA reductase 1	9	5	52	5	0.61
Q9JJ89	Ccdc86	Coiled-coil domain-containing protein 86	4	2	26	2	0.61
Q7TQH0-2	Atxn2l	Isoform 2 of Ataxin-2-like protein	13	13	298	12	0.61
Q9CXE7	Tmed5	Transmembrane emp24 domain-containing protein 5	13	3	27	3	0.61
P60710	Actb	Actin, cytoplasmic 1	52	17	4580	6	0.61
P23116	Eif3a	Eukaryotic translation initiation factor 3 subunit A	30	39	436	39	0.61
Q8VDM4	Psmd2	26S proteasome non-ATPase regulatory subunit 2	23	19	235	19	0.61
Q5XJY5	Arcn1	Coatomer subunit delta	14	7	133	7	0.61
O35286	Dhx15	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	16	14	223	14	0.61
P97930	Dtymk	Thymidylate kinase	18	4	27	4	0.61
Q8CI94	Pygb	Glycogen phosphorylase, brain form	4	4	29	4	0.61
Q3TLH4	Prrc2c	Protein PRRC2C	5	16	182	15	0.61

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q3TAQ9	Wdr36	Protein Wdr36	7	5	32	5	0.61
Q3TEA8	Hp1bp3	Heterochromatin protein 1-binding protein 3	16	9	150	9	0.60
H9KV04	Mcmbp	Mini-chromosome maintenance complex-binding protein	4	3	21	3	0.60
P08228	Sod1	Superoxide dismutase [Cu-Zn]	52	8	190	8	0.60
Q8BLH7	Hirip3	HIRA-interacting protein 3	5	3	30	3	0.60
P61255	Rpl26	60S ribosomal protein L26	31	8	459	8	0.60
E9PY39	Gm20431	Protein Gm20431	11	5	120	5	0.60
P68037	Ube2l3	Ubiquitin-conjugating enzyme E2 L3	36	6	137	6	0.60
G3X928	Sec23ip	SEC23-interacting protein	5	6	69	6	0.60
P54823	Ddx6	Probable ATP-dependent RNA helicase DDX6	14	5	43	5	0.60
P31938	Map2k1	Dual specificity mitogen-activated protein kinase kinase 1	12	5	47	3	0.60
P21107-2	Tpm3	Isoform 2 of Tropomyosin alpha-3 chain	38	11	253	10	0.60
Q61335	Bcap31	B-cell receptor-associated protein 31	33	12	303	12	0.60
Q9JIF0	Prmt1	Protein arginine N-methyltransferase 1	8	3	40	3	0.60
Q9JHU9	Isyna1	Inositol-3-phosphate synthase 1	4	3	100	3	0.59
Q3V117	Acly	ATP-citrate synthase	14	16	159	16	0.59
P27546	Map4	Microtubule-associated protein 4	14	15	152	15	0.59
Q64737	Gart	Trifunctional purine biosynthetic protein adenosine-3	8	10	194	10	0.59
Q9D0E1	Hnrnpm	Heterogeneous nuclear ribonucleoprotein M	54	39	1564	39	0.59
E9PVC5	Eif4g1	Eukaryotic translation initiation factor 4 gamma 1	18	29	515	1	0.59
Q61233	Lcp1	Plastin-2	43	25	1018	22	0.59
Q6PFD9	Nup98	Nuclear pore complex protein Nup98-Nup96	6	11	184	11	0.59
Q8VDD5	Myh9	Myosin-9	40	75	1531	75	0.59
Q8BH80	Vapb	Vesicle-associated membrane protein, associated protein B and C	33	8	117	7	0.59
O09110	Map2k3	Dual specificity mitogen-activated protein kinase kinase 3	10	4	72	4	0.59
Q8CH25	Sltm	SAFB-like transcription modulator	3	4	17	4	0.59
Q9CQN1	Trap1	Heat shock protein 75 kDa, mitochondrial	23	15	428	14	0.59
E9QML5	Zfp638	Zinc finger protein 638	3	7	44	7	0.59
Q8BGR2	Lrrc8d	Volume-regulated anion channel subunit LRRC8D	2	2	14	2	0.59
A2A4J8	Vps25	Vacuolar protein-sorting-associated protein 25	15	3	42	3	0.59
P99024	Tubb5	Tubulin beta-5 chain	33	11	733	4	0.59
Q9WTP7	Ak3	GTP:AMP phosphotransferase AK3, mitochondrial	16	4	29	4	0.59
E9PXY8	Usp7	Ubiquitin carboxyl-terminal hydrolase 7	2	4	39	4	0.59
Q99L47	St13	Hsc70-interacting protein	25	10	169	10	0.59
P50446	Krt6a	Keratin, type II cytoskeletal 6A	7	5	128	2	0.58
Q8BP47	Nars	Asparagine--tRNA ligase, cytoplasmic	14	6	56	5	0.58
Q60648	Gm2a	Ganglioside GM2 activator	25	4	20	4	0.58
A2ANY6	Mdn1	Protein Mdn1	3	17	174	17	0.58
O70318	Epb41l2	Band 4.1-like protein 2	16	15	173	15	0.58
Q8VCB1	Ndc1	Nucleoporin NDC1	6	5	63	5	0.58

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
F8WHU5	Pds5b	Sister chromatid cohesion protein PDS5 homolog B	3	4	38	4	0.58
F7ACR9	Macf1	Microtubule-actin cross-linking factor 1 (Fragment)	10	48	358	14	0.58
Q91VC3	Eif4a3	Eukaryotic initiation factor 4A-III	29	14	313	11	0.58
E9QMN5	Gatad2a	Transcriptional repressor p66 alpha	8	5	43	5	0.58
P17710	Hk1	Hexokinase-1	17	17	220	16	0.58
Q91VE6	Nifk	MKI67 FHA domain-interacting nucleolar phosphoprotein	11	4	87	4	0.58
Q60631	Grb2	Growth factor receptor-bound protein 2	31	7	82	7	0.58
Q9CYG7	Tomm34	Mitochondrial import receptor subunit TOM34	13	4	74	4	0.58
Q80YV2	Zc3hc1	Nuclear-interacting partner of ALK	7	3	35	3	0.58
Q8BH24	Tm9sf4	Transmembrane 9 superfamily member 4	6	4	30	4	0.58
Q6A0D4	Rftn1	Raftlin	4	2	33	2	0.58
O54825	Bysl	Bystin	11	5	75	5	0.58
Q99JY9	Actr3	Actin-related protein 3	21	7	170	7	0.58
D3YWJ3	Rps2	40S ribosomal protein S2	18	6	216	6	0.58
P08905	Lyz2	Lysozyme C-2	16	2	96	2	0.57
Q9D051	Pdhb	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	9	3	41	3	0.57
Q99LE6	Abcf2	ATP-binding cassette sub-family F member 2	11	7	66	7	0.57
Q61990	Pcbp2	Poly(rC)-binding protein 2	22	6	406	3	0.57
Q61510	Trim25	E3 ubiquitin/ISG15 ligase TRIM25	6	4	37	4	0.57
E9Q7G0	Numa1	Protein Numa1	13	27	348	27	0.57
Q01853	Vcp	Transitional endoplasmic reticulum ATPase	35	28	648	28	0.57
Q9CQI6	Cotl1	Coactosin-like protein	27	5	172	5	0.57
P35700	Prdx1	Peroxiredoxin-1	49	10	636	8	0.57
Q7M6Y3-5	Picalm	Isoform 5 of Phosphatidylinositol-binding clathrin assembly protein	19	10	280	10	0.57
O70194	Eif3d	Eukaryotic translation initiation factor 3 subunit D	13	6	72	6	0.57
P70460	Vasp	Vasodilator-stimulated phosphoprotein	27	10	204	10	0.57
A2AEM2	Clcc1	Chloride channel CLIC-like 1, isoform CRA_a	9	4	52	4	0.57
Q8BH43	Wasf2	Wiskott-Aldrich syndrome protein family member 2	8	4	48	4	0.57
Q3TXS7	Psmd1	26S proteasome non-ATPase regulatory subunit 1	12	12	88	12	0.57
Q6PGC1	Dhx29	ATP-dependent RNA helicase Dhx29	4	5	42	5	0.57
Q9ERF3	Wdr61	WD repeat-containing protein 61	5	2	8	2	0.57
Q9CQR2	Rps21	40S ribosomal protein S21	30	3	291	3	0.57
Q8BTI8	Srrm2	Serine/arginine repetitive matrix protein 2	9	23	273	23	0.57
F8VQC9	Slc4a7	Anion exchange protein	3	4	19	4	0.57
O88738	Birc6	Baculoviral IAP repeat-containing protein 6	1	4	27	4	0.56
A0A0R4J1I3	Men1	Menin	4	2	6	2	0.56
P62918	Rpl8	60S ribosomal protein L8	28	11	476	11	0.56
P42669	Pura	Transcriptional activator protein Pur-alpha	8	3	63	3	0.56
P46978	Stt3a	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	7	5	210	5	0.56
P27773	Pdia3	Protein disulfide-isomerase A3	54	27	1106	27	0.56

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q76MZ3	Ppp2r1a	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	23	11	269	10	0.56
E0CYV0	Pcmt1	Protein-L-isoaspartate O-methyltransferase	7	2	9	2	0.56
P42208	Sep-02	Septin-2	24	8	130	8	0.56
Q8C156	Ncaph	Condensin complex subunit 2	4	4	42	4	0.56
Q9JHU4	Dync1h1	Cytoplasmic dynein 1 heavy chain 1	9	44	427	44	0.56
A2A841	Epb41	Protein 4.1	4	4	20	4	0.56
Q9ERE7	Mesdc2	LDLR chaperone MESD	16	4	41	4	0.56
Q8BWY3	Etf1	Eukaryotic peptide chain release factor subunit 1	16	6	72	6	0.56
Q9DC51	Gnai3	Guanine nucleotide-binding protein G(k) subunit alpha	12	4	98	2	0.56
Q8CAQ8-5	Immt	Isoform 5 of MICOS complex subunit Mic60	34	27	579	7	0.56
Q9JL26	Fmnl1	Formin-like protein 1	12	13	196	13	0.56
E9PU96	Urb1	Nucleolar pre-ribosomal-associated protein 1	1	3	25	3	0.56
Q99P88	Nup155	Nuclear pore complex protein Nup155	7	10	111	10	0.56
Q9JII6	Akr1a1	Alcohol dehydrogenase [NADP(+)]	18	6	92	6	0.55
P33611	Pola2	DNA polymerase alpha subunit B	5	3	18	3	0.55
Q9JIH2	Nup50	Nuclear pore complex protein Nup50	11	6	87	6	0.55
P70168	Kpnb1	Importin subunit beta-1	19	17	316	17	0.55
O88531	Ppt1	Palmitoyl-protein thioesterase 1	14	4	58	4	0.55
P67778	Phb	Prohibitin	54	14	616	14	0.55
Q9WUR9	Ak4	Adenylate kinase 4, mitochondrial	9	2	47	2	0.55
P35922	Fmr1	Synaptic functional regulator FMR1	11	6	61	5	0.55
G3X9B1	Heatr1	HEAT repeat containing 1	7	17	219	17	0.55
Q9Z0H1	Wdr46	WD repeat-containing protein 46	8	5	60	5	0.55
D3Z4J3	Myo5a	Unconventional myosin-Va	3	7	49	7	0.55
Q9CX56	Psmd8	26S proteasome non-ATPase regulatory subunit 8	9	4	42	4	0.55
Q9D071	Mms19	MMS19 nucleotide excision repair protein homolog	1	2	10	2	0.55
Q8C854	Myef2	Myelin expression factor 2	15	10	222	10	0.55
Q9CQC9	Sar1b	GTP-binding protein SAR1b	15	3	46	1	0.55
P57759	Erp29	Endoplasmic reticulum resident protein 29	19	5	227	5	0.55
Q8C147	Dock8	Dedicator of cytokinesis protein 8	2	6	38	6	0.55
P14148	Rpl7	60S ribosomal protein L7	35	18	505	18	0.55
Q8VDN2	Atp1a1	Sodium/potassium-transporting ATPase subunit alpha-1	30	30	848	21	0.55
P27659	Rpl3	60S ribosomal protein L3	30	14	659	14	0.55
Q8BMJ2	Lars	Leucine--tRNA ligase, cytoplasmic	11	12	140	12	0.55
Q9D8S9	Bola1	BolA-like protein 1	40	4	33	4	0.55
P80315	Cct4	T-complex protein 1 subunit delta	39	17	388	17	0.55
P38060	Hmgcl	Hydroxymethylglutaryl-CoA lyase, mitochondrial	14	4	90	4	0.54
Q6P5F9	Xpo1	Exportin-1	3	4	23	4	0.54
Q8BGZ6	Gla	Alpha-galactosidase A	4	2	12	2	0.54
Q05D44	Eif5b	Eukaryotic translation initiation factor 5B	8	10	96	10	0.54

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
G5E895	Akr1b10	MCG142264, isoform CRA_b	5	2	37	1	0.54
Q3U741	Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a	16	10	326	6	0.54
Q9D8B3	Chmp4b	Charged multivesicular body protein 4b	29	8	85	8	0.54
Q9DC37	Mfsd1	Major facilitator superfamily domain-containing protein 1	4	2	33	2	0.54
Q9R0U0	Srsf10	Serine/arginine-rich splicing factor 10	11	3	32	3	0.54
Q8BYB9	Poglut1	Protein O-glucosyltransferase 1	5	2	15	2	0.54
G3X963	Atad2	ATPase family AAA domain-containing protein 2	2	4	40	4	0.54
Q9CWJ9	Atic	Bifunctional purine biosynthesis protein PURH	28	14	213	14	0.54
Q9WUK2	Eif4h	Eukaryotic translation initiation factor 4H	40	9	211	9	0.54
Q8CG47	Smc4	Structural maintenance of chromosomes protein 4	10	14	145	14	0.54
P46061	Rangap1	Ran GTPase-activating protein 1	21	10	170	10	0.54
P59999	Arpc4	Actin-related protein 2/3 complex subunit 4	23	4	106	4	0.54
P70698	Ctps1	CTP synthase 1	7	4	22	4	0.53
O08788	Dctn1	Dynactin subunit 1	5	6	51	6	0.53
Q80X50-5	Ubap2l	Isoform 5 of Ubiquitin-associated protein 2-like	21	17	364	17	0.53
Q8VDP4	Ccar2	Cell cycle and apoptosis regulator protein 2	10	10	82	10	0.53
Q8BH95	Echs1	Enoyl-CoA hydratase, mitochondrial	15	5	44	5	0.53
E9QNN1	Dhx9	ATP-dependent RNA helicase A	22	25	564	25	0.53
O55142	Rpl35a	60S ribosomal protein L35a	52	7	241	7	0.53
P62814	Atp6v1b2	V-type proton ATPase subunit B, brain isoform	16	8	239	8	0.53
P57784	Snrpa1	U2 small nuclear ribonucleoprotein A'	36	7	78	7	0.53
Q8R574	Prpsap2	Phosphoribosyl pyrophosphate synthase-associated protein 2	9	4	31	4	0.53
Q8BFQ4	Wdr82	WD repeat-containing protein 82	6	2	28	2	0.53
Q9D2G2	Dlst	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	18	7	112	7	0.53
Q8R5K4	Nol6	Nucleolar protein 6	2	3	19	3	0.53
F6WIU1	Kri1	Protein KRI1 homolog	6	5	45	5	0.53
Q62376	Snrnp70	U1 small nuclear ribonucleoprotein 70 kDa	24	12	197	12	0.53
Q61584	Fxr1	Fragile X mental retardation syndrome-related protein 1	8	6	56	4	0.53
Q9QYL7	Abt1	Activator of basal transcription 1	10	3	34	3	0.53
A0A0R4J083	Acadl	Long-chain-specific acyl-CoA dehydrogenase, mitochondrial	10	5	87	5	0.53
Q6P8X1	Snx6	Sorting nexin-6	11	5	96	4	0.53
Q9CSH3	Dis3	Exosome complex exonuclease RRP44	3	3	27	3	0.53
P59708	Sf3b6	Splicing factor 3B subunit 6	19	3	82	3	0.53
Q3TCH7	Cul4a	Cullin-4A	5	5	38	4	0.53
P62313	Lsm6	U6 snRNA-associated Sm-like protein LSm6	35	3	31	3	0.53
Q9CZR8	Tsfm	Elongation factor Ts, mitochondrial	8	2	6	2	0.53
Q9JHS9	Cwc15	Spliceosome-associated protein CWC15 homolog	13	3	41	3	0.52
Q91YH5	Atl3	Atlastin-3	13	6	92	6	0.52
P61089	Ube2n	Ubiquitin-conjugating enzyme E2 N	28	4	111	4	0.52

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9DBG5	Plin3	Perilipin-3	16	6	29	6	0.52
E9Q481	Smek1	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	7	6	88	6	0.52
E9Q6J5-3	Bod1l	Isoform New of Biorientation of chromosomes in cell division protein 1-like 1	1	4	57	4	0.52
Q9CQ49	Ncbp2	Nuclear cap-binding protein subunit 2	25	4	26	4	0.52
D3Z0B9	Aldh16a1	Aldehyde dehydrogenase family 16 member A1	4	3	24	3	0.52
Q62167	Ddx3x	ATP-dependent RNA helicase DDX3X	28	20	588	5	0.52
P35279	Rab6a	Ras-related protein Rab-6A	25	6	116	5	0.52
Q3UMA3	Hgs	Hepatocyte growth factor-regulated tyrosine kinase substrate	4	4	75	4	0.52
F8WHL2	Copa	Coatomer subunit alpha	9	10	114	10	0.52
Q5SQ20	Pes1	Pescadillo homolog	20	11	149	11	0.52
Q9CSU0	Rprd1b	Regulation of nuclear pre-mRNA domain-containing protein 1B	7	2	14	2	0.52
Q9WV55	Vapa	Vesicle-associated membrane protein-associated protein A	38	9	176	8	0.52
P60229	Eif3e	Eukaryotic translation initiation factor 3 subunit E	15	6	122	6	0.52
P80316	Cct5	T-complex protein 1 subunit epsilon	28	13	297	13	0.52
O08547	Sec22b	Vesicle-trafficking protein SEC22b	38	7	108	7	0.51
Q99KR7	Ppif	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	14	4	35	4	0.51
Q9QZQ8	H2afy	Core histone macro-H2A.1	20	6	51	6	0.51
Q8K224	Nat10	RNA cytidine acetyltransferase	15	16	203	16	0.51
Q9Z2X2	Psmd10	26S proteasome non-ATPase regulatory subunit 10	7	2	9	2	0.51
Q922H4	Gmppa	Mannose-1-phosphate guanyltransferase alpha	7	3	20	3	0.51
Q9CXW2	Mrps22	28S ribosomal protein S22, mitochondrial	13	5	42	5	0.51
A2AAY5	Sh3pxd2b	SH3 and PX domain-containing protein 2B	6	5	27	5	0.51
Q9CQ06	Mrpl24	39S ribosomal protein L24, mitochondrial	11	3	38	3	0.51
Q99LP6	Grpel1	GrpE protein homolog 1, mitochondrial	27	6	126	6	0.51
Q8VH51	Rbm39	RNA-binding protein 39	11	5	134	5	0.51
P54731	Faf1	FAS-associated factor 1	3	2	12	2	0.51
Q8K2V6-2	Ipo11	Isoform 2 of Importin-11	4	4	33	4	0.51
P38647	Hspa9	Stress-70 protein, mitochondrial	50	37	1373	35	0.51
E9QMK9	9030617O03Rik	Protein 9030617O03Rik	5	4	32	4	0.51
Q3U0V1	Khsrp	Far upstream element-binding protein 2	38	24	713	21	0.51
Q9D662	Sec23b	Protein transport protein Sec23B	8	6	68	5	0.51
Q9D1Q6	Erp44	Endoplasmic reticulum resident protein 44	7	3	56	3	0.51
Q91VR5	Ddx1	ATP-dependent RNA helicase DDX1	10	8	124	8	0.51
P70195	Psmb7	Proteasome subunit beta type-7	14	5	100	5	0.51
E9Q4Q2	Sf1	Splicing factor 1	8	5	79	5	0.50
G5E866	Sf3b1	Splicing factor 3B subunit 1	20	24	361	24	0.50
P97855	G3bp1	Ras GTPase-activating protein-binding protein 1	31	10	302	9	0.50
Q9CXY6	Ilf2	Interleukin enhancer-binding factor 2	12	3	29	3	0.50
P24668	M6pr	Cation-dependent mannose-6-phosphate receptor	14	4	70	4	0.50
Q11011	Npepps	Puromycin-sensitive aminopeptidase	2	3	37	3	0.50

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
P37040	Por	NADPH--cytochrome P450 reductase	12	9	302	9	0.50
P62281	Rps11	40S ribosomal protein S11	27	7	280	7	0.50
Q3TUQ5	Pnn	Pinin	17	14	241	14	0.50
Q8BM55	Tmem214	Transmembrane protein 214	9	6	48	6	0.50
Q8VE91	Fam134b	Reticulophagy receptor Fam134b	7	3	15	3	0.50
Q61093	Cybb	Cytochrome b-245 heavy chain	11	5	79	5	0.50
Q9R0E1	Plod3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	5	4	75	4	0.50
Q9DBG7	Srpra	Signal recognition particle receptor subunit alpha	8	6	71	6	0.50
O08583	Alyref	THO complex subunit 4	29	6	90	6	0.50
Q5SSZ5	Tns3	Tensin-3	2	4	27	4	0.50
Q9JM90	Stap1	Signal-transducing adaptor protein 1	13	6	56	6	0.50
Q9QY81	Nup210	Nuclear pore membrane glycoprotein 210	7	13	119	13	0.50
Q9Z2U0	Psma7	Proteasome subunit alpha type-7	29	7	127	7	0.50
P18572	Bsg	Basigin	10	5	193	5	0.50
Q8QZY1	Eif3l	Eukaryotic translation initiation factor 3 subunit L	20	12	243	12	0.50
Q62425	Ndufa4	Cytochrome c oxidase subunit NDUFA4	32	4	192	4	0.50
Q9CY50	Ssr1	Translocon-associated protein subunit alpha	18	3	50	3	0.50
Q61686	Cbx5	Chromobox protein homolog 5	14	3	26	3	0.50
P67984	Rpl22	60S ribosomal protein L22	19	2	98	2	0.49
Q9CWK8	Snx2	Sorting nexin-2	14	8	65	7	0.49
Q6P9P6	Kif11	Kinesin-like protein KIF11	2	3	19	3	0.49
P63280	Ube2i	SUMO-conjugating enzyme UBC9	13	3	28	3	0.49
Q9D3D9	Atp5d	ATP synthase subunit delta, mitochondrial	13	2	153	2	0.49
P70670	Naca	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	2	4	131	4	0.49
G3X8Y3	Naa15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	11	11	120	11	0.49
Q9ES97	Rtn3	Reticulon-3	1	2	68	2	0.49
H7BX95	Srsf1	Serine/arginine-rich-splicing factor 1	26	8	291	8	0.49
E9QP00	Tra2a	Transformer-2 protein homolog alpha	21	6	96	4	0.49
P62835	Rap1a	Ras-related protein Rap-1A	26	6	141	6	0.49
Q3U3K9	Aup1	Ancient ubiquitous protein 1	5	3	44	3	0.49
P40124	Cap1	Adenylyl cyclase-associated protein 1	34	13	373	13	0.49
P43276	Hist1h1b	Histone H1.5	35	11	536	10	0.49
Q9JM76	Arpc3	Actin-related protein 2/3 complex subunit 3	21	4	73	4	0.49
Q62418	Dbnl	Drebrin-like protein	14	6	124	6	0.49
P23591	Tsta3	GDP-L-fucose synthase	6	2	15	2	0.49
O54941	Smarce1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	9	4	88	3	0.49
Q9D883	U2af1	Splicing factor U2AF 35 kDa subunit	8	2	76	2	0.49
Q921K2	Parp1	Poly [ADP-ribose] polymerase	14	14	309	14	0.49
P63017	Hspa8	Heat shock cognate 71 kDa protein	61	36	2589	25	0.49

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q8BIJ7	Rufy1	RUN and FYVE domain-containing protein 1	9	7	95	7	0.48
Q99PM9	Uck2	Uridine-cytidine kinase 2	9	3	38	3	0.48
O88325	Naglu	Alpha-N-acetylglucosaminidase	5	4	66	4	0.48
Q64012-2	Raly	Isoform 1 of RNA-binding protein Raly	35	11	238	11	0.48
Q9D8W5	Psmd12	26S proteasome non-ATPase regulatory subunit 12	7	4	70	4	0.48
Q3UE92	Xpnpep1	X-prolyl aminopeptidase (Aminopeptidase P) 1, soluble, isoform CRA_b	6	5	47	5	0.48
Q8BWT1	Acaa2	3-ketoacyl-CoA thiolase, mitochondrial	14	4	53	4	0.48
A2APB8	Tpx2	Targeting protein for Xklp2	14	10	91	10	0.48
Q9CY66	Gar1	H/ACA ribonucleoprotein complex subunit 1	7	2	53	2	0.48
Q80UM7	Mogs	Mannosyl-oligosaccharide glucosidase	16	12	142	12	0.48
Q61753	Phgdh	D-3-phosphoglycerate dehydrogenase	17	9	384	9	0.48
A0A140T8K6	Rpl36-ps3	60S ribosomal protein L36	19	2	141	2	0.48
P47757-4	Capzb	Isoform 3 of F-actin-capping protein subunit beta	28	10	244	10	0.48
Q07417	Acads	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	10	4	27	4	0.48
Q62189	Snrpa	U1 small nuclear ribonucleoprotein A	19	4	161	3	0.48
P19783	Cox4i1	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	35	5	172	5	0.48
A0A0A6YX26	Rpl31	60S ribosomal protein L31	24	4	265	4	0.48
Q8BTW3	Exosc6	Exosome complex component MTR3	18	4	48	4	0.48
A2AIX1	Sec16a	Protein Sec16a	3	7	48	7	0.48
P09405	Ncl	Nucleolin	46	43	2027	43	0.48
Q8BY02	Nkrf	NF-kappa-B-repressing factor	5	4	31	4	0.48
P50247	Ahcy	Adenosylhomocysteinase	29	11	126	10	0.48
P33174	Kif4	Chromosome-associated kinesin KIF4	4	5	25	5	0.48
D3YX79	Gm8394	Proteasome subunit alpha type	17	3	87	3	0.47
Q9R0Q7	Ptges3	Prostaglandin E synthase 3	6	2	27	2	0.47
P58252	Eef2	Elongation factor 2	36	32	1390	31	0.47
Q80SY5	Prpf38b	Pre-mRNA-splicing factor 38B	2	2	24	2	0.47
Q61792	Lasp1	LIM and SH3 domain protein 1	35	11	262	11	0.47
E9Q070	Gm8730	60S acidic ribosomal protein P0	31	8	343	8	0.47
Q9JKX6	Nudt5	ADP-sugar pyrophosphatase	14	3	33	3	0.47
Q542V3	Srsf4	Serine/arginine-rich-splicing factor 4	10	5	148	2	0.47
Q8BKZ9	Pdhx	Pyruvate dehydrogenase protein X component, mitochondrial	9	5	133	5	0.47
Q9EQI8	Mrpl46	39S ribosomal protein L46, mitochondrial	7	2	20	2	0.47
Q8BUE4-2	Aifm2	Isoform 2 of Apoptosis-inducing factor 2	4	2	10	2	0.47
Q3TLR7-2	Dtl	Isoform 2 of Denticleless protein homolog	3	2	11	2	0.47
Q9WTR1	Trpv2	Transient receptor potential cation channel subfamily V member 2	5	3	16	3	0.47
Q3UW66	Mpst	Sulfurtransferase	9	3	41	3	0.47
Q6NS46	Pdcd11	Protein RRP5 homolog	9	17	148	17	0.47
Q6P1F6	Ppp2r2a	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	11	5	40	5	0.47
P53026	Rpl10a	60S ribosomal protein L10a	33	7	156	7	0.47

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9WUQ2	Preb	Prolactin regulatory element-binding protein	10	3	12	3	0.47
Q9WUU7	Ctsz	Cathepsin Z	5	2	209	2	0.47
Q9Z2X1	Hnrnpf	Heterogeneous nuclear ribonucleoprotein F	33	10	556	8	0.47
Q8C052	Map1s	Microtubule-associated protein 1S	10	9	140	9	0.47
Q9Z2I0	Letm1	LETM1 and EF-hand domain-containing protein 1, mitochondrial	9	6	107	6	0.47
P40630	Tfam	Transcription factor A, mitochondrial	12	5	73	5	0.47
O08528	Hk2	Hexokinase-2	16	12	113	11	0.47
P70279	Surf6	Surfeit locus protein 6	15	6	65	6	0.47
F6ZDS4	Tpr	Nucleoprotein TPR	18	44	552	44	0.47
Q8VDF2	Uhrf1	E3 ubiquitin-protein ligase UHRF1	11	9	173	9	0.47
P70388	Rad50	DNA repair protein RAD50	2	4	16	4	0.46
Q9CZU6	Cs	Citrate synthase, mitochondrial	17	8	207	8	0.46
Q6ZWN5	Rps9	40S ribosomal protein S9	57	14	248	14	0.46
P62855	Rps26	40S ribosomal protein S26	20	2	91	2	0.46
Q9WUA2	Farsb	Phenylalanine–tRNA ligase beta subunit	10	7	116	7	0.46
Q8BTT6	Diexf	Digestive organ expansion factor homolog	5	4	39	4	0.46
E9PZC3	Blvrb	Flavin reductase (NADPH)	24	4	51	4	0.46
S4R1S4	Ptprc	Receptor-type tyrosine-protein phosphatase C	5	8	78	8	0.46
Q99K28-2	Arfgap2	Isoform 2 of ADP-ribosylation factor GTPase-activating protein 2	14	8	183	8	0.46
Q9CWL8	Ctnnbl1	Beta-catenin-like protein 1	5	3	26	3	0.46
P62702	Rps4x	40S ribosomal protein S4, X isoform	46	14	554	14	0.46
P20029	Hspa5	78 kDa glucose-regulated protein	61	41	2492	38	0.46
Q9DCD0	Pgd	6-phosphogluconate dehydrogenase, decarboxylating	25	11	361	11	0.46
D3Z7P3-2	Gls	Isoform 2 of Glutaminase kidney isoform, mitochondrial	16	7	145	7	0.46
Q62351	Tfrc	Transferrin receptor protein 1	29	21	674	21	0.46
P33609	Pola1	DNA polymerase alpha catalytic subunit	3	5	28	5	0.46
O35129	Phb2	Prohibitin-2	51	15	525	15	0.46
Q8CCM6-2	Timm21	Isoform 2 of Mitochondrial import inner membrane translocase subunit Tim21	7	2	24	2	0.46
P60521	Gabarapl2	Gamma-aminobutyric acid receptor-associated protein-like 2	12	2	38	2	0.45
Q8K124	Plekho2	Pleckstrin homology domain-containing family O member 2	6	3	59	3	0.45
Q9Z315	Sart1	U4/U6.U5 tri-snRNP-associated protein 1	20	15	158	15	0.45
Q02053	Uba1	Ubiquitin-like modifier-activating enzyme 1	23	19	339	19	0.45
Q08943-2	Ssrp1	Isoform 2 of FACT complex subunit SSRP1	7	5	38	5	0.45
P18654	Rps6ka3	Ribosomal protein S6 kinase alpha-3	4	3	16	3	0.45
Q62318	Trim28	Transcription intermediary factor 1-beta	13	9	191	9	0.45
Q9WTP6	Ak2	Adenylate kinase 2, mitochondrial	35	7	197	7	0.45
P58064	Mrps6	28S ribosomal protein S6, mitochondrial	14	2	41	2	0.45
Q8CD76	Klc1	Kinesin light chain 1	3	2	16	2	0.45
Q9EPL9	Acox3	Peroxisomal acyl-coenzyme A oxidase 3	3	3	9	3	0.45
P12787	Cox5a	Cytochrome c oxidase subunit 5A, mitochondrial	16	2	22	2	0.45

Accession	**Gene**	**Description**	**Coverage**	**Peptides**	**Unique Peptides**	**PSMs**	**[1]*pksP*/wt**
B1AXP6-4	Tomm5	Isoform 4 of Mitochondrial import receptor subunit TOM5 homolog	14	3	36	3	0.45
Q8BHN3-2	Ganab	Isoform 2 of Neutral alpha-glucosidase AB	18	16	174	16	0.45
P11983	Tcp1	T-complex protein 1 subunit alpha	36	15	224	15	0.45
P51660	Hsd17b4	Peroxisomal multifunctional enzyme type 2	15	11	186	11	0.45
Q3V3R1	Mthfd1l	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	31	28	478	27	0.45
Q5SWT9	Ikzf1	DNA-binding protein Ikaros	12	7	87	6	0.45
P11499	Hsp90ab1	Heat shock protein HSP 90-beta	48	35	1801	19	0.45
Q31125	Slc39a7	Zinc transporter SLC39A7	7	3	55	3	0.45
P70296	Pebp1	Phosphatidylethanolamine-binding protein 1	44	5	136	5	0.45
P12970	Rpl7a	60S ribosomal protein L7a	41	14	390	14	0.45
P24547	Impdh2	Inosine-5'-monophosphate dehydrogenase 2	20	10	214	9	0.45
P14206	Rpsa	40S ribosomal protein SA	23	5	224	5	0.44
Q9DCW4	Etfb	Electron transfer flavoprotein subunit beta	38	9	300	9	0.44
Q8R0X7	Sgpl1	Sphingosine-1-phosphate lyase 1	23	13	203	13	0.44
Q9CQF0	Mrpl11	39S ribosomal protein L11, mitochondrial	11	3	18	3	0.44
Q9JKR6	Hyou1	Hypoxia up-regulated protein 1	33	29	662	29	0.44
Q9DB05	Napa	Alpha-soluble NSF attachment protein	10	3	60	3	0.44
P63276	Rps17	40S ribosomal protein S17	51	7	200	7	0.44
P80318	Cct3	T-complex protein 1 subunit gamma	35	18	391	18	0.44
A0A0R4J0D3	Stt3b	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	4	3	42	3	0.44
P80313	Cct7	T-complex protein 1 subunit eta	29	15	292	15	0.44
Q9D2L9	Fam111a	Protein FAM111A	3	2	30	2	0.44
Q99K85	Psat1	Phosphoserine aminotransferase	27	11	138	11	0.44
Q9Z1Z2	Strap	Serine-threonine kinase receptor-associated protein	34	10	109	10	0.44
Q8VI75	Ipo4	Importin-4	2	3	16	3	0.44
S4R270	Bin2	Bridging integrator 2	17	9	147	8	0.44
E9PV41	Diaph1	Protein diaphanous homolog 1	3	4	38	4	0.44
Q9DB77	Uqcrc2	Cytochrome b-c1 complex subunit 2, mitochondrial	28	11	379	11	0.44
G3X8T2	Zc3h18	RIKEN cDNA 5830416A07, isoform CRA_c	8	8	136	8	0.44
Q99N87	Mrps5	28S ribosomal protein S5, mitochondrial	10	5	94	5	0.44
Q3U7R1	Esyt1	Extended synaptotagmin-1	3	4	39	4	0.44
P08775	Polr2a	DNA-directed RNA polymerase II subunit RPB1	8	14	149	14	0.44
Q9QYG0	Ndrg2	Protein NDRG2	6	2	17	2	0.44
Q9R059	Fhl3	Four and a half LIM domains protein 3	14	3	34	3	0.44
P62242	Rps8	40S ribosomal protein S8	35	8	301	8	0.44
P30204	Msr1	Macrophage scavenger receptor types I and II	11	5	167	5	0.43
P62264	Rps14	40S ribosomal protein S14	39	8	352	8	0.43
Q3THE2	Myl12b	Myosin regulatory light chain 12B	29	5	87	5	0.43
Q9D8V0-4	Hm13	Isoform 4 of Minor histocompatibility antigen H13	4	2	82	2	0.43
Q5SWU9-2	Acaca	Isoform 2 of Acetyl-CoA carboxylase 1	2	6	37	6	0.43

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9DBH5	Lman2	Vesicular integral-membrane protein VIP36	21	6	63	6	0.43
Q00612	G6pdx	Glucose-6-phosphate 1-dehydrogenase X	27	16	278	16	0.43
Q9Z1R2	Bag6	Large proline-rich protein BAG6	8	7	67	7	0.43
P35564	Canx	Calnexin	37	28	752	28	0.43
Q6NZJ6	Eif4g1	Eukaryotic translation initiation factor 4 gamma 1	18	29	520	1	0.43
H3BL08	Cers6	Ceramide synthase 6	4	2	30	2	0.43
Q8VCT3	Rnpep	Aminopeptidase B	4	3	62	3	0.43
Q8JZZ5	Pitpnb	Phosphatidylinositol transfer protein beta isoform	13	4	42	3	0.43
P48962	Slc25a4	ADP/ATP translocase 1	31	11	921	5	0.43
O88569	Hnrnpa2b1	Heterogeneous nuclear ribonucleoproteins A2/B1	44	16	1690	12	0.43
Q6P9L6	Kif15	Kinesin-like protein KIF15	5	6	43	6	0.43
Q9CQS8	Sec61b	Protein transport protein Sec61 subunit beta	38	3	143	3	0.43
Q80UU9	Pgrmc2	Membrane-associated progesterone receptor component 2	15	2	26	2	0.43
Q99PV0	Prpf8	Pre-mRNA-processing-splicing factor 8	14	29	298	29	0.43
Q7TPD0	Ints3	Integrator complex subunit 3	3	4	27	4	0.43
Q99LL5	Pwp1	Periodic tryptophan protein 1 homolog	2	2	41	2	0.43
Q9D2V8	Mfsd10	Major facilitator superfamily domain-containing protein 10	4	2	30	2	0.43
Q9JHF5	Tcirg1	V-type proton ATPase subunit a	16	7	44	7	0.43
Q69ZA1	Cdk13	Cyclin-dependent kinase 13	2	3	25	2	0.43
O08795-2	Prkcsh	Isoform 2 of Glucosidase 2 subunit beta	14	9	139	9	0.42
Q6GQT9	Nomo1	Nodal modulator 1	7	8	159	8	0.42
A0A0R4J140	Cluh	Clustered mitochondria protein homolog	9	13	76	13	0.42
G3X9M0	Dap3	28S ribosomal protein S29, mitochondrial	11	4	17	4	0.42
Q8K4Z5	Sf3a1	Splicing factor 3A subunit 1	26	18	335	18	0.42
Q3U319	Rnf40	E3 ubiquitin-protein ligase BRE1B	4	5	42	5	0.42
P29758	Oat	Ornithine aminotransferase, mitochondrial	16	5	125	5	0.42
D3Z4B2	Napg	Gamma-soluble NSF attachment protein (Fragment)	7	3	23	3	0.42
Q569Z6	Thrap3	Thyroid hormone receptor-associated protein 3	21	19	257	19	0.42
Q8CGC7	Eprs	Bifunctional glutamate/proline--tRNA ligase	17	25	335	24	0.42
P49717	Mcm4	DNA replication licensing factor MCM4	11	13	114	13	0.42
A0A0R4J093	Cmpk1	UMP-CMP kinase	15	3	82	3	0.42
F8VQE9	Agap3	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	2	2	13	2	0.42
Q8BVE3	Atp6v1h	V-type proton ATPase subunit H	7	3	85	3	0.42
P61021	Rab5b	Ras-related protein Rab-5B	15	3	79	1	0.42
Q78YY6	Dnajc15	DnaJ homolog subfamily C member 15	13	2	21	2	0.42
A0A140T8M7	Rpl23a-ps3	Protein Rpl23a-ps3	41	10	414	10	0.42
Q9WV03	Fam50a	Protein FAM50A	6	2	13	2	0.42
A0A0R4J0G0	Pck2	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	7	5	56	5	0.42
G3UZA7	Sumo3	Small ubiquitin-related modifier	18	2	73	1	0.42
Q9D7W5	Med8	Mediator of RNA polymerase II transcription subunit 8	8	2	23	2	0.42

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q924T2	Mrps2	28S ribosomal protein S2, mitochondrial	11	2	43	2	0.42
A0A0G2JGW9	Fubp1	Far upstream element-binding protein 1	33	20	769	16	0.42
Q569Z5	Ddx46	Probable ATP-dependent RNA helicase DDX46	9	11	108	11	0.41
Q3UA06	Trip13	Pachytene checkpoint protein 2 homolog	3	2	19	2	0.41
Q8BH59	Slc25a12	Calcium-binding mitochondrial carrier protein Aralar1	17	10	100	8	0.41
P24270	Cat	Catalase	12	6	75	6	0.41
Q9Z2N8	Actl6a	Actin-like protein 6A	10	4	27	4	0.41
Q80UW8	Polr2e	DNA-directed RNA polymerases I, II, and III subunit RPABC1	23	5	70	5	0.41
Q8K1Z0	Coq9	Ubiquinone biosynthesis protein COQ9, mitochondrial	9	3	23	3	0.41
Q8BI84	Mia3	Melanoma inhibitory activity protein 3	3	8	64	8	0.41
Q9R1C7	Prpf40a	Pre-mRNA-processing factor 40 homolog A	10	9	95	9	0.41
Q8K2C7	Os9	Protein -9	9	7	79	7	0.41
P30681	Hmgb2	High mobility group protein B2	40	8	231	8	0.41
P24369	Ppib	Peptidyl-prolyl cis-trans isomerase B	33	8	280	8	0.41
P62852	Rps25	40S ribosomal protein S25	36	6	257	6	0.41
P11438	Lamp1	Lysosome-associated membrane glycoprotein 1	5	2	55	2	0.41
Q8R5H1	Usp15	Ubiquitin carboxyl-terminal hydrolase 15	3	4	27	4	0.41
P08113	Hsp90b1	Endoplasmin	33	30	1387	29	0.41
H9KV00	Son	Protein SON	4	8	123	8	0.41
Q9Z1Q9	Vars	Valine--tRNA ligase	19	20	288	20	0.41
Q9D172	D10Jhu81e	ES1 protein homolog, mitochondrial	10	3	38	3	0.41
P62830	Rpl23	60S ribosomal protein L23	24	3	160	3	0.41
Q9JIW9	Ralb	Ras-related protein Ral-B	21	6	116	6	0.41
O35379	Abcc1	Multidrug resistance-associated protein 1	1	3	33	3	0.41
Q8CG48	Smc2	Structural maintenance of chromosomes protein 2	12	16	130	16	0.41
Q3U186	Rars2	Probable arginine--tRNA ligase, mitochondrial	5	3	20	3	0.41
A0A0R4J1G5	Erlin1	Erlin-1	19	8	108	5	0.41
Q8BJU0	Sgta	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	17	6	87	6	0.40
Q99P31	Hspbp1	Hsp70-binding protein 1	7	3	15	3	0.40
P60766	Cdc42	Cell division control protein 42 homolog	19	3	110	3	0.40
P19096	Fasn	Fatty acid synthase	17	38	502	38	0.40
Q8CGF7	Tcerg1	Transcription elongation regulator 1	8	11	90	11	0.40
P18242	Ctsd	Cathepsin D	17	7	156	7	0.40
Q8CIN4	Pak2	Serine/threonine-protein kinase PAK 2	19	9	87	8	0.40
Q5F2E7-2	Nufip2	Isoform 2 of Nuclear fragile X mental retardation-interacting protein 2	6	4	56	4	0.40
O70503	Hsd17b12	Very-long-chain 3-oxoacyl-CoA reductase	10	4	112	4	0.40
Q9D0B0	Srsf9	Serine/arginine-rich splicing factor 9	17	4	66	4	0.40
Q8BX10	Pgam5	Serine/threonine-protein phosphatase PGAM5, mitochondrial	25	8	132	8	0.40
Q8K2T8	Paf1	RNA polymerase II-associated factor 1 homolog	6	3	24	3	0.40
E9QN31	Nop2	Probable 28S rRNA (cytosine-C(5))-methyltransferase	17	13	278	13	0.40

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q1HFZ0	Nsun2	tRNA (cytosine(34)-C(5))-methyltransferase	17	11	151	11	0.40
Q9CXT8	Pmpcb	Mitochondrial-processing peptidase subunit beta	9	5	143	4	0.40
Q03265	Atp5a1	ATP synthase subunit alpha, mitochondrial	45	24	1124	24	0.40
E9QM77	Atxn2	Ataxin-2	1	2	14	1	0.40
A0A0R4J1W7	Cdc23	CDC23 (Cell division cycle 23, yeast, homolog), isoform CRA_c	4	2	8	2	0.40
B2RXS4	Plxnb2	Plexin-B2	4	8	61	8	0.40
Q8BFZ9	Erlin2	Erlin-2	13	5	81	2	0.40
P47738	Aldh2	Aldehyde dehydrogenase, mitochondrial	40	16	358	16	0.40
Q9CQF4	N/A	Uncharacterized protein C6orf203 homolog	8	2	13	2	0.40
Q99020	Hnrnpab	Heterogeneous nuclear ribonucleoprotein A/B	35	9	287	9	0.40
Q9D8S4	Rexo2	Oligoribonuclease, mitochondrial	7	2	23	2	0.40
E9PVX6	Mki67	Protein Mki67	26	72	1287	72	0.40
A2AH85	Eftud2	116 kDa U5 small nuclear ribonucleoprotein component	17	15	188	14	0.40
Q8R3N1	Nop14	Nucleolar protein 14	7	7	38	7	0.40
Q9QYJ0	Dnaja2	DnaJ homolog subfamily A member 2	12	6	143	6	0.40
G3X8T3	Ctsa	Carboxypeptidase	6	3	186	3	0.39
Q9Z1Z0	Uso1	General vesicular transport factor p115	3	3	19	3	0.39
Q68FH4	Galk2	N-acetylgalactosamine kinase	4	2	18	2	0.39
Q9CR00	Psmd9	26S proteasome non-ATPase regulatory subunit 9	13	3	21	3	0.39
Q9WUM3	Coro1b	Coronin-1B	3	2	39	2	0.39
G5E924	Hnrnpl	Heterogeneous nuclear ribonucleoprotein L (Fragment)	35	17	694	17	0.39
P56382	Atp5e	ATP synthase subunit epsilon, mitochondrial	30	2	54	2	0.39
Q810V0	Mphosph10	U3 small nucleolar ribonucleoprotein protein MPP10	6	4	43	4	0.39
Q07813	Bax	Apoptosis regulator BAX	13	2	42	2	0.39
E9PW66	Nap1l1	Nucleosome assembly protein 1-like 1	6	2	34	1	0.39
P35991	Btk	Tyrosine-protein kinase BTK	2	2	14	2	0.39
Q9DBZ5	Eif3k	Eukaryotic translation initiation factor 3 subunit K	11	2	13	2	0.39
Q5SFM8	Rbm27	RNA-binding protein 27	3	3	15	3	0.39
Q80UG5	Sep-09	Septin-9	6	4	52	4	0.39
Q9ERA6	Tfip11	Tuftelin-interacting protein 11	2	2	20	2	0.39
Q8K310	Matr3	Matrin-3	23	18	435	18	0.39
Q8BLN5	Lss	Lanosterol synthase	6	5	49	5	0.39
Q61033	Tmpo	Lamina-associated polypeptide 2, isoforms alpha/zeta	26	14	264	6	0.39
P70404	Idh3g	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	9	4	98	4	0.39
P40142	Tkt	Transketolase	35	20	676	20	0.39
Q80ZS3	Mrps26	28S ribosomal protein S26, mitochondrial	18	4	74	4	0.39
A0A0R4IZW7	Trmt1	tRNA (guanine(26)-N(2))-dimethyltransferase	6	4	38	4	0.39
Q8CGY8	Ogt	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	4	5	35	5	0.39
Q8R180	Ero1a	ERO1-like protein alpha	9	4	42	4	0.39
Q9CYA6	Zcchc8	Zinc finger CCHC domain-containing protein 8	8	4	41	4	0.38

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9CQI3	Gmfb	Glia maturation factor beta	14	2	38	2	0.38
P84096	Rhog	Rho-related GTP-binding protein RhoG	17	3	24	3	0.38
Q921G7	Etfdh	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	4	3	32	3	0.38
Q3UHX9	D2Wsu81e	Putative methyltransferase C9orf114 homolog	5	2	35	2	0.38
Q80VL1	Tdrkh	Tudor and KH domain-containing protein	6	4	63	4	0.38
Q921T2	Tor1aip1	Torsin-1A-interacting protein 1	10	5	64	5	0.38
Q8BMS1	Hadha	Trifunctional enzyme subunit alpha, mitochondrial	23	16	274	16	0.38
P21958	Tap1	Antigen peptide transporter 1	4	3	31	3	0.38
P84099	Rpl19	60S ribosomal protein L19	35	8	255	8	0.38
P97868	Rbbp6	E3 ubiquitin-protein ligase RBBP6	3	6	36	6	0.38
Q9JI75	Nqo2	Ribosyldihydronicotinamide dehydrogenase [quinone]	8	2	19	2	0.38
Q922Q4	Pycr2	Pyrroline-5-carboxylate reductase 2	23	8	138	8	0.38
A2A432	Cul4b	Cullin-4B	8	8	80	7	0.38
P43275	Hist1h1a	Histone H1.1	23	5	392	3	0.38
P56960	Exosc10	Exosome component 10	6	6	89	6	0.38
Q80WJ7	Mtdh	Protein LYRIC	32	17	256	17	0.38
Q3UDW8	Hgsnat	Heparan-alpha-glucosaminide N-acetyltransferase	3	2	21	2	0.38
G5E870	Trip12	E3 ubiquitin-protein ligase TRIP12	4	7	59	7	0.38
Q8BL97	Srsf7	Serine/arginine-rich splicing factor 7	18	5	124	4	0.38
Q5SYD0	Myo1d	Unconventional myosin-Id	9	11	157	11	0.38
Q61102	Abcb7	ATP-binding cassette sub-family B member 7, mitochondrial	4	3	55	3	0.38
P83917	Cbx1	Chromobox protein homolog 1	18	3	25	2	0.38
P50516	Atp6v1a	V-type proton ATPase catalytic subunit A	20	12	258	12	0.38
Q8BG15	Ctdspl2	CTD small phosphatase-like protein 2	2	2	30	2	0.38
P61161	Actr2	Actin-related protein 2	16	5	54	5	0.38
Q9Z1J3	Nfs1	Cysteine desulfurase, mitochondrial	12	5	59	5	0.38
P35980	Rpl18	60S ribosomal protein L18	37	6	344	6	0.38
P14152	Mdh1	Malate dehydrogenase, cytoplasmic	19	8	202	8	0.38
Q99JX3	Gorasp2	Golgi reassembly-stacking protein 2	6	3	69	3	0.38
Q9EPU0	Upf1	Regulator of nonsense transcripts 1	12	12	70	12	0.37
E9Q5C9	Nolc1	Protein Nolc1	24	22	792	22	0.37
Q8BW10	Nob1	RNA-binding protein NOB1	9	5	77	5	0.37
Q9CY57	Chtop	Chromatin target of PRMT1 protein	10	2	87	2	0.37
P62259	Ywhae	14-3-3 protein epsilon	52	14	333	12	0.37
Q8BK72	Mrps27	28S ribosomal protein S27, mitochondrial	4	2	28	2	0.37
P10852-2	Slc3a2	Isoform 2 of 4F2 cell-surface antigen heavy chain	21	11	200	11	0.37
Q61881	Mcm7	DNA replication licensing factor MCM7	20	14	168	14	0.37
Q9EQH2	Erap1	Endoplasmic reticulum aminopeptidase 1	4	4	57	4	0.37
Q8K078	Slco4a1	Solute carrier organic anion transporter family member 4A1	4	3	54	3	0.37
Q91VR2	Atp5c1	ATP synthase subunit gamma, mitochondrial	22	7	269	7	0.37

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
A2ADY9	Ddi2	Protein DDI1 homolog 2	4	2	28	2	0.37
P61750	Arf4	ADP-ribosylation factor 4	27	4	168	2	0.37
P97369	Ncf4	Neutrophil cytosol factor 4	7	2	11	2	0.37
Q9D1D4	Tmed10	Transmembrane emp24 domain-containing protein 10	31	6	111	6	0.37
P62137	Ppp1ca	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	15	4	25	2	0.37
Q9CPQ8	Atp5l	ATP synthase subunit g, mitochondrial	33	2	21	2	0.37
Q9CQ92	Fis1	Mitochondrial fission 1 protein	8	2	43	2	0.36
P18155	Mthfd2	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	13	5	101	5	0.36
Q99L04	Dhrs1	Dehydrogenase/reductase SDR family member 1	9	3	40	3	0.36
P59325	Eif5	Eukaryotic translation initiation factor 5	12	7	87	7	0.36
Q61425	Hadh	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	14	6	65	6	0.36
Q9JK81	Myg1	UPF0160 protein MYG1, mitochondrial	7	3	33	3	0.36
O08579	Emd	Emerin	29	6	66	6	0.36
Q6PFB2	Rcc1	Rcc1 protein	17	6	113	6	0.36
Q9R0A0	Pex14	Peroxisomal membrane protein PEX14	8	4	24	4	0.36
Q6PR54-3	Rif1	Isoform 3 of Telomere-associated protein RIF1	4	10	99	10	0.36
P26369	U2af2	Splicing factor U2AF 65 kDa subunit	25	6	102	6	0.36
P61087	Ube2k	Ubiquitin-conjugating enzyme E2 K	24	4	30	4	0.36
P42125	Eci1	Enoyl-CoA delta isomerase 1, mitochondrial	13	4	12	4	0.36
Q9EP69	Sacm1l	Phosphatidylinositide phosphatase SAC1	12	8	90	8	0.36
Q9CQR4	Acot13	Acyl-coenzyme A thioesterase 13	15	2	19	2	0.36
P84091	Ap2m1	AP-2 complex subunit mu	13	7	100	7	0.36
Q921M3	Sf3b3	Splicing factor 3B subunit 3	11	13	245	13	0.36
P21279	Gnaq	Guanine nucleotide-binding protein G(q) subunit alpha	17	6	61	5	0.36
Q8K1B8	Fermt3	Fermitin family homolog 3	17	12	169	12	0.36
Q9Z1F9	Uba2	SUMO-activating enzyme subunit 2	13	7	82	7	0.36
Q8CFI7	Polr2b	DNA-directed RNA polymerase II subunit RPB2	8	11	134	11	0.36
P35585	Ap1m1	AP-1 complex subunit mu-1	3	2	22	2	0.36
G3XA17	Eif4g2	Eukaryotic translation initiation factor 4 gamma 2	13	11	176	11	0.36
B2RY56	Rbm25	RNA-binding protein 25	7	6	55	6	0.36
P17742	Ppia	Peptidyl-prolyl cis-trans isomerase A	42	8	332	8	0.36
Q7TPV4	Mybbp1a	Myb-binding protein 1A	22	26	805	26	0.36
P62827	Ran	GTP-binding nuclear protein Ran	22	7	293	7	0.36
Q8C5N3	Cwc22	Pre-mRNA-splicing factor CWC22 homolog	7	7	56	7	0.36
Q8CGK3	Lonp1	Lon protease homolog, mitochondrial	6	8	133	8	0.36
E9QAZ2	Gm10020	Ribosomal protein L15	44	11	320	11	0.36
Q99KI0	Aco2	Aconitate hydratase, mitochondrial	34	23	484	23	0.36
Q922D8	Mthfd1	C-1-tetrahydrofolate synthase, cytoplasmic	17	18	212	17	0.36
Q8K019	Bclaf1	Bcl-2-associated transcription factor 1	10	11	141	11	0.36

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q8VCY6	Utp6	U3 small nucleolar RNA-associated protein 6 homolog	11	7	53	7	0.36
Q8WTY4	Ciapin1	Anamorsin	16	3	11	3	0.36
Q9D8N0	Eef1g	Elongation factor 1-gamma	29	16	396	16	0.36
Q922F4	Tubb6	Tubulin beta-6 chain	22	8	300	3	0.36
P52503	Ndufs6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	15	2	11	2	0.36
P61082	Ube2m	NEDD8-conjugating enzyme Ubc12	25	5	90	5	0.35
O35381	Anp32a	Acidic leucine-rich nuclear phosphoprotein 32 family member A	19	6	93	3	0.35
Q01320	Top2a	DNA topoisomerase 2-alpha	20	34	622	27	0.35
Q8BKC5	Ipo5	Importin-5	10	9	86	9	0.35
O35955	Psmb10	Proteasome subunit beta type-10	11	3	36	3	0.35
Q5NCR9	Nsrp1	Nuclear speckle splicing regulatory protein 1	7	3	27	3	0.35
Q9CQA3	Sdhb	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	16	6	99	6	0.35
Q9CPQ1	Cox6c	Cytochrome c oxidase subunit 6C	30	4	112	4	0.35
Q8BGS2	Bola2	BolA-like protein 2	18	2	32	2	0.35
A2A7S7	Yars	Tyrosine--tRNA ligase	18	11	197	11	0.35
Q6P5E4	Uggt1	UDP-glucose:glycoprotein glucosyltransferase 1	10	17	230	17	0.35
Q9CYH6	Rrs1	Ribosome biogenesis regulatory protein homolog	29	11	242	11	0.35
P61804	Dad1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	26	3	44	3	0.35
Q6P8I4	Pcnp	PEST proteolytic signal-containing nuclear protein	40	7	111	7	0.35
O88532	Zfr	Zinc finger RNA-binding protein	8	8	64	8	0.35
Q9QYC0	Add1	Alpha-adducin	6	4	32	4	0.35
Q8QZT1	Acat1	Acetyl-CoA acetyltransferase, mitochondrial	36	13	299	13	0.35
Q80X41	Vrk1	Serine/threonine-protein kinase VRK1	9	4	26	4	0.35
D3Z7M5	Nop16	Nucleolar protein 16	22	5	103	5	0.35
Q91YK2	Rrp1b	Ribosomal RNA processing protein 1 homolog B	16	10	107	10	0.35
Q9ERK4	Cse1l	Exportin-2	9	8	86	8	0.35
A0A087WR52	Agfg1	Arf-GAP domain and FG repeat-containing protein 1 (Fragment)	12	4	107	4	0.35
E9PX68	Slc4a1ap	Protein Slc4a1ap	3	3	18	3	0.35
P63038	Hspd1	60 kDa heat shock protein, mitochondrial	55	29	1813	29	0.35
Q8BHB4	Wdr3	WD repeat-containing protein 3	3	3	24	3	0.35
P26516	Psmd7	26S proteasome non-ATPase regulatory subunit 7	16	5	103	5	0.35
Q06138	Cab39	Calcium-binding protein 39	4	2	24	2	0.35
P56959	Fus	RNA-binding protein FUS	22	10	222	8	0.35
P28033	Cebpb	CCAAT/enhancer-binding protein beta	13	3	20	3	0.34
Q9Z1X4-3	Ilf3	Isoform 3 of Interleukin enhancer-binding factor 3	16	14	123	14	0.34
P60843	Eif4a1	Eukaryotic initiation factor 4A-I	49	19	403	16	0.34
Q3TFK5	Gpatch4	G patch domain-containing protein 4	8	3	76	3	0.34
Q3UQ84	Tars2	Threonine--tRNA ligase, mitochondrial	6	5	70	5	0.34
P30993	C5ar1	C5a anaphylatoxin chemotactic receptor 1	6	2	65	2	0.34
Q5H8C4	Vps13a	Vacuolar protein sorting-associated protein 13A	1	2	12	2	0.34

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
E9Q4S7	Ptprj	Receptor-type tyrosine-protein phosphatase eta	1	2	15	2	0.34
E9Q8Z5	Ctnnd1	Catenin delta-1	10	10	87	10	0.34
Q9CZE3	Rab32	Ras-related protein Rab-32	17	3	60	3	0.34
O35465-2	Fkbp8	Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP8	11	5	88	5	0.34
Q9D7N3	Mrps9	28S ribosomal protein S9, mitochondrial	8	4	59	4	0.34
Q9CZ30	Ola1	Obg-like ATPase 1	14	6	86	6	0.34
P63085	Mapk1	Mitogen-activated protein kinase 1	19	7	63	7	0.34
A0A0G2JGL0	Ube2d3	Ubiquitin-conjugating enzyme E2 D3	12	2	37	2	0.34
E9PXU2	Adam17	Disintegrin and metalloproteinase domain-containing protein 17	3	3	20	3	0.34
Q9CQU1	Mfap1	Microfibrillar-associated protein 1	9	3	76	3	0.34
Q8CH18	Ccar1	Cell division cycle and apoptosis regulator protein 1	5	6	69	6	0.34
Q8VCM8	Ncln	Nicalin	12	8	125	8	0.34
Q9Z2I9	Sucla2	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	19	9	166	9	0.34
P11835	Itgb2	Integrin beta-2	12	8	123	8	0.34
Q9CZW5	Tomm70	Mitochondrial import receptor subunit TOM70	9	6	137	6	0.34
Q9JHP7	Kdelc1	KDEL motif-containing protein 1	8	4	52	3	0.34
Q9EPE9	Atp13a1	Manganese-transporting ATPase 13A1	7	7	72	7	0.34
P54103	Dnajc2	DnaJ homolog subfamily C member 2	9	5	61	5	0.34
Q8BNW9	Kbtbd11	Kelch repeat and BTB domain-containing protein 11	7	4	24	4	0.34
E9Q3X0	Mvp	Major vault protein	14	12	147	12	0.34
Q9DC70	Ndufs7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	7	2	87	2	0.34
O55023	Impa1	Inositol monophosphatase 1	9	3	20	3	0.34
Q6IRU5-2	Cltb	Isoform 2 of Clathrin light chain B	19	5	67	5	0.33
Q3UI84	Rfc4	Replication factor C subunit 4	17	7	73	7	0.33
Q9D6R2	Idh3a	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	21	9	282	9	0.33
Q6P5B0	Rrp12	RRP12-like protein	10	12	136	12	0.33
Q6Y7W8	Gigyf2	PERQ amino acid-rich with GYF domain-containing protein 2	3	5	41	5	0.33
Q8C7K6	Pcyox1l	Prenylcysteine oxidase-like	4	2	30	2	0.33
Q9CQV8	Ywhab	14-3-3 protein beta/alpha	32	9	639	3	0.33
Q8BG81	Poldip3	Polymerase delta-interacting protein 3	17	8	81	8	0.33
Q9CZ13	Uqcrc1	Cytochrome b-c1 complex subunit 1, mitochondrial	17	8	138	7	0.33
P05213	Tuba1b	Tubulin alpha-1B chain	42	15	668	4	0.33
Q6NTA4	Rragb	Ras-related GTP-binding protein B	5	2	12	2	0.33
Q62523	Zyx	Zyxin	10	5	64	5	0.33
Q3UDM0	Mob1b	MOB kinase activator 1B	10	2	19	2	0.33
Q6P069	Sri	Sorcin	14	3	87	3	0.33
Q8R4X3	Rbm12	RNA-binding protein 12	7	6	52	6	0.33
P30416	Fkbp4	Peptidyl-prolyl cis-trans isomerase FKBP4	27	15	251	15	0.33
P97371	Psme1	Proteasome activator complex subunit 1	16	4	25	4	0.33
P49722	Psma2	Proteasome subunit alpha type-2	16	4	61	4	0.33

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
E9PVA8	Gcn1	eIF-2-alpha kinase activator GCN1	5	16	99	16	0.33
Q7TMK9	Syncrip	Heterogeneous nuclear ribonucleoprotein Q	17	11	183	9	0.33
Q9D0R8	Lsm12	Protein LSM12 homolog	5	2	21	2	0.33
A0A0N4SUH4	Pum3	Pumilio homolog 3	10	8	130	8	0.33
Q5SXR6	Cltc	Clathrin heavy chain	24	34	651	34	0.33
Q62426	Cstb	Cystatin-B	39	3	21	3	0.33
Q9DCT2	Ndufs3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	17	4	35	4	0.33
Q8VEH3	Arl8a	ADP-ribosylation factor-like protein 8A	14	3	48	1	0.33
Q8C7R4	Uba6	Ubiquitin-like modifier-activating enzyme 6	4	4	38	4	0.33
Q9DBR1	Xrn2	5'-3' exoribonuclease 2	8	9	100	9	0.32
Q9Z1K5	Arih1	E3 ubiquitin-protein ligase ARIH1	5	2	6	2	0.32
E9PUU4	Gemin5	Gem-associated protein 5	1	2	11	2	0.32
P53995	Anapc1	Anaphase-promoting complex subunit 1	1	2	27	2	0.32
Q9D8E6	Rpl4	60S ribosomal protein L4	35	15	699	15	0.32
Q6PB66	Lrpprc	Leucine-rich PPR motif-containing protein, mitochondrial	15	22	229	22	0.32
Q924Z4	Cers2	Ceramide synthase 2	8	3	38	3	0.32
Q8BYA0	Tbcd	Tubulin-specific chaperone D	1	2	12	2	0.32
F6VW30	Ywhaq	14-3-3 protein theta (Fragment)	24	8	412	3	0.32
G3X8R0	Reep5	Receptor expression-enhancing protein	14	3	101	3	0.32
Q8K297	Colgalt1	Procollagen galactosyltransferase 1	8	6	45	6	0.32
Q8BL66	Eea1	Early endosome antigen 1	8	10	77	10	0.32
Q91VD9	Ndufs1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	28	18	311	18	0.32
Q9CZN7	Shmt2	Serine hydroxymethyltransferase	32	15	541	15	0.32
Q8R050	Gspt1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	15	9	128	9	0.32
Q6P1Y9	Exoc1	Exocyst complex component 1	2	2	14	2	0.32
E9Q035	Gm20425	Protein Gm20425	7	6	106	6	0.32
Q9JMG1	Edf1	Endothelial differentiation-related factor 1	41	6	113	6	0.32
Q9Z1P6	Ndufa7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	17	2	65	2	0.32
O70492	Snx3	Sorting nexin-3	25	4	68	4	0.32
Q8R3C6	Rbm19	Probable RNA-binding protein 19	10	8	100	8	0.32
Q8BP27	Sfr1	Swi5-dependent recombination DNA repair protein 1 homolog	6	2	28	2	0.31
E9PYH2	Acot7	Cytosolic acyl coenzyme A thioester hydrolase	10	3	18	3	0.31
P61205	Arf3	ADP-ribosylation factor 3	34	5	213	3	0.31
P83741-3	Wnk1	Isoform 3 of Serine/threonine-protein kinase WNK1	2	6	50	6	0.31
P97379	G3bp2	Ras GTPase-activating protein-binding protein 2	8	4	59	3	0.31
A2AL50	Agps	Alkyldihydroxyacetonephosphate synthase, peroxisomal	2	3	56	3	0.31
Q8K205	Pop1	Blood vessel epicardial substance	2	3	31	3	0.31
A2A9Q2	Nrd1	Nardilysin	1	2	33	2	0.31
Q9DBG6	Rpn2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	27	11	197	11	0.31
Q8BTS0	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	36	25	729	21	0.31

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
A4QPD3	Rel	Proto-oncogene c-Rel	6	4	70	2	0.31
Q8K2B3	Sdha	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	14	8	169	8	0.31
P54116	Stom	Erythrocyte band 7 integral membrane protein	39	9	473	9	0.31
P07901	Hsp90aa1	Heat shock protein HSP 90-alpha	40	28	1330	13	0.31
O35316	Slc6a6	Sodium- and chloride-dependent taurine transporter	5	3	61	3	0.31
Q810U5	Ccdc50	Coiled-coil domain-containing protein 50	6	2	16	2	0.31
Q9DCD2	Xab2	Pre-mRNA-splicing factor SYF1	12	11	69	11	0.31
Q9DB20	Atp5o	ATP synthase subunit O, mitochondrial	29	6	112	6	0.31
Q3UH70	Brd4	Bromodomain-containing protein 4	2	5	48	5	0.31
F8VQ95	Tacc1	Transforming acidic coiled-coil-containing protein 1	2	2	15	2	0.31
G3UWS4	Ppp2r1b	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	4	3	55	2	0.31
P52293	Kpna2	Importin subunit alpha-1	24	9	89	9	0.31
O89053	Coro1a	Coronin-1A	28	13	396	13	0.31
Q91YW3	Dnajc3	DnaJ homolog subfamily C member 3	19	10	156	10	0.31
Q9JHI5	Ivd	Isovaleryl-CoA dehydrogenase, mitochondrial	7	3	37	3	0.31
Q9Z110	Aldh18a1	Delta-1-pyrroline-5-carboxylate synthase	19	15	222	15	0.31
Q6NZF1	Zc3h11a	Zinc finger CCCH domain-containing protein 11A	15	11	137	11	0.31
Q62383	Supt6h	Transcription elongation factor SPT6	3	6	65	6	0.31
A0A0R4J0B7	Sdad1	Protein SDA1 homolog	7	5	56	5	0.31
Q9CQI7	Snrpb2	U2 small nuclear ribonucleoprotein B''	27	6	219	5	0.31
Q99LC5	Etfa	Electron transfer flavoprotein subunit alpha, mitochondrial	27	7	235	7	0.31
P29416	Hexa	Beta-hexosaminidase subunit alpha	5	3	46	3	0.30
Q99N89	Mrpl43	39S ribosomal protein L43, mitochondrial	9	2	46	2	0.30
P29351-2	Ptpn6	Isoform 2 of Tyrosine-protein phosphatase non-receptor type 6	27	16	335	16	0.30
P18760	Cfl1	Cofilin-1	42	10	373	9	0.30
Q99KC8	Vwa5a	von Willebrand factor A domain-containing protein 5A	9	6	43	6	0.30
Q9QZE5	Copg1	Coatomer subunit gamma-1	6	5	59	3	0.30
Q5SUF2-2	Luc7l3	Isoform 2 of Luc7-like protein 3	10	6	67	6	0.30
F6YVP7	Gm10260	Protein Gm10260	48	12	592	12	0.30
Q8K1R7	Nek9	Serine/threonine-protein kinase Nek9	3	3	19	3	0.30
Q8BYC6	Taok3	Serine/threonine-protein kinase TAO3	8	9	37	9	0.30
Q6NV83	U2surp	U2 snRNP-associated SURP motif-containing protein	9	9	100	9	0.30
O55098	Stk10	Serine/threonine-protein kinase 10	10	10	97	9	0.30
O55143	Atp2a2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	23	19	319	17	0.30
P57787	Slc16a3	Monocarboxylate transporter 4	7	3	25	3	0.29
P45952	Acadm	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	13	5	50	5	0.29
P19253	Rpl13a	60S ribosomal protein L13a	38	10	308	10	0.29
Q9Z0M5	Lipa	Lysosomal acid lipase/cholesteryl ester hydrolase	4	2	18	2	0.29
P68372	Tubb4b	Tubulin beta-4B chain	27	10	685	2	0.29
Q64378	Fkbp5	Peptidyl-prolyl cis-trans isomerase FKBP5	9	4	48	4	0.29

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
F8WGM5	Stxbp2	Syntaxin-binding protein 2 (Fragment)	5	3	45	3	0.29
Q91ZW3	Smarca5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	21	24	393	24	0.29
Q60668	Hnrnpd	Heterogeneous nuclear ribonucleoprotein D0	23	9	308	9	0.29
Q8K4P0	Wdr33	pre-mRNA 3' end processing protein WDR33	3	4	68	4	0.29
Q3U1J4	Ddb1	DNA damage-binding protein 1	12	14	174	14	0.29
P52633	Stat6	Signal transducer and transcription activator 6	5	5	57	4	0.29
Q3V1V3	Esf1	ESF1 homolog	7	7	35	7	0.29
P62869	Tceb2	Transcription elongation factor B polypeptide 2	27	4	60	4	0.29
Q9DCC4	Pycrl	Pyrroline-5-carboxylate reductase 3	6	2	17	2	0.29
Q8R1B4	Eif3c	Eukaryotic translation initiation factor 3 subunit C	14	16	158	16	0.29
Q80Y44	Ddx10	Probable ATP-dependent RNA helicase DDX10	3	4	38	4	0.29
Q99LC8	Eif2b1	Translation initiation factor eIF-2B subunit alpha	5	2	19	2	0.29
P58242	Smpdl3b	Acid sphingomyelinase-like phosphodiesterase 3b	7	3	62	3	0.29
O89017	Lgmn	Legumain	11	3	37	3	0.29
Q9CZU3	Skiv2l2	Superkiller viralicidic activity 2-like 2	7	8	104	8	0.29
P17047-2	Lamp2	Isoform LAMP-2B of Lysosome-associated membrane glycoprotein 2	4	2	34	2	0.29
Q9CPP6	Ndufa5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	8	2	28	2	0.29
P54071	Idh2	Isocitrate dehydrogenase [NADP], mitochondrial	17	8	195	8	0.29
Q6P4T2	Snrnp200	U5 small nuclear ribonucleoprotein 200 kDa helicase	12	25	315	25	0.28
Q99PL5	Rrbp1	Ribosome-binding protein 1	41	41	702	41	0.28
Q60771	Cldn11	Claudin-11	11	2	15	2	0.28
P05202	Got2	Aspartate aminotransferase, mitochondrial	27	15	372	15	0.28
P14211	Calr	Calreticulin	44	19	881	19	0.28
P47963	Rpl13	60S ribosomal protein L13	33	8	434	8	0.28
E9Q317	Sap18b	Histone deacetylase complex subunit SAP18	26	6	137	6	0.28
Q9CX86	Hnrnpa0	Heterogeneous nuclear ribonucleoprotein A0	33	11	287	9	0.28
P97384	Anxa11	Annexin A11	11	6	79	6	0.28
Q9JI11	Stk4	Serine/threonine-protein kinase 4	8	4	41	4	0.28
Q9DBE9	Ftsj3	pre-rRNA processing protein FTSJ3	13	10	68	10	0.28
A0A0R4J0I4	Chtf18	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae), isoform CRA_a	2	2	6	2	0.28
P70677	Casp3	Caspase-3	6	2	30	2	0.28
Q8K2Z4-2	Ncapd2	Isoform 2 of Condensin complex subunit 1	6	9	77	9	0.28
Q8CBB7	Ap1g1	AP-1 complex subunit gamma-1	3	3	38	3	0.28
Q8VIJ6	Sfpq	Splicing factor, proline- and glutamine-rich	33	26	1090	25	0.28
B2RQC6	Cad	CAD protein	9	18	236	18	0.28
Q922R8	Pdia6	Protein disulfide-isomerase A6	42	14	416	14	0.28
Q9WTI7-3	Myo1c	Isoform 3 of Unconventional myosin-Ic	7	7	69	7	0.28
Q9CY16	Mrps28	28S ribosomal protein S28, mitochondrial	11	2	7	2	0.28

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
E9PUB7	Msto1	Protein misato homolog 1	5	3	18	3	0.28
P07742	Rrm1	Ribonucleoside-diphosphate reductase large subunit	16	11	106	11	0.28
Q9CQM9	Glrx3	Glutaredoxin-3	5	2	41	2	0.28
P46460	Nsf	Vesicle-fusing ATPase	13	12	173	11	0.28
Q9WV70	Noc2l	Nucleolar complex protein 2 homolog	7	6	63	6	0.28
Q9CRD0	Ociad1	OCIA domain-containing protein 1	31	6	74	6	0.28
Q9DAW6	Prpf4	U4/U6 small nuclear ribonucleoprotein Prp4	5	3	53	3	0.28
Q8K4Q8	Colec12	Collectin-12	5	5	41	5	0.27
P29341	Pabpc1	Polyadenylate-binding protein 1	30	16	336	14	0.27
P17426	Ap2a1	AP-2 complex subunit alpha-1	9	11	113	7	0.27
Q6PGF5	Bms1	BMS1 homolog, ribosome assembly protein (Yeast)	2	3	63	3	0.27
Q8C7X2	Emc1	ER membrane protein complex subunit 1	12	11	68	11	0.27
Q0VG62	1	Uncharacterized protein C8orf59 homolog	16	2	24	2	0.27
Q7TNV0	Dek	Protein DEK	13	6	123	6	0.27
P34884	Mif	Macrophage migration inhibitory factor	15	2	30	2	0.27
O35387	Hax1	HCLS1-associated protein X-1	8	2	21	2	0.27
Q9CY21	Wbscr22	Probable 18S rRNA (guanine-N(7))-methyltransferase	6	2	12	2	0.27
Q6PGB6-4	Naa50	Isoform 4 of N-alpha-acetyltransferase 50	27	6	41	6	0.27
P61027	Rab10	Ras-related protein Rab-10	43	8	313	6	0.27
Q99ME9	Gtpbp4	Nucleolar GTP-binding protein 1	23	16	270	16	0.27
Q99JY0	Hadhb	Trifunctional enzyme subunit beta, mitochondrial	21	11	215	11	0.27
E9QK83	Utp20	Small subunit processome component 20 homolog	3	10	87	10	0.27
Q8R001	Mapre2	Microtubule-associated protein RP/EB family member 2	10	3	61	3	0.27
Q91YR7	Prpf6	Pre-mRNA-processing factor 6	11	11	141	11	0.27
Q9JI13	Utp3	Something about silencing protein 10	7	4	34	4	0.27
Q5EBP8	Hnrnpa1	Heterogeneous nuclear ribonucleoprotein A1	39	15	624	11	0.27
Q60872	Eif1a	Eukaryotic translation initiation factor 1A	19	3	46	3	0.27
P80317	Cct6a	T-complex protein 1 subunit zeta	30	15	426	15	0.26
Q99KG3	Rbm10	RNA-binding protein 10	4	4	51	4	0.26
Q9JMH6	Txnrd1	Thioredoxin reductase 1, cytoplasmic	16	9	82	9	0.26
Q61035	Hars	Histidine--tRNA ligase, cytoplasmic	14	8	92	6	0.26
Q78IK4	Apool	MICOS complex subunit Mic27	13	4	29	4	0.26
P03975	Iap	IgE-binding protein	7	4	60	4	0.26
P60335	Pcbp1	Poly(rC)-binding protein 1	26	7	538	4	0.26
Q9CXL3	1	Uncharacterized protein C7orf50 homolog	22	4	33	4	0.26
P14733	Lmnb1	Lamin-B1	54	38	1599	33	0.26
P49710	Hcls1	Hematopoietic lineage cell-specific protein	33	15	340	15	0.26
Q9D104	Srp19	Signal recognition particle 19 kDa protein	11	2	40	2	0.26
O54950	Prkag1	5'-AMP-activated protein kinase subunit gamma-1	4	2	15	2	0.26
Q8VE80	Thoc3	THO complex subunit 3	4	2	24	2	0.26

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
Q3UVK0	Ermp1	Endoplasmic reticulum metallopeptidase 1	2	2	12	2	0.26
Q6PHQ9	Pabpc4	Polyadenylate-binding protein	14	9	142	7	0.26
Q3UZ35	Cd72	B-cell differentiation antigen CD72	5	2	14	2	0.26
Q91YQ5	Rpn1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	32	20	642	20	0.26
P52825	Cpt2	Carnitine O-palmitoyltransferase 2, mitochondrial	7	5	39	5	0.26
G3UVU2	Sf3a2	Splicing factor 3A subunit 2	10	4	21	4	0.26
Q69ZR2	Hectd1	E3 ubiquitin-protein ligase HECTD1	2	5	27	5	0.26
P62996	Tra2b	Transformer-2 protein homolog beta	21	6	187	4	0.26
P50431	Shmt1	Serine hydroxymethyltransferase, cytosolic	5	3	27	3	0.26
E9PUQ7	Trmt2a	tRNA (uracil-5-)-methyltransferase homolog A	5	4	30	4	0.26
P61620	Sec61a1	Protein transport protein Sec61 subunit alpha isoform 1	11	7	175	7	0.25
P97807	Fh	Fumarate hydratase, mitochondrial	22	10	239	10	0.25
P58059	Mrps21	28S ribosomal protein S21, mitochondrial	31	2	18	2	0.25
P15532	Nme1	Nucleoside diphosphate kinase A	38	5	245	1	0.25
Q8BG94	Commd7	COMM domain-containing protein 7	10	2	12	2	0.25
P51881	Slc25a5	ADP/ATP translocase 2	27	10	957	4	0.25
Q9DC69	Ndufa9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	15	4	54	4	0.25
Q921F2	Tardbp	TAR DNA-binding protein 43	14	7	409	7	0.25
Q8CGC6	Rbm28	RNA-binding protein 28	16	12	146	12	0.25
O88696	Clpp	ATP-dependent Clp protease proteolytic subunit, mitochondrial	16	4	21	4	0.25
P97372	Psme2	Proteasome activator complex subunit 2	15	4	46	4	0.25
Q6DFW4	Nop58	Nucleolar protein 58	12	6	118	6	0.25
Q04447	Ckb	Creatine kinase B-type	25	7	91	7	0.25
Q921H8	Acaa1a	3-ketoacyl-CoA thiolase A, peroxisomal	39	12	168	12	0.25
E9PWG6	Ncapg	Protein Ncapg	3	3	18	3	0.25
Q8K003	Tma7	Translation machinery-associated protein 7	30	2	76	2	0.25
Q8BGA9	Oxa1l	Mitochondrial inner membrane protein OXA1L	8	4	50	4	0.25
Q6ZWV3	Rpl10	60S ribosomal protein L10	15	3	109	3	0.25
Q8BH74	Nup107	Nuclear pore complex protein Nup107	7	6	57	6	0.25
P62858	Rps28	40S ribosomal protein S28	30	2	356	2	0.24
Q99LC2	Cstf1	Cleavage stimulation factor subunit 1	7	3	36	3	0.24
A2AEW1	Tfe3	Transcription factor E3	4	3	37	3	0.24
P61028	Rab8b	Ras-related protein Rab-8B	44	9	289	4	0.24
Q91ZV0	Mia2	Melanoma inhibitory activity protein 2	5	9	72	9	0.24
Q6ZPR5	Smpd4	Sphingomyelin phosphodiesterase 4	5	4	33	4	0.24
E9PV22	Lrrc47	Leucine-rich repeat-containing protein 47	6	3	31	3	0.24
P56480	Atp5b	ATP synthase subunit beta, mitochondrial	48	19	659	19	0.24
P62843	Rps15	40S ribosomal protein S15	30	3	94	3	0.24
Q8BJW5	Nol11	Nucleolar protein 11	6	5	25	5	0.24
Q9WVA3	Bub3	Mitotic checkpoint protein BUB3	17	6	138	6	0.24

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
E9QAQ7	Arid1a	AT-rich interactive domain-containing protein 1A	6	9	94	9	0.24
Q99MU3	Adar	Double-stranded RNA-specific adenosine deaminase	2	3	14	3	0.24
Q8BT07	Cep55	Centrosomal protein of 55 kDa	11	5	28	5	0.24
P97496	Smarcc1	SWI/SNF complex subunit SMARCC1	11	13	164	11	0.24
Q8BML9	Qars	Glutaminyl-tRNA synthetase	14	12	188	11	0.24
P51859	Hdgf	Hepatoma-derived growth factor	53	9	68	8	0.24
P00920	Ca2	Carbonic anhydrase 2	29	6	318	6	0.23
Q9CXW3	Cacybp	Calcyclin-binding protein	18	4	84	4	0.23
Q9D6K9	Cers5	Ceramide synthase 5	4	2	21	2	0.23
Q9JIK5	Ddx21	Nucleolar RNA helicase 2	36	33	619	33	0.23
Q5RKN9	Capza1	Capping protein (Actin filament) muscle Z-line, alpha 1	32	6	74	5	0.23
A2AWA9	Rabgap1	Rab GTPase-activating protein 1	2	2	14	2	0.23
Q922U1	Prpf3	U4/U6 small nuclear ribonucleoprotein Prp3	14	10	100	10	0.23
Q80YR5	Safb2	Scaffold attachment factor B2	9	9	82	8	0.23
Q8BJ71	Nup93	Nuclear pore complex protein Nup93	17	14	144	14	0.23
G3UW85	Erh	Enhancer of rudimentary homolog	15	3	49	3	0.23
Q9CYA0	Creld2	Cysteine-rich with EGF-like domain protein 2	8	3	21	3	0.23
Q8VHZ7	Imp4	U3 small nucleolar ribonucleoprotein protein IMP4	10	3	35	3	0.23
Q9D1G1	Rab1b	Ras-related protein Rab-1B	46	9	259	3	0.23
A0A0J9YUD5	Nup205	Protein Nup205	7	16	244	16	0.23
Q8VBT6	Apobr	Apolipoprotein B receptor	8	8	86	8	0.23
Q91WD5	Ndufs2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	6	3	16	3	0.23
Q9DBS1	Tmem43	Transmembrane protein 43	10	2	13	2	0.23
Q3UEB3	Puf60	Poly(U)-binding-splicing factor PUF60	20	8	137	8	0.23
Q9CXK8	Nip7	60S ribosome subunit biogenesis protein NIP7 homolog	10	2	18	2	0.23
Q8JZR0	Acsl5	Long-chain-fatty-acid--CoA ligase 5	2	2	32	1	0.23
Q9D964	Gatm	Glycine amidinotransferase, mitochondrial	5	3	33	3	0.23
Q9Z0E0	Ncdn	Neurochondrin	2	2	13	2	0.22
P48999	Alox5	Arachidonate 5-lipoxygenase	2	2	19	2	0.22
Q9R0Q3	Tmed2	Transmembrane emp24 domain-containing protein 2	18	4	145	4	0.22
Q9R190	Mta2	Metastasis-associated protein MTA2	15	11	142	10	0.22
Q8R323	Rfc3	Replication factor C subunit 3	17	6	93	6	0.22
P62267	Rps23	40S ribosomal protein S23	30	6	258	6	0.22
Q8CB77	Tceb3	Transcription elongation factor B polypeptide 3	5	4	21	4	0.22
Q8K0C4	Cyp51a1	Lanosterol 14-alpha demethylase	7	4	44	4	0.22
Q9D0M3	Cyc1	Cytochrome c1, heme protein, mitochondrial	5	3	33	3	0.22
Q9R1Q6	Tmem176b	Transmembrane protein 176B	9	3	78	3	0.22
Q921S7	Mrpl37	39S ribosomal protein L37, mitochondrial	8	3	39	3	0.22
Q9D0K2	Oxct1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	23	9	221	9	0.22
Q9D7N6	Mrpl30	39S ribosomal protein L30, mitochondrial	12	2	24	2	0.22

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q8K301	Ddx52	Probable ATP-dependent RNA helicase DDX52	4	3	45	3	0.22
A0A0R4J275	Ndufa12	MCG11204, isoform CRA_b	14	2	37	2	0.22
H3BJW3	Cpsf6	Cleavage and polyadenylation-specificity factor subunit 6	7	4	38	4	0.22
Q61550	Rad21	Double-strand-break repair protein rad21 homolog	16	8	62	8	0.22
Q91VC9	Ghitm	Growth hormone-inducible transmembrane protein	6	2	24	2	0.22
Q922I7	Ptbp1	MCG13402, isoform CRA_c	34	13	522	10	0.22
Q9D1M4	Eef1e1	Eukaryotic translation elongation factor 1 epsilon-1	25	5	43	5	0.22
A0A0R4J049	Prmt5	Protein arginine N-methyltransferase 5	4	3	24	3	0.22
E9Q411	Nbas	Protein Nbas	1	2	24	2	0.22
G5E8I8	Cherp	Calcium homeostasis endoplasmic reticulum protein	5	6	52	6	0.22
S4R1W5	Rbm6	Protein Rbm6	3	3	15	3	0.21
Q8R344	Ccdc12	Coiled-coil domain-containing protein 12	25	3	32	3	0.21
P14131	Rps16	40S ribosomal protein S16	50	9	184	9	0.21
A0A087WNT1	Tceb1	Transcription elongation factor B polypeptide 1	14	2	27	2	0.21
A2AGT5	Ckap5	Cytoskeleton-associated protein 5	3	6	44	6	0.21
Q6ZQL4	Wdr43	WD repeat-containing protein 43	6	5	80	5	0.21
G3X8U3	2210016F16Rik	MCG6895	5	2	9	2	0.21
P62245	Rps15a	40S ribosomal protein S15a	36	5	170	5	0.21
Q8BJW6	Eif2a	Eukaryotic translation initiation factor 2A	9	5	35	5	0.21
Q8C4J7	Tbl3	Transducin beta-like protein 3	5	5	39	5	0.21
Q9CQH3	Ndufb5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	15	3	42	3	0.21
Q8VEK3	Hnrnpu	Heterogeneous nuclear ribonucleoprotein U	19	19	697	19	0.21
Q9D881	Cox5b	Cytochrome c oxidase subunit 5B, mitochondrial	21	3	103	3	0.21
P61358	Rpl27	60S ribosomal protein L27	43	6	151	6	0.21
Q91YI4-2	Arrb2	Isoform 2 of Beta-arrestin-2	4	2	11	2	0.21
Q9R0E2	Plod1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	5	5	48	5	0.21
Q63850	Nup62	Nuclear pore glycoprotein p62	6	3	23	3	0.20
Q8JZX4	Rbm17	Splicing factor 45	4	2	18	2	0.20
Q9D6Z1	Nop56	Nucleolar protein 56	26	14	262	14	0.20
F7DCH5	Clasp2	CLIP-associating protein 2	2	3	24	3	0.20
Q9WU40-2	Lemd3	Isoform 2 of Inner nuclear membrane protein Man1	4	2	12	2	0.20
Q9D1J3	Sarnp	SAP domain-containing ribonucleoprotein	29	6	84	6	0.20
Q99KF1	Tmed9	Transmembrane emp24 domain-containing protein 9	7	2	47	2	0.20
P47968	Rpia	Ribose-5-phosphate isomerase	11	3	15	3	0.20
Q9QYF1	Rdh11	Retinol dehydrogenase 11	14	4	30	4	0.20
Q61263	Soat1	Sterol O-acyltransferase 1	4	3	22	3	0.20
Q9D7N9	Apmap	Adipocyte plasma membrane-associated protein	6	3	22	3	0.20
O09172	Gclm	Glutamate--cysteine ligase regulatory subunit	10	3	24	3	0.20
F8VQ28	Pxn	Paxillin	3	2	40	2	0.19
P27870	Vav1	Proto-oncogene vav	7	6	77	6	0.19

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q09200	B4galnt1	Beta-1,4 N-acetylgalactosaminyltransferase 1	21	9	110	9	0.19
Q9Z0W3	Nup160	Nuclear pore complex protein Nup160	3	5	51	5	0.19
Q7TT37	Ikbkap	Elongator complex protein 1	2	4	22	4	0.19
O35218	Cpsf2	Cleavage and polyadenylation specificity factor subunit 2	5	5	29	5	0.19
Q9WTM5	Ruvbl2	RuvB-like 2	32	15	197	15	0.19
Q8BVY0	Rsl1d1	Ribosomal L1 domain-containing protein 1	28	12	245	12	0.19
Q9D903	Ebna1bp2	Probable rRNA-processing protein EBP2	19	9	133	9	0.19
Q8K1X4	Nckap1l	NCK associated protein 1 like	2	3	24	3	0.19
Q9Z1B5	Mad2l1	Mitotic spindle assembly checkpoint protein MAD2A	12	3	33	3	0.19
Q8R0G9	Nup133	Nuclear pore complex protein Nup133	9	11	110	11	0.19
Q80VA0	Galnt7	N-acetylgalactosaminyltransferase 7	11	8	103	8	0.19
P23198	Cbx3	Chromobox protein homolog 3	28	4	41	3	0.19
Q8VHE0	Sec63	Translocation protein SEC63 homolog	7	6	46	6	0.19
Q61941	Nnt	NAD(P) transhydrogenase, mitochondrial	3	4	32	4	0.19
E9Q3G8	Nup153	Protein Nup153	11	14	215	14	0.19
Q923D5	Wbp11	WW domain-binding protein 11	9	7	88	7	0.18
Q99LD9	Eif2b2	Translation initiation factor eIF-2B subunit beta	7	2	11	2	0.18
Q9R1P3	Psmb2	Proteasome subunit beta type-2	24	4	39	4	0.18
Q9D1P4	Chordc1	Cysteine and histidine-rich domain-containing protein 1	12	3	43	3	0.18
F8WJD4	Sympk	Symplekin	4	5	21	5	0.18
Q9DCM0	Ethe1	Persulfide dioxygenase ETHE1, mitochondrial	10	2	26	2	0.18
Q9CW46	Raver1	Ribonucleoprotein PTB-binding 1	8	5	93	5	0.18
Q9CR47	Nsa2	Ribosome biogenesis protein NSA2 homolog	6	2	29	2	0.18
Q8BPU7	Elmo1	Engulfment and cell motility protein 1	9	7	85	7	0.18
Q9JLV5	Cul3	Cullin-3	2	3	10	2	0.18
Q99LS3	Psph	Phosphoserine phosphatase	16	4	28	4	0.18
P62806	Hist1h4a	Histone H4	54	9	2172	9	0.18
Q80SW1	Ahcyl1	Putative adenosylhomocysteinase 2	9	5	30	4	0.18
Q9D024	Ccdc47	Coiled-coil domain-containing protein 47	10	6	56	6	0.18
E9PVZ8	Golgb1	Protein Golgb1	3	8	36	8	0.18
Q3TIX6	Fubp3	Protein Fubp3	20	12	216	10	0.17
J3QMG3	Vdac3	Voltage-dependent anion-selective channel protein 3	14	4	30	4	0.17
P13864	Dnmt1	DNA (cytosine-5)-methyltransferase 1	15	25	280	25	0.17
A0A0R4J0R1	Vamp8	Vesicle-associated membrane protein 8	26	3	81	3	0.17
O35857	Timm44	Mitochondrial import inner membrane translocase subunit TIM44	19	10	116	10	0.17
Q8C483	Sars	Serine--tRNA ligase, cytoplasmic	18	6	100	6	0.17
Q5SUS9	Ewsr1	RNA-binding protein EWS	11	6	292	6	0.17
Q9ESX5	Dkc1	H/ACA ribonucleoprotein complex subunit 4	25	10	128	10	0.17
P63163	Snrpn	Small nuclear ribonucleoprotein-associated protein N	9	2	84	2	0.17
Q9D0T1	Snu13	NHP2-like protein 1	18	2	61	2	0.17

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q04207	Rela	Transcription factor p65	3	2	29	1	0.17
P45878	Fkbp2	Peptidyl-prolyl cis-trans isomerase FKBP2	37	3	23	3	0.16
Q9JJU8	Sh3bgrl	SH3 domain-binding glutamic acid-rich-like protein	17	2	22	2	0.16
Q924C1	Xpo5	Exportin-5	1	2	24	2	0.16
Q9D0I8	Mrto4	mRNA turnover protein 4 homolog	17	4	34	4	0.16
P43274	Hist1h1e	Histone H1.4	37	12	783	4	0.16
Q8BU88	Mrpl22	39S ribosomal protein L22, mitochondrial	15	3	13	3	0.16
Q8R4U7	Luzp1	Leucine zipper protein 1	3	4	19	4	0.16
P52480-2	Pkm	Isoform M1 of Pyruvate kinase PKM	48	27	2348	1	0.16
P97310	Mcm2	DNA replication licensing factor MCM2	16	13	132	13	0.16
D3YWX2	Ylpm1	YLP motif-containing protein 1	2	5	53	5	0.15
Q3UV17	Krt76	Keratin, type II cytoskeletal 2 oral	4	3	175	2	0.15
Q03963	Eif2ak2	Interferon-induced, double-stranded RNA-activated protein kinase	3	2	36	2	0.15
Q61578	Fdxr	NADPH:adrenodoxin oxidoreductase, mitochondrial	10	4	45	4	0.15
Q5SSI6	Utp18	U3 small nucleolar RNA-associated protein 18 homolog	11	5	73	5	0.15
F8WJA0	Ddx24	ATP-dependent RNA helicase DDX24	15	12	115	12	0.15
P63323	Rps12	40S ribosomal protein S12	13	2	70	2	0.15
Q9CU62	Smc1a	Structural maintenance of chromosomes protein 1A	11	15	149	15	0.15
Q8K2P7	Slc38a1	Sodium-coupled neutral amino acid transporter 1	3	2	12	2	0.15
E9QAS5	Chd4	Chromodomain-helicase-DNA-binding protein 4	9	19	232	19	0.15
Q8BX70	Vps13c	Vacuolar protein sorting-associated protein 13C	7	24	155	24	0.15
Q8R2M2	Dnttip2	Deoxynucleotidyltransferase terminal-interacting protein 2	9	8	90	8	0.15
Q60596	Xrcc1	DNA repair protein XRCC1	7	4	41	4	0.15
Q8R1Q8	Dync1li1	Cytoplasmic dynein 1 light intermediate chain 1	3	2	13	2	0.14
Q9D1J1	Necap2	Adaptin ear-binding coat-associated protein 2	9	2	6	2	0.14
Q9DC71	Mrps15	28S ribosomal protein S15, mitochondrial	15	4	60	4	0.14
Q8JZN5	Acad9	Acyl-CoA dehydrogenase family member 9, mitochondrial	10	6	26	6	0.14
D3Z780	Eif2b4	Translation initiation factor eIF-2B subunit delta	4	2	12	2	0.14
Q9JJA4	Wdr12	Ribosome biogenesis protein WDR12	11	4	29	4	0.14
Q8BP67	Rpl24	60S ribosomal protein L24	19	4	50	4	0.14
P04184	Tk1	Thymidine kinase, cytosolic	8	2	11	2	0.13
Q06185	Atp5i	ATP synthase subunit e, mitochondrial	42	3	68	3	0.13
Q8BFY9	Tnpo1	Transportin-1	4	4	69	4	0.13
Q8R5F3	Oard1	O-acetyl-ADP-ribose deacetylase 1	13	2	9	2	0.13
P02535	Krt10	Keratin, type I cytoskeletal 10	10	6	296	4	0.13
Q99K48	Nono	Non-POU domain-containing octamer-binding protein	42	17	367	15	0.13
Q99N84	Mrps18b	28S ribosomal protein S18b, mitochondrial	7	2	13	2	0.13
P97287	Mcl1	Induced myeloid leukemia cell differentiation protein Mcl-1 homolog	23	6	85	6	0.13
B1AUX2	Hcfc1	Host cell factor 1	5	10	93	10	0.13
Q3U9G9	Lbr	Lamin-B receptor	15	11	320	11	0.13

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9JMA1	Usp14	Ubiquitin carboxyl-terminal hydrolase 14	19	8	92	8	0.13
Q4WWC5	htb1	Histone H2B	22	4	294	1	0.13
P10605	Ctsb	Cathepsin B	17	5	238	5	0.13
Q9CY27	Tecr	Very-long-chain enoyl-CoA reductase	14	6	51	6	0.13
Q80YD1	Supv3l1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	3	3	15	3	0.12
Q9D787	Ppil2	Peptidyl-prolyl cis-trans isomerase-like 2	6	3	14	3	0.12
Q9QWL7	Krt17	Keratin, type I cytoskeletal 17	14	7	178	4	0.12
Q80TJ7	Phf8	Histone lysine demethylase PHF8	2	2	10	2	0.12
Q91VA7	Idh3b	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	20	7	54	7	0.12
Q9CR98	Fam136a	Protein FAM136A	13	2	16	2	0.12
P08752	Gnai2	Guanine nucleotide-binding protein G(i) subunit alpha-2	20	6	122	4	0.12
Q9ERU9	Ranbp2	E3 SUMO-protein ligase RanBP2	9	29	369	29	0.12
Q8BXC6	Commd2	COMM domain-containing protein 2	9	2	17	2	0.12
P97760	Polr2c	DNA-directed RNA polymerase II subunit RPB3	12	3	24	3	0.12
Q9DBR7	Ppp1r12a	Protein phosphatase 1 regulatory subunit 12A	5	5	36	5	0.12
Q8BXV2	Bri3bp	BRI3-binding protein	6	2	50	2	0.12
O35134	Polr1a	DNA-directed RNA polymerase I subunit RPA1	2	4	42	3	0.12
Q640M1	Utp14a	U3 small nucleolar RNA-associated protein 14 homolog A	11	8	65	8	0.12
Q9D6J6	Ndufv2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	8	2	24	2	0.12
Q80XU3	Nucks1	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	10	2	17	2	0.11
Q60770	Stxbp3	Syntaxin-binding protein 3	3	2	9	2	0.11
P83870	Phf5a	PHD finger-like domain-containing protein 5A	20	3	62	3	0.11
O35680	Mrps12	28S ribosomal protein S12, mitochondrial	13	2	13	2	0.11
E9PZF0	Gm20390	Nucleoside diphosphate kinase	34	5	228	1	0.11
Q91ZA3	Pcca	Propionyl-CoA carboxylase alpha chain, mitochondrial	6	5	27	5	0.11
Q8K0D5	Gfm1	Elongation factor G, mitochondrial	6	6	37	6	0.11
Q8C2Q3	Rbm14	RNA-binding protein 14	23	16	306	16	0.11
A0A0R4J0W6	Lrrc40	Leucine rich repeat containing 40, isoform CRA_a	2	2	27	2	0.11
P17095-1	Hmga1	Isoform HMG-Y of High mobility group protein HMG-I/HMG-Y	30	4	129	1	0.11
Q921J2	Rheb	GTP-binding protein Rheb	8	2	70	2	0.10
Q6P9R1	Ddx51	ATP-dependent RNA helicase DDX51	7	4	38	4	0.10
Q8K221	Arfip2	Arfaptin-2	8	2	9	2	0.10
Q8BG05	Hnrnpa3	Heterogeneous nuclear ribonucleoprotein A3	30	12	683	10	0.10
E9PYN1	Cadm1	Cell adhesion molecule 1	4	2	9	2	0.09
A6H611	Mipep	Mitochondrial intermediate peptidase	3	3	12	3	0.09
Q91WN1	Dnajc9	DnaJ homolog subfamily C member 9	11	3	11	3	0.09
Q9CQJ4	Rnf2	E3 ubiquitin-protein ligase RING2	13	3	27	3	0.09
Q9CQT2	Rbm7	RNA-binding protein 7	12	3	11	3	0.09
Q62511	Zfp91	E3 ubiquitin-protein ligase ZFP91	3	2	9	2	0.09
O54774	Ap3d1	AP-3 complex subunit delta-1	2	3	9	3	0.09

Accession	**Gene**	**Description**	**Coverage**	**Peptides**	**Unique Peptides**	**PSMs**	**[1]*pksP*/wt**
Q9D1P0	Mrpl13	39S ribosomal protein L13, mitochondrial	29	6	33	6	0.09
P17095	Hmga1	High mobility group protein HMG-I/HMG-Y	37	4	125	1	0.09
Q91WV0	Dr1	Protein Dr1	15	3	14	3	0.09
O70145	Ncf2	Neutrophil cytosol factor 2	8	6	30	6	0.09
P58742	Aaas	Aladin	9	4	15	4	0.09
Q8BU14	Sec62	Translocation protein SEC62	5	3	35	3	0.08
P47754	Capza2	F-actin-capping protein subunit alpha-2	11	3	72	2	0.08
Q3B7Z2	Osbp	Oxysterol-binding protein 1	2	2	10	2	0.08
P50544	Acadvl	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	10	6	28	6	0.08
Q04750	Top1	DNA topoisomerase 1	22	17	220	17	0.07
Q9Z204	Hnrnpc	Heterogeneous nuclear ribonucleoproteins C1/C2	38	15	351	15	0.07
Q8CI51	Pdlim5	PDZ and LIM domain protein 5	6	3	33	3	0.07
Q9Z103	Adnp	Activity-dependent neuroprotector homeobox protein	3	3	18	3	0.07
P99027	Rplp2	60S acidic ribosomal protein P2	77	7	149	7	0.07
Q8JZM7	Cdc73	Parafibromin	12	7	69	7	0.07
O55106	Strn	Striatin	3	3	25	3	0.07
Q61462	Cyba	Cytochrome b-245 light chain	31	4	94	4	0.06
Q9D880	Timm50	Mitochondrial import inner membrane translocase subunit TIM50	16	5	93	5	0.06
Q91Z49	Fyttd1	UAP56-interacting factor	6	2	21	2	0.06
Q60848	Hells	Lymphocyte-specific helicase	2	2	21	2	0.06
Q8BMF4	Dlat	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	14	7	85	7	0.06
F7C846	Mtx1	Metaxin-1	7	4	62	4	0.06
Q14C51	Ptcd3	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	5	4	13	4	0.06
Q7TSC1	Prrc2a	Protein PRRC2A	2	5	36	4	0.06
D3YY09	Drap1	Dr1-associated corepressor	9	2	9	2	0.05
Q64511	Top2b	DNA topoisomerase 2-beta	7	13	127	6	0.05
P62075	Timm13	Mitochondrial import inner membrane translocase subunit Tim13	36	3	28	3	0.05
Q8R3Y8	Irf2bp1	Interferon regulatory factor 2-binding protein 1	4	2	28	2	0.05
A0A0N4SVL0	Eif4g3	Eukaryotic translation initiation factor 4 gamma 3	3	6	53	5	0.04
Q9ERS2	Ndufa13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	13	2	22	2	0.04
A0A0R4J008	Hdac2	Histone deacetylase	7	4	29	2	0.04
P17809	Slc2a1	Solute carrier family 2, facilitated glucose transporter member 1	4	2	36	2	0.04
P97822	Anp32e	Acidic leucine-rich nuclear phosphoprotein 32 family member E	8	3	31	3	0.04
Q8R332	Nup58	Nucleoporin p58/p45	5	4	89	4	0.04
Q05144	Rac2	Ras-related C3 botulinum toxin substrate 2	17	4	81	1	0.04
Q9CWW7	Cxxc1	CXXC-type zinc finger protein 1	3	2	8	2	0.03
Q8BHC4	Dcakd	Dephospho-CoA kinase domain-containing protein	9	2	16	2	0.02
Q8R5L1	C1qbp	Complement component 1 Q subcomponent-binding protein, mitochondrial	11	2	47	2	0.01
P62737	Acta2	Actin, aortic smooth muscle	27	11	3673	1	0.01

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q99LI7	Cstf3	Cleavage stimulation factor subunit 3	5	3	9	3	n.a.
B0QZN5	Vamp2	Vesicle-associated membrane protein 2	14	2	31	1	n.a.
E0CYM8	Sirpa	Tyrosine-protein phosphatase non-receptor type substrate 1	3	2	12	2	n.a.
P48453	Ppp3cb	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform	4	2	10	1	n.a.
Q8BRG8	Tmem209	Transmembrane protein 209	4	2	24	2	n.a.
Q8R307	Vps18	Vacuolar protein sorting-associated protein 18 homolog	3	3	12	3	n.a.
Q8R2U2	Nepro	Protein nepro	3	2	9	2	n.a.
E9QKD1	Nol8	Nucleolar protein 8	2	3	9	3	n.a.
A2A7F4	Rlf	MCG122876	1	2	9	2	n.a.
Q8R2U0	Seh1l	Nucleoporin SEH1	8	2	7	2	n.a.
Q9ET26	Rnf114	E3 ubiquitin-protein ligase RNF114	7	2	10	2	n.a.
Q9Z329	Itpr2	Inositol 1,4,5-trisphosphate receptor type 2	1	2	5	1	n.a.
Q6PGG2	Gmip	GEM-interacting protein	2	2	9	2	n.a.
Q61009	Scarb1	Scavenger receptor class B member 1	3	2	4	2	n.a.
Q9CQ22	Lamtor1	Ragulator complex protein LAMTOR1	27	2	7	2	n.a.
Q9QYS9-7	Qki	Isoform 7 of Protein quaking	8	2	10	2	n.a.
P11881	Itpr1	Inositol 1,4,5-trisphosphate receptor type 1	1	3	8	2	n.a.
Q8QZS1	Hibch	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	5	2	6	2	n.a.
Q62311	Taf6	Transcription initiation factor TFIID subunit 6	3	2	6	2	n.a.
Q6KCD5	Nipbl	Nipped-B-like protein	2	7	30	7	n.a.
P33610	Prim2	DNA primase large subunit	5	2	6	2	n.a.
Q60855	Ripk1	Receptor-interacting serine/threonine-protein kinase 1	6	4	48	4	n.a.
Q91WC9	Daglb	Sn1-specific diacylglycerol lipase beta	2	2	12	2	n.a.
Q80WQ6	Rhbdf2	Inactive rhomboid protein 2	2	2	6	2	n.a.
Q4FZC9	Syne3	Nesprin-3	5	5	27	5	n.a.
Q9Z2A5	Ate1	Arginyl-tRNA--protein transferase 1	4	2	6	2	n.a.
A2A484	Zmynd8	Protein Zmynd8	3	4	12	4	n.a.
A2ASZ8-3	Slc25a25	Isoform 3 of Calcium-binding mitochondrial carrier protein SCaMC-2	5	3	11	3	n.a.
B1AR13	Cisd3	CDGSH iron-sulfur domain-containing protein 3, mitochondrial	10	2	13	2	n.a.
Q8BKT7	Thoc5	THO complex subunit 5 homolog	2	2	7	2	n.a.
Q64525	Hist2h2bb	Histone H2B type 2-B	65	10	1600	1	n.a.
P63024	Vamp3	Vesicle-associated membrane protein 3	22	2	28	1	n.a.
Q8R3F5	Mcat	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	6	2	23	2	n.a.
A0A0U1RNX8	Bcl7c	B-cell CLL/lymphoma 7 protein family member C	7	2	9	2	n.a.
Q8BX09	Rbbp5	Retinoblastoma-binding protein 5	4	2	12	2	n.a.
Q9CZ83-2	Mrpl55	Isoform 2 of 39S ribosomal protein L55, mitochondrial	18	2	15	2	n.a.
Q6NXI6	Rprd2	Regulation of nuclear pre-mRNA domain-containing protein 2	3	5	18	5	n.a.
P70336-2	Rock2	Isoform 2 of Rho-associated protein kinase 2	1	3	11	1	n.a.
Q80UJ7	Rab3gap1	Rab3 GTPase-activating protein catalytic subunit	1	2	9	2	n.a.
A0A0R4J0M9	Vcpip1	Deubiquitinating protein VCIP135	2	2	8	2	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
F8VQ93	Phip	PH-interacting protein	1	2	6	2	n.a.
E9Q2I4	Elmsan1	Protein Elmsan1	2	2	18	2	n.a.
Q8CC88	Vwa8	von Willebrand factor A domain-containing protein 8	1	2	12	2	n.a.
E9PVA6	Git2	ARF GTPase-activating protein GIT2	2	2	11	2	n.a.
Q8C3Y4	Kntc1	Kinetochore-associated protein 1	1	2	6	1	n.a.
Q3UKJ7	Smu1	WD40 repeat-containing protein SMU1	8	3	21	3	n.a.
P40336-2	Vps26a	Isoform 2 of Vacuolar protein sorting-associated protein 26A	8	3	12	3	n.a.
K3W4Q9	Gopc	Golgi-associated PDZ and coiled-coil motif-containing protein	6	2	9	2	n.a.
Q8VCV2	Ndrg3	Ndrg3 protein	6	2	9	2	n.a.
A2A654	Bptf	Protein Bptf	1	2	12	2	n.a.
P32233	Drg1	Developmentally-regulated GTP-binding protein 1	7	3	28	2	n.a.
Q8K4Z3	Naxe	NAD(P)H-hydrate epimerase	9	2	17	2	n.a.
B2RXC6	Polr3a	DNA-directed RNA polymerase subunit	1	2	9	1	n.a.
Q7JJ13	Brd2	Bromodomain-containing protein 2	4	3	15	3	n.a.
F8WHT3	Prrc2b	Protein PRRC2B	1	4	27	2	n.a.
E9PWW9	Rsf1	Protein Rsf1	2	3	20	3	n.a.
Q6P5H2	Nes	Nestin	1	2	12	2	n.a.
Q9QUR7	Pin1	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	9	2	11	2	n.a.
O08915	Aip	AH receptor-interacting protein	8	2	6	2	n.a.
Q6IFZ6	Krt77	Keratin, type II cytoskeletal 1b	5	5	77	1	n.a.
Q61210-5	Arhgef1	Isoform 5 of Rho guanine nucleotide exchange factor 1	5	5	31	1	n.a.
E9Q634	Myo1e	Unconventional myosin-Ie	5	4	30	2	n.a.
Q6Q477	Atp2b4	Plasma membrane calcium-transporting ATPase 4	1	2	6	2	n.a.
A0A0R4J174	Ecsit	Evolutionarily conserved-signaling intermediate in Toll pathway, mitochondrial	4	2	15	2	n.a.
A0A0M3HEP2	Zeb2	Zinc finger E-box-binding homeobox 2	2	2	11	2	n.a.
O35405	Pld3	Phospholipase D3	3	2	9	2	n.a.
O09131	Gsto1	Glutathione S-transferase omega-1	14	3	9	3	n.a.
P43406	Itgav	Integrin alpha-V	2	3	20	3	n.a.
Q11136	Pepd	Xaa-Pro dipeptidase	5	3	17	3	n.a.
Q9JJF3	No66	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	4	2	17	2	n.a.
Q6NZR5	Skiv2l	Protein Skiv2l	1	2	4	2	n.a.
Q69ZQ2	Isy1	Pre-mRNA-splicing factor ISY1 homolog	11	2	12	2	n.a.
Q61187	Tsg101	Tumor susceptibility gene 101 protein	9	4	56	4	n.a.
Q3TXZ6	Pde2a	Phosphodiesterase	4	4	21	4	n.a.
Q9ESE1	Lrba	Lipopolysaccharide-responsive and beige-like anchor protein	1	2	12	2	n.a.
Q8VE99	Ccdc115	Coiled-coil domain-containing protein 115	35	5	57	5	n.a.
Q9QXV1	Cbx8	Chromobox protein homolog 8	5	2	17	2	n.a.
P63328	Ppp3ca	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	5	3	13	2	n.a.
E9QLG3	Mga	MAX gene-associated protein	1	2	6	2	n.a.
Q8VCD5	Med17	Mediator of RNA polymerase II transcription subunit 17	3	2	5	2	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q9CQX2	Cyb5b	Cytochrome b5 type B	31	2	19	2	n.a.
Q61048	Wbp4	WW domain-binding protein 4	8	3	42	3	n.a.
P52431	Pold1	DNA polymerase delta catalytic subunit	2	3	9	3	n.a.
P35235	Ptpn11	Tyrosine-protein phosphatase non-receptor type 11	2	2	12	2	n.a.
Q8BNU0	Armc6	Armadillo repeat-containing protein 6	5	2	8	2	n.a.
A0A0A6YW53	Map4k4	Mitogen-activated protein kinase kinase kinase kinase 4	1	2	16	1	n.a.
Q9JHK5	Plek	Pleckstrin	9	2	9	2	n.a.
Q9D0D5	Gtf2e1	General transcription factor IIE subunit 1	6	2	18	2	n.a.
Q99MN9	Pccb	Propionyl-CoA carboxylase beta chain, mitochondrial	4	2	12	2	n.a.
Q8R366	Igsf8	Immunoglobulin superfamily member 8	3	2	11	2	n.a.
P70452	Stx4	Syntaxin-4	6	2	6	2	n.a.
Q02819	Nucb1	Nucleobindin-1	3	2	8	2	n.a.
Q80U72-3	Scrib	Isoform 3 of Protein scribble homolog	2	3	21	3	n.a.
O08900	Ikzf3	Zinc finger protein Aiolos	3	2	14	1	n.a.
P70362	Ufd1l	Ubiquitin fusion degradation protein 1 homolog	8	2	12	2	n.a.
P28658	Atxn10	Ataxin-10	5	2	24	2	n.a.
E9Q6E5	Srsf11	Protein Srsf11	5	2	13	2	n.a.
A0A0R4J099	2210016L21Rik	Protein 2210016L21Rik	6	2	6	2	n.a.
P22682	Cbl	E3 ubiquitin-protein ligase CBL	2	2	12	2	n.a.
Q3TYA6	Mphosph8	M-phase phosphoprotein 8	6	4	12	4	n.a.
Q91YP2	Nln	Neurolysin, mitochondrial	2	2	6	2	n.a.
Q6PD26	Pigs	GPI transamidase component PIG-S	16	6	24	6	n.a.
P35951	Ldlr	Low-density lipoprotein receptor	3	3	18	3	n.a.
Q9CZW4	Acsl3	Long-chain-fatty-acid--CoA ligase 3	5	3	15	2	n.a.
F8VQD1	Pbrm1	Protein polybromo-1	1	2	12	2	n.a.
Q9CQX6	Gm16286	MCG141091, isoform CRA_a	11	3	24	1	n.a.
Q8BXZ1	Tmx3	Protein disulfide-isomerase TMX3	7	3	18	3	n.a.
Q8K3A9	Mepce	7SK snRNA methylphosphate capping enzyme	5	2	27	2	n.a.
Q8CJF7	Ahctf1	Protein ELYS	3	6	49	6	n.a.
Q05769	Ptgs2	Prostaglandin G/H synthase 2	3	2	9	2	n.a.
Q99J47	Dhrs7b	Dehydrogenase/reductase SDR family member 7B	7	2	9	2	n.a.
Q9QXK7	Cpsf3	Cleavage and polyadenylation specificity factor subunit 3	5	4	31	4	n.a.
Q99N69	Lpxn	Leupaxin	15	5	52	5	n.a.
O88379	Baz1a	Bromodomain adjacent to zinc finger domain protein 1A	2	4	19	4	n.a.
E9PYH6	Setd1a	Protein Setd1a	1	2	12	2	n.a.
Q8R5A3	Apbb1ip	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	3	2	11	2	n.a.
Q497V5	Srbd1	S1 RNA-binding domain-containing protein 1	1	2	5	2	n.a.
Q6PDI5	Ecm29	Proteasome-associated protein ECM29 homolog	3	5	33	5	n.a.
Q8BMQ2	Gtf3c4	General transcription factor 3C polypeptide 4	2	2	6	2	n.a.
Q7TQK5	Ccdc93	Coiled-coil domain-containing protein 93	6	4	15	4	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
P40201	Chd1	Chromodomain-helicase-DNA-binding protein 1	2	3	16	3	n.a.
P55937	Golga3	Golgin subfamily A member 3	1	2	9	2	n.a.
Q9D162-2	Ccdc167	Isoform 2 of Coiled-coil domain-containing protein 167	8	2	7	2	n.a.
Q9DC48	Cdc40	Pre-mRNA-processing factor 17	3	2	11	2	n.a.
Q9WTK3	Gpaa1	Glycosylphosphatidylinositol anchor attachment 1 protein	2	2	9	2	n.a.
Q8C6G8	Wdr26	WD repeat-containing protein 26	3	2	9	2	n.a.
P22366	Myd88	Myeloid differentiation primary response protein MyD88	6	2	8	2	n.a.
E9PWW6	Zc3h7a	Protein Zc3h7a	1	2	6	2	n.a.
Q8K1R3	Pnpt1	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	6	5	20	5	n.a.
Q91YP3	Dera	Deoxyribose-phosphate aldolase	11	3	9	3	n.a.
Q63932	Map2k2	Dual specificity mitogen-activated protein kinase kinase 2	6	3	35	1	n.a.
V9GX74	Trps1	Zinc finger transcription factor Trps1	1	2	10	2	n.a.
Q9D1K2	Atp6v1f	V-type proton ATPase subunit F	17	2	10	2	n.a.
Q6A065	Cep170	Centrosomal protein of 170 kDa	1	3	12	3	n.a.
P63037	Dnaja1	DnaJ homolog subfamily A member 1	5	2	10	2	n.a.
Q8BTX9	Hsdl1	Inactive hydroxysteroid dehydrogenase-like protein 1	6	2	9	2	n.a.
E9Q8I7	Nfxl1	Protein Nfxl1	5	4	24	4	n.a.
P48758	Cbr1	Carbonyl reductase [NADPH] 1	6	2	12	2	n.a.
Q9QZS3	Numb	Protein numb homolog	3	2	5	2	n.a.
B7ZNL8	Pus7	Protein Pus7	2	2	9	2	n.a.
O70551	Srpk1	SRSF protein kinase 1	3	2	12	2	n.a.
Q8BN21	Vrk2	Serine/threonine-protein kinase VRK2	3	2	6	2	n.a.
Q9JLI8	Sart3	Squamous cell carcinoma antigen recognized by T-cells 3	3	3	15	3	n.a.
D3YTQ3	Hnrnpdl	Heterogeneous nuclear ribonucleoprotein D-like	3	3	38	3	n.a.
O88643	Pak1	Serine/threonine-protein kinase PAK 1	3	2	36	1	n.a.
Q8CFQ3	Aqr	Intron-binding protein aquarius	2	4	23	4	n.a.
Q3URQ0	Tex10	Testis-expressed sequence 10 protein	3	3	17	3	n.a.
P60670	Nploc4	Nuclear protein localization protein 4 homolog	4	3	17	3	n.a.
A2AWI7	Sh3glb2	Endophilin-B2	3	2	39	1	n.a.
Q91VZ6	Smap1	Stromal membrane-associated protein 1	5	2	32	2	n.a.
Q8K298	Anln	Actin-binding protein anillin	3	3	12	3	n.a.
O08800	Serpinb8	Serpin B8	4	2	9	2	n.a.
E9QPD7	Pcx	Pyruvate carboxylase	1	2	6	2	n.a.
D3YYI8	Gm10093	Histone deacetylase	6	3	21	1	n.a.
E9Q0Y4	Sipa1	Signal-induced proliferation-associated protein 1	5	5	31	5	n.a.
Q5SXY1	Specc1	Cytospin-B	3	4	18	4	n.a.
Q91VN6	Ddx41	Probable ATP-dependent RNA helicase DDX41	4	3	17	3	n.a.
Q8VBV7	Cops8	COP9 signalosome complex subunit 8	13	2	10	2	n.a.
Q8BHL8	Psmf1	Proteasome inhibitor PI31 subunit	11	3	34	3	n.a.
D3Z627	Itgal	Integrin alpha-L	3	4	23	4	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q6PAC3	Dcaf13	DDB1- and CUL4-associated factor 13	7	4	23	4	n.a.
Q9CPW7	Zmat2	Zinc finger matrin-type protein 2	14	3	11	3	n.a.
Q3URE1	Acsf3	Acyl-CoA synthetase family member 3, mitochondrial	3	3	10	2	n.a.
O54833	Csnk2a2	Casein kinase II subunit alpha'	6	2	6	2	n.a.
Q56A08	Gpkow	G patch domain and KOW motifs-containing protein	6	3	15	3	n.a.
Q62095	Ddx3y	ATP-dependent RNA helicase DDX3Y	24	17	471	2	n.a.
Q810B6	Ankfy1	Rabankyrin-5	3	3	11	3	n.a.
A0A0B4J1E7	Kpna4	Importin subunit alpha-3	4	3	29	1	n.a.
Q8R149	Bud13	BUD13 homolog	3	2	9	2	n.a.
Q8VCX5-2	Micu1	Isoform 2 of Calcium uptake protein 1, mitochondrial	4	2	8	2	n.a.
Q9DBY8	Nvl	Nuclear valosin-containing protein-like	2	2	15	2	n.a.
Q3U9N4	Grn	Granulins	2	2	8	2	n.a.
K4DI59	Lig3	DNA ligase	2	2	14	2	n.a.
Q8CFE6	Slc38a2	Sodium-coupled neutral amino acid transporter 2	7	2	11	2	n.a.
Q9D1E8	Agpat5	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	8	3	16	3	n.a.
Q9D1I6	Mrpl14	39S ribosomal protein L14, mitochondrial	18	2	9	2	n.a.
Q9WTK5	Nfkb2	Nuclear factor NF-kappa-B p100 subunit	2	2	5	1	n.a.
O88508	Dnmt3a	DNA (cytosine-5)-methyltransferase 3A	7	5	48	5	n.a.
Q61466	Smarcd1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	3	2	12	2	n.a.
Q99M28	Rnps1	RNA-binding protein with serine-rich domain 1	8	2	9	2	n.a.
Q9D198	Syf2	Pre-mRNA-splicing factor SYF2	9	2	21	2	n.a.
Q8BFP9	Pdk1	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	4	2	16	2	n.a.
Q8CCP0	Nemf	Nuclear export mediator factor Nemf	3	3	20	3	n.a.
O54790	Mafg	Transcription factor MafG	12	2	6	2	n.a.
P97376	Frg1	Protein FRG1	8	2	18	2	n.a.
Q6PGG6	Gnl3l	Guanine nucleotide-binding protein-like 3-like protein	5	3	15	3	n.a.
Q99J09	Wdr77	Methylosome protein 50	7	2	7	2	n.a.
E9Q555	Rnf213	E3 ubiquitin-protein ligase RNF213	1	5	18	5	n.a.
F8VPK0	Ttc37	Protein Ttc37	1	2	5	2	n.a.
Q9DC16	Ergic1	Endoplasmic reticulum-Golgi intermediate compartment protein 1	18	4	30	4	n.a.
Q8BYW1	Arhgap25	Rho GTPase-activating protein 25	11	8	57	7	n.a.
P35821	Ptpn1	Tyrosine-protein phosphatase non-receptor type 1	6	3	24	3	n.a.
Q791T5	Mtch1	Mitochondrial carrier homolog 1	4	2	18	2	n.a.
Q6QD59	Bnip1	Vesicle transport protein SEC20	8	2	9	2	n.a.
D0QMC3	Mndal	Myeloid cell nuclear differentiation antigen-like protein	4	2	17	2	n.a.
Q3UM45	Ppp1r7	Protein phosphatase 1 regulatory subunit 7	6	2	14	2	n.a.
Q3TBT3-2	Tmem173	Isoform 2 of Stimulator of interferon genes protein	8	3	11	3	n.a.
B2RUP0	Rbm34	RNA binding motif protein 34	12	5	36	5	n.a.
Q9CPX6	Atg3	Ubiquitin-like-conjugating enzyme ATG3	11	3	16	3	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
B2RRE7	Otud4	OTU domain-containing protein 4	2	2	13	2	n.a.
O08912	Galnt1	Polypeptide N-acetylgalactosaminyltransferase 1	3	2	13	2	n.a.
Q8BIJ6	Iars2	Isoleucine--tRNA ligase, mitochondrial	4	4	18	4	n.a.
Q8BKE6	Cyp20a1	Cytochrome P450 20A1	8	4	29	4	n.a.
Q6PAR5-4	Gapvd1	Isoform 4 of GTPase-activating protein and VPS9 domain-containing protein 1	1	3	22	3	n.a.
A0A0R4J100	Gpr84	G-protein-coupled receptor 84	17	4	30	4	n.a.
Q9CR80	Fam32a	Protein FAM32A	16	2	10	2	n.a.
J3QNE8	Slc38a10	Putative sodium-coupled neutral amino acid transporter 10	2	2	23	2	n.a.
E9QKD9	Gtf2h1	General transcription factor IIH subunit 1	4	2	6	2	n.a.
P61961	Ufm1	Ubiquitin-fold modifier 1	25	2	8	2	n.a.
Q91X20	Ash2l	Set1/Ash2 histone methyltransferase complex subunit ASH2	2	2	8	2	n.a.
Q8C1D8	Iws1	Protein IWS1 homolog	2	2	11	2	n.a.
O08539	Bin1	Myc box-dependent-interacting protein 1	3	2	16	1	n.a.
Q921E6-2	Eed	Isoform 2 of Polycomb protein EED	8	3	32	3	n.a.
Q3TIX9	Usp39	U4/U6.U5 tri-snRNP-associated protein 2	6	3	20	3	n.a.
Q9QWF0	Chaf1a	Chromatin assembly factor 1 subunit A	2	2	19	2	n.a.
Q9JKF7	Mrpl39	39S ribosomal protein L39, mitochondrial	7	3	17	3	n.a.
Q00899	Yy1	Transcriptional repressor protein YY1	3	2	13	2	n.a.
Q9D2V7	Coro7	Coronin-7	2	2	8	2	n.a.
Q9D1H7	Get4	Golgi to ER traffic protein 4 homolog	8	2	6	2	n.a.
Q60967	Papss1	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	4	2	6	2	n.a.
Q8BU03	Pwp2	Periodic tryptophan protein 2 homolog	5	4	27	4	n.a.
P01897	H2-L	H-2 class I histocompatibility antigen, L-D alpha chain	12	4	93	1	n.a.
O70480	Vamp4	Vesicle-associated membrane protein 4	18	2	9	2	n.a.
Q9D0D4	Dimt1	Probable dimethyladenosine transferase	9	3	15	3	n.a.
Q8BGA5	Krr1	KRR1 small subunit processome component homolog	6	3	24	3	n.a.
Q8K3Z9	Pom121	Nuclear envelope pore membrane protein POM 121	3	4	48	4	n.a.
Q61029-3	Tmpo	Isoform Epsilon of Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	42	14	509	2	n.a.
Q9DCS9	Ndufb10	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	36	5	27	5	n.a.
Q91V61	Sfxn3	Sideroflexin-3	12	2	14	1	n.a.
Q9QYJ3	Dnajb1	DnaJ homolog subfamily B member 1	8	3	51	3	n.a.
B2RQG2	Phf3	PHD finger protein 3	1	3	24	3	n.a.
P70699	Gaa	Lysosomal alpha-glucosidase	2	2	21	2	n.a.
P17439	Gba	Glucosylceramidase	2	2	15	2	n.a.
Q3SXA6	Tnip3	Protein Tnip3	9	2	9	2	n.a.
Q61704	Itih3	Inter-alpha-trypsin inhibitor heavy chain H3	2	2	5	2	n.a.
Q3UM18	Lsg1	Large subunit GTPase 1 homolog	3	2	23	2	n.a.
Q99NB8	Ubqln4	Ubiquilin-4	5	2	18	1	n.a.
Q5SWD9	Tsr1	Pre-rRNA-processing protein TSR1 homolog	4	3	11	3	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	^{1}*pksP*/wt
Q61164	Ctcf	Transcriptional repressor CTCF	2	2	13	2	n.a.
Q8R1N0	Znf830	Zinc finger protein 830	6	2	9	2	n.a.
P17427	Ap2a2	AP-2 complex subunit alpha-2	6	7	72	3	n.a.
Q91VJ5	Pqbp1	Polyglutamine-binding protein 1	6	2	6	2	n.a.
A0A0R4J027	Acod1	Cis-aconitate decarboxylase	9	4	18	4	n.a.
Q8BWM0	Ptges2	Prostaglandin E synthase 2	4	2	9	2	n.a.
D3YYT1	Glyr1	Putative oxidoreductase GLYR1	6	3	21	3	n.a.
Q80U70	Suz12	Polycomb protein Suz12	4	3	14	3	n.a.
B1AU74	Mospd2	Motile sperm domain-containing protein 2	3	2	9	2	n.a.
Q6PA06	Atl2	Atlastin-2	4	3	21	3	n.a.
P09450	Junb	Transcription factor jun-B	33	8	62	8	n.a.
Q8BJ05	Zc3h14	Zinc finger CCCH domain-containing protein 14	2	2	15	2	n.a.
Q3UE37	Ube2z	Ubiquitin-conjugating enzyme E2 Z	7	2	20	2	n.a.
A0A0R4J046	Cebpz	CCAAT/enhancer-binding protein zeta	4	4	35	4	n.a.
Q9D517	Agpat3	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	5	2	12	2	n.a.
Q6NSQ7	Ltv1	Protein LTV1 homolog	3	2	9	2	n.a.
P97329	Kif20a	Kinesin-like protein KIF20A	5	4	31	4	n.a.
E9Q7E2	Arid2	Protein Arid2	1	3	22	3	n.a.
Q9D0N7	Chaf1b	Chromatin assembly factor 1 subunit B	9	5	26	5	n.a.
Q8CEC0	Nup88	Nuclear pore complex protein Nup88	5	4	26	4	n.a.
Q5DW34	Ehmt1	Histone-lysine N-methyltransferase EHMT1	4	4	37	4	n.a.
G3UZM1	Jmjd1c	Probable JmjC domain-containing histone demethylation protein 2C	1	2	9	2	n.a.
G5E911	Fam3c	DNA segment, Chr 6, Wayne State University 176, expressed, isoform CRA_f	14	4	27	4	n.a.
Q60960	Kpna1	Importin subunit alpha-5	4	3	20	2	n.a.
O88286-3	Wiz	Isoform 2 of Protein Wiz	4	4	40	4	n.a.
P30285	Cdk4	Cyclin-dependent kinase 4	6	2	22	1	n.a.
Q6ZQH8	Nup188	Nucleoporin NUP188 homolog	1	3	15	3	n.a.
Q9CYZ6	N/A	Uncharacterized protein C19orf60 homolog	10	2	14	2	n.a.
A0A0R4J0B4	Cmas	Cytidine monophospho-N-acetylneuraminic acid synthetase	4	2	6	2	n.a.
Q9DCZ4-3	Apoo	Isoform 3 of MICOS complex subunit Mic26	9	2	13	2	n.a.
A0A0R4J098	Zfp326	DBIRD complex subunit ZNF326	5	3	34	3	n.a.
Q5U4D9	Thoc6	THO complex subunit 6 homolog	13	4	25	4	n.a.
Q69Z99	Znf512	Zinc finger protein 512	2	2	20	2	n.a.
Q8BG07	Pld4	Phospholipase D4	12	5	35	5	n.a.
P24860	Ccnb1	G2/mitotic-specific cyclin-B1	6	3	14	3	n.a.
Q9Z1G4	Atp6v0a1	V-type proton ATPase 116 kDa subunit a isoform 1	2	2	9	2	n.a.
Q9WV54	Asah1	Acid ceramidase	6	3	13	3	n.a.
Q9D3L3	Snap23	Synaptosomal-associated protein	9	2	4	2	n.a.
Q9D1B9	Mrpl28	39S ribosomal protein L28, mitochondrial	13	3	20	3	n.a.
Q01147	Creb1	Cyclic AMP-responsive element-binding protein 1	8	3	17	3	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
E9Q0F0	Krt78	Protein Krt78	1	2	81	1	n.a.
E9Q1P8	Irf2bp2	Interferon regulatory factor 2-binding protein 2	8	3	26	3	n.a.
A2ATU9	Hat1	Histone acetyltransferase type B catalytic subunit	5	2	16	2	n.a.
Q64FW2	Retsat	All-trans-retinol 13,14-reductase	3	2	12	2	n.a.
P60762	Morf4l1	Mortality factor 4-like protein 1	4	2	9	2	n.a.
Q80U78	Pum1	Pumilio homolog 1	4	4	52	1	n.a.
P97452	Bop1	Ribosome biogenesis protein BOP1	9	6	24	6	n.a.
Q6ZQI3	Mlec	Malectin	16	4	49	4	n.a.
Q61733	Mrps31	28S ribosomal protein S31, mitochondrial	7	3	22	3	n.a.
Q8K2C9	Hacd3	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	5	2	15	2	n.a.
Q9CQZ5	Ndufa6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	14	2	9	2	n.a.
Q8CCJ3	Ufl1	E3 UFM1-protein ligase 1	3	3	18	3	n.a.
Q61127	Nab2	NGFI-A-binding protein 2	5	3	14	3	n.a.
Q9Z120	Mettl1	tRNA (guanine-N(7)-)-methyltransferase	7	2	12	2	n.a.
Q99K01-4	Pdxdc1	Isoform 4 of Pyridoxal-dependent decarboxylase domain-containing protein 1	3	2	6	2	n.a.
Q8R2N2	Utp4	U3 small nucleolar RNA-associated protein 4 homolog	9	7	37	7	n.a.
Q80X85	Mrps7	28S ribosomal protein S7, mitochondrial	18	3	17	3	n.a.
Q91YT0	Ndufv1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	17	7	56	7	n.a.
Q9DB96	Ngdn	Neuroguidin	11	3	11	3	n.a.
Q8R3N6	Thoc1	THO complex subunit 1	2	2	6	2	n.a.
Q5RJG1	Nol10	Nucleolar protein 10	2	2	28	2	n.a.
Q8C2Q7	Hnrnph1	Heterogeneous nuclear ribonucleoprotein H	25	8	216	3	n.a.
Q99JR8	Smarcd2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	9	5	27	5	n.a.
P55264	Adk	Adenosine kinase	6	2	8	2	n.a.
P67871	Csnk2b	Casein kinase II subunit beta	7	2	10	2	n.a.
D3Z3N4	Hnrnph3	MCG11326, isoform CRA_a	10	3	178	3	n.a.
O35855	Bcat2	Branched-chain-amino-acid aminotransferase, mitochondrial	5	2	13	2	n.a.
Q3TTY5	Krt2	Keratin, type II cytoskeletal 2 epidermal	6	5	211	4	n.a.
Q9CRD2	Emc2	ER membrane protein complex subunit 2	9	3	50	3	n.a.
Q60973	Rbbp7	Histone-binding protein RBBP7	14	6	91	2	n.a.
Q99N94	Mrpl9	39S ribosomal protein L9, mitochondrial	10	3	31	3	n.a.
Q9D287	Bcas2	Pre-mRNA-splicing factor SPF27	9	2	17	2	n.a.
Q8K2Y7	Mrpl47	39S ribosomal protein L47, mitochondrial	7	2	12	2	n.a.
Q9DCS3	Mecr	Trans-2-enoyl-CoA reductase, mitochondrial	5	2	12	2	n.a.
Q9Z0H3	Smarcb1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	4	2	30	2	n.a.
Q9R112	Sqrdl	Sulfide:quinone oxidoreductase, mitochondrial	5	3	20	3	n.a.
P42227	Stat3	Signal transducer and activator of transcription 3	2	2	15	2	n.a.
O35704	Sptlc1	Serine palmitoyltransferase 1	7	4	28	4	n.a.

Accession	Gene	Description	Coverage	Peptides	Unique Peptides	PSMs	[1]*pksP*/wt
Q91VY9	Znf622	Zinc finger protein 622	4	2	11	2	n.a.
Q8VI93	Oas3	2'-5'-oligoadenylate synthase 3	2	2	6	2	n.a.
Q3TLP8	Rac1	RAS-related C3 botulinum substrate 1, isoform CRA_a	16	5	61	2	n.a.
Q8C6B9	Rps19bp1	Active regulator of SIRT1	15	2	21	2	n.a.
Q921N6	Ddx27	Probable ATP-dependent RNA helicase DDX27	11	9	57	9	n.a.
Q99JX4	Eif3m	Eukaryotic translation initiation factor 3 subunit M	5	2	12	2	n.a.
Q9JKB1	Uchl3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	12	2	9	2	n.a.
P21460	Cst3	Cystatin-C	25	3	19	3	n.a.
Q3UFM5	Nom1	Nucleolar MIF4G domain-containing protein 1	3	3	15	3	n.a.
Q9DC28	Csnk1d	Casein kinase I isoform delta	7	3	16	3	n.a.
Q9JJ80	Rpf2	Ribosome production factor 2 homolog	10	3	19	3	n.a.
P62849	Rps24	40S ribosomal protein S24	30	4	29	4	n.a.
P63166	Sumo1	Small ubiquitin-related modifier 1	20	2	9	2	n.a.
Q9Z1A1	Tfg	Protein Tfg	11	3	30	3	n.a.
P62315	Snrpd1	Small nuclear ribonucleoprotein Sm D1	36	3	12	3	n.a.
P56395	Cyb5a	Cytochrome b5	22	2	18	2	n.a.
Q9JIY5	Htra2	Serine protease HTRA2, mitochondrial	4	2	24	2	n.a.
Q3V2H3	Snx12	Sorting nexin-12	10	2	22	2	n.a.
Q9DBG3-2	Ap2b1	Isoform 2 of AP-2 complex subunit beta	10	9	69	2	n.a.
Q9D868-2	Ppih	Isoform 2 of Peptidyl-prolyl cis-trans isomerase H	17	3	18	3	n.a.
O70252	Hmox2	Heme oxygenase 2	6	2	15	2	n.a.
Q9Z1N5	Ddx39b	Spliceosome RNA helicase Ddx39b	18	7	90	2	n.a.
Q920A7	Afg3l1	AFG3-like protein 1	3	3	22	1	n.a.
P63087-2	Ppp1cc	Isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	16	4	37	2	n.a.
Q8C570	Rae1	mRNA export factor	11	3	39	3	n.a.
Q60737	Csnk2a1	Casein kinase II subunit alpha	4	2	36	2	n.a.
Q9D050	Mtch2	Mitochondrial carrier homolog 2	10	3	48	3	n.a.
P04104	Krt1	Keratin, type II cytoskeletal 1	5	4	47	2	n.a.
Q922U2	Krt5	Keratin, type II cytoskeletal 5	11	9	207	4	n.a.
P62897	Cycs	Cytochrome c, somatic	14	2	29	2	n.a.
E9PUF7	Arhgef1	Rho guanine nucleotide exchange factor 1	6	5	43	1	n.a.
Q3THK7	Gmps	GMP synthase [glutamine-hydrolyzing]	5	4	27	4	n.a.
A0A140LHG8	Spcs2	Signal peptidase complex subunit 2	13	3	18	3	n.a.
Q70FJ1	Akap9	A-kinase anchor protein 9	1	3	12	3	n.a.
Q9D823	Rpl37	60S ribosomal protein L37	15	2	11	2	n.a.
P62309	Snrpg	Small nuclear ribonucleoprotein G	25	2	20	2	n.a.