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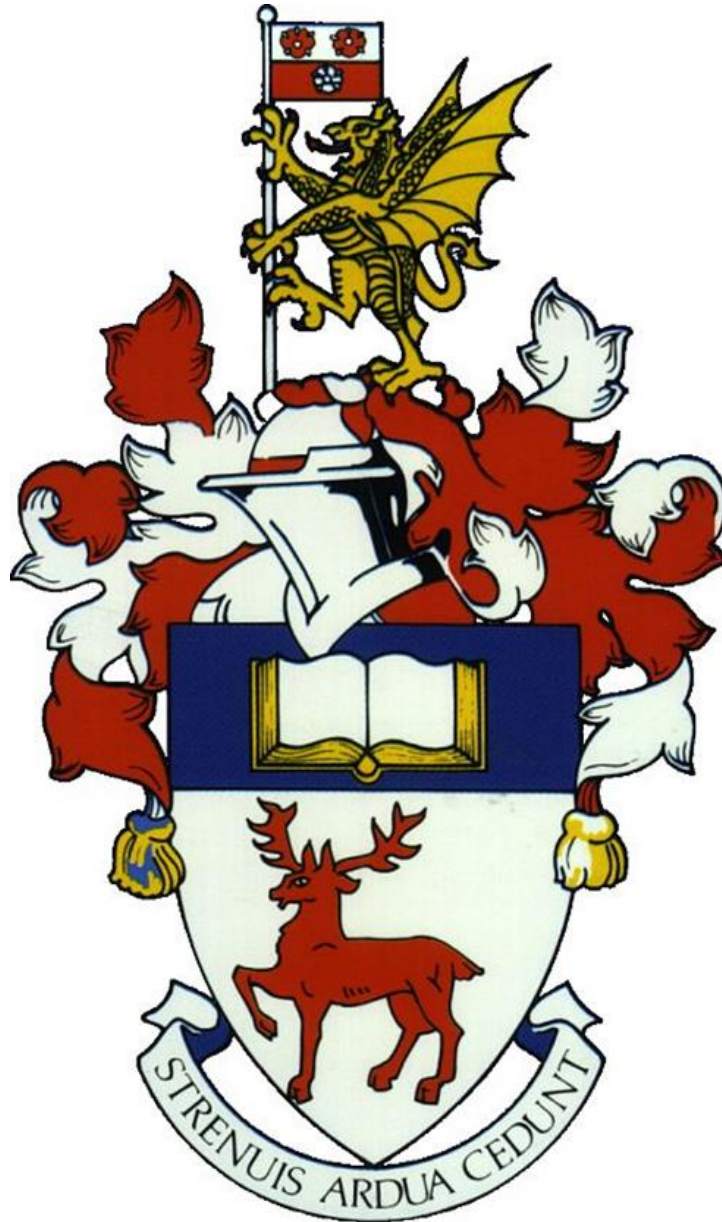
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Faculty of Environmental and Life Sciences

School of Biological Sciences

**Investigation of cellular responses to specific protein haptentation by low
molecular weight chemical sensitisers**



Alexander Lester *MSci MRSB*

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Abstract

Allergies resulting from exposure to small (low M_w) organic chemicals are a public health concern, manifesting as varied clinical outcomes. Skin sensitiser chemicals generally induce relatively mild T cell-mediated hypersensitivity, whereas chemical respiratory allergies are often IgE-mediated and potentially life-threatening. Mechanistic understanding of sensitisation to these low molecular weight chemicals is such that all involve a protein haptenation molecular initiation event (MIE). In the MIE, the electrophilic chemical sensitisers covalently modify nucleophilic amino acid residues of endogenous proteins, thereby becoming immunogenic. The key events following the MIE form the basis of Adverse Outcome Pathways (AOPs) for skin and respiratory sensitisation¹⁻³. This thesis uses proteomics-based methods to characterise the differences in reactivity of chemical sensitisers in the context of the haptenome, proteome and immunopeptidome for the identification of potential molecular drivers of downstream immunological divergence.

The proliferative and cytotoxic effects of skin sensitisers (Dinitrochlorobenzene - DNCB, Diphenylcyclopropenone - DPCP) and respiratory sensitisers (Phthalic anhydride - PA, Toluene diisocyanate - 2,4-TDI) on human epithelial cell lines at different concentrations *in vitro* were initially investigated. Acute changes in cell viability were observed following exposure to skin sensitisers, whereas no such change was observed following exposure to respiratory sensitizer chemicals. The same concentrations of chemical sensitisers were investigated in terms of reactivity and peptide adduct formation with synthetic hexapeptides *in chemico* using a targeted mass spectrometry method. The resulting peptide reactivity data confirmed specificity for each chemical sensitizer predominantly for cysteine- or lysine-containing peptides, consistent with existing evidence in the literature⁴⁻⁷. These results also provided further understanding of haptenation reaction mechanisms for each individual chemical.

Following optimisation of sub-cytotoxic chemical sensitizer concentrations demonstrating maximum peptide reactivity, living alveolar (A549) and bronchial epithelial cells (16HBE14o-) were exposed to equimolar concentrations of deuterated and un-deuterated chemical sensitizers *in vitro* using established dual isotope labelling and tandem mass spectrometry methods⁸. Label-free quantitation of the proteome reproducibly identified significant differences in protein abundance observed between different sensitizer exposure groups. Exposure to respiratory sensitizer chemicals induced a greater magnitude of differential protein expression relative to skin sensitizer chemical exposure. Further, proteins and pathways related to cellular stress (particularly oxidative stress), genotoxicity & proteotoxicity, the ubiquitin proteasome system, and several other potential drivers of immunological divergence were a significant feature of this cellular response.

Additionally, small proportions of the proteome were observed to be haptenated, generating haptenomes of sizes similar to previous experiments in our laboratory⁸⁻¹⁰. The haptenomes were further found to demonstrate more haptenated cysteine residues following skin sensitiser exposure compared to more haptenated lysine residues following exposure to respiratory sensitisers.

Finally, A549 cell cultures exposed to DNCB or PA were subjected to immunoprecipitation of antigen-presenting major histocompatibility complex I (MHC class I) proteins. An immuno-peptidomics workflow and analysis of the presented peptides followed for comparison to similar experiments on human keratinocytes performed in our laboratory¹¹. These results did not provide compelling support for hapten-protein conjugates identified previously forming peptide antigens on MHC class I complexes under these experimental conditions. However, methodological insight was provided for improving the efficiency of experiments investigating haptenation of the immuno-peptidome by respiratory sensitiser chemicals.

Overall, the results in this thesis characterise haptenation and the associated cellular response based on the specific reactivity of select skin and respiratory chemical sensitisers. The insights presented here also demonstrate a progression from the initial hypotheses regarding interplay between these aspects. Furthermore, the data provides a contribution to the weight-of-evidence approach of the AOPs, as well as generation of new hypotheses for further research in this area.

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List of Abbreviations

ACD	Allergic contact dermatitis
AOP	Adverse outcome pathway
APC	Antigen-presenting cell
ARE/EpRE	Antioxidant/electrophile response element
BCA	Bicinchoninic acid
BPI	Base peak intensity chromatogram
CA	Cinnamaldehyde
CLIP	Class II associated invariant chain peptide
DAMP	Danger-associated molecular pattern
DC	Dendritic cell
DDA	Data-dependent acquisition
DIA	Data-independent acquisition
DNCB	2,4-Dinitrochlorobenzene
DPCP	Diphenylcyclopropenone
DPRA	Direct peptide reactivity assay
EA	Ethyl Acrylate
ESI	Electrospray ionisation
FBS	Foetal bovine serum
GSH	Glutathione
GST	Glutathione S-transferase
HDI	Hexamethylene diisocyanate
HDMS ^E	High-definition MS ^E
HLA	Human leukocyte antigen
HSA	Human serum albumin
HSP	Heat-shock protein
IFN	Interferon
IL	Interleukin
IMS	Ion mobility separation
iTRAQ	Isobaric tags for relative and absolute quantification
Keap1	Kelch-like ECH-associated protein 1

LC	Liquid chromatography
MALDI	Matrix-associated laser desorption/ionisation
MCI	5-Chloro-2-methyl-4-isothiazolin-3-one
MHC	Major Histocompatibility Complex
MHCI/MHCII	Major histocompatibility complex I/II
MIE	Molecular initiating event
MIIC	Late endosomal MHC class II compartment
MRM	Multiple reaction monitoring
MS	Mass spectrometry
MS ^E	Elevated energy mode
MS/MS	Tandem mass spectrometry
M _w	Molecular weight
NFATC	Nuclear Factor of Activated T Cells
NGRA	Next Generation Risk Assessment
NLR	Nucleotide-binding domain leucine-rich repeat containing receptor
Nrf2	Nuclear erythroid 2-related factor 2
OA	Occupational asthma
OECD	Organisation for economic co-operation and development
PA	Phthalic anhydride
PPIN	Protein-protein interaction network
PSTAT-5	Phosphorylated signal transducer and activator of transcription - 5
PTM	Post-translational modification
qRT-PCR	Quantitative reverse transcription polymerase chain reaction (real-time)
QSAR	Quantitative structure-activity relationship
QToF	Quadrupole time-of-flight mass analyser
SDS	Sodium Dodecyl Sulphate
SILAC	Stable isotope labelling with amino acids in cell culture
TDI	Toluene 2,4-diisocyanate
Tfh	T follicular helper cell
Th1	T-helper type 1
Th2	T-helper type 2
THP-1	Tohoku Hospital Pediatrics – 1 (spontaneously immortalised cell line)

TLR	Toll-like receptor
ToF	Time-of-flight mass analyser
TSLP/TSLPr	Thymic stromal lymphopoietin/Thymic stromal lymphopoietin receptor
6-MC	6-methyl coumarin

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Research Thesis: Declaration of Authorship

Print name:	Alexander Michael Thomas Lester

Title of thesis:	Investigation of cellular responses to specific protein haptentation by low molecular weight chemical sensitizers

I declare that this thesis and the work presented in it are my own and has been generated by me as the result of my own original research.

I confirm that:

1. This work was done wholly or mainly while in candidature for a research degree at this University;
2. Where any part of this thesis has previously been submitted for a degree or any other qualification at this University or any other institution, this has been clearly stated;
3. Where I have consulted the published work of others, this is always clearly attributed;
4. Where I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work;
5. I have acknowledged all main sources of help;
6. Where the thesis is based on work done by myself jointly with others, I have made clear exactly what was done by others and what I have contributed myself;
7. None of this work has been published before submission.

Signature:		Date:	

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Chapter 1 Background and Literature Review

1.1 Introduction to Chemical Sensitisation

Many cell-mediated immune responses, such as allergies, develop in two phases¹². The first stage is referred to as the sensitisation phase in which the predominant observations generally centre on differentiation of antigen-presenting cells^{1,2} and lesser physiological symptoms^{12,13}. This stage occurs following exposure to a chemical capable of causing sensitisation through a number of subsequent processes, therefore emphasising the importance of cells of different epithelia as the main point of exposure to such chemicals. Following the chemical sensitisation phase (also referred to simply as “sensitisation”, or becoming “sensitised”), is the more severe effector phase in which molecular and cellular interactions lead to a notably larger immune response than during sensitisation. This knowledge aids in highlighting why sensitisation to small organic chemicals represents a considerable public health concern¹⁴, particularly due to the manifestation of the resulting allergies as differing clinical outcomes. The major outcomes show an immunological divergence resulting in Allergic Contact Dermatitis (ACD) and Occupational Asthma (OA) due to skin and respiratory sensitisation¹⁵ respectively, though evidence has also emerged to show that the two outcomes are not necessarily mutually exclusive and is discussed further herein.

It has previously been shown that the effector phase is the more clinically-apparent stage, and crucially is a direct result of interactions in the more covert sensitisation phase^{1,13}. This by extension presents the underpinning reason for the level of interest in the cellular causes and interactions leading to the divergent development of skin and respiratory sensitisation, in which specific protein modification and associated peptide presentation logically would be significant contributing or driving factors.

1.1.1 Skin Sensitisation

The adverse outcome pathway (AOP) of skin sensitisation¹ refers to the sequential process following the structure-reactivity relationships between specific sensitizer chemicals and carrier proteins in the molecular initiating event (MIE) at the cellular level. The AOP collates current knowledge and data into a series of additional stages/events resulting in the *in vivo* adverse outcome of delayed hypersensitivity associated with skin sensitisation. Understanding, weight, and confidence of both qualitative and quantitative evidence used to build the AOP has developed greatly over the last 20 years, providing a robust composition of 11 events, of which 4 are consistently considered key events in leading to the adverse outcome^{1,3,13,16}.

Skin sensitisation has been illustrated as an immunological process adhering to the aforementioned sensitisation and elicitation/effector phases. The initial phase of skin sensitisation demonstrates the sequence of events leading from the MIE to the rest of the AOP (Figure 1.1). The structure of the AOP has garnered agreement in terms of events included¹; though it still remains, to an extent, unclear the impact of the underlying biology on the importance of each stage outside of the key stages.

In the skin sensitisation AOP representation of the sensitisation phase (Figure 1.1), the chemical sensitizer/hapten exhibits epidermal penetration where it (or a derivatised metabolite) undergoes stable conjugation to a host protein which acts as a carrier. This covalent interaction between electrophilic sensitizer chemical and nucleophilic carrier protein is referred to as Haptenation^{1,13,17}. The conjugate is subsequently internalised and processed for antigen presentation by dendritic cells (referred to as Langerhans cells for the epidermal sub-type) and keratinocytes^{1,18,19}, before maturation and migration of the dendritic antigen-presenting cells (APCs) to local lymph nodes. Keratinocytes have the potential to interact with dendritic cells prior to migration^{19,20}, and also possess the ability to secrete cytokines which have often been the subject of cytokine profiling associated with the sensitisation phase^{1,4,12,13,21}.

Once in the local lymph nodes, the APCs present the previously-internalised haptenated peptides to naïve T-lymphocytes by virtue of the major histocompatibility complex (MHC) molecules on the cell surface of APCs. This provokes maturation and proliferation of memory T cells specifically targeting the hapten-protein conjugate, some of which remain in the local lymph nodes and some of which enter circulation for availability upon re-exposure (Figure 1.1).

The sensitisation phase proceeds into the elicitation/effector phase after re-exposure to the same sensitizer chemical^{1,13}, where the large population of keratinocytes shows further importance. The hapten-complex is once again internalised and presented by the MHC molecules of cells in the region of exposure¹. The conjugate-specific memory T cells are activated to release cytokines to induce release of inflammatory cytokines from cells of the epidermis (e.g. keratinocytes) and chemokine-recruited inflammatory cells, leading to the characteristic redness and irritation symptoms of allergic contact dermatitis^{1,13,22,23}.

Evidently, covalent interactions are critical in the MIE, and whilst reactions with proteins and low molecular weight (Mw) inorganic chemicals have been identified^{6,24–26}, much interest remains focused on initiation of the AOP by low Mw organic chemicals^{1,3,27,28} bonding predominantly to primary amino groups and thiol groups of host proteins. It is understood that the details and intricacies of the AOP will vary in regard to chemical-specific target residues and reactivity in the upstream molecular stages. The downstream cellular processes show relatively more elucidation

and greater similarity thus far^{1,3,29}. This, alongside the previously described biological complexities, provides some explanation for the historical emphasis on *in vivo* tests and assays at the back end of the AOP.

The AOP is useful in highlighting the quantity and strength of available evidence in an understandable, linear process. However, it is also understood that the linear demonstration of the AOP suffers from some degree reductionism and a simplification of the overall process. This is largely due to significant variation in the level of detail and linearity between the initial MIE and the end-point adverse outcome as a result of multiple molecular/cellular interactions in various tissues in response to the sensitisation process^{1,3}. For example, it has been suggested that during epidermal penetration by the sensitiser, the chemical(s) may undergo transformation/modification which alters the sensitisation potential^{1,30,31}.

In partial counter to these issues, AOPs generally consider available quantitative structure-activity relationships (QSARs) to acknowledge chemical relationships are concerned with molecular interactions, and not necessarily the whole tissue/organism. This also provides the additional benefit of accounting for missingness in the available data via traditional read-across and trend analysis methods¹. Therefore, the adverse outcome is considered both as a function of the downstream biological responses in association with the molecular interactions of the chemicals in the upstream MIE and allows organisation of chemicals into categories reflecting the specific links between reaction and response^{1,31–33}.

Ultimately the skin sensitisation AOP does suffer from a number of issues highlighted above, however it continues to be a useful qualitative tool for which experiments can be designed to interrogate the key events quantitatively. As will be discussed later, there are a number of studies at each of the key events in which quantitative interpretations have been made to indirectly assess the robustness of the AOP structure. Crucially, there is demonstration of extensive strength, consistency and specificity of the link between *in vivo* skin sensitisation and *in chemico* molecular initiating events involving specific chemical groups and associated sensitiser molecules¹, though the reasons remain unclear.

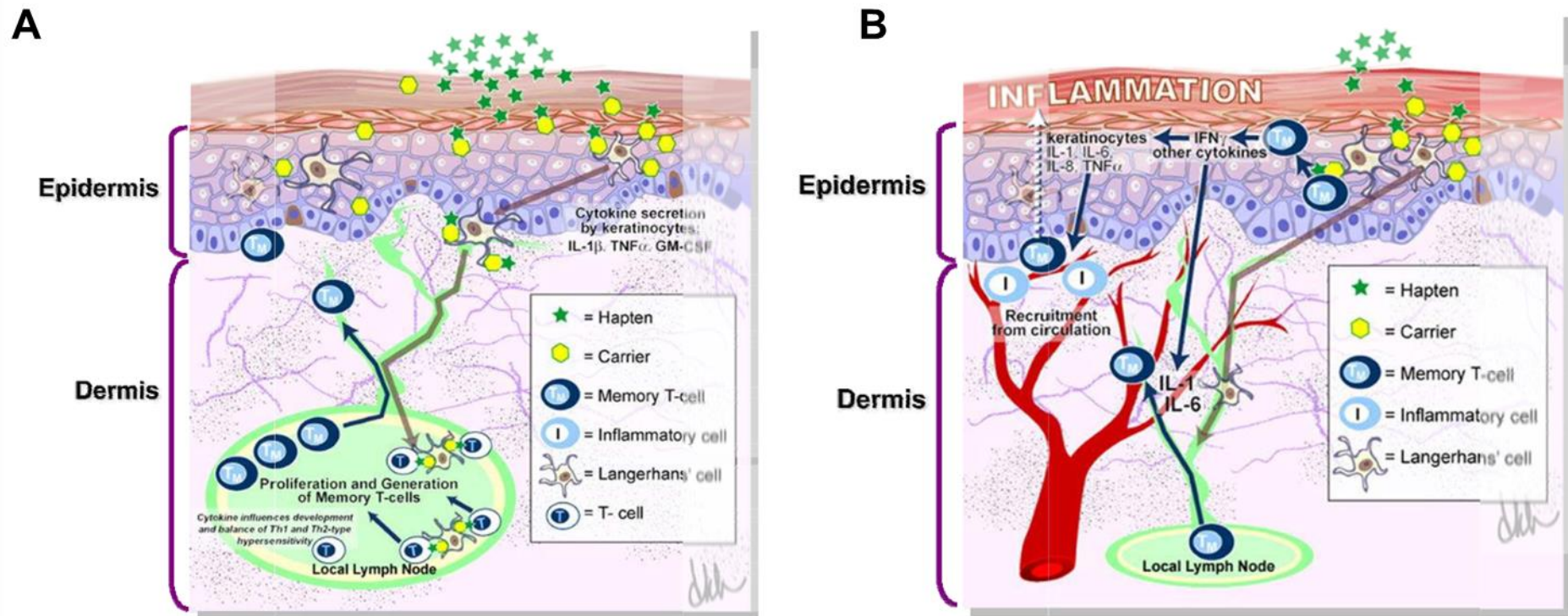


Figure 1.1: The skin sensitisation adverse outcome pathway – The initial induction/sensitisation phase (A) compared to the elicitation/effector phase (B).

Obtained from Organisation for Economic Co-operation and Development¹

1.1.2 Respiratory Sensitisation

Similar to (and developing on) the skin sensitisation AOP, there is an AOP of respiratory sensitisation referring to the sequential process following haptentation in the MIE at the cellular level². The respiratory AOP focuses on sensitisation by low molecular weight chemicals in the respiratory tract; it also collates current knowledge and data into a series of key events to give a systematic overview and evaluation of research methodology guiding predictive testing.

The respiratory AOP reflects the same general structure of the skin sensitisation AOP, though there are some subtle yet distinct differences in sensitiser selectivity, cellular response, and cytokine profiles. The respiratory sensitisation AOP demonstrates the sequence of key events and reactions leading from the MIE to the adverse outcome (Figure 1.2), as well as highlighting the parallels to the skin sensitisation AOP. The literature evidence supporting haptentation as the MIE for respiratory sensitisation, similar to the extent of support for the skin sensitisation AOP, is expansive^{1–3,6,26,34–38}. The most informative explanation of variations in the MIE between the skin and respiratory AOP can be gained from the dedicated sections herein.

Following the MIE in this model of respiratory sensitisation are dual events, of which one is not equally demonstrated as a substantial component in the dermal sensitisation AOP, but more recently shows great importance³⁸ suggesting understatement in the original dermal sensitisation AOP. The first of these key events, and less represented in the dermal sensitisation AOP, is the induction of cellular danger signals, including cytoprotective gene pathways and a range of inflammatory cytokines & chemokines^{2,4,22,38}. This stage reinforces the importance of the innate immune system in induction of an adaptive immune response^{19,22}, which is a common feature to both the main models of sensitisation and their effector phase. Summarily, the innate immune system is induced through a variety of pattern recognition receptors which are complementary for conserved surface patterns of different pathogens. Such patterns include the NLR family of nucleotide-binding domain receptors³⁹, and toll-like receptors (TLRs)⁴⁰ which have a particularly key role in the innate immune system due to their presence on the surface of dendritic cells – the bridge between innate and adaptive immunity⁴¹.

Pattern recognition receptors can also be activated by internal danger-associated molecular patterns (DAMPs), released as a result of oxidative stress and cellular damage. These patterns commonly feature constituents of damaged extracellular matrix, such as keratins – a component of cytoskeletal structural filaments – as well as interferons and intracellular proteins e.g. heat-shock proteins (HSP)^{2,22,40}. Following stimulation, toll-like receptors and some sub-classes of NLR

proteins in turn stimulate signaling pathways of the innate immune system, resulting in release of pro-inflammatory cytokines and chemokines^{39,40}.

These processes and pathways demonstrate reason for the increased consideration of innate immune system signaling by pathogen-associated and danger-associated molecular patterns in asthma. This is also one of the central themes used to describe key events in respiratory sensitisation, e.g. dendritic cell stimulation and migration, and exposes the importance of immune signaling alongside antigen presentation in processes of chemical respiratory sensitisation^{2,38}. This event is granted increased relevance due to identification of a key reaction whereby protein binding in the MIE induces the cellular danger signals described previously; therefore presenting a point of comparison between the two main AOP models discussed later (section 1.2).

The second of the aforementioned dual events is the induction and migration of dendritic cells, a crucial event in sensitisation of the respiratory tract^{20,42,43} (and to an extent skin sensitisation as well). The most critical changes in DCs following sensitisation-induced maturation include antigen presentation, increased major histocompatibility complex (MHCII) expression, and elevated co-stimulatory molecules and receptors necessary for migration to local lymph nodes and antigen presentation to T helper cells^{2,38}. Despite not being a major component of the dermal sensitisation AOP, presently available *in vitro* and *in vivo* evidence reveals haptenated protein conjugates are able to induce cellular danger signals whilst also being able to interact directly with dendritic cells to trigger antigen presentation^{2,3,19,42} – a potentially two-pronged induction.

Subsequent events in the respiratory sensitisation generally mirror the dermal AOP quite well. Maturation and migration of DCs to lymph nodes once again results in the activation, proliferation, and polarisation of T cells via antigen presentation by MHC molecules. This however presents a challenge and a gap in the current literature. There is currently limited understanding of a number of aspects of antigen processing in respiratory sensitisation, specifically the uptake process, peptide processing, and MHC-peptide characterisation and relative stabilities^{2,38}. It has been suggested that there may be differences between dermal and respiratory sensitisers in regards to these antigen presentation-related processes that may provide vital data for a meaningful distinction^{2,3,38}. The field of immunopeptidomics is recently expanding, partly in pursuit of addressing the gap in our knowledge for dermal sensitisation. These pursuits have not yet however been performed for models of respiratory sensitisation.

Processes occurring in lymphatic T cells as a result of sensitisation are here also considered to be the primary event preceding the adverse outcome^{2,3,12,38} (sensitisation of the respiratory tract) as it was also with dermal sensitisation. However, antigen presentation to T helper cells this time results in T-cell clonal expansion and differentiation into a Th2 cytokine immune response^{2,4} which

also induces immunoglobulin class-switching by B cells, resulting in production of antigen-specific immunoglobulin-E (IgE) antibodies and further clonal expansion of memory B cells^{2,3,38,44}. Processes defined in section 1.2.4 highlight the importance of this IgE production and cross-linking in the differential severity of symptoms and clinical outcomes between dermal and respiratory sensitisation.

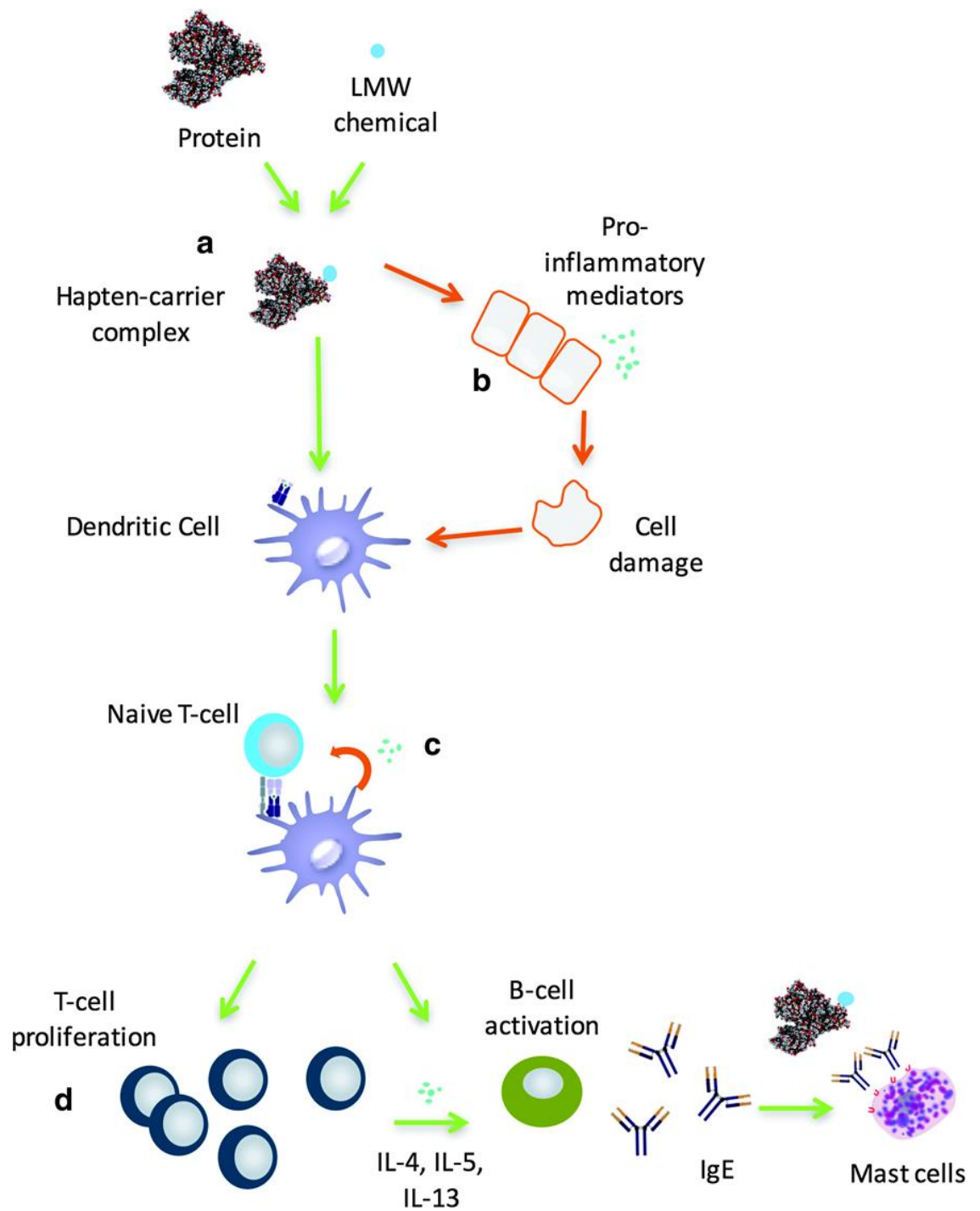


Figure 1.2: Respiratory sensitisation adverse outcome pathway – Obtained from Sullivan et al²

1.2 Distinguishing between Sensitisation Mechanisms

It is evident that we have a better mechanistic understanding of the events necessary for the development of dermal sensitisation. However, our knowledge of mechanistic events inducing respiratory sensitisation is significantly less complete and presents a major challenge in defining the causes of both known and proposed divergence between the processes which will be discussed here.

The AOP for both dermal and respiratory sensitisation exhibit the same overall structure and can be briefly summarised as beginning with covalent haptentation of protein nucleophilic sites in the skin or lung cells/tissue after exposure to an electrophilic, low-molecular-weight organic chemical. This binding event provokes the activation of stress response pathways and cellular danger signals, including oxidative stress and cytokine/chemokine secretion by epithelial cells (plus other cell types). Both the molecular initiation and danger signalling events lead to DC maturation and migration to the draining lymph nodes, though the interactions between these three events are incompletely understood¹⁻³. Following DC antigen presentation to local T cell populations, a skewed T cell proliferation response has been demonstrated and categorised into either a T-helper 1 response representing dermal sensitisation, or a T-helper 2 representing respiratory sensitisation^{3,4,29}.

The advantage of the dual existing AOPs is that it allows for a natural comparison between them which highlights the overarching sequence of key events, as well as the differences between the two. Indeed, this concept has been embraced by Kimber et al to produce a hybrid AOP in which the previously published dermal and respiratory sensitisation AOPs are viewed more as a single common pathway, with specific points where divergence has either been found to occur or where there is potential for it to occur³. However, it should still be remembered that AOPs are largely evidence-based and are therefore only as reliable as the wealth and depth of evidence they are based on.

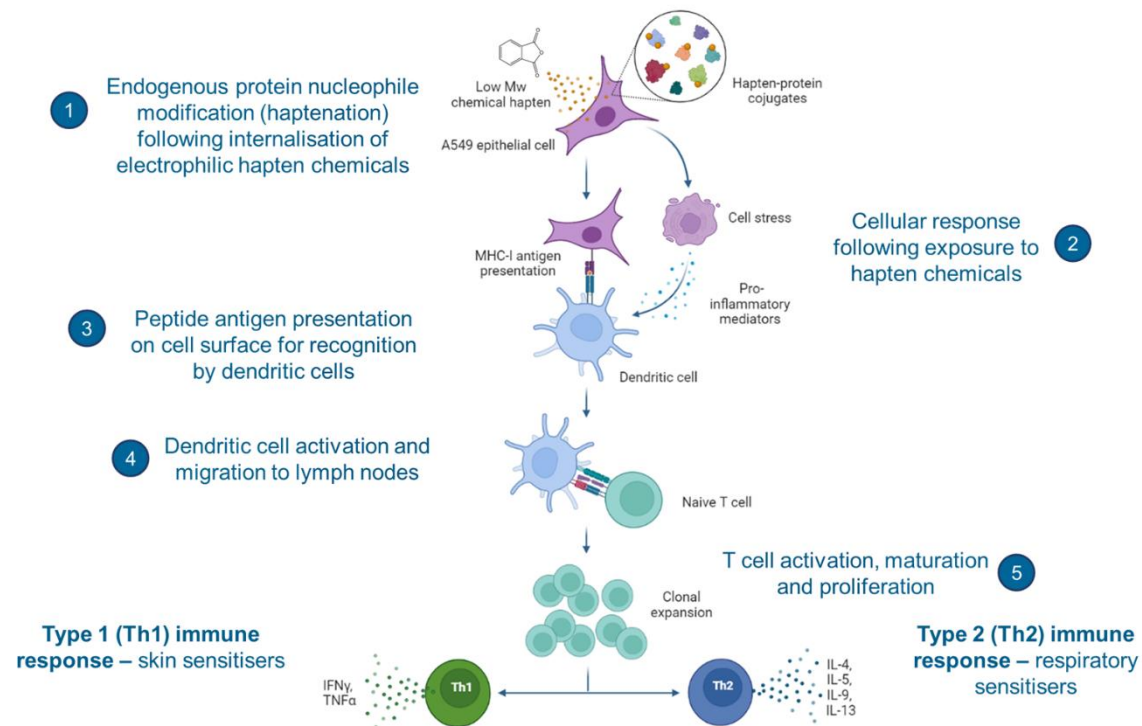


Figure 1.3: Combined adverse outcome pathway based on published versions – Published adverse outcome pathways are broadly similar for both skin and respiratory sensitisation, in that both require a molecular initiation event whereby small chemicals (which are too small to inherently cause an immune response) penetrate cells and covalently modify intracellular protein in a process termed ‘haptentation’ (1). From this haptentation event, a series of further key events are stimulated, these being; cellular signalling responses (2), endogenous protein-derived peptides being presented on the cell surface and recognition by dendritic cells (3), dendritic cell activation and migration to lymph nodes (4), and finally T cell activation & proliferation (5). The important distinction is that this final immune response diverges into a Th1 immune response following skin sensitizer exposure, or a Th2 immune response following respiratory sensitizer exposure.

1.2.1 Cellular Pathways

Cellular responses to sensitisation and elicitation most notably include induction of inflammatory cytokine pathways, such as the oxidative stress response pathway, particularly in keratinocytes^{1,45–48} and feasibly other dense epithelial cell populations. The Nrf2-Keap1 antioxidant response element (ARE) has been singled out and considered here separately due to featuring in both the dermal and respiratory sensitisation AOPs, as well as other hybrid pathways, and also represents a potential tool for distinction between dermal and respiratory sensitisers^{46,48}. The Keap1 component is a cysteine-rich sensor protein which is ordinarily bound to the transcription factor Nrf2⁴⁹. This Nrf2 component is known to dissociate from Keap1 following covalent interaction between an electrophile and the Keap1 constituent cysteine residues^{50,51}. For this reason, the antioxidant response element is also sometimes referred to as the electrophile response element (EpRE)⁵². This dissociation event causes Nrf2 to gather in the nucleus, resulting in increased expression of genes found to contain ARE in the promoter region^{46,48,49}.

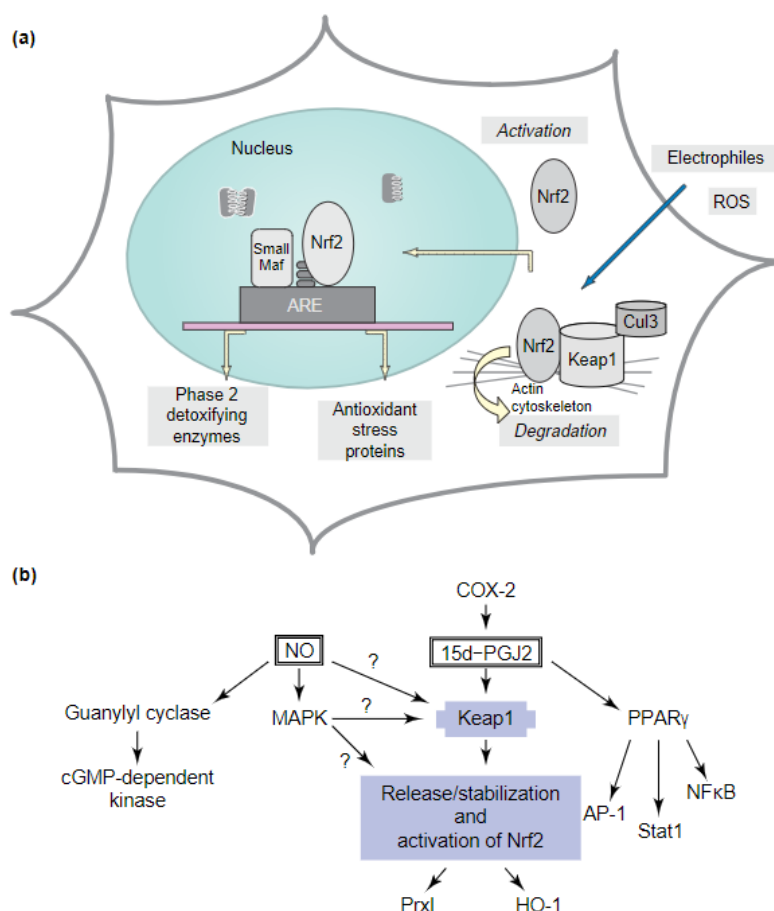


Figure 1.4: The Nrf2-Keap1 pathway – (a) Nrf2-Keap1 ARE pathway overview demonstrating transcriptional induction (a). Nrf2-Keap1 interactions with other relevant biochemical pathways (b). Obtained from Motohashi & Yamamoto⁴⁷.

Further demonstrating its utility, the Nrf2-Keap1 has been proposed as the basis of a predictive assay for the indication of dermal sensitisation by virtue of dermal sensitisers having some affinity towards cysteine residues^{46,48,50} that appears to be absent with respiratory sensitisers^{3,7} (covered in more detail later). If dermal sensitisers are indeed able to selectively up-regulate the Nrf2-Keap1 ARE pathway, then logically this may result in increased gene expression of gene sets related to a Th1 immune response and dermal sensitisation. The relative inability of respiratory sensitisers to dissociate Nrf2 would mean they are unable to up-regulate expression of these gene sets and therefore would lead to an alternative immune response⁴⁶, i.e. Th2-induced respiratory sensitisation. This relative difference in gene expression can serve as a means of distinguishing the sensitiser classes, as well as linking them to their associated T-helper immune response⁴⁸.

Unfortunately, more research is required for this pathway to reliably serve as a discrimination between dermal and respiratory sensitisers. The importance and activation of this pathway is considerably more elucidated for dermal sensitisation compared to respiratory sensitisation, though progress is being made to characterise *in vitro* Nrf2-Keap1 activation following exposure of dermal and respiratory epithelium to selected respiratory sensitisers⁵³.

The importance of DAMPs and danger signals in this context were originally outlined by Matzinger *et al*⁵⁴, with the explanation that an adaptive immune response to sensitisers is reliant upon endogenous danger signal activity and inflammation in the innate immune response^{22,54}. This offers some explanation for the lack of robust understanding of the differences between sensitiser and irritant chemicals and the effects they exert on the downstream pathways discussed here; exacerbating this further is the observation of sensitisers being capable of inducing irritation, initially found in the 1930s³⁶ with supporting publications since^{55,56}.

Information is available demonstrating the importance of danger signals to sensitisation acquisition primarily as a result of up-regulated cytokine expression with potentially important downstream effects depending on differential expression of PRR types^{2,57}. It has been suggested previously that dermal and respiratory sensitisers potentially infer different damage/stress responses and therefore differential danger signals reflected by the divergent immune responses and antigen presentation. This represents a current knowledge gap with results comparing DAMP induction (and associated danger signals) with immune response to dermal and respiratory sensitisers being unavailable¹⁻³. It is incompletely understood which cells have the most importance in skin and respiratory sensitisation as the sources of danger signals, though it has been noted the main candidates include keratinocytes, alveolar epithelial and bronchial epithelial cells^{18,58-60}.

A number of other inducible biochemical pathways have been identified following treatment with dermal sensitiser chemicals. For example, a number of kinase signalling pathways have received demonstrated activation following exposure to haptenation-capable chemical structures^{61–64}. This has generally been achieved through studying alterations in expression of different kinases in the p38 MAPK, PGK, NFkB, and ERK signalling pathways, as well as other N-terminal kinases^{61,62}. Miyazawa *et al* further demonstrated activation of ERK and MAPK in THP1 cells⁶⁴, which while not keratinocytes, do provide some insight on the underlying stimulation in danger signalling pathways and more crucially in antigen presentation processes involved in the development of dermal sensitisation. It was determined from these studies that DNCB has a dual effect on the cells in which the two aforementioned pathways are activated alongside stimulation of TNF- α ⁶³.

The majority of the studies discussed here have been identified in response only to a limited group of sensitisers, and often extreme model sensitisers such as DNCB. This therefore represents a potential pitfall. The findings are clearly informative of the underlying processes that could be contributing to dermal sensitisation, though there is a pronounced relative lack of information on the specific target proteins in these pathways. Furthermore, the limited range of sensitisers analysed thus far also limits the transferability of the findings to other cells, chemicals, and respiratory sensitisation pathways. However, efforts have recently been made to characterise additional pathways and components associated with a wider range of sensitisers^{28,65}, though there is still considerable room for growth – particularly in terms of differential targeting of components of signaling pathways.

1.2.2 Dendritic Cells

Differences in the two-pronged induction of DC development & migration by the MIE and/or cellular danger signals is considered a major possible avenue towards identifying the underlying mechanism skewing the respiratory sensitisation immune response in favour of Th2^{2,3,66}.

The current understanding on roles of DCs as professional APCs has great importance in explaining each sensitisation mechanism discretely, though a relatively lesser importance for explaining divergence between responses when compared to the other aspects discussed here. This is in part due to high density epithelial cell populations, such as keratinocytes, which also perform this role as previously discussed. However, the more important consideration here is that biased DC subsets are implicated in either sensitisation AOPs but also show a plasticity to allow them to be trained to either a Th1 or Th2 response^{38,67,68}. It is also becoming increasingly apparent that DC functionality is actively influenced by cross-talk with neighbouring epithelial cells^{20,42,43}. Dendritic cells are therefore considered to act more as facilitators of immune response

divergence based on specific interactions in the earlier events, with some body of evidence to support this perception.

It has been suggested that differential induction of DC migration could result in differences promoting either of the divergent immune responses³. There is also supporting evidence highlighting DC subsets with an inherent Th2 bias, as well as principles of DC to T-cell ratio influencing the immune outcome^{68–71}. However, it has also been proposed that the uptake, processing, and presentation of the hapten-conjugate antigen can be attributed more to specific interaction biochemistry of the conjugate and associated danger signals³ inferring a Th1/Th2 bias, rather than inherent differences in DCs themselves. Though these subsets should not be ignored, and may be especially relevant when considering sensitisation at the tissue level. Ultimately, it remains unclear what processes result in a Th1/Th2 bias, though it currently appears more probable that one or more of the other upstream processes are responsible and therefore present themselves as better candidates for driving immunological divergence, e.g. specific targeting of proteins by different sensitiser chemicals.

1.2.3 T Cell Regulation & Proliferation

The original Gell & Coombs classification of allergic hypersensitivity reactions^{72,73} is subdivided into four categories based on their respective mechanisms of pathophysiology. Type I-III are rapid reactions and generally antibody-mediated, occurring within 24 hours post-exposure. However, type IV represents delayed hypersensitivity reactions and as such are non-immediate. Type IV reactions are T-cell mediated and generally do not include a direct antibody effector mechanism – these are the main type of response distinguishing skin and respiratory sensitisation pathology.

T cells are lymphocytes which mature in the thymus and are instrumental in the mediation of immune response mechanisms. Most T cells are defined as either CD4⁺ helper or CD8⁺ cytotoxic cells, named for the glycoproteins expressed on their cell surface. However, there are also subsets of these cells, as well as other types of T cells including memory T cells, regulatory T cells (T_{reg}), natural killer T cells (NKTs), mucosal associated invariant T cells (MAIT), and gamma-delta T cells⁷⁴ (see figure/table). There are also further types of co-receptors that infer different levels of activation specificity as well as increased stability of binding interaction with MHC-peptide antigen complexes.

CD8⁺ cytotoxic T cells can directly kill target cells presenting foreign MHC peptide antigens, though may also secrete specific cytokines to recruit other types of immune cells in this process⁷⁴. Unlike CD8⁺, CD4⁺ helper T cells (T_h) generally function through activation of memory B lymphocytes and CD8⁺ cytotoxic T cells, leading to a stronger immune response. Differential induction of CD8⁺ and CD4⁺ mediated immune processes is believed to be a likely reason for differences in the severity of clinical outcomes of skin and respiratory sensitisation, with the former being milder in terms of symptoms and the latter being more severe. The reason for this appears to lie in different regulation of the adaptive immune response regulated by T_h subsets.

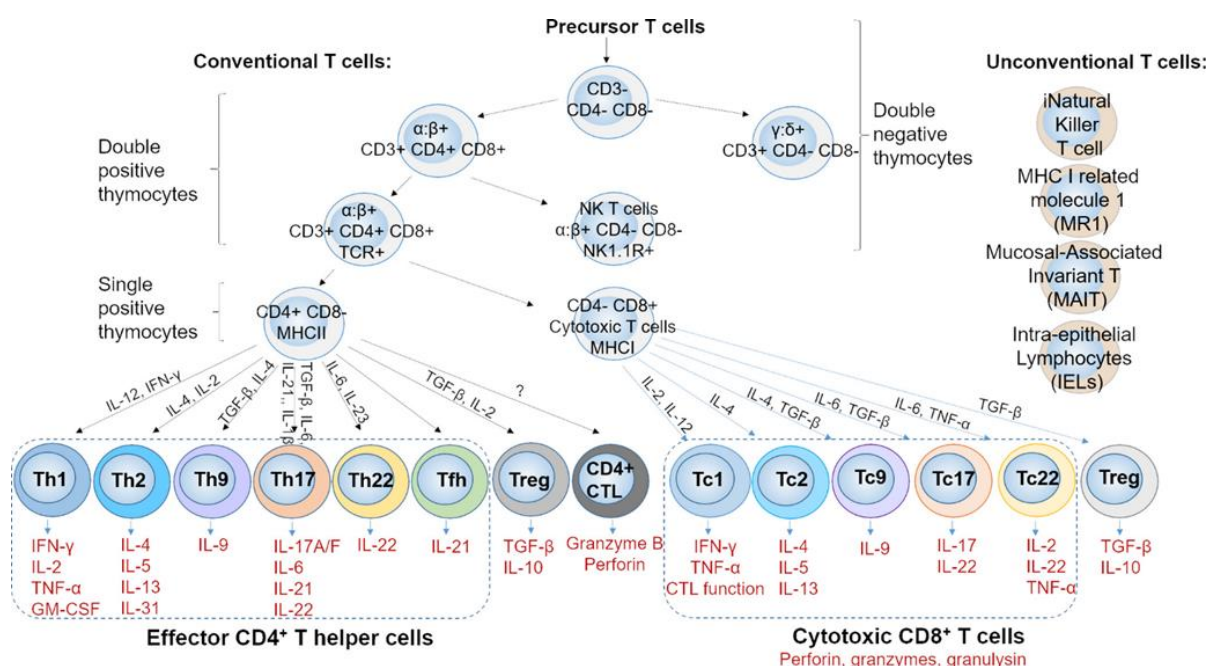


Figure 1.5: Overview of the array of conventional and unconventional T-cell subsets.

During processes of maturation and selection in the thymus, T-cell surface markers are expressed differently amongst the T-cell subtypes. Naïve T cells are dependent upon local cytokines for further differentiation into the mature states. Obtained from Krohn et al (2021)⁷⁴.

The activation of T cells is determined by the interaction of T-cell receptors (TCRs) with major histocompatibility complex proteins presenting peptide antigens (see previous section). Direct activation of naïve T cells that interact with specific foreign peptide antigens (e.g. haptenated peptides) results in positive selection and subsequent clonal expansion of cells with the TCR structure specifically complementary to the MHC peptide antigen. Secondary cytokine signals and differences in co-stimulatory molecules of different T cell subsets are not necessarily antigen-specific, but contribute to T cell proliferation and augment the clonal expansion of T cells recognising the specific peptide antigen (see differential cytokine section and figure below). CD4⁺ Th subsets are differentiated from naïve CD4⁺ T cells by specific cytokines. For example: Th1 by IL-

12 and IFN- γ , Th-2 by IL-4, and T_{reg} by IL-2 and TGF- β (Figure 1.5). Each Th subset is also capable of releasing specific cytokines with a variety of pro- or anti-inflammatory functions, survival or cytoprotective functions. For example, Th1 is typically associated with skin sensitisation and secretes IL-12, IFN- γ and TNF- α with roles including increased Toll-like receptors (TLRs), macrophage activation, and induction of CD8+ cytotoxic T cell differentiation and proliferation⁷⁵. For further comparison, Th2 is associated with respiratory sensitisation and releases IL-4 (among others), which is an important survival factor for B cells and class switching to IgE⁷⁶. T_{reg} cells secrete IL-10 and TGF- β , with functions in immunosuppression⁷⁷. Tfh secretes IL-21 and has roles in aiding the antibody production of B lymphocytes, as well as being implicated in asthma pathology⁴⁴ (see section 1.2.4).

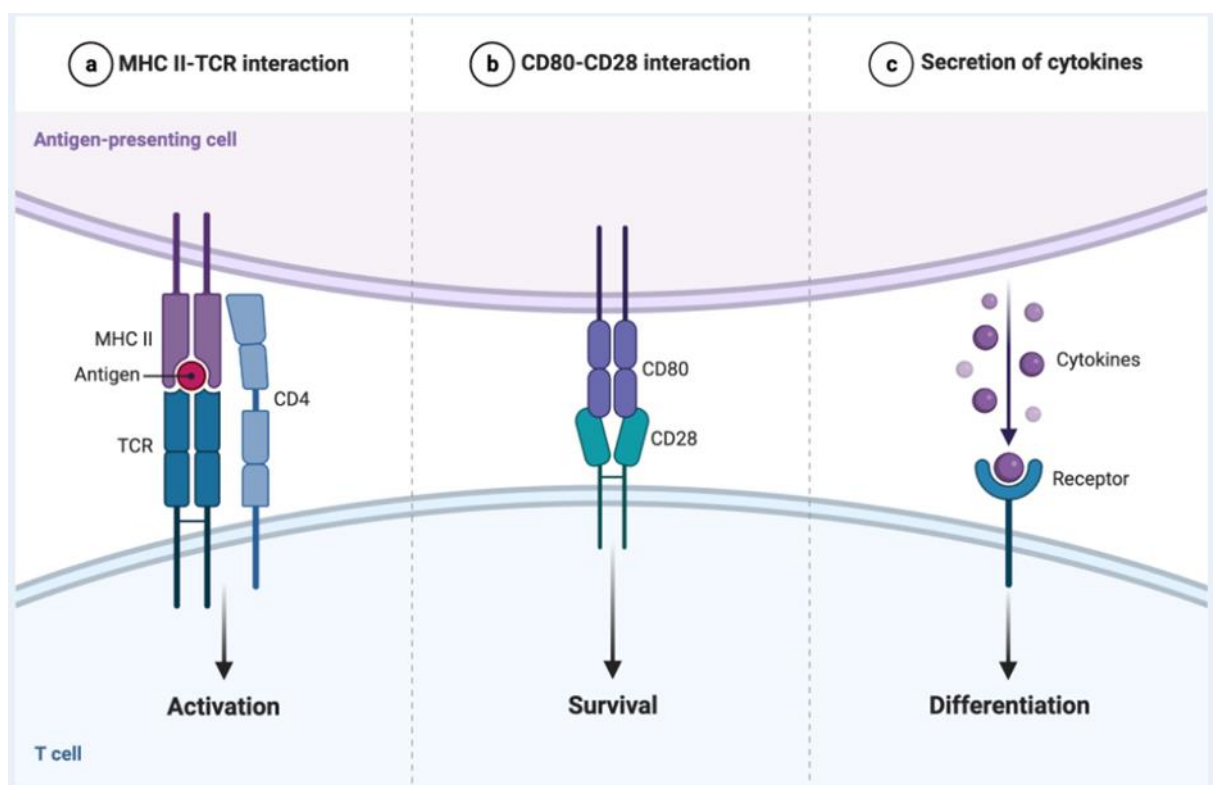


Figure 1.6: T-cell activation signalling pathways. The activation of T cells proceeds by three concurrent processes at the cell surface. The first is the interaction between T cell receptors (TCRs) and the MHC-bound immunopeptide – shown here as MHC class II, but analogous to MHC class I (a). The second component of activation involves co-stimulatory signalling between CD receptors on T cells and co-stimulatory molecules of the cell presenting the MHC-peptide complex (b). The third signal is the secretion of cytokines from the cell presenting the MHC-peptide complex which bind to complementary cytokine receptors on the T cell surface (c).

These processes provide an extra level of selection on which types of T cells mediate the immune response between skin and respiratory sensitisation. Additionally, there is evidence for signals

negatively regulating certain T cell responses through inhibitory pathways⁷⁸, potentially skewing T cell responses towards one type of response over another based on negative selection of T cell subsets for clonal expansion. For example, signaling resulting in negative selection of Th2 subsets, therefore resulting in clonal expansion of Th1 subsets and effector mechanisms associated with skin sensitisation rather than respiratory and vice versa.

The T-cell subset and effector mechanism differs within the Gell & Coombs Type IV classification, allowing an additional level of subdivision. Type IVa refers to a Th1 (skin sensitisation) response characterised predominantly by monocytic inflammation with interferon effectors, whereas Type IVb is a Th2 response and is characterised predominantly by eosinophilic inflammation with interleukin effectors (respiratory sensitisation). CD4⁺ helper T cells and CD8⁺ cytotoxic T cells mediate apoptosis in Type IVc responses and Type IVd reactions involve neutrophilic inflammation^{79,80}. It is noted within the literature there is likely to be interindividual overlap and variation in the type of T cell responses observed, resulting in the suggestion that more modern classification systems are needed⁷³. Regardless, Th1 and Th2 are the primary ones of concern in the sensitisation AOPs, but others are potentially of importance – such as Type I IgE effector mechanisms in respiratory sensitisation (refer to relevant IgE section of literature review).

A number of factors have already been referred to previously to explain the likely most influential factors affecting divergence of T-cell population proliferation mainly inducing either Th1 or Th2 responses. The factors with the most likely influence pertaining to T-cell proliferation include the structure of presented antigens (i.e hapten-carrier structure), the cellular danger signals elicited, and mechanisms of antigen processing and presentation by T-cells. Therefore, even minor differences in any of these aspects could potentially yield a profound effect on the category of immune response subsequently elicited by the T-cells³. Furthermore, combinations/interplay between these aspects could serve to amplify any divergence-driving factors potentially at work in the system.

Focusing on T cell proliferation and responses for each AOP discussed has two substantial advantages. Firstly, it is well-accepted that chemical sensitisation allergy (as well as all other forms of allergy) depend on induction of an adaptive immune response, almost all of which are related to T cell responses^{1-3,38}. Secondly, elicitation of IgE is also dependent on and associated with T-cell responses^{2,3,44,81}. There is strong evidence for the stimulation of a T-helper 1 proliferation response in the development of dermal sensitisation^{4,82,83}, as well as a CD8 cytotoxic T-cell response^{13,84}. Conversely, T-helper 2 immune responses are necessary for the induction of respiratory sensitisation²⁻⁴. Th2 cells are a primary source of cytokines promoting development of hypersensitivity and IgE production⁴⁴.

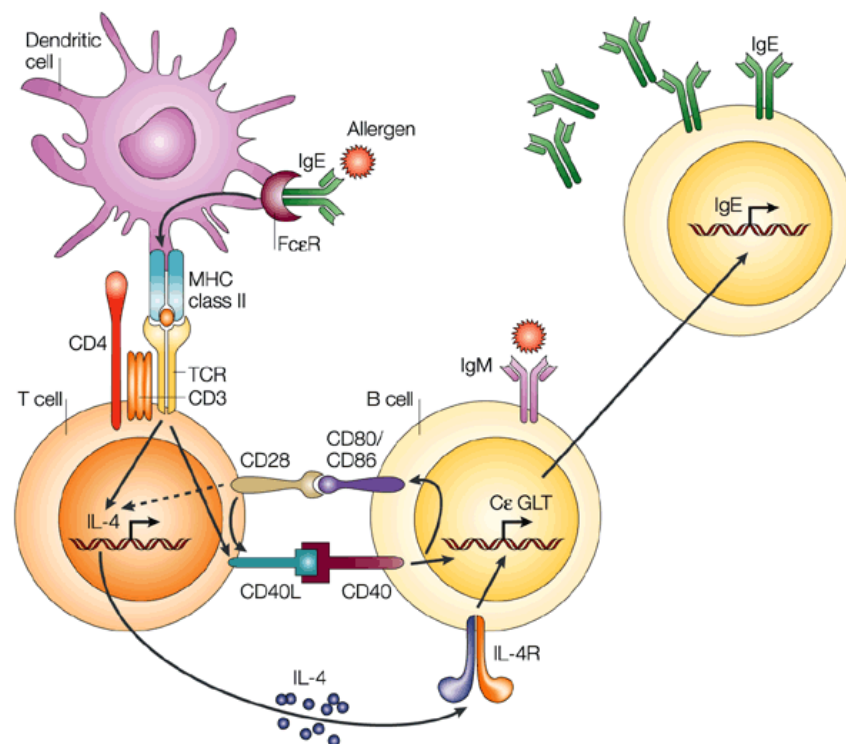
The categorisation of the divergent T cell responses into Th1 and Th2 is a useful simplification of what is believed to be the actual case, the most probable situation is more complex and less clear-cut including a number of cellular subsets^{3,44,85,86}. Dermal sensitisers have never been associated with the development of respiratory sensitisation, however in some cases select respiratory sensitisers have been associated with dermal sensitisation whereas other respiratory sensitisers such as phthalic anhydride have not^{3,87,88}. Currently the primary difference between the sensitisation mechanisms is accepted to be the type and magnitude of T cell proliferation required for sensitisation development, which is partly determined through the balance of local T-cell sub-populations^{4,18,89}.

Rodent studies have provided interesting results showing that different T-cell sub-populations (and their associated cytokines) determine the subsequent outcome of adaptive immune response, i.e. dermal or respiratory sensitisation. This has been corroborated by studies in humans, though to a much lesser extent, to also indicate the proposed association between Th2 responses and respiratory sensitisation^{90,91}. Overall, understanding of the mechanisms underlying hapten-specific activation of T cell subsets by different antigen presentation processes remains incompletely understood, especially with respect to the antigenic determinants⁸⁰. Observation of the differences in determinant peptide antigens could shed light on the cause of divergence between the primary skin and respiratory sensitisation effector mechanisms Th1 and Th2 respectively.

1.2.4 Immunoglobulin E and its links to T cell proliferation

The hypothesis of molecular-driven divergence between the two AOPs being determined as a predominantly 'front end' process between the MIE, cellular danger signals, and DC activation/migration is reinforced by the previously discussed observation that the rest of the respiratory AOP is generally analogous with the dermal AOP. However, an additional site of distinction is present in cytokine release at the 'back end' of the respiratory AOP in a distinct IgE-mediated phase^{2,38,44} which is not a component of dermal sensitisation⁹².

Following sensitisation of the respiratory tract, haptenated protein-specific IgE antibodies have been found in circulation as well as bound to receptors on mast cells within respiratory tissues, specifically the alveolar and bronchial epithelium^{29,93}. This means upon re-exposure to the sensitizer chemical, the subsequently produced hapten-protein antigen is able to cross-link with the pre-produced IgE and induce degranulation of surrounding mast cells. This releases mediators, such as histamines, that cause the inflammation and other symptoms associated with respiratory anaphylaxis and the more severe adverse outcome of respiratory sensitisation relative to dermal sensitisation^{2,44,81} (which lacks the IgE-mediated processes, as *in vivo* skin prick tests have inferred⁹⁴). IgG does not display the mast cell degranulation-associated symptoms, though hapten-specific IgG has been detected in response to both dermal and respiratory sensitizers. However, comparative analysis of IgG subclasses, and how they may reflect specificity of respiratory-exclusive IgE, has yet to be performed².



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Figure 1.7: Immunoglobulin E class switching regulation – An overview with particular focus on IL-4 induction of class-switching for IgE production and the gap in understanding of the causal signal(s). Obtained from Geha et al⁷⁶.

It has been argued that selective Th2 cytokine responses support both respiratory sensitisation and IgE production in a synergistic but exclusive manner³⁸, i.e. Th2 is suitable for development of respiratory sensitisation regardless of whether IgE is produced or not. The main advantage of this current proposal is that a common mechanism for development of respiratory sensitisation can be identified supporting both IgE mediated and non-IgE mediated sensitisation mechanisms. This is of interest given other forms of allergy, e.g. protein allergy, uses IgE as the primary effector mechanism⁹⁵. Additionally, this represents a crucial benefit considering the conflicting evidence for the necessity of IgE.

Discrepancies in the necessity and involvement of IgE stems mainly from difficulties in identifying an IgE component in *in vivo* studies in response to different classes of respiratory sensitizer chemicals. Diisocyanate sensitizer chemicals have shown very limited levels of sensitizer-specific IgE^{96–99} relative to the strong association between acid anhydrides and discernibly specific IgE^{100–102}. However, in light of these observations it has also been suggested that different respiratory sensitizer chemicals can have differential reliance on IgE for the development of sensitisation^{96,97}. This has led to the proposal that IgE plays an important role in respiratory sensitisation but is more pivotal following exposure to some sensitizer classes over others³.

Another point of uncertainty has arrived with the discovery of a transcriptionally distinct IL-4⁺ follicular T helper cell type (Tfh2) revealing Th2 cells are not the sole drivers of IgE induction as previously believed^{44,103,104}. This Tfh2-derived IL-4 is necessary for low affinity IgE production by class-switching of B cells, but also requires high affinity IgE production capabilities provided by secretion of IL-13 and IL-5 by the newly discovered Tfh13 cell population⁴⁴. This landmark discovery provides additional hypothetical routes of IgE elicitation to reach the respiratory sensitisation/anaphylaxis adverse outcome. For example, DOCK8, increased IL-13 and reduced IL-21 associated with Tfh13 have been found to prevent inappropriate IgE induction during type 1 immune responses⁴⁴, thus offering a novel downstream point of distinction between type 1 & 2 responses to protein haptening and danger signalling upstream.

Further to the considerations above, it is putatively accepted that preparation of representative hapten-protein conjugates comes with great difficulty and inconsistencies between studies^{105–109}. One of the main issues here is that likely target proteins for a select group of dermal sensitizers have only recently been proposed^{28,110}, whereas the *in vitro* target proteins for respiratory sensitizers have not yet been elucidated at all. This observation offers some reason for the high variability in hapten-protein conjugates following preparation. IgE levels have also been found to diminish soon after exposure^{30,84} therefore confounding the skin prick methods used in the past.

This may potentially be due to the demonstrable interchange between Th2 cells and Tfh cell subtypes⁴⁴.

Overall, the above points offer an explanation why some assays may have struggled to produce conclusive data and that, as suggested by Kimber et al, IgE may be a more crucial factor than is currently recognised^{3,30}.

1.2.5 Antigen Presentation

Major histocompatibility complex proteins (MHC), also commonly referred interchangeably to as human leukocyte antigens (HLA), are transmembrane glycoproteins presenting peptide antigens to the cells of the immune system (e.g. dendritic cells and T cells) for regulation of different types of immune response. The MHC proteins are crucial to the adaptive immune response due to their role in cell surface presentation of the peptide antigens for recognition by professional antigen-presenting cells such as dendritic cells and T cells. Importantly, both 'self' and 'non-self' peptides are presented by MHC proteins, allowing constant surveillance of the immune system by APCs. However, 'self' peptides generally do not stimulate the immune system under normal physiological conditions.

Human MHC proteins are divided predominantly into two groups: Class I (encoded by the HLA-A, HLA-B, and HLA-C genes) and Class II (encoded by the HLA-DR, HLA-DP, and HLA-DQ genes). Both classes are involved primarily in antigen presentation, but there are a number of important differences in the structures and processes. Variation in the specific peptide antigen structure presented by each protein class generally results in the activation of different types of T cells and associated immune response.

MHC class I proteins are expressed on the surface of all nucleated cells and are usually associated with presentation of intracellularly-derived peptides from endogenous proteins. This often results in a CD8⁺ mediated effector response. MHC class II proteins are typically restricted to the surface of professional APCs, often resulting in a CD4⁺ effector response. MHC class I and II are both heterodimers with a similar folded structure and four extracellular domains (refer to figure). The two membrane-distal domains comprise the peptide-binding cleft in both protein classes, with a pair of α -helices situated above a β -sheet. One of the major differences between MHC class I and II is that the peptide-binding cleft is formed by different domains. The MHC class I binding cleft is created by two α -chains ($\alpha 1$ and $\alpha 2$), whereas the MHC class II binding cleft is assembled from a α -chain and β -chain. These differences confer different peptide-binding properties and therefore result in notable differences between MHC class I immunopeptides compared to those of class II. For example, the relatively 'closed' conformation of the MHC class I peptide binding cleft means

the length of presented immunopeptides is usually restricted to 8-10 amino acids. However, the MHC class II binding cleft is relatively more 'open' and usually presents peptides of 12 or more amino acids in length¹¹¹.

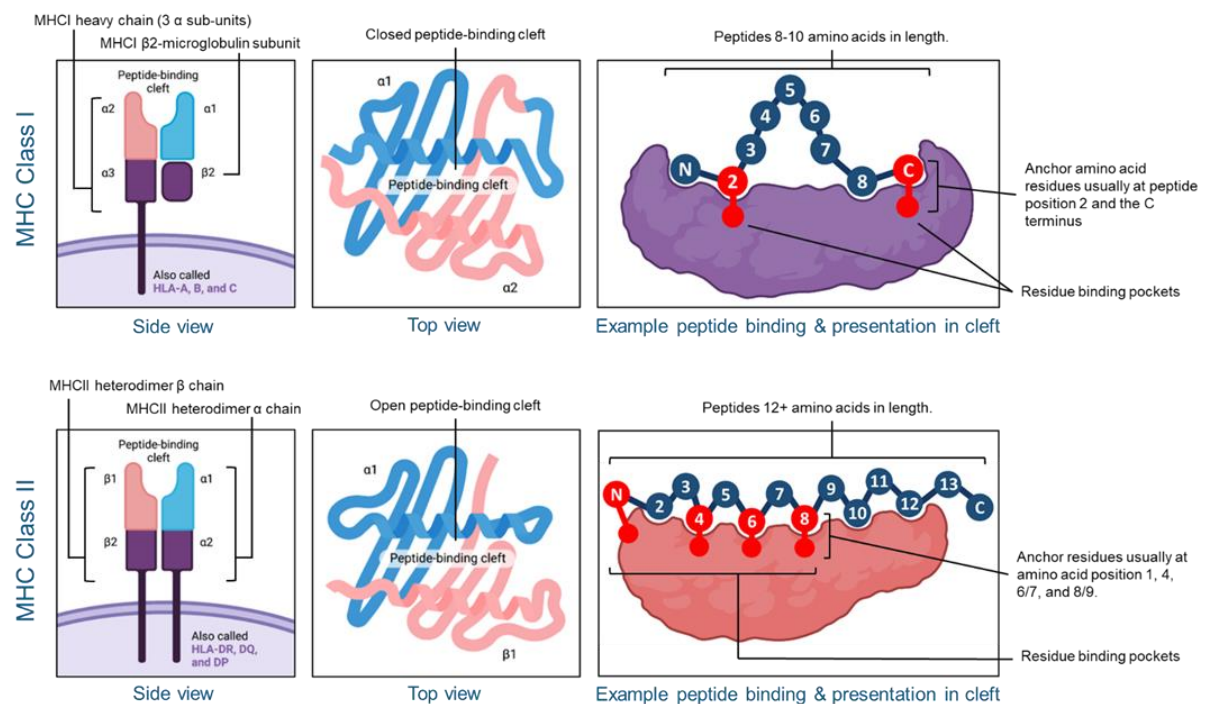


Figure 1.8: MHC class I and II structures. MHC class I protein molecules (above) are heterodimers comprised of a membrane-bound α 'heavy' chain ($\alpha 1$, $\alpha 2$, $\alpha 3$) and a soluble $\beta 2$ -microglobulin subunit. Peptides are presented by MHC class I in a relatively 'closed' peptide-binding cleft, restricting the length of presented peptides to 8-10 amino acid residues in length. Anchor residues are normally at the second amino acid position and the C-terminus of the peptide. MHC class II protein molecules (below) are heterodimers comprised of a membrane-bound α chain paired with a membrane-bound β chain (both with two subunits each). Peptides are presented by MHC class II in a relatively 'open' peptide-binding cleft, with the length of presented peptides being 12+ amino acid residues in length. Anchor residues are normally at positions 1, 4, 6/7 and 8/9 of the peptide amino acid sequence.

The immunopeptidome refers to the entire repertoire of peptides associated with MHC proteins. Immunopeptides are also subdivided into two groups alongside the MHC protein classes. MHC class I immunopeptides are typically derived from fragmented endogenous proteins which have been subjected to proteolytic digestion in the proteasome. MHC class II peptides are typically derived from exogenous proteins that have been endocytosed and undergone digestion by proteases. The human HLA gene is incredibly polymorphic and the diversity of alleles leads to immunopeptidomes of great complexity given that the polymorphism is predominantly in the

peptide binding cleft¹¹¹. It is understandable then that there is a large amount of variation in the peptide repertoires comprising immunopeptidomes – greater than 10,000 forms making up 14 distinct allotypes¹¹².

Each distinct HLA allele consists of a peptide binding groove, referred to as the HLA binding motif. The pair of α -helices are positioned in such a conformation as to form the groove in between them where individual pockets for peptide binding are situated. Each pocket demonstrates affinity for preferential amino acids, meaning peptides will bind to the groove through complementary interactions, including hydrogen bond formation between the HLA molecule side chains, the peptide backbone peptide backbone, and the pockets of the MHC binding groove peptide side chains – commonly known as anchor residues¹¹³. The position of the anchor residues in a peptide varies between MHC class I and II molecules. MHC class I peptide anchor residues are typically found at position 2 and the C-terminal residue within the peptide amino acid sequence, whereas MHC class II peptide anchor residues are typically located at positions 1, 4, 6, and 9¹¹². The binding affinity of a peptide to the MHC binding groove is dependent upon particular amino acids at these positions, which varies between the HLA alleles.

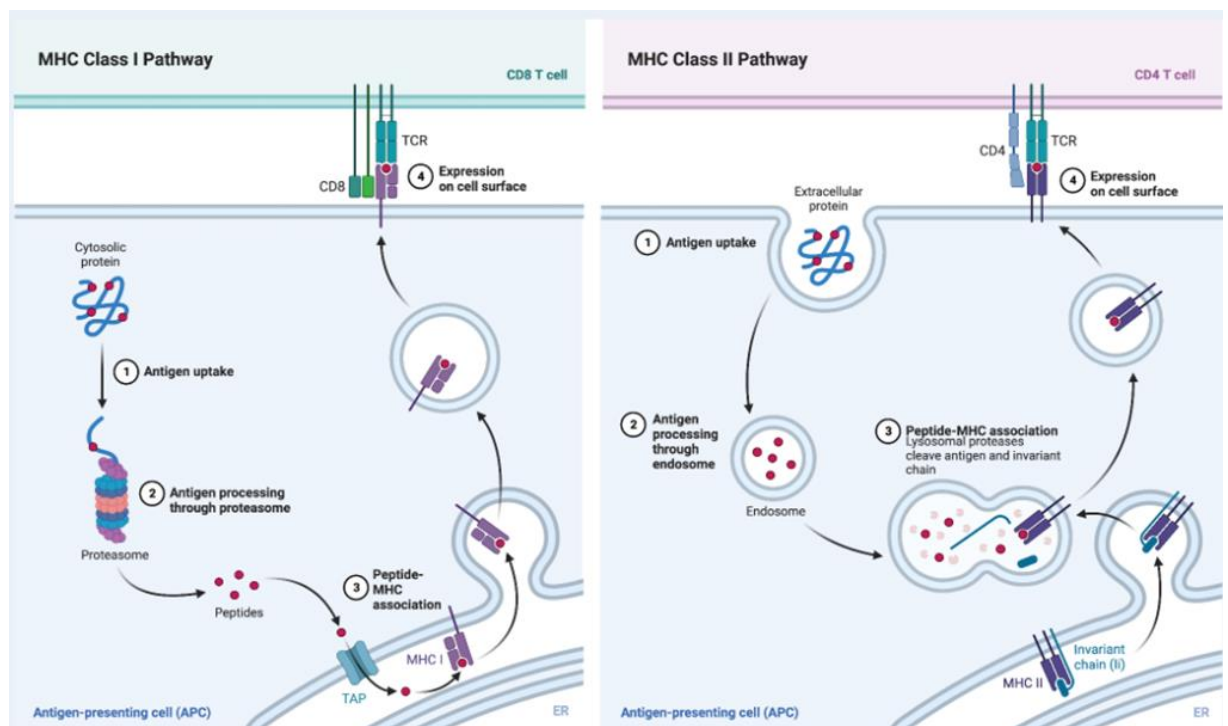


Figure 1.9: MHC antigen processing and presentation pathways. MHC class I complexes are formed through proteolytic digestion of endogenous proteins by the proteasome (**left**). This results in peptides which are transported to the ER by a transporter associated with antigen processing (TAP) for further cleavage into smaller peptides suitable for MHC-loading. Peptides with high MHC class I binding affinity are loaded into the peptide binding cleft via chaperone proteins. MHC class I proteins presenting the peptide antigen are

transported to the cell membrane via the Golgi, therefore resulting in antigen presentation on the cell surface. MHC class II complexes are formed through endocytosis of exogenous proteins and lysosomal cleavage into peptides (**right**). MHC class II molecules are assembled in the ER with invariant chain stabilisation, then transported to the late endosomal MIIC via the Golgi. Cathepsins generate class-II associated invariant chain peptide (CLIP) by cleavage of the invariant chain. HLA-DM and HLA-DO then assist in CLIP dissociation from the binding cleft, with the high affinity MHC class II peptide replacing it. MHC class II proteins presenting the peptide antigen are then transported to the cell membrane, resulting in antigen presentation on the cell surface.

Three non-mutually exclusive models of antigen presentation are available¹¹⁴. The first is direct presentation of peptide antigens through the standard HLA pathways (Figure 5.1 and the new pathways one). The second model highlights hapten modification of external regions of MHC proteins on the cell surface without internalisation of haptenated peptide antigens. The third concerns differences in global proteome regulation causing subsequent variation in the immunopeptidome. These processes have been initially delineated using the skin sensitiser DNCB¹¹, which has frequently been utilised as a model skin sensitiser, partly for its propensity to sensitise immunocompetent individuals^{115,116}. However, direct modification and the resulting conformational change of the peptide binding groove has been observed in immunopeptidomics studies of pharmacological agents¹¹⁷. Therefore, all three models should be considered when investigating the immunopeptidome of cells exposed to different chemical sensitisers.

1.2.6 Routes of Exposure

It is well-accepted that dermal sensitisers need to have certain characteristics that allow them to penetrate the stratum corneum to reach the site of action in the epidermis^{3,118}, such as low M_w in this case. However, given that it has been shown respiratory sensitisation can be acquired through the skin also, it seems unlikely that the ability of a dermal/respiratory sensitiser to penetrate skin would confer a different immune response^{3,29,92}. However, it could be a factor that logically affects potency, given that respiratory sensitisers would logically reach more potential exposure sites than skin sensitisers. Additionally, it proposes an interesting question of what intracellular proteins and pathways might be affected as a result of alternative sites of exposure, e.g. keratinocytes are a potential site of exposure for both dermal and respiratory sensitisers and arguably should be treated experimentally as such.

The respiratory AOP accounts for this phenomenon by collating information from models of respiratory sensitisation from both *in vivo* skin and lung exposure, and *in vitro* dermal and

respiratory cells, thus further improving its applications and usefulness^{92,119}. It has also been suggested that the two routes of exposure for respiratory sensitisation provides support for the importance of IgE in development of respiratory sensitisation³⁰. This is because IgE activity is systemic and therefore would logically facilitate respiratory sensitisation at points of exposure other than lung tissue, assuming IgE is indeed a key facilitator of the adverse outcome. A more concentrated exposure to a respiratory sensitizer, such as splashing onto skin, has been suggested to induce (in some cases) more efficient respiratory sensitisation than the logical exposure route of inhalation^{92,120}. This could hypothetically be due to more intense IgE induction at the concentrated exposure site, though this suggestion would benefit from further research incorporating more recent methods and knowledge to improve our understanding of the IgE component in respiratory sensitisation.

1.2.7 Divergent Cytokine Profiles

Despite early work identifying formation of covalent haptenation as a *primary* event in the stimulation of downstream T-cell immune responses³⁶, the specific sites of covalent binding (and by extension, parameters of antigen formation) remained unknown in terms of the effect on T-cell divergence for some time. Hopkins et al addressed this by examining the polarised cytokine profiles in mice resulting from treatment with different classes of dermal/respiratory sensitizers and categorised the regions of hapten-protein antigen formation⁴. However, it was noted more research would be necessary to identify specific target proteins associated with the observed responses and divergence.

Hopkins et al compared the cytokine secretion profiles, induced following skin exposure to various dermal and respiratory sensitizers, with *in vitro* distribution of cellular and serum protein. It was further demonstrated that dermal sensitizers induce a Th1 response (high levels of type 1 cytokines) whereas respiratory sensitizers induce a Th2 response (high levels of type 2 cytokines)^{4,86,93,121}, with the aim of identifying whether the ability to induce a polarised immune response is an inherent result of protein interaction. Interestingly, it was illustrated that both classes of sensitizer bind with cellular and serum protein when incubated with cells or serum separately. However, when incubated with both cells and serum combined, dermal sensitizers bound selectively to cellular protein whereas respiratory sensitizers bound selectively to serum protein⁴.

Table 1.1: Cytokine differentiation – Th1 response cytokine secretion profile (left) and Th2 response cytokine secretion profile (right) with supporting literature evidence for each.

Th1 Cytokines		Th2 Cytokines	
IFN- γ	Lucey et al ¹²²	TNF- α	Lauenstein et al ¹²³
TNF- β	Lucey et al ¹²²	IL-1 α	Lauenstein et al ¹²³
IL-1 β	Cumberbatch et al ¹²⁴	IL-4	Kimber et al ³⁸ , Gowthaman et al ⁴⁴
IL-2	Lucey et al ¹²²	IL-5	Kimber et al ³⁸
IL-12	Lucey et al ¹²²	IL-6	Lucey et al ¹²²
IL-18	Van Och et al ¹²⁵	IL-10	Lucey et al ¹²²
IL-21	Gowthaman et al ⁴⁴	IL-13	Lucey et al ¹²²
		IL-17	Kim et al ¹²⁶

The two main T cell responses have historically been split into two main phenotypes; a type 1 cytokine profile (IFN- γ secretion) and type 2 cytokine profile (IL-4, IL-5, IL-10, and IL-13 secretion). These are putatively considered to be the main cytokines associated with each secretion profile, however there are a number of others determined from more recent studies utilising model respiratory sensitisers (provided in table 1). As previously explained, sensitiser chemicals usually display a preference for one of the profiles, identified by increased cytokine secretion of one phenotype generally paired with decreased cytokine secretion of the other^{4,121}. For example, IL-12 has demonstrated importance in dendritic cells facilitating a Th1 response concurrent with dermal sensitisation^{127,128}. In contrast, a lack of IL-12 secretion has been linked with skewing in favour of a Th2 response¹²⁹. These observations serve to highlight the interest in differential cytokine secretion, and more specifically the causes.

It is true that preference/selectivity for one secretion profile may not be the sole determining factor, due to suppression of one secretion profile *indirectly* leading to up-regulation of the other¹²⁸. Furthermore, there is conflicting evidence for some cytokines as to which resultant Th cell response they are associated with, e.g. IL-18^{4,58}. The majority of cytokine profiling discussed thus far has been performed using well characterised dermal/respiratory sensitisers in animal models, with some supporting human data¹³⁰. Though this has also presented an interesting, albeit confusing, case; reduced dermal sensitisation has been observed in subjects exhibiting ACD who have a pre-existing Th2 bias¹³⁰, potentially due to altered production capacity of the necessary cytokines¹²⁸. Such findings suggest *in vitro* model systems have good value, though realistically *in vivo* population and genetic differences also have a potentially decisive role in Th response skewing associated with the two AOPs^{130,131}.

It cannot be ignored that there are some flaws in the methods for these key findings. The concentration of protein in the serum component was 50x higher than the protein concentration in the cellular component, therefore suggesting the overabundance of potential haptenation sites suggests predominant serum binding, particularly for chemicals with low-to-null selectivity⁴. Furthermore, the cells studied are known to be thiol-rich on the cell surface¹³², with thiol groups generally having more reactivity towards dermal sensitisers than respiratory sensitisers due to the abundance of cysteine residues^{4,7}. Conversely, serum predominantly contains albumin with an abundance of lysine groups^{133,134} generally possessing greater reactivity towards respiratory sensitisers⁷.

These points present a potential explanation that the results demonstrate differential competition for binding sites rather than differential selectivity in cellular protein residues/sites, i.e. respiratory sensitisers bind to serum protein more rapidly than cellular protein due to more ample opportunity⁴. This finding was supported by immunoblot analysis suggesting binding intensity was representative of protein abundance, as well as serum albumin being previously identified as a major immunologically relevant haptenated protein from *in vivo* animal and human exposure studies¹³⁴.

However, this logic is built upon the assumption that the relationship between sensitiser chemical and haptenation sites is stoichiometric, which has more recently been suggested to not be the case through use of more sensitive methods providing evidence binding is more specific than previously believed^{27,28}. In addition, it was previously suggested that a number of sensitisers had the ability to bind to both cellular and serum protein, though still inducing type 1 cytokine secretion exclusively⁴. There is also a lack of amino acid or protein selectivity distinguished from the different sensitiser classes, a point which spurred recent research into these aspects (see chapter 3).

Ultimately, it has been demonstrated the distribution of *in vitro* antigen formation can be differentiated through comparison to the *in vivo* divergent cytokine secretion profiles in mice⁴, though the differential haptenation specificity and target proteins remains largely unknown. Also, despite these landmark observations, there remains no known or accepted cause for the divergence in cytokine secretion profiles (and associated T cell response) induced following protein haptenation.

1.2.8 Risk Factors for Chemical Sensitisation

It is evident from the literature that there is a level of inter-individual variance in susceptibility to chemical sensitisation. However, not all of those exposed to chemicals identified as sensitisers will

develop the ACD or occupational asthma associated with skin or respiratory sensitisation. It now appears there are important genetic, epigenetic, and environmental factors contributing to the risk, with there likely being a combination of such factors determining the likelihood of acquiring skin/respiratory sensitisation in any individual case¹³⁵.

Each of the chemicals utilised in this project represent an exposure risk for the acquisition and development of skin or respiratory sensitisation. Therefore, any conditions under which contact with the chemicals is more frequent can be considered risk factors. DNCB is a well-characterised model skin sensitizer mainly used for mechanistic validation purposes. Generally, this does not present much of an exposure risk presently outside of research. DPCP is a skin sensitizer topically administered as an experimental treatment for alopecia areata¹³⁶. DPCP is believed to trigger immune responses countering the action of autoreactive cells that cause hair loss symptoms in alopecia, albeit in a counter-intuitive fashion. The contact immunotherapy basis generally follows the expected principle that the body will attempt to downregulate inflammation at the DPCP application site, and therefore indirectly also down-regulate the autoimmune response at hair follicles¹³⁷.

PA is the anhydride of phthalic acid, and is a potent respiratory sensitizer^{32,33,138}. This organic chemical is important in the industrial-scale production of plasticizers for plastics and in composition of spray paints, with several million tonnes produced worldwide annually¹³⁹. The organic compound TDI is also a potent respiratory sensitizer^{32,33,138}. Of the six possible isomers, 2,4-TDI is produced in the pure state, with approximately 1.5 billion tonnes produced annually¹⁴⁰. Commercial TDI is commonly used in the production of polyurethane foams for purposes such as cushioning in domestic furniture¹⁴¹.

Human and animal studies of atopic dermatitis have identified skin epithelial barrier dysfunction (direct physical trauma such as irritation, but also things like gene mutations), which may facilitate allergen entry, as a key factor in the development of adverse outcomes of atopic dermatitis and asthma¹⁴². Filaggrin is a skin protein facilitating terminal differentiation of keratinocytes and is also important in formation of the epidermal barrier^{143,144}. Genetic studies of several populations have revealed mutations in the filaggrin gene, hypothetically resulting in impaired barrier function, correlating with an increased risk of developing atopic dermatitis and asthma via allergen sensitisation^{144,145}.

Atopy (predisposition to mounting an IgE response), gender and pre-existing non-specific bronchial hypersensitivity are not associated with the development of chemical respiratory allergy¹⁴⁶. However, polymorphisms in anti-oxidant enzyme systems have been shown to be a risk factor for sensitisation¹⁴⁶, hence the interest in characterisation of cellular oxidative stress

responses following exposure to chemical sensitisers. Naturally, an individual's native expression of antioxidant enzymes, as well as any factors suppressing their activity, would be of clinical interest.

Recently, the "barrier hypothesis" has suggested that increased epithelial barrier damage can be related to industrialisation, urbanisation, and lifestyle factors. This implies that not only allergens, but also infections, pollutants, and other environmental triggers impact allergic inflammation¹⁴⁷. Cigarette smoking has been associated with increased risk of respiratory sensitisation^{101,148}. A variety of studies have been undertaken to investigate how tobacco smoke skews immune responses towards the development of lung diseases. For example, environmental tobacco smoke has been linked with asthma and allergic diseases in children, leading to a skewed inflammatory profile with increased inflammation, promotion of infections, tissue damage, and potentially the development of allergy¹⁴⁹. The imbalance of oxidants and anti-oxidants caused by tobacco smoke exposure results in oxidative stress, mucosal inflammation, and increased expression of inflammatory cytokines associated with chemical sensitisation. Furthermore, the direct effects of tobacco smoke exposure on epithelial cells have been shown to include increased cellular permeability (facilitating allergen entry into cells), impaired mucociliary clearance, secretion of proinflammatory cytokines, and a skewed T lymphocyte balance towards Th2 responses¹⁴⁹.

MHC class II polymorphisms have also shown association with increased risk of respiratory sensitisation¹⁴⁶. There is evidence for an association between specific HLA alleles and respiratory sensitisation to acid anhydrides¹⁵⁰, as well as between antioxidant genes and HLA alleles with diisocyanate-induced occupational asthma^{151–153}. The influence of genetic polymorphisms on susceptibility to respiratory sensitisation has important implications for the determination of relevant exposure thresholds.

In line with all types of allergic immune response, there are thresholds representing the exposure requirements for an antigen to cause sensitisation. Any individual predisposition that lowers this threshold could be considered a risk factor for sensitisation of either the skin or airways. Indeed, there are a variety of other factors in addition to the specific ones discussed previously that could contribute to increased risk of sensitisation.

Thresholds for evaluation of respiratory sensitisation acquisition have been reviewed¹⁴⁶, including: lymphocyte proliferative response (see section), induced changes in cytokine expression (see section), induced IgE antibody production or changes in the total serum concentration of IgE (see section), and data from human studies/clinical experience.

Available exposure-response human data for the development of sensitisation of the respiratory tract by protein allergens is well-documented and shows defined thresholds¹⁴⁶. This is not necessarily the case for all classes of low Mw chemical sensitisers such as acid anhydrides and diisocyanates. It is also important to consider that whilst informative, such studies possess limitations such as sample sizes and participant selection biases (i.e. examined populations often do not provide a good representation of the general population).

Among the acid anhydrides shown to cause respiratory sensitisation are: phthalic anhydride, trimellitic anhydride, hexahydrophthalic anhydride and maleic anhydride^{146,154}. Dose-response relationships related to sensitisation by various acid anhydrides have been outlined, most commonly the relationship between acid anhydride specific IgE levels in the body and workplace exposure concentrations to acid anhydrides in human cohort studies^{155–157}. However, clear thresholds have been challenging to define in this regard¹⁴⁶.

A variety of diisocyanates have been established as respiratory allergens, including (but limited to) toluene diisocyanate, hexamethylene diisocyanate, and diphenylmethane diisocyanate¹⁵⁸.

Occurrence of IgE specific for various diisocyanates examined in human workforce populations have shown results even more inconclusive than for acid anhydrides in terms of determining thresholds. Indeed, such studies have in places demonstrated a lack of any detectable IgE for the chemical allergen¹⁵⁹. Other studies differentiate between high and low exposure concentrations^{158,160,161}. However, these studies exclusively investigated clinical parameters such as lung function and self-reporting symptoms, meaning no verification of sensitisation at the molecular level was available.

It has been determined that cases of occupational asthma due to respiratory sensitisation are associated mainly with acute over-exposure to chemical allergens, or routine short-term exposure to lower concentrations >20ppb¹⁴⁶. As with all other forms of adaptive immune responses (including allergy), there is an exposure threshold an antigen must reach to cause skin or respiratory sensitisation. Further, there is a minimum level of antigen exposure below which an immune response or acquisition of sensitisation will not be stimulated. Evidence in this regard is largely available from allergen-specific IgE levels and clinical observations in human cohort studies. However, identification of the thresholds under various conditions and in different populations remains incomplete for the different chemical sensitiser classes. It remains clear though that the threshold requirements (and by extension the risk factors) vary greatly based on the inherited/acquired responsiveness and susceptibility of an individual to sensitisation, the conditions of exposure (concentration, duration, frequency and route of exposure), and the inherent immunogenicity of the antigen itself.

1.3 Methods of Identifying Haptenation Target Proteins by Mass Spectrometry

The first documented recognition of the necessity of chemical interaction with host proteins in the induction of sensitisation was proposed by Landsteiner and Jacobs³⁶. It has since been agreed that low M_w organic sensitizer chemicals are not inherently immunogenic and thus do not elicit an immune response themselves. As highlighted by the various AOPs, haptenation of host carrier proteins by the sensitizer chemicals is necessary to produce the immunogenic hapten-protein conjugates. Therefore such sensitizer chemicals must be protein-reactive, or readily converted to a protein-reactive species in close proximity to the site of exposure³⁸. The previously discussed studies have also inferred that sensitizers are expected to be primarily (though not exclusively) cysteine-reactive and/or lysine-reactive^{4,7,26}, with lysine (primary amines) generally being favoured more by respiratory sensitizers and cysteine (thiol groups) being preferred by dermal sensitizers³². This hypothesis has garnered further support from evidence of differences in coverage of mechanistic domains showing typical respiratory sensitizers reacting via acylation and Schiff base formation rather than nucleophilic substitution and Michael addition demonstrated by typical dermal sensitizers^{6,32,33}.

The above findings had led to the suggestion that proteins with greater availability of these residues for modification would demonstrate increased abundance in the total amount of haptenated residues in a sample, i.e. the haptenome. However, as previously explained, it has recently been proposed that the nature of haptenation is likely to be non-stoichiometric, in as much as the percentage coverage of the proteome by the haptenome is not proportional to the number of available residues, in addition to coverage generally falling between 1-3%²⁸. It is therefore now believed that specificity of residue binding, and the proteins they are situated on, has the greater influence over inclusion in the haptenome. Further support for this proposition is evident through studies on the model protein HSA demonstrating that not every available site is modified by a hapten, indeed only seven specific lysine residues were modified by the respiratory sensitizer hexahydrophthalic anhydride¹⁶². In light of these recent insights into sensitizer chemical reactivity and characteristics, there remains one critical point at which distinction has great potential to be derived – differences in reactivity between specific sensitizer chemicals and specific protein targets. Proteomics approaches have been developed and shown to be instrumental in studying such processes.

1.3.1 Protein Biomarkers

Biomarkers have been defined as features that are “objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacological responses to a therapeutic intervention”¹⁶³. In the context of this review, this includes biochemical analyses of biological molecules (proteins) within cells/tissues that are indicative of either dermal or respiratory sensitisation, allowing potential identification of molecular processes occurring exclusively in one or the other and therefore proposing divergence driving factors.

There are currently no validated protein biomarkers specific to either pathway, and as such also no biomarkers distinguishing the two, though efforts have been made to provide a range of haptenation target proteins²⁸ that may serve as biomarkers for dermal sensitisation, alongside significant shifts in abundance within global cell proteomes induced by exposure to skin sensitisers. It is also logical that identifying a set of target proteins associated with respiratory sensitisation would reinforce the assignment of biomarkers for both sensitisation pathways through comparative analysis. Ideal protein biomarkers would need to be accurately measurable and reproducible¹⁶⁴, and ideally be suitably abundant and stable so as to allow validation with measurements from assays interrogating related key events within the adverse outcome pathway, e.g. immunopeptidomics for peptide antigen presentation or differential cytokine profiling.

There are five accepted phases of biomarker discovery and development which are transferable from the original disease of cancer to other diseases and disorders. The experiments alluded to thus far would be of the first of these phases, the preclinical exploratory phase¹⁶⁴, i.e. identifying features unique to dermal or respiratory sensitisation such as differentially haptenated proteins or differential protein abundance. Candidate protein biomarkers identified in such experiments would ideally satisfy the subsequent four phases of biomarker development for future use in clinical and computational diagnostics. A current lack of validated target protein biomarkers may possibly be associated with the lack of validated assays for detection of sensitisers and sensitisation highlighted in the AOPs^{1,2}.

There are two methods of biomarker identification; highlighting candidate biomarkers based on existing evidence, and using omics techniques to essentially screen for molecules that could be presented as biomarker candidates¹⁶⁵. The first method has the obvious benefit of targeting research, though a lack of evidence is often the reason for interest in identifying candidate biomarkers, particularly in this case. The second method is generally more associated with omics technologies and offers the benefits of multiple candidates as well as the potential for *de novo* biomarker identification across a whole cell/tissue proteome.

1.3.2 Background of Proteomics and Mass Spectrometry

The proteome refers to the entire range of proteins expressed in a cell or tissue at a particular time under specific conditions. Proteomics refers to the study of the proteome, often aiming to identify, quantify, and characterise a set of proteins to relate them back to changes in cellular function/response¹⁶⁶. Various protein isoforms, modifications, and interaction networks also commonly feature in proteomics research and highlight the complexity of the proteome. Increasing the complexity further, is the propensity of the proteome to dynamically change in response to both internal and external stimuli. Hence proteomics experiments and resultant datasets provide only a snapshot of processes occurring in samples at the time of extraction for analysis.

Studies frequently isolate sub-proteomes based on cellular localisation or labelling techniques to simplify the complex mixtures to analyse specific protein sub-sets of interest based on additional features^{28,166,167}. There are also an array of proteomics experiments employing a high throughput 'shotgun' proteomics approach in which the whole proteome is analysed, as opposed to a more targeted method¹⁶⁸. These type of bottom-up proteomics experiments allow global protein identification and quantification.

Mass spectrometry (MS) is an analytical technique used to identify and quantify the protein components of the proteome. Mass spectrometry is perhaps the most prevalent proteomics technique used today and provides information about cellular composition, protein interactions, and post-translational modifications such as acetylation and phosphorylation¹⁶⁹. Protein samples are usually digested into peptides by a series of reagents that reduce, alkylate, and digest samples. This reaction sequence is favoured for MS analysis due to whole proteins providing limited data when compared to the relatively easy sequencing and protein identification^{167,169}.

Liquid chromatography (LC) is often twinned with MS to improve separation of peptide samples and simplifying the samples in terms of composition. Furthermore, LC systems also allow the exploitation of peptide characteristics for separation by reversible binding to a very low diameter (μm scale) column via high pressure motility. As an example, peptides are highly hydrophobic which allows LC columns to separate peptides based on their relative hydrophobicity (polarity) before eluting them off the column with an organic solvent gradient prior to MS injection.

MS analysis requires the travel of charged molecules through electromagnetic fields under a vacuum, therefore peptides must be ionised prior to analysis. Peptides are usually positively ionised and in the gaseous phase before input into the MS instrument^{169,170}. These ions get separated according to respective mass-to-charge ratios (m/z) by one or more mass analysers.

The resulting mass spectra are processed by dedicated software and searched against databases housing protein sequences for protein identification.

The field of proteomics has progressed rapidly since its inception as relatively simple one- and two-dimensional gel electrophoresis experiments¹⁶⁹, to the advanced high resolution mass spectrometry instruments used today. Clearly the field of proteomics is expansive, therefore the remainder of this review will focus on the methods most applicable for assessing global abundance changes in the proteome and the identification of haptenated target proteins with specific labelling techniques.

1.3.3 Ionisation Methods

There are a pair of peptide sample ionisation methods commonly used, referred to as electrospray ionisation (ESI) and matrix-assisted laser desorption/ionisation (MALDI). Both are referred to as 'soft' ionisation methods due to generating ions in the gaseous phase without bond breaking¹⁶⁹. The ionisation method used in a particular experiment depends on the complexity and phase of the sample, amongst other features. ESI has become more popular than MALDI recently, and is particularly instrumental in addressing questions of sensitisation pathway distinction due to its efficiency in ionising complex samples such as cell lysates.

The ESI method produces gaseous ions from solution phase samples, hence its high compatibility with LC separation methods. A positive potential high voltage is applied to solution-based samples following LC column elution during transport through a conductive capillary, and results in samples being drawn out in an elliptical shape. This forms a more conical shape, referred to as a 'Taylor cone', when the voltage is further increased¹⁷¹. Charged parent droplets begin to form and are sprayed into a chamber where the droplets move towards an electrode by virtue of their positive charge¹⁶⁹. The solvent undergoes evaporation during this process, with further evaporation occurring as a result of droplets passing through a heated nitrogen curtain or

capillary¹⁷¹. This results in charged droplets of an even smaller size, eventually losing their solvent sheath and accelerating the ions into the mass analyser^{166,169}.

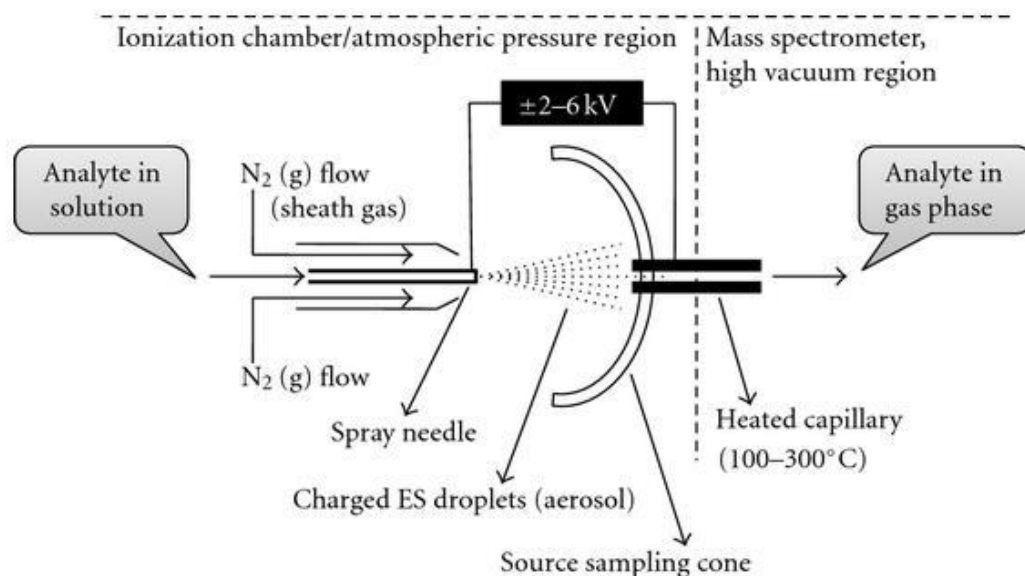


Figure 1.10: Overview of the electrospray ionisation method. Obtained from Banerjee and Mazumdar¹⁷¹.

ESI can be used in combination with LC systems to analyse highly complex sample mixtures. In addition, depending on the type of mass analyser used there may be no discernible limit in mass, allowing large protein complexes to be examined. Another benefit of the ionisation efficiency of ESI is that low abundance proteins can be identified¹⁷², increasing the throughput capability of the system and allowing the low abundance target proteins associated with haptentation to be detected.

1.3.4 Mass Analysers

There are four major categories of mass analysers, which are responsible for separation and detection of peptide ion analytes within the MS instrument. These include quadrupole, time of flight (ToF), ion trap, and fourier-transform. Generally multiple mass analysers are coupled to perform tandem mass spectrometry (MS/MS). One example of this is a triple-quadrupole instrument in which the second quadrupole acts as a collision cell for ion fragmentation, and the flanking quadrupoles perform scanning processes^{166,170}. Another example is coupling of an ion trap to an orbitrap mass analyser. Two each of these are components of the advanced Waters Synpat G2-S (Figure 1.7) and Thermo Scientific Orbitrap Fusion (Figure 1.8) LC-MS/MS instruments, which are covered in more detail below.

A quadrupole mass analyser is composed of four parallel rods, situated equidistant from a central axis along which the analyte ions travel from the electrospray ionisation source. One set of opposing rods have a positive voltage applied, whereas the other two have a negative voltage applied. When combined, these rods produce overlapping mass filters, requiring analyte ions to be above or below a critical m/z threshold to traverse the filters¹⁶⁹. Ions not meeting the requirements of the critical threshold are dispersed onto the rods, therefore allowing the quadrupole to select ions with a specific m/z ¹⁷⁰. The m/z ratio is proportional to the voltage applied, meaning if the voltage is increased the m/z selected will also be increased. Scanning the quadrupole voltage allows a full mass spectrum to be produced¹⁶⁶.

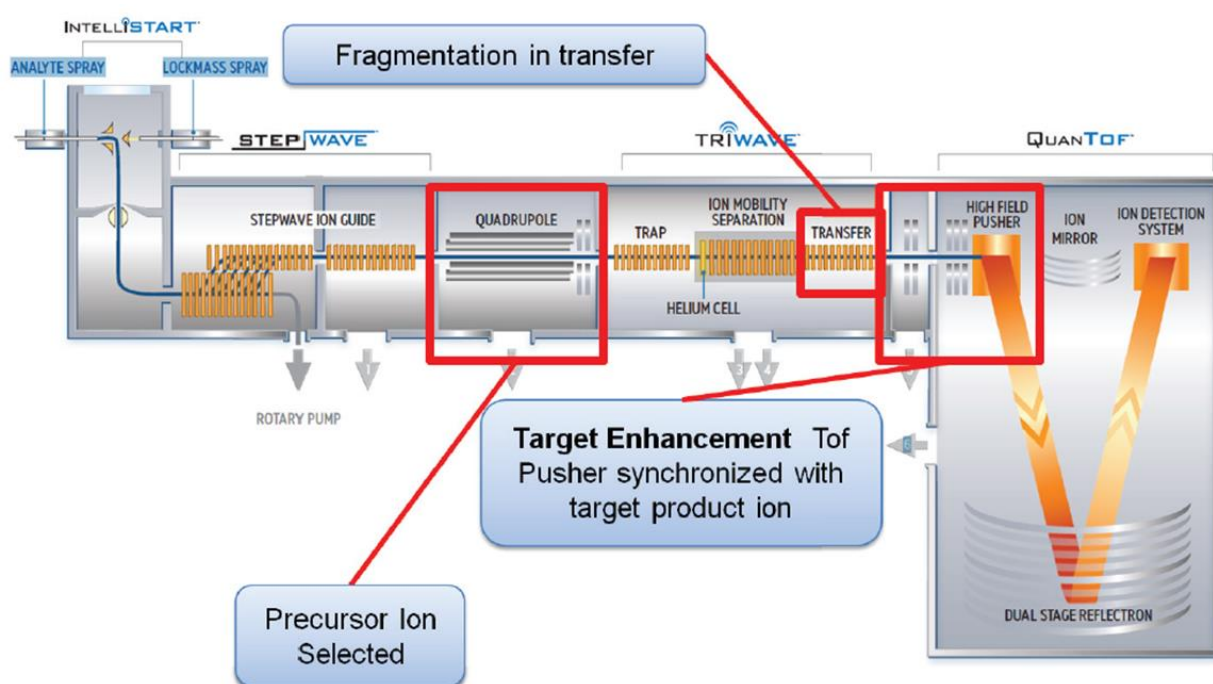


Figure 1.11: Waters Synapt G2-S HD mass spectrometer schematic overview – StepWave technology is incorporated for filtering neutral ions, an ion mobility cell for separating ions according to shape before fragmentation in the transfer cell. Also included are a quadrupole and ToF mass analyser. Obtained from Alelyunas *et al*¹⁷³.

The guiding principle of a ToF mass analyser is that when ions of different mass are accelerated through a vacuum, they will travel a fixed distance in a different amount of time relative to their mass¹⁷⁰. For example, an ion of lower mass will travel faster than an ion of larger mass, and therefore reach the end of the flight path sooner. The analyser measures the time taken for ions to reach the end of the flight path from the ion source as a measure of their relative m/z . Ions are pushed down into the ToF analyser and their flight path is deflected by a reflectron located at the base of the analyser. Ions possessing greater energy penetrate deeper into the reflective surface and therefore take longer before being forced upwards towards the ion detector. A quadrupole mass analyser can also be coupled with a ToF mass analyser (QToF). This QToF hybrid mass

analyser identifies ion analytes according to their arrival time at the detector^{169,170}. Combining these two mass analysers provides increased mass accuracy, as well as high resolution and sensitivity¹⁶⁶ (Figure 1.7).

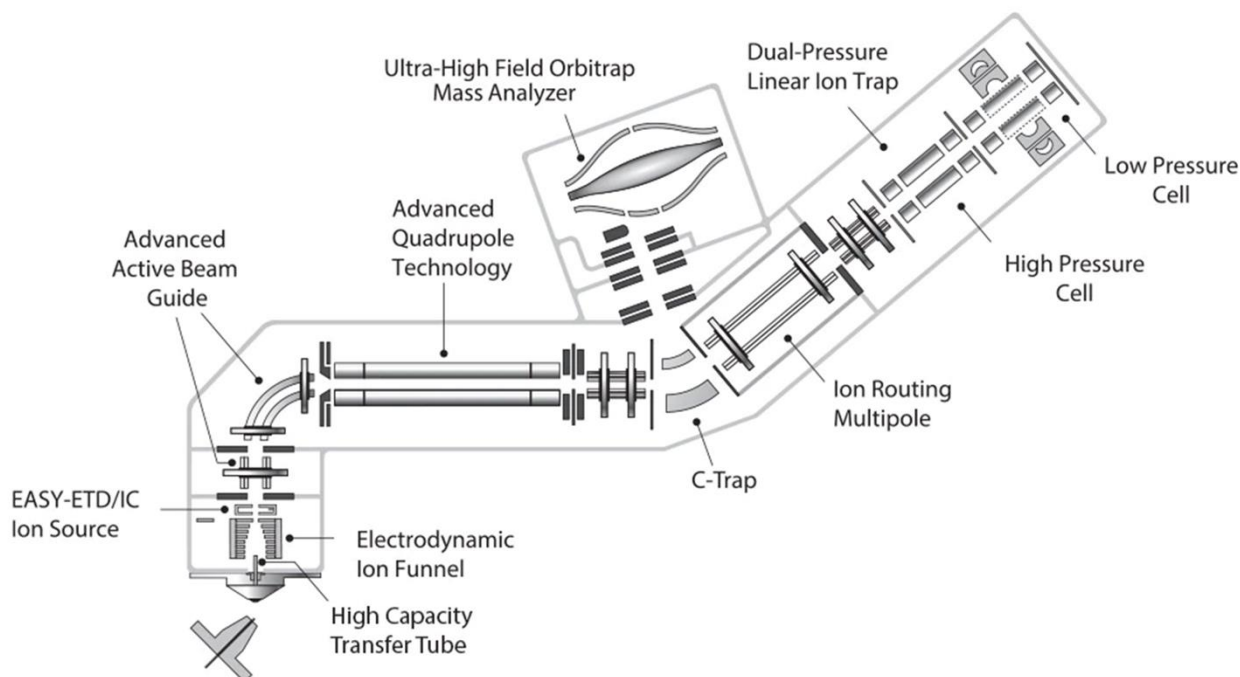


Figure 1.12: ThermoScientific Orbi-trap Fusion LC-MS/MS instrument schematic overview.

Electrospray ionisation at sample source generates positive peptide ions in an evaporative process for acceleration of ions to the quadrupole mass filter. Specific voltages applied allows selection of a range of ion m/z values to be allowed to proceed to further analysis. Ions are focused in the C-trap and ion-routing multipole to where parallel analysis is possible by ion accumulation & rerouting of precursor and fragmentation ions. Parent ions (precursors) are sent to the orbitrap mass analyser where the MS spectra is obtained by oscillation signal frequency amplification. Ions can then be selectively transferred from the orbi-trap to the collision cell for collision-induced dissociation (CID) and fragment (daughter) ion analysis by the ion trap. Fragmentation spectra analyses and bioinformatic comparison to precursor MS spectra allows identification of amino acid sequence in each peptide for protein identification by database searching¹⁷⁴.

An orbitrap is a form of ion trap mass analyser assembly composed of an outer barrel-like electrode and a coaxial inner spindle-like electrode¹⁷⁵ (Figure 1.8). Ions are trapped based on electrostatic attraction to the coaxial inner electrode, and cyclically balanced around it in elliptical trajectories that extend back and forth along the electrode. Injection of ions from an external source (often ESI) as ion packets occurs tangentially into the space between the inner and outer electrodes using a curved-linear trap (C-trap). Each of these packets contains a range of ions moving with different velocities in the inter-electrode space. The ion packets move with the same

axial frequency but different elliptical rotation frequencies. Increasing the voltage of the inner electrode tightens the elliptical trajectories of ions until a desired orbit pattern is achieved. Ions of a specific m/z ratio separate into oscillating rings that move back and forth along the inner electrode. The voltage ramping of the inner electrode is then ceased, causing the field to become static and conducive to detection¹⁷⁵. Oscillating ion packet rings are detected by sensors on the outer electrode and converted to a mass spectrum using a Fourier transform of the resultant data¹⁷⁶.

1.3.5 Data Acquisition

Two modes of data acquisition exist for MS instruments; data-dependent acquisition (DDA) and data-independent acquisition (DIA). MS/MS is traditionally performed using DDA, with precursor peptide ions being scanned upon input into the MS instrument. Precursor peptide ion peaks are subsequently selected by the first mass analyser according to select criteria including charge state and ion intensity. Ions matching the criteria are then extracted from the quadrupole and are subjected to fragmentation, with the m/z of the fragmented ions being measured via the second mass analyser. Once the initial fragment ions are analysed, those with specific m/z can be selectively excluded from the subsequent cycles, thus allowing lower abundance peptide ions to be fragmented and analysed¹⁷⁷.

Data pertaining to fragment ions and precursor ion m/z is used for identification of precursor peptide sequences, possible by virtue of the difference in mass between consecutive fragment ions being equivalent to the exact mass of an individual amino acid¹⁷⁰. It is therefore evident that fragmentation data yields more information on the peptide ions from which protein identification is derived. Despite the efficiency of MS/MS in peptide isolation and sequencing within complex mixtures¹⁷⁷, a number of low abundance peptides may be missed due to DDA non-selection¹⁷⁸ – a missingness feature that must be considered during data analysis and interpretation.

LC-MS/MS is a modified tandem MS method that incorporates liquid chromatography to aid in identifying precursor ions for MS analysis. The instrument switches between survey scanning in MS mode and MS/MS mode to selectively fragment and measure precursor ions. Due to the instrument not performing MS survey scans in MS/MS mode, precursor ions are not identified and selected for fragmentation, therefore these analyses are missed due to the continual sample spray into the instrument. The reason these ions may be missed is because the switch to MS/MS mode is generally triggered by the intensity of ions being analysed in the form of an elution peak exceeding a threshold defined by the operator^{179,180}. This form of data-dependence generally results in under-sampling and irregular sampling intervals¹⁸¹, which results in reduced

chromatographic peak quality. The point at which the peak reaches the threshold to initiate the switch to MS/MS mode may also not necessarily be at the apex of the peak where the precursor ion has the greatest intensity, therefore further reducing the quality of product peaks¹⁷⁹. If the frequencies of the MS survey scanning and ion intensity threshold are increased, less ions are selected for fragmentation and thus producing reduced sequence coverage. This understanding means the operator must choose how to balance the benefits and drawbacks¹⁷⁹.

DDA has proven to be a powerful discovery tool, despite the inherent drawbacks resulting from the semi-stochastic nature of precursor ion selection (e.g. run-run reproducibility and detection of low abundance ions)¹⁸². DIA has shown substantial advancement within the last 20 years in terms of data acquisition and analysis since its inception^{183,184}. During DIA, all peptide ions in a defined m/z range are fragmented and subjected to iterative sampling until the full m/z range is covered. The peptide fragments are then computationally interrogated for protein identification.

MS^E was developed following initial shotgun CID and DIA methods¹⁸⁵ and represents a DIA method in which the MS instrument continually switches between low energy MS mode and elevated energy mode (MS^E) without ion selectivity¹⁸⁶. This method involves peptide separation by an LC system before introduction into a QToF MS instrument operating in the MS^E mode (Figure 1.7). A quadrupole mass analyser allows passage of all precursor ions to the ToF analyser without incorporating any selectivity. The collision cell has a continuous energy cycling between low energy (MS) and elevated energy (MS^E). This presents the advantage of precursor ions both being analysed in both low energy mode and fragmented in high energy mode in a single process. The resulting fragment ions are matched with the precursors based on retention time and ion intensity through the Ion Accounting Algorithm in Waters corporation instruments in order to produce reconstituted fragment ion spectra for each individual precursor ion. These spectra can then be passed to peptide/protein identification methods.

A number of other derivatised methods have been introduced since the initial development of MS^E. These are numerous and have been reviewed elsewhere¹⁸², but they include: precursor acquisition independent from ion count (PACIFIC)¹⁸⁷, all ion fragmentation (AIF)¹⁸⁸, electron transfer dissociation and CID (XDIA)¹⁸⁹, sequential window acquisition of all theoretical fragment ion spectra (SWATH)¹⁹⁰, multiplex MS (MSX)¹⁹¹, wide selected-ion monitoring (WiSIM)¹⁹², pSMART¹⁹³, scanning quadrupole DIA (SONAR)¹⁹⁴, BoxCar¹⁹⁵, precursor ion and small slice-DIA (PASS-DIA), and multi-injection pulsed gas-phase fractionation DIA (Pulse DIA)¹⁹⁶. This sequential development in DIA methods has seen a variety of acquisition window, m/z range and analysis software parameters employed. This has provided greater identification coverage, quantification, and reproducibility (e.g. absolute quantification) and less missingness than DDA in general.

However, DIA requires complex computational data analysis tools relative to DDA as well as requiring selection of precursor m/z isolation windows and scan durations. Ultimately, the different types of instrumentation (ionisation methods, mass analysers etc.) and data acquisition modes (DDA vs DIA) should be considered and evaluated in terms of specific experimental needs and desired data outputs for a given study.

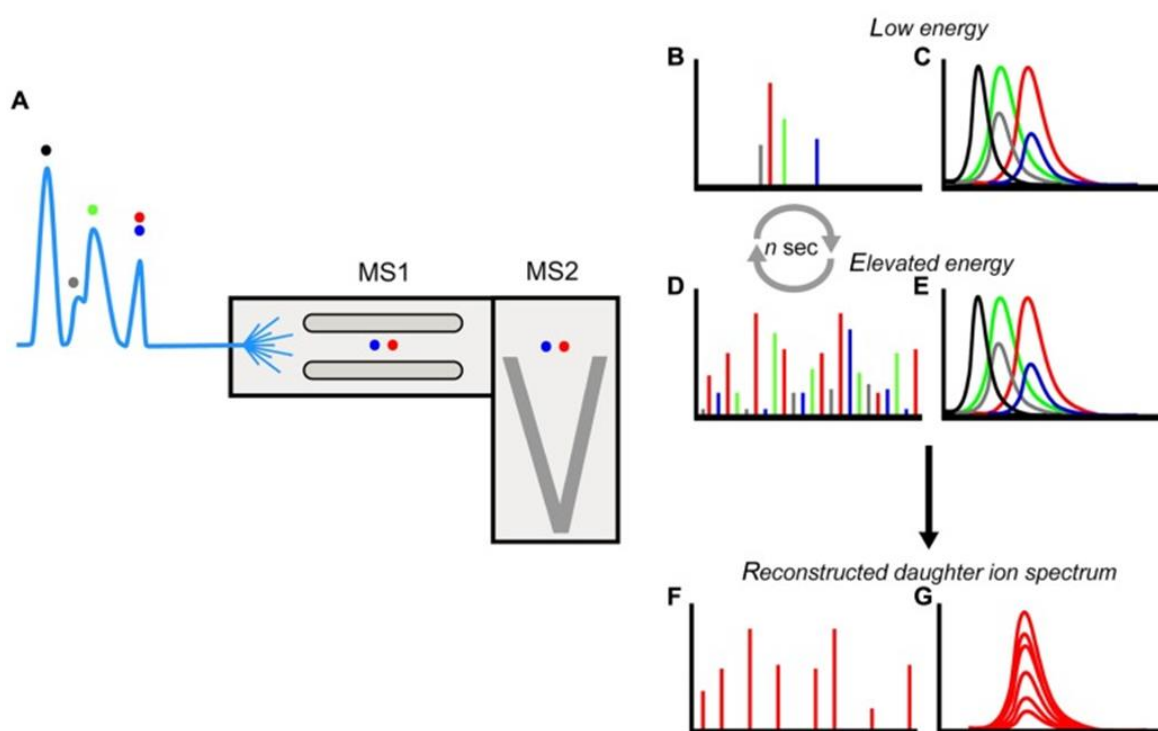


Figure 1.13: LC-MS^E data-independent acquisition diagrammatic overview – Peptides separation occurs in an LC system and are sprayed into the MS instrument via electrospray ionisation (A). A quadrupole (MS1) allows all precursor ions to reach the ToF mass analyser (MS2). Continuous cycling between low and elevated energy states occurs in the collision cell (B) to fragment ions indiscriminately (D). The Ion Accounting Algorithm is employed to match parent and daughter ions by comparison of retention times and ion intensity (C, E). The algorithm subsequently produces a reconstituted daughter ion spectrum from which peptide/protein identification can be performed (F, G). Obtained from Kramer et al (2012).

The aforementioned under-sampling issue is negated by using MS^E as all precursors are fragmented simultaneously and indiscriminately across the entire peak profile. Furthermore, the regular switching between MS and MS^E modes mitigates sampling irregularity observed with MS/MS methods¹⁷⁹. This also means less sample is required as the sample does not need to be run multiple times to obtain data for the full range of ions as it otherwise would with MS/MS¹⁹⁷. MS^E methods are not immune to limitations, however. Precursor ion intensity is regularly below the limit of detection¹⁷⁹, and the quantity of correctly assigned fragment ions to precursors by the dedicated matching software has its own set of inherent limitations discussed elsewhere¹⁹⁸. Additionally, the software packages generate large raw datasets at the gigabyte level for each individual sample, which is a large amount of data needing to be converted to a database-friendly format before use in protein identification. There also understandably limitations in data storage associated with such large datasets. The Waters QToF instrument (Figure 1.7) also possesses an ion mobility separation component (IMS) which is often referred to as HDMS^E to emphasise the

high definition capabilities¹⁹⁸. This component improves the quality of data by causing further gas-phase separation according to cross-sectional area, and providing specific drift times for each individual ion.

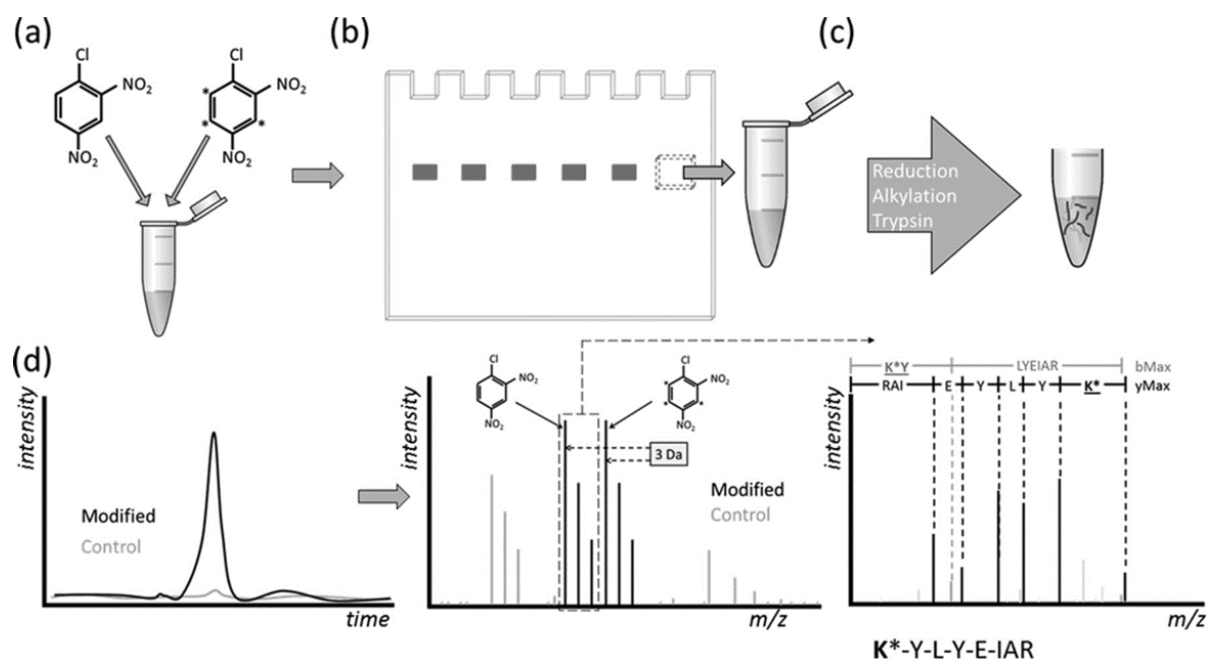


Figure 1.14: Overview of dual isotope labelling method and detection in MS samples – Complex protein samples (e.g. cell lysates) are haptenated with a 50:50 molar ratio of unlabelled and stable deuterated sensitisers (A). Proteins are resolved by polyacrylamide gel electrophoresis to remove excess sensitiser (B) before being excised and subjected to reduction, alkylation, and trypsin digestion (C). Digested peptides are injected onto an LC column before being eluted into the MS instrument operating in MS^E mode. Peptide pairs at the same retention time separated by a mass change equal to the incorporated deuterium mass confirms a hapten-modified peptide during analysis of the fragmentation spectra (D). Obtained from Parkinson *et al* (2014)²⁷.

Dual isotope labelling is a method employed by Parkinson *et al*^{27,28}, originally built upon HDMS^E but with principles transferable to data-dependent acquisition methods. The process uses a solution of labelled sensitiser chemical (e.g. stable deuterium labelling) with a solution of unlabelled sensitiser chemical in a 50/50 ratio before dosing cells and extracting them for MS. This results in twin peaks being evident in the spectral data at the same retention time for exposed samples where one peak represents the m/z (as a measure of M_w) of peptide/protein plus unlabelled sensitiser, and where the second peak represents the same m/z with a peak shift equating to the mass difference of the number of incorporated deuterium atoms. Pairing of these associated peaks provides increased confidence in subsequent identification of the hapten-modified proteins sub-set, i.e. the haptenome.

1.3.6 Protein Identification

The initial stage of protein identification requires raw data processing before searching against relevant protein sequence databases. During this initial stage for HDMS^E data processing, factors such as m/z , IMS drift time, retention time, and peak apex are identified for all MS peaks prior to lock mass correction. Lock mass is any compound of known m/z used as an internal mass standard to counter calibration drifting of the MS instrument¹⁹⁹; an example of a lock mass compound is [Glu1]-Fibrinopeptide B (Glu-Fib). The previous methods produce a list of precursor and fragment ions necessary for further analysis. Deconvolution of isotopes and charge states is the next phase. Following from this, a time alignment algorithm is applied to match fragment ions with corresponding parent precursor ions based on the parent ion apex retention time. This then produces a list of accurate mass retention times for precursor/product pairs of ions necessary for database searching and assignment to a protein for identification.

The Ion Accounting Algorithm available with Waters corporation instruments is used for searching HDMS^E data¹⁷⁹, which is an iterated process with each iteration being more selective, specific, and sensitive to provide confident identification²⁰⁰. There are other additional methods of improving identification confidence depending on experimental aims and design, such as dual isotope labelling (Figure 1.10). False positives are identified and mitigated through use of a decoy database containing both positive and reverse sequences, with only peptides identified with the reverse database being assumed as false positives¹⁶⁷. These software and databases also allow fixed and variable modifications to be included in the search, such as acetylation, though the stable isotope labelling currently cannot be included. Reliable and successful protein identification is dependent on a number of factors, including mass accuracy and protein coverage¹⁶⁷. This coverage is further dependent on the sequencing, sensitivity, speed, and range of the MS instrument¹⁷⁸, as well as sample complexity – hence samples are often simplified by being subjected to reverse-phase peptide purification prior to MS analysis.

1.3.7 Quantification Methods

It is logical that for a more meaningful comparison of two or more proteomes or sub-proteomes the proteins should be quantified in addition to identification. Mass spectrometry is not inherently quantitative due to a number of reasons, but most notably due to differences in ionisation efficiency between peptides. Current technology allows this inherent limitation to be overcome, enabling protein quantification relatively within a sample, and in several cases also quantifying absolutely. As such, there are two overarching types of quantification methods,

relative quantification and absolute quantification, with each further diverging into their own methods for quantifying protein samples.

Multiple methods provide relative quantification of proteins alongside identification, which are commonly used in shotgun proteomics approaches¹⁶⁸. These methods often deploy labelling techniques such as SILAC, iTRAQ, and TMT, though label-free techniques have more recently been adopted^{110,168}. This shift in focus can be attributed to a number of limitations with labelling methods such as incomplete labelling, complex culture/sample preparation, time consumption, and the relatively high cost of reagents. Label-free methods are generally based either upon a comparison of spectral counts between samples, or a comparison of precursor intensities. Research has been undertaken to assess the efficiency of label-free methods compared to labelling methods. The major beneficial observations of label-free methods were identifying a larger number of proteins compared to labelling methods, whilst also doing so in a shorter amount of time with a smaller amount of sample needed¹⁶⁸. The major disadvantage highlighted by these comparative studies was that the datasets for label-free methods were up to 10 times larger than labelling methods¹⁶⁸. However, as early as 2011 it has been shown that label-free methods of relative protein quantification have overtaken labelling methods in proteomics research^{198,201}.

Absolute quantification has a distinct advantage over relative quantification as it allows a direct comparison of proteins in one sample with proteins in multiple other independent samples, an attribute that is not available with relative quantification¹⁸⁶. The ideal method of absolute quantification is multiple reaction monitoring (MRM) which can be combined with labelling techniques such as SILAC, and is favoured for its narrow mass ranges providing high selectivity^{202,203}. However, MRM methods are a targeted approach requiring prior knowledge of the identity of analytes. This makes MRM better suited towards experiments focused on specific protein(s) of interest, rather than exploratory experiments needed for comparing haptenation in global proteomes. MRM assays also require specific design and synthesis of a labelled internal standard, as well as using expensive reagents^{203,204}.

A relatively simple method for absolute quantification in shotgun global proteomics experiments is to spike in a protein digest internal standard into the analysed sample at a defined concentration. This is evident in the Hi3 method in which during data analysis, the MS signal response of the three most intense tryptic peptides of the internal standard comprise a universal signal response factor²⁰⁵. This response factor is compared to the MS signal response of the three most tryptic peptides from each protein in the sample, providing quantification of those proteins¹⁸⁶. The internal standard used in this process does not require matching to endogenous

proteins in the sample and also does not require labelling. In fact, it should be distinct from the endogenous proteins so that it can be distinguished during data analysis. A common distinction is for the internal standard to be derived from a different species to the sample. The Hi3 method has reduced cost compared to the previously discussed methods and requires no pre-existing knowledge of sample peptide composition. However, the method is also less accurate than the previously discussed methods, and therefore is considered an estimate of absolute abundance.

Again, the operator must decide which methods are the most appropriate given their experimental design, though Hi3 currently appears to be the most applicable method for studying haptenation in epithelial cells. Assuming there is a quantifiable difference in protein expression between healthy cells and skin/respiratory sensitised cells, or between the skin and respiratory sensitised cells themselves, potential biomarkers or factors driving divergence may be identified. Such a hypothesis would likely also benefit from differential analysis of known protein-protein interaction networks (PPIN) in which haptenation target proteins are included, as well as the potential metabolic effects this may have in driving divergence of the sensitisation immune response.

1.4 Key Findings from Haptenation Studies

1.4.1 The Research Environment

Haptens are ubiquitous in nature in the form of sensitisers or compounds that are readily metabolised to sensitisers^{1,2}. These are also often found in domestic, cosmetic, and medical products which results in wide-ranging exposure risk to large portions of the population⁹. In the current period of Next Generation Risk Assessments (NGRA), distancing from animal studies has resulted in a priority for understanding the molecular mechanisms (MIE) underpinning skin and respiratory sensitisation, including the potential of cross-reactivity³.

In chemico evidence is predicated upon relatively simple models as proxies for complex *in-vitro* protein nucleophile systems, such as amino acids residues of peptides, and model proteins^{26,206–208}. Several considerations are needed to gain a more physiologically relevant understanding of haptenation reactions during sensitisation. These considerations include (but are not limited to) competition for binding sites on different nucleophiles, differences in protein nucleophile expression in cells and tissues, differences in local pH of the reaction, and steric constraints. The majority of these model systems incorporate a single nucleophilic haptenation site on each molecule, which whilst useful for initial characterisation of the different haptenation reactions,

are too limited for direct characterisation in multi-dimensional nucleophile systems such as cell lysates and tissue homogenates.

In-vivo studies most commonly implicate animal models and human participants, e.g. skin-prick or skin-patch tests, with some advancement made in the direction of population studies^{94,101,102}. However, such investigations generally aim to characterise physiological cytokine and antibody responses derived from incompletely understood upstream processes. Furthermore, they typically suffer from inconsistencies due to variance in the sample groups, as well as considerable ethical considerations.

As alluded to during evaluation of the AOPs, the key knowledge gap preventing clear connection between upstream *in chemico* and downstream *in vivo* observations is the nature of haptentation in complex *in vitro* and *ex vivo* systems. Such studies are expected to initially identify protein nucleophile targets haptentated in the MIE, as well as inform classification of sensitiser chemicals based on characteristic haptenomes. Of further interest is the question of whether model peptide/protein reactivity profiles remain comparable with these haptenomes.

1.4.2 Proteome Surveillance

Parkinson *et al* produced the first comprehensive, qualitative and quantitative survey of the human skin proteome using shotgun proteomics methods with an isobaric tagging strategy to characterise the response of macerated tissue samples to the irritant SDS¹¹⁰. Whilst the SDS-induced changes were not statistically significant, quite likely due to variation between individual sample donations, the study did define the repertoire of nucleophilic amino acids within the proteome.

This initial dataset provided crucial knowledge on the type and abundance of proteins for experimental design discounting higher abundance proteins (e.g. serum albumin) in order to pinpoint lower abundance protein hapten targets. The importance of low abundance nucleophile targets has been emphasised previously, based on modifications inferred from 3D model peptide/protein systems. Data for the nucleophilic make-up also generated here (5.7% Lys, 0.9% Cys) would be instrumental for in-depth comparison between specific haptentation events on model proteins, and within the complexity of the human skin proteome. To date, no such in-depth surveillance of the lung tissue proteome is known of.

1.4.3 Pinpointing Low Abundance Modifications

There are some select investigations previously addressing specific protein haptenation in complex mixtures. Largely these have either been based on the intrinsic properties of certain haptenation products (e.g. fluorescent adducts), or interactions with biotin. However, the majority of investigation into global haptenation reactions has been performed by Parkinson *et al*^{9,10,27,28}, as a remedy to the lack of knowledge of the localisation and identity of haptenated proteins within the complexity of the human skin proteome.

Parkinson *et al* also improved upon previous 3D model protein haptenation studies by incorporating novel stable dual-isotope deuterium labelling into an established geLC-MS/MS method²⁷. This innovative combination of techniques allows the pinpointing of low abundance haptenated proteins with improved confidence. The 3D model protein HSA was modified in solution through exposure to the skin sensitisers DNCB, MCI, cinnamaldehyde, and the non- (or weak) sensitiser 6-MC over a series of time points. Peptide modifications were confirmed, and false positives mitigated, by virtue of the fixed mass shift between paired ion peaks corresponding to the deuterium mass in a 50/50 labelled-unlabelled sensitiser exposure.

1.4.3.1 Model Protein Haptenation

Human serum albumin (HSA) has been the subject of numerous haptenation studies due to being well-characterised as well as its prevalence in human tissues²⁰⁹, namely the skin. A further point of interest is that HSA has also been implicated in haptenation studies where it has been observed to stimulate T-cell responses. The suggestion here is that HSA may play an important role as a carrier protein mediating T-cell activation within sensitisation processes²⁷.

Some common observations were made between the different sensitisers used in these experiments. Both MCI and DNCB preferentially modified lysine, with the majority of DNCB modifications being observed throughout the time course from the earliest time points. The suggestion has been made that the same residues susceptible to haptenation at the earliest time points continue to be modified over time. However, haptenation of a number of residues has only been observed at later time points. This led to the hypothesis that conformational changes are induced by initial haptenation events, allowing subsequent haptenation of usually obscured or unavailable haptenation residues – there is some degree of precedence for this^{210,211}. However, later modifications may have been due to overcoming constraints imposed by the reaction mixture composition at earlier time points, e.g. depletion of other non-protein nucleophiles. Also, the extensive incubation time could result in methylation or oxidation masking the haptenated peptides from database searches. This progressive haptenation was generally observed

indiscriminately with all the sensitisers, suggesting that denaturation was being induced by the experimental conditions rather than chemical interaction.

Four HSA lysine residues were commonly haptenated by a range of skin sensitisers, suggesting some general influence in sensitisation, though clearly not in terms of specificity. Conversely, a number of residues were only modified by DNCB with a single mass adduct of +166 $\Delta m/z$ and present good examples for further investigation into residue specificity in modification. Furthermore, many of these are cysteine residues, despite being a low proportion of the nucleophile repertoire.

Results from DPCP modification also showed reaction predominantly with lysine, rather than the typical cysteine reactivity expected from a dermal sensitiser^{4,206}. In addition to this, DPCP was found here to produce three mass adducts of +206, +222, and +224 $\Delta m/z$ over a range of different sites on HSA. This highlights the importance of specific hapten reaction mechanism with different residues/structures, as the multiple mass adducts are explained as resulting from further oxidation and ring-opening modifications to the initial adduct, at some sites differing from those previously identified in HSA reactivity studies. This is in notable contrast to the other haptens explored in these studies, which generally all formed only a single mass adduct. The only unique modification with DPCP was at His228, previously shown to be a target residue for trans-4-hydroxy nonenal, generated by lipid peroxidation²¹².

The HSA haptenation data summarily reviewed here has demonstrated the utility of dual isotope labelling in combination with the improvements of modern MS to identify low abundance haptenation target residues, also supporting the non-stoichiometric concept of haptenation.

1.4.3.2 Haptenation in Complex Protein Mixtures – Cell Lysates and Tissue Homogenates

Following the success of the skin proteome surveillance and HSA dual isotope labelling in providing a dataset of proteins and novel method of modification, the techniques were combined to assess haptenation within the complex mixtures of keratinocyte (HaCaT) cell lysates compared to skin tissue homogenates.

HaCaT keratinocyte cell lysates and skin tissue homogenates were exposed to skin sensitisers DNCB, cinnamaldehyde, MCI, and 6-MC in 100-fold excess for 4 weeks at 37°C before fractionation and analysis by LC-MS with ion mobility (HDMS^E)²⁸. The investigation has also since been extended to characterising the haptenome of DPCP and EA in HaCaT cell lysates¹⁰. The high, non-clinical concentration of sensitisers and prolonged exposure time used in these experiments were utilised to hypothetically provide as much haptenation as possible, with the explanation that

an inability to detect any considerable haptenation under these conditions would render *in vitro* investigations with clinical-relevant concentrations futile.

The total number of proteins identified was approximately 3-fold greater for cell lysates compared to the skin tissue, though gene ontology analysis revealed 70% agreement with the total number of modifications generally being equal as well. These observations were used as the basis for determining the satisfactory utility of the HaCaT cell line as a model representative of global proteome haptenation in skin tissue.

DNCB was found to modify 2.5% of the cellular proteome and 1.8% of the skin tissue proteome, with haptenated proteins being observed over a range of abundance levels. The proteins with the greatest number of DNCB modifications included complement C3, pyruvate kinase, prelamin-A/C, and serum albumin among others haptenated to various extents. These represent proteins of interest for further analysis and comparison with findings from other studies, though the importance of the number of modifications on a given protein remains relatively unclear compared to the specificity of binding. Several proteins were also found to be modified in *both* cells and tissue, including; keratins, heat shock protein 90, annexins, alpha actinins, and glutathione S-transferase.

The data analysed for DPCP and EA modification in HaCaT cell lysates showed 1.2% and 0.1% proteome coverage. These observations are comparable to those of previously investigated haptens within the same nucleophile system. Despite different reaction mechanisms DNCB and DPCP generally showed concurrence in proteins modified within HaCaT cell lysates, as well as again sharing a preference for lysine rather than cysteine. There are some proteins which were specifically modified by DPCP on tyrosine residues, including Ubiquitin carboxyl-terminal hydrolase 7, Ezrin, and Desmoplakin. An unprecedented finding was that DPCP also modified tyrosine residues on a number of proteins, a capability that had never been reported in peptide or model protein reactivity studies.

The methods and analyses reviewed thus far have successfully located and identified low abundance protein haptenation in 3D model proteins, and also within the complexity of cellular and skin tissue proteomes. However, no such in-depth analyses yet exist for respiratory sensitisation to allow a successful comparison of the MIE, in terms of localisation and specificity of protein nucleophile targets, and subsequent comparison to evidence of divergent downstream cellular processes. However, working at the forefront of instrument sensitivity also means working at the lower limit of detection. In these studies, this has meant many of the haptenated proteins were only identifiable in a single replicate or in duplicate at maximum.

Surprisingly, a lack of adherence of multiple sensitisers in complex models to the precedent of Cys/Lys modification duality in peptide reactivity studies was displayed. This is most likely a result of differences in nucleophile composition between the different systems. Peptide reactivity studies employ a fixed concentration of single nucleophile targets. Complex protein mixtures like lysates, and to an extent HSA, have an array of different nucleophile targets including a much larger proportion of amine nucleophiles (Lys) relative to thiols (Cys). This is compounded by not all nucleophile sites being conformationally available for haptenation in protein models, as well as incomplete understanding of the importance of this steric constraint.

In spite of high non-clinical doses, prolonged incubation time, and pre-lysed/macerated samples, haptenation analyses have shown both low levels of modified residues (as in HSA) *and* low levels of modification of all proteins in general. As illustrated by Parkinson *et al*, mapping haptenated cell-derived proteins to a ranked list according to their nucleophile content shows a correlation between haptenation and nucleophile content, though this was not corroborated by the tissue-derived proteins^{10,28}. These findings appear independent of abundance, and therefore in contradiction to the hypothesis of Hopkins *et al* that more abundant proteins would be favoured. This suggests a significant role for specificity or *de facto* specificity due to alterations in steric constraints or further haptenation events. The fundamental proposal arising from these results is that haptenation *in vitro* is not driven solely by abundance, i.e. it is a non-stoichiometric process.

1.4.3.3 Haptenation in Living Epithelial Cell Systems

Haptenation studies have generally utilised a high molar ratio of hapten-to-nucleophile, which in conjunction with data-independent acquisition, maximises the detection of low abundance haptenation. However, this demonstrates a key issue facing this area currently. The hapten-to-nucleophile ratio is reversed in a live cell haptenation model to maintain cell viability, with the nucleophilic residues far outnumbering the number of hapten molecules. This is where the hypothesis of haptenation target specificity and differential cellular processes comes into play. Such selectivity advances the logic behind non-stoichiometric modification of cellular proteins.

The low proteome coverages observed with even the most potent dermal haptens within cellular and tissue proteomes, in a 100-fold excess^{10,28}, offers some plausibility for the criticality of specific and dynamic cellular processes in response to protein haptenation. However, identification of haptenation sites, and quantification of the haptenated proteins within a complex living system remained challenging. Using the proteome previously surveyed, Parkinson *et al* again employed the dual isotope labelling HDMS^E method with the addition of Top3 quantitation for proteome changes in living HaCaT keratinocytes over 48 hours at a sub-cytotoxic exposure (10µM) of DNCB for 4 hours.

Only 28 haptenated proteins were found in common between this living cell dataset and the previous cell lysate dataset²⁸, with only a single specific haptenation residue identified in both – Cys489 of keratin type II cytoskeletal 2 epidermal protein. Two other hapten targets have been named, mitochondrial heat shock protein and heat shock cognate. However, a number of other targets identified in previous literature were not modified here. A preference for amine nucleophiles (lysine) was once again observed, but considerable modification of thiols (cysteine) was also evident, with proportions differing over the range of time points. Of the available residues, cysteines were more frequently modified than lysine relative to the total theoretically available nucleophiles of each type. This may indicate a greater affinity for cysteine modification despite the far greater abundance of lysine, though a more robust group of samples would be needed to confirm this ideally.

It was noted by the authors that some proteins are ‘certainly’ haptenated due to their abundance, with the example of basal epidermal keratins having readily available cysteine residues and being extensively modified whereas upper epidermal keratins are equally abundant, but do not have readily available cysteines and remained unmodified. Additionally, the majority of highly abundant proteins identified were not haptenated. Overall, these observations are in line with the hypothesis that abundance is not the sole driver of haptenation, and it appears steric constraints indeed appear more important than initially realised.

The haptenation of low abundance proteins is much more complex. The minimal changes in differential expression of the proteome matches the expectation of the authors that at sub-toxic doses, cells respond to the electrophilic insult by employing defence mechanisms to minimise detrimental cellular effects of the haptenation. Potentially, these defences would not produce a substantial signal in the analysis methods employed here. Moreover, proteome shifts would hypothetically only be detected once the capacity of the cells to counteract the haptenation has been exceeded – whether due to exposure duration or chemical concentration.

There are explanations provided for the low numbers of haptenated proteins in the haptenome. The experimental design omitted some additional elements of the cellular response, such as changes in the quantity of small intracellular nucleophile molecules like glutathione (GSH) and other thiol-rich molecules. It has also previously been demonstrated that concentrations of DNCB capable of causing sensitisation physiologically (10 μ M) depletes >50% of GSH in HaCaT cells within 1 hour and fully recovers by 24 hours²¹³. This provides further support to the detoxification concept for DNCB haptens previously highlighted, with the potential for differential regulation in respiratory sensitisation. This would also explain the minimal cellular response measured in the Parkinson *et al* paper.

Further investigation in living cell systems is necessary for determination of specific rules and conditions necessary for different skin and respiratory sensitisers. Such investigations could also identify differential induction of specific pathways and interaction networks between skin and respiratory sensitisation. For example, the same experimental concentration of DNCB has previously been shown to activate the Nrf2 pathway²¹³. However, the associated Keap1 protein was not modified here as would be expected to initiate dissociation and activate the pathway. This represents an interesting process to monitor in respiratory sensitisation-focused experiments to compare the potential for divergent induction of the pathway by either skin or respiratory sensitisers. Another process of interest for differential pathway induction would stem from differences in redox imbalance due to differences in reactive oxygen species induced by different sensitizer chemicals. Lipid peroxidation has been shown to be initiated by increased reactive oxygen species²¹⁴, which have the capacity to produce further endogenous electrophiles with potential to further modify. Differential induction of this pathway would yield signals indicative of differential competition in skin and respiratory sensitisation.

It would be prudent to assess the wealth of haptenation methods and data produced by Parkinson *et al* in congruence with other mechanistic studies, particularly those attempting to delineate skin and respiratory sensitisation from the perspective of other key sensitisation events.

1.4.3.4 Haptenation in Other Living Cell Systems

Chary *et al* aimed to develop an *in vitro* living cell model mimicking the alveolar capillary barrier to allow assessment of the respiratory sensitisation potential of a variety of compounds, including low M_w organic chemicals such as phthalic anhydride²¹⁵. The methods compared monocultures of dendritic-like THP-1 cells with a co-culture model of alveolar epithelial cells (A549), endothelial cells, and macrophages.

Both cultures were exposed to nebulised chemical respiratory sensitisers and irritants at concentrations inducing 25% cytotoxicity (where solubility allowed). Data was generated for cell surface markers of THP-1 cells via flow cytometry methods and a multiplex array. Cytokine profiling and gene expression of THP-1 cells were also assessed, via qRT-PCR of extracted RNA.

Exposure to phthalic anhydride induced DC activation. Cell surface markers TSLPr and IL7-R α were upregulated in both cultures, with CD54 and to an extent CD86 also being upregulated in coculture. TSLP and its receptor TSLPr are heavily implicated in OX40L upregulation on DCs, though the quantification of OX40L does not provide a good basis for the prediction of respiratory sensitisation due to only minor modulation at the protein level, though it is often found in epithelial expression of asthma patients²¹⁶. TSLPr combines with IL7-R α as a high affinity binding

complex for TSLP, which triggers phosphorylation signalling via signal transducer and activator of transcription 5 (PSTAT-5), whereas TSLPr alone does not have high affinity for its ligand²¹⁷.

Phthalic anhydride also demonstrated a specific cytokine release pattern, with statistical significance identified for CCL20, GM-CSF, and IL-10 release. CCL20 recruits DCs to the alveolar barrier whereas epithelial-derived GM-CSF has been described as a critical early signal in respiratory sensitisation²¹⁸. IL-10 is a cytokine characteristic of a Th2 response, as previously illustrated¹²². Analysis of PA-induced gene expression showed up-regulation of *IL1RL1* which encodes the IL-33 receptor, and reduced expression of *CIITA* encoding MHCII – representing a potentially important finding for related immunopeptidomics investigations.

The authors noted that a considerable improvement would be the testing of chemicals exclusively inducing skin sensitisation (e.g. DNCB) to establish suitable markers for discrimination from those regulated by respiratory sensitisers. Conceivably, disparity between such markers would reflect differences in proteins modified and/or cellular response. The study would gain added benefit from expanded understanding on the individual key events (especially the MIE and cellular responses) that have perhaps been prematurely combined in the study.

A cell viability of 75% is historically useful for cell surface marker analysis^{219–221}, however, the use of sub-cytotoxic concentrations was cited as being more appropriate for gene expression and cytokine measurement²¹⁵. Findings from these improvements would aid in delineating the effects and markers associated with cytotoxicity rather than sensitisation. This would also further represent an improvement in terms of test chemical solubility due to CV75 often being beyond the maximum achievable solubility. Sub-toxic doses would also be advantageous for comparison to the MIE research by Parkinson *et al*, in fact similar studies to Chary *et al* have already begun moving closer to sub-cytotoxic concentrations⁶⁵. There is limited transferability to other diisocyanates though, due chiefly to polymerisation at higher concentration in aqueous environments making nebulisation especially challenging. Sensitisation and related processes could occur after recurrent exposure to the same (or similar) chemicals; however, this cannot be assessed above a sub-toxic dose as cell viability would need to be maintained.

In summary, the analyses of Chary *et al* represents a multi-faceted approach to assessing the extracellular interactions and dendritic cell gene expression involved in the determination of respiratory sensitisation potential. The study also successfully demonstrated the discriminating factors between respiratory sensitisers and irritant, serving as a reflection of the skin sensitiser/irritant comparison by Parkinson *et al*¹¹⁰, and offering insights into the utility of sensitiser nebulisation methods for respiratory haptenation studies.

Finally, examination of the epithelial cellular proteome after exposure to the respiratory sensitisers in this study would be of considerable interest due to being the principle site of exposure, and for comparison to haptenated skin proteome data. To date, such an examination has not been performed, with the nearest fulfilments being *in vivo* animal studies. For example, Wisniewski *et al* identified reaction products of hexamethylene diisocyanate (HDI) vapours with self-molecules in the airways of rabbits using LC-MS and MS/MS methods²²².

The major findings confirmed previous *in vitro* studies presenting HDI reactivity with GSH across a vapour-/liquid-phase boundary and suggest it acts as a point of chemical access to the lower respiratory tract²²³. The data also demonstrated haptenation of the rabbit homologue club cell protein, and albumin at a site previously identified as being preferred for diisocyanate conjugation, as proteins susceptible to HDI modification following aerosol inhalation^{224–226}. Notwithstanding the obvious difficulties in translating data from animal studies to human samples, this study outlined valuable methods for determining the solution concentration following aerosol exposure with potential for inoculating living cell cultures in future.

1.4.4 Summary and Further Research Scope

Many of the earlier studies reviewed here realistically represent upscaled *in chemico* studies, with physiologically relevant hapten targets likely being a subset of those identified. This therefore emphasises the importance of advancement to more complex *in vitro* systems such as live cell haptenation and *ex vivo* tissue models.

Moreover, determination of the extent of haptenation depends upon a host of other factors, a number of which have already been discussed. Reaction mechanism, route and role of detoxification, electrophile concentration, nucleophile type & concentration, electrophilicity, solubility and volatility are all important practical considerations for the development of more complex haptenation models. It is also plausible that the extent of proteome haptenation correlates with the diversity and number of available T-cell epitopes²²⁷ – a credible indicator of hapten potency.

For the sensitisers studied thus far, haptenation in increasingly complex nucleophilic models appears to not be completely random, rather it is a low-level and reproducible event. The argument of stoichiometry vs non-stoichiometry appears more compelling in favour of the latter, though potentially differs on a chemical-by-chemical basis. And perhaps most importantly, the improved sensitivity, resolution, and modes of data acquisition of modern MS combined with stable dual isotope-labelling have established the methods of Parkinson *et al* as the method of choice for analysing *in vitro* haptenation resulting from the MIE.

It is important to remember that the apparent preference for a specific nucleophilic residue in these studies may not be universally representative of haptentation under different conditions. Discussed here have been a number of examples of the many complications introduced between relatively simple *in chemico* investigations and clinical *in vivo* studies and the assumptions that have been tentatively developed as a remedy – which are further outlined here:

- Analysis of haptentation within cellular proteome models allows the most in-depth analysis to date, but still has inherent detection limitations that must be considered.
- Combination or comparison with studies targeting other key events is important for meaningful *in silico* prediction of sensitisation potential.
- Degree of specificity of some chemicals towards binding certain nucleophilic amino acid residues, predominantly cysteine or lysine.
- Possible effect of the protein tertiary structure on the likelihood of haptentation, which may be circumvented for some nucleophile target residues.
- Sensitiser potency does not necessarily equal extent of haptentation, but often appears to.
- Theoretical hapten-to-nucleophile ratio may be determinant in the *extent of in vitro* haptentation, the *specificity* is another matter for further review.
- Protein abundance can be determinant, but just as often (if not more often) is not.

Based on all the above, the process cannot be considered stoichiometric *or* random at this time. Hapten target identification appears to persist in its importance for understanding the consequences of binding specificity, cellular proteome response, and interaction with divergent stages of the skin and respiratory AOPs. The conceptual importance of specific cellular processes following sensitiser exposure introduces a host of further questions; is the hapten internalised by cells before modifying native proteins? Or is it that extracellular proteins are haptentated and then internalised by cells? Are haptentated proteins internalised from cell debris following apoptosis of sensitised cells? These questions are historically beyond the scope of haptentation studies, but the incorporation of proteomics, immuno-peptidomics, and bioinformatics techniques would expectedly widen the scope and aid in elucidating the most plausible pathway(s).

Chapter 2 Aims and Objectives

Allergies to low molecular weight organic chemicals are a public health concern and can manifest as a variety of clinical outcomes. For example, allergic contact dermatitis (ACD) is a T-cell mediated, delayed hypersensitivity typically resulting in skin symptoms, which can be severe but generally not life-threatening. By contrast, chemical respiratory allergies can be IgE-mediated in a number of cases and potentially fatal. Mechanistic understanding of allergies to these chemicals is such that all involve an initial protein haptenation event in which a small electrophilic chemical covalently modifies nucleophilic residues of endogenous proteins. There remains a number of uncertainties which appear to be crucial for a distinction between skin and respiratory sensitisation; such as structural/chemical cut-offs between measured and theoretical reactivity²²⁸ and what drives subsequent divergent adverse immunological outcomes⁴.

However, a major route yet to be fully explored is the significance of differential targeting of protein nucleophiles by different chemical sensitizer structures and reactivity. A number of adverse outcome pathways (AOPs) for chemical respiratory sensitisation have been published^{2,3,38}, building on the earlier AOP for skin sensitisation^{1,3}. Common key events of the AOPs identify driving factors underpinning divergence between T_H1 and T_H2 polarisation as a key knowledge gap. Much *in chemico* research is available and ongoing regarding the chemicals and modification chemistry of haptenation, and a wealth of *in vivo* animal studies indirectly measuring activity of pathways leading to the divergent adverse outcomes have been performed. Crucially however, little human-derived *in vitro* evidence is available for final target proteins forming the hapten-carrier complex, specific cellular proteome response, or the nature of antigens presented to T-cells potentially causing divergent downstream immune responses.

Capitalising upon novel mass spectrometry techniques recently developed at the University of Southampton, this project aims to characterise quantitatively the covalent modifications^{27,28}, specific cellular response, and the peptide antigens presented by selected skin and respiratory sensitizers (Figure 2.1). Extending these research methods to respiratory chemical allergens will hypothetically allow a meaningful comparison between skin and respiratory sensitisation at the molecular and cellular level.

This research project aims primarily to test the hypothesis that skin and respiratory sensitizers differ in haptenation targets, cellular response and antigen presentation. To this end, a series of experiments are proposed here for the *in vitro* characterisation of sensitizer-elicited differences in the haptenome, proteome, and immunopeptidome in human respiratory epithelial cells. The associations identified in this work would hypothetically be instrumental in identifying and

discriminating proteins, pathways, and specific peptide antigens associated with either downstream immune response pathway (T_h1/T_h2).

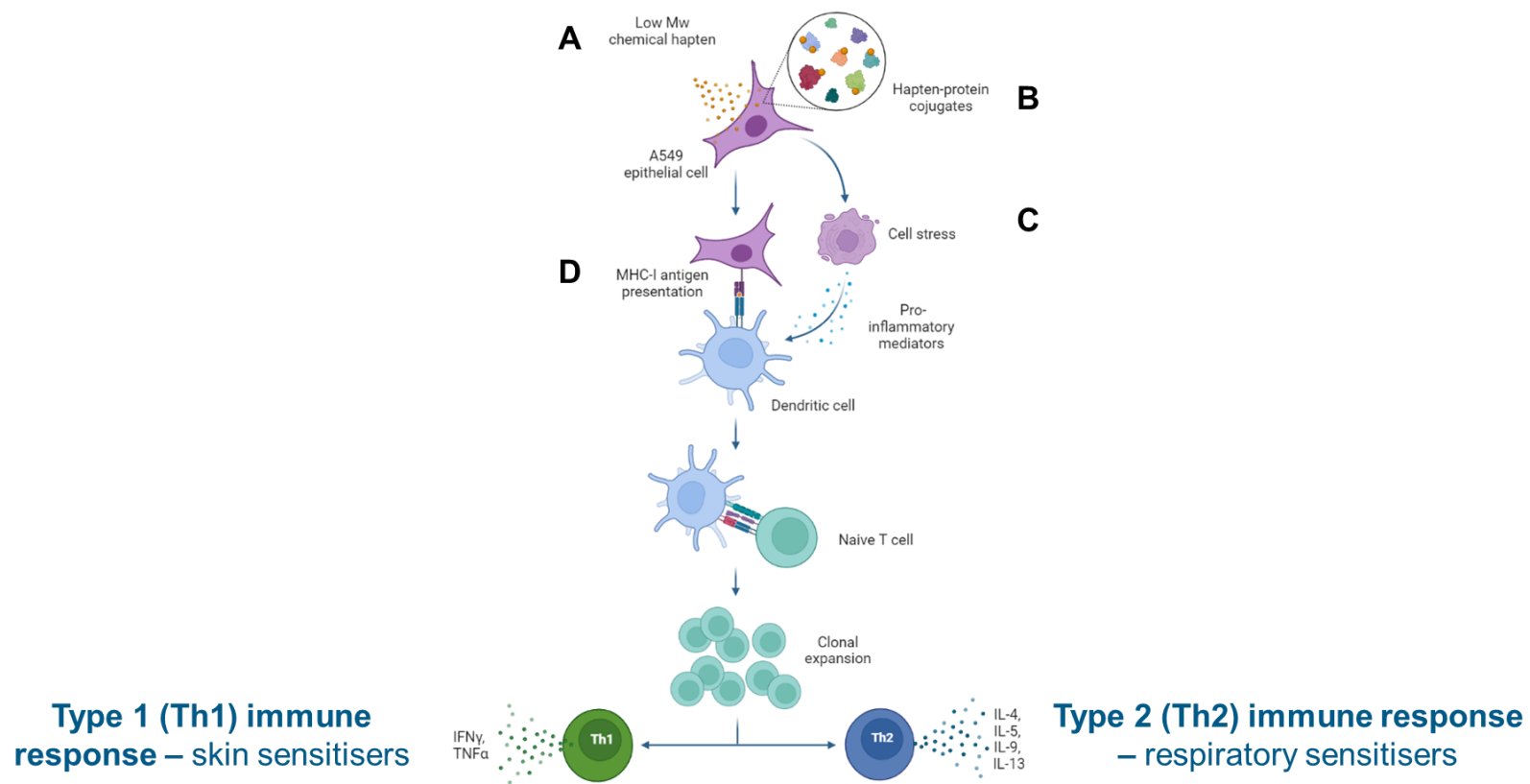


Figure 2.1: Project research aims in the context of the combined adverse outcome pathways – differences in specific reaction mechanisms and adducts for different skin and respiratory chemical sensitizers (A) are investigated in the context of specific protein haptentation targets in human respiratory epithelial cells (B), the associated downstream exposed cell signaling & pathway induction response (C), and haptentated peptide presentation on the surface of exposed cells by major histocompatibility complex proteins within the immunopeptidome (D).

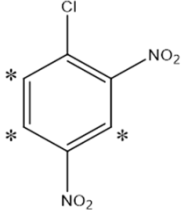
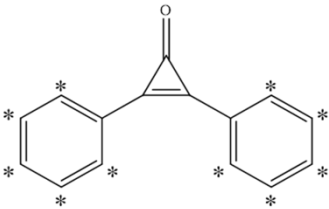
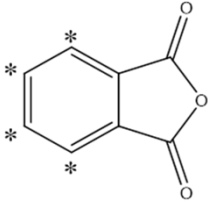
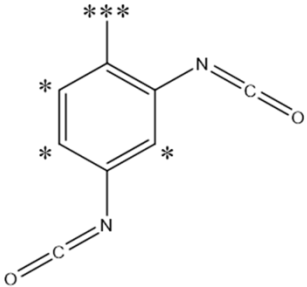
Chapter 3 Peptide reactivity and cell viability following exposure to select skin and respiratory sensitisers

3.1 Introduction

Mechanistic understanding of skin sensitisation is such that covalent modification of self-proteins by low molecular weight organic chemicals is a necessary molecular initiation event (MIE). This leads to the cell-mediated delayed hypersensitivity adverse outcome of allergic contact dermatitis through a series of key events outlined in an adverse outcome pathway (AOP)²²⁹. This covalent molecular initiation was originally termed ‘haptentation’ in the pioneering work of Landsteiner & Jacobs³⁶. These processes are also reflected in the AOP for respiratory sensitisation through a number of divergent key events, resulting in the potentially IgE-mediated adverse outcomes of rhinitis, respiratory anaphylaxis, and other allergic asthma symptoms of varying severity². Due to increasingly important public health consequences, and the necessity of developing alternatives to animal-based testing, characterisation and delineation of selective skin and respiratory sensitizer chemical action is of growing interest.

Following the work of Hopkins *et al* in demonstrating selective haptentation of cellular thiol groups (cysteine) and serum amines (lysine)⁴, predictive methods for the characterisation and risk assessment of chemicals inducing skin sensitisation has been well-documented. Such methods included the guinea pig maximisation test²³⁰ and local lymph node assay (LLNA)²²⁰. In the last 10-20 years, a number of adaptations to the direct peptide reactivity assay (DPRA)⁵ have been made, presenting it as an increasingly valid identification & confirmation method for assessing amino acid selectivity of skin sensitisers. More recently, assessment of selectivity of other nucleophilic amino acids (His, Arg, Tyr) have been applied to the DPRA²⁰⁸, with selectivity being lower than for Cys/Lys. The analytical methods of the DPRA (and its adaptations) generally rely either on quantitative peptide nucleophile depletion or qualitative mass spectrometric identification of specific peptide adducts¹⁶. In certain studies, both these methodologies have been combined²⁰⁸. Extension of these methods into more complex nucleophile models, e.g. human serum albumin (HSA)^{26,27}, has contributed to increased understanding of the biochemical mechanisms of skin sensitisation^{1,3,16}.

Table 3.1: Sensitiser chemical structures – the molecular mass, potency category (EC3 from Local Lymph Node Assay), reaction mechanism, Δ mass (Da) from haptenation, expected adduct type, and relevant references for each sensitiser chemical investigated in this study.

Chemical Compound	M _w (Da)	Potency (%EC3)	Reaction Mechanism	Δ Mass (<i>m/z</i>) unlabelled (& deuterated)	Expected Adduct Type	Reference(s)
2,4-Dinitrochlorobenzene	202.552	Extreme (0.05)	S _N Ar	166.092 (169.092)	Single Adduct	Parkinson <i>et al</i> ^{8,9,27}
						
Diphenylcyclopropanone	206.244	Extreme (0.00009)	Michael Addition	206.244 (216.244)	Single adduct	Parkinson <i>et al</i> ¹⁰
				222.243 (232.243)	Oxidation of single adduct	Parkinson <i>et al</i> ¹⁰
				224.259 (234.259)	Ring opening of single adduct	Parkinson <i>et al</i> ¹⁰
				412.488 (432.488)	Double adduct	Natsch & Gfeller ⁸⁸
				430.503 (450.503)	Double adduct partially hydrolysed	
				448.518 (468.518)	Double adduct fully hydrolysed	
Phthalic Anhydride	148.117	Strong (0.16)	Acylation	148.117 (152.117)	Single adduct	Natsch & Gfeller ⁸⁸
				149.125 (153.117)	Tautomeric single adduct	
				164.116 (168.116)	Oxidation of single adduct	
				130.102 (134.102)	Imide-like single adduct	Khong <i>et al</i> ²³¹
				296.234 (304.234)	Double adduct	Natsch & Gfeller ⁸⁸ , Reichardt <i>et al</i> ²³²
				298.250 (306.250)	Tautomeric double adduct	
2,4-Toluene diisocyanate	174.159	Strong (0.109)	Acylation	174.159 (180.159)	Single adduct	Reichardt <i>et al</i> ²³² , Keough <i>et al</i> ²³³
				148.165 (154.165)	Single adduct hydrolysed	Reichardt <i>et al</i> ²³² , Keough <i>et al</i> ²³³
				174.159 (180.159)	Intramolecular cross-link single adduct	Reichardt <i>et al</i> ²³²
				[2M+dNCO+2H] ²⁺	Intermolecular cross-link	Hettick <i>et al</i> ²²⁴
				348.318 (360.318)	Double adduct	
				322.324 (334.324)	Double adduct partially hydrolysed	
				296.330 (308.330)	Double adduct fully hydrolysed	Hettick <i>et al</i> ²²⁴

By comparison, there remains a relative lack of validated assays for the identification and characterisation of chemicals causing respiratory sensitisation, with most data arising from *in vivo* occupational exposure studies^{94,101,102}. To date, perhaps the most compelling assays for MIE characterisation of respiratory sensitisation are adaptations of the DPRA. In such cases, comparisons have been drawn between skin and respiratory sensitizer chemicals based on characteristics such as, suitable bioavailability, direct-acting electrophilicity (or readily metabolised to electrophiles), specific mechanistic domains, potency, and nucleophile selectivity^{1-3,16,234}.

The work of Lalko *et al*²⁰⁶ demonstrated that respiratory sensitizer chemicals could be identified in a modified peptide reactivity assay by differential reactivity with peptides containing a single nucleophilic residue of either cysteine or lysine. Importantly, these studies assessed the major classes of respiratory sensitizers, including acid anhydrides and diisocyanates. Respiratory sensitizers were found to react preferentially with lysine, in direct contrast to cysteine selectivity commonly observed with skin sensitizers. These observations were further validated in the context of direct nucleophile competition²³⁵.

Differential specificity has been demonstrated with both skin and respiratory sensitizers^{26,27,207,231}, however not in equal amount and exclusively in model skin proteins rather than respiratory. These studies have also illustrated haptentation as a highly specific event, which is non-stoichiometric with respect to nucleophile/protein abundance based upon three main factors: electrophilicity of the hapten, nucleophilicity of the target(s), and in particular steric constraints.

It is established that protein haptentation can occur and activate responses in keratinocytes as a result of sensitizer exposure²³⁶⁻²³⁸. Such responses include, but are not limited to, release of pro-inflammatory cytokines and induction of cytoprotective pathways^{1,24,46,52}. Furthermore, keratinocytes are epithelial cells making up more than 90% of the highly keratinised epidermis²³⁹, therefore providing a high number of cells capable of antigen presentation after T cells have been primed by dendritic cells in the adverse outcome pathway (AOP). Keratinocytes also make up a large proportion of the site of exposure for skin sensitisation. Therefore, they are logically the most likely to stimulate the characteristic T cell sub-populations (T_H1) created after the initial sensitisation phase^{58,125}. Overall, keratinocytes can be considered the main effector cells following sensitizer re-exposure.

Proceeding from the mouth and nose, via the trachea, are a pair of cilia- and mucus-lined bronchi which enter the lungs at each hilum. Each bronchus in turn branches into narrower secondary and tertiary bronchi, the narrowest of which are referred to as bronchioles²⁴⁰. Despite

the ability of bronchioles to constrict and dilate to alter the surface area, bronchioles still only provide a relatively small 0.5-50mm² of surface area²⁴¹. The main appeal of utilising bronchial epithelial cells for comparison to human keratinocytes is that they form the earliest interface between external sensitiser chemicals and the internal microenvironments of the skin or lungs respectively²⁴².

Alveoli are the principle, and smallest, unit of gaseous exchange in the lung and are situated mainly (though not exclusively) in ducts at the end of terminal and respiratory bronchioles. Each alveolus consists primarily of squamous epithelial cells that make up more than 90% of the alveolar surface, with approximately 70m² provided by all alveoli collectively²⁴³. Thus these cells provide extensive availability for exposure and antigen presentation after T cells have initially been primed by dendritic cells in the sensitisation phase²⁴⁴ of the AOPs. As with keratinocytes and bronchial epithelial cells, alveolar epithelial cells are similarly capable of signalling and cytokine/chemokine secretion in response to sensitiser exposure². As such, the human alveolar epithelial cell line A549 has been used previously in cytokine profiling experiments⁶⁰, and investigation of reactive oxygen species²⁴⁵ produced following exposure to respiratory sensitisers.

Considering the growing wealth of evidence surrounding the differential selectivity of skin and respiratory sensitisers, assessment of both skin and respiratory sensitisers over the full range of concentrations possible under different reaction conditions relevant to more complex assays would be ideal. This would allow inference to reaction environments comparable to *in vitro* cell-based assays, especially when incorporating the principles of competing nucleophiles introduced by salt solutions and cell culture supplements. To this end, methods of functional peptide reactivity analysis²⁰⁸ have been adapted here for investigation of the skin sensitisers DNCB and DPCP and the respiratory sensitisers PA and TDI at a range of concentrations under different reaction conditions.

The weight-of-evidence based approach employed by adverse outcome pathways to characterise skin and respiratory sensitisation demonstrates the importance of living cellular responses to sensitiser exposure. Toxicological assessment of *in vitro* human cell lines, representing the most abundant cell types at the purported site of sensitiser exposure *in vivo*, is a logical starting point for more complex cellular assays. To this end, dose concentrations of skin and respiratory sensitiser chemicals must be determined which are sub-cytotoxic. Ideally the selected dose should remain as concentrated as possible to elicit maximum cellular response for investigation in later proteomics analyses. The selected dose concentration should also still demonstrate maximal nucleophile reactivity, especially where a cytotoxic concentration cannot be observed. Therefore,

peptide reactivity has also been investigated in the context of a cell medium reaction environment here.

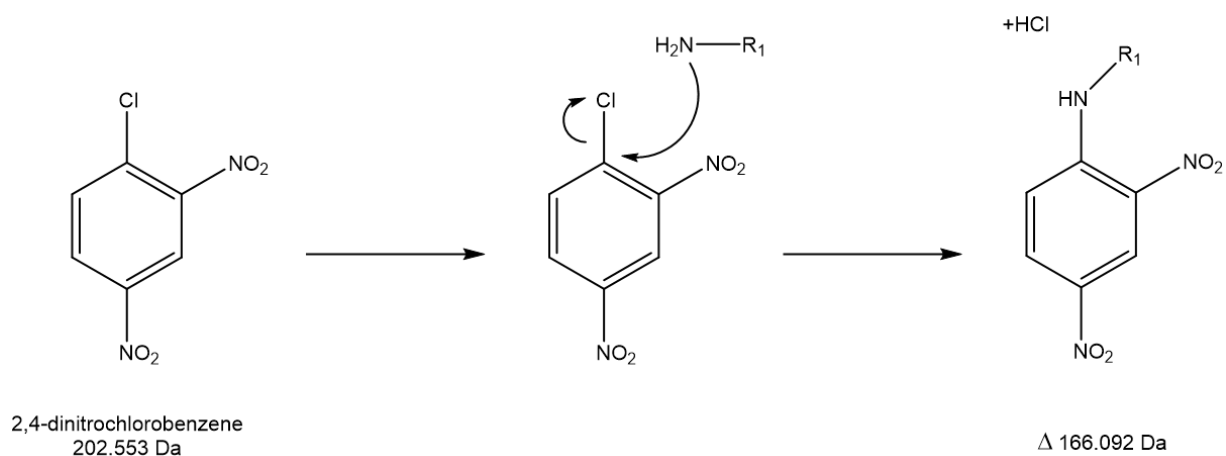


Figure 3.1: 2,4-dinitrochlorobenzene reaction chemistry. Nucleophilic substitution reaction to form a single adduct

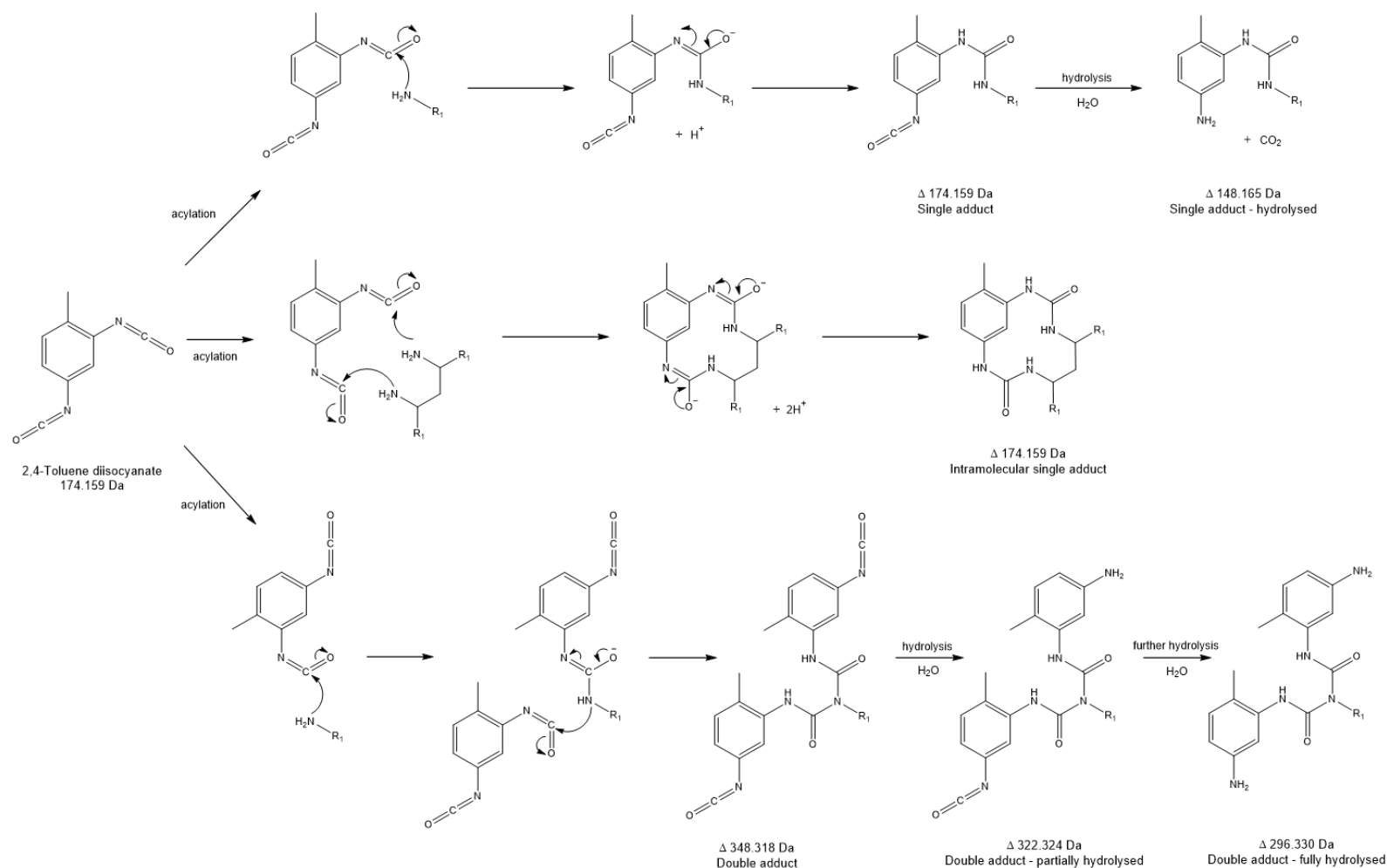


Figure 3.2: 2,4-Toluene diisocyanate theoretical reaction chemistry. Acylation reaction forming a single hydrolysed adduct. Also demonstrated are proposed mechanisms by which intramolecular single adducts may form, as well as incompletely hydrolysed single and double adducts.

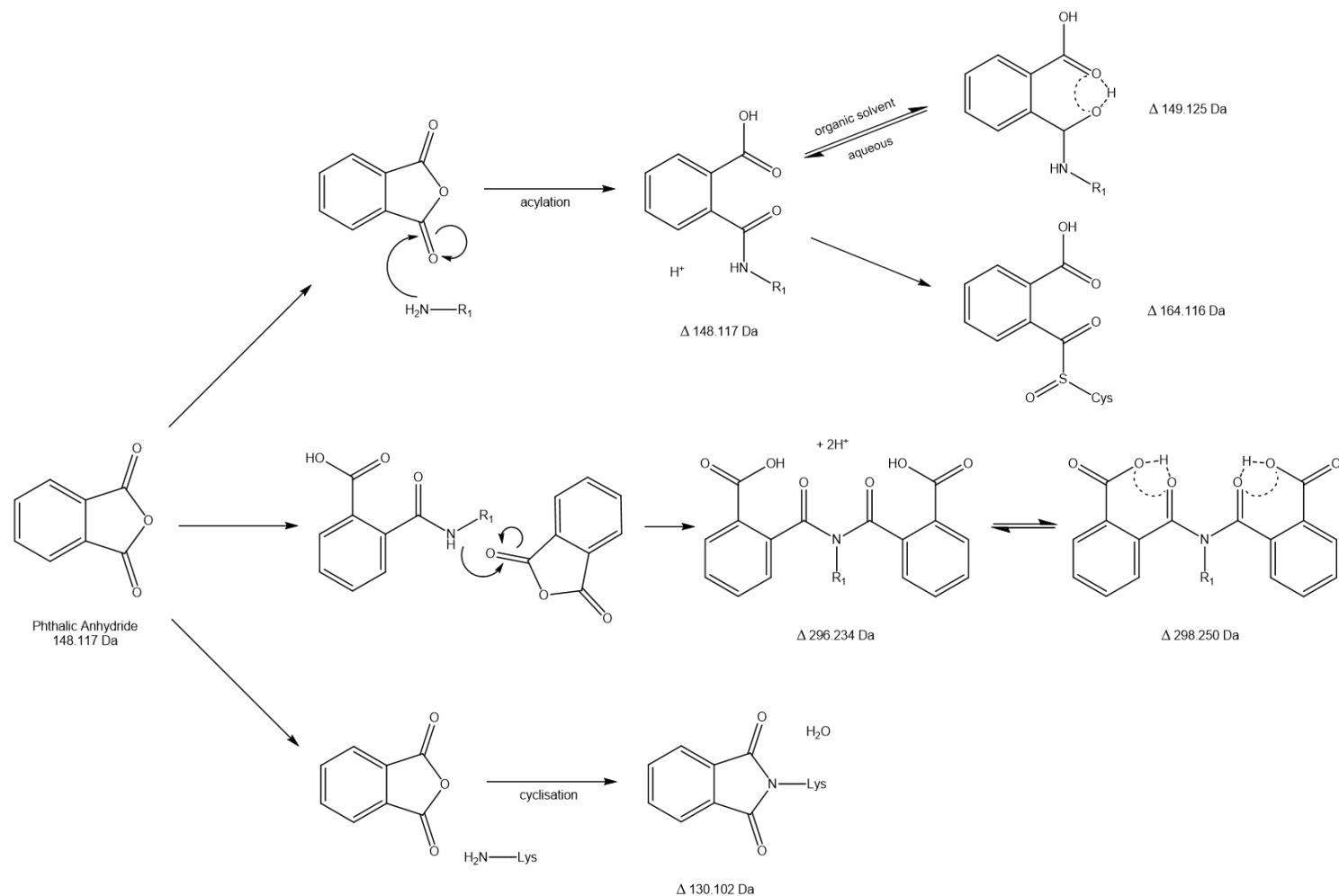


Figure 3.3: Phthalic anhydride theoretical reaction chemistry. Acylation adduct formation, with proposed mechanisms for undergoing oxidation (with cysteine) or forming tautomeric structures. Also demonstrated is a cyclisation reaction to produce an imide-like adduct by loss of water.

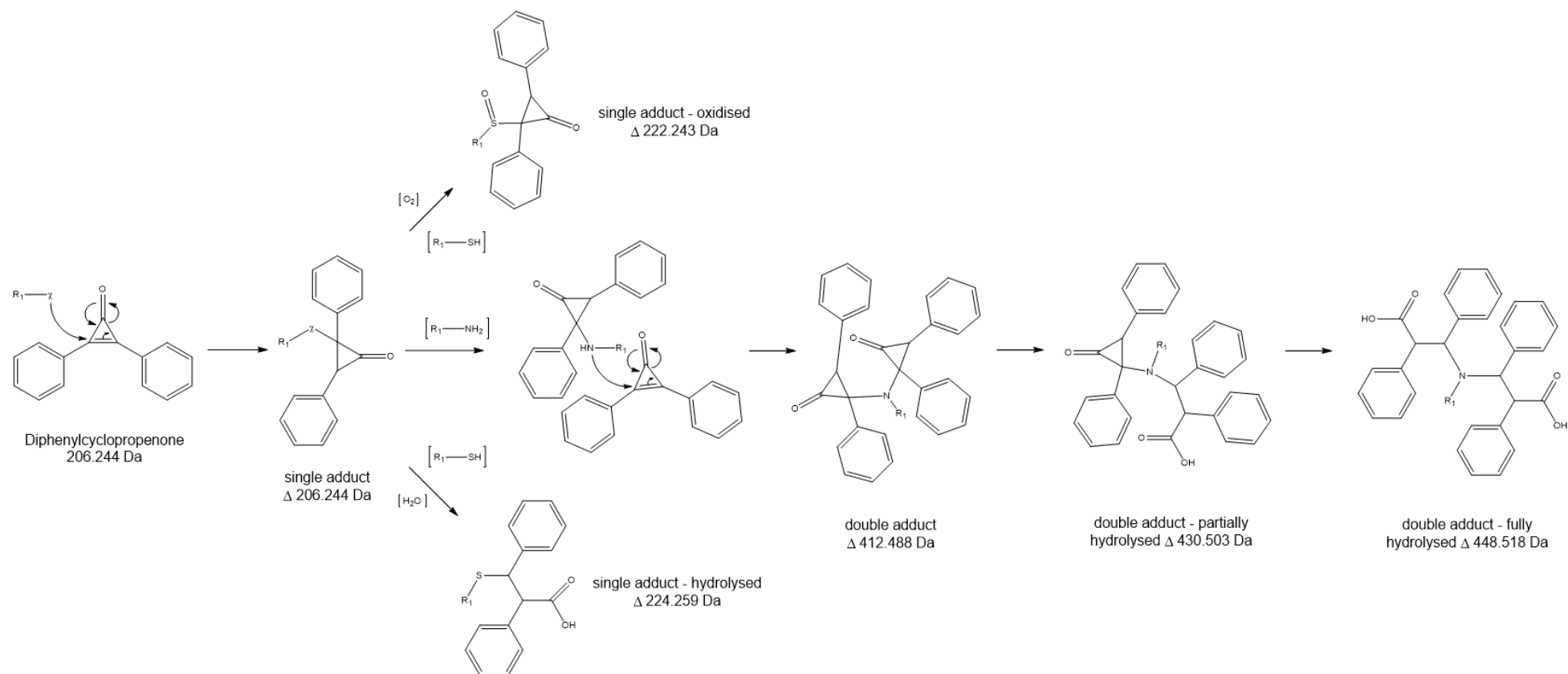


Figure 3.4: Diphenylcyclopropanone theoretical reaction chemistry. Michael addition to form single adduct, followed by further proposed reactions for production of a number of different adducts.

3.2 Methods

3.2.1 Materials & reagents

The following chemical sensitisers were purchased from Sigma-Aldrich (purities included); 2,4-dinitrochlorobenzene (DNCB, >99%), diphenylcyclopropenone (DPCP, 98%), phthalic anhydride (PA, >99%), and 2,4-toluene diisocyanates (TDI, >98%). The following chemicals were also purchased from Sigma-Aldrich; dimethyl sulfoxide (DMSO), potassium phosphate monobasic (KH_2PO_4 , >99%), potassium phosphate dibasic (K_2HPO_4 , >98%), potassium carbonate (K_2CO_3 , >99%), potassium hydrogencarbonate (KHCO_3 , >99.5%). 50mM pH 7.4 phosphate buffer was prepared with potassium phosphate monobasic and potassium phosphate dibasic. 50mM pH10 carbonate buffer was also prepared with potassium carbonate and potassium hydrogencarbonate. Dulbecco's modified Eagle medium/Ham's nutrient mixture F12 (L-glutamine, HEPES, no phenol red) and penicillin-streptomycin (100X) were purchased from Fisher Scientific.

Synthetic peptides with N-terminal acetylation were prepared by Cambridge Research Biochemicals, purified to >90% by HPLC with molecular weight confirmation conducted by flow injection mass spectrometry with electrospray ionisation (positive mode), performed by the Unilever PLC supervisory team. All peptides were of the generic structure (Ac)FAAnAA, where the *n* group represents a single nucleophilic amino acid residue of; cysteine (594 g/mol), lysine (619 g/mol), histidine (628 g/mol), arginine (647 g/mol), or tyrosine (654 g/mol). All solutions were used within 1 week of preparation. Peptide stock solutions were prepared from lyophilised powder to a final concentration of 2mM in 18.2MΩ ultrapure water (MilliQ), with (Ac)FAACAA being prepared in 50mM pH7.4 phosphate buffer to aid stability in dissolution. Test chemical stock solutions were prepared at 100mM in DMSO, with additional stock solutions being prepared at 3M DNCB, 1M DPCP, 2M PA, and 3M TDI – deemed to be maximum solubilities in DMSO, with the exception of TDI which was instead limited by relative cost.

Cell culture reagents were purchased from Fisher Scientific; Dulbecco's phosphate-buffered saline (DPBS), Dulbecco's modified Eagle medium (DMEM), Corning foetal bovine serum supplement (FBS, 10X), penicillin-streptomycin (P/S, 100X), Dulbecco's modified Eagle medium/Ham's nutrient mixture F12 (DMEM/F12, with L-glutamine, HEPES, no phenol red), trypsin-EDTA dissociation reagent (0.25%). CellTiter96® AQueous non-radioactive cell proliferation assay kits and CytoTox96® non-radioactive cytotoxicity assay kits were purchased from Promega.

3.2.2 Cell culture and cryogenic storage of cell lines

Establishment of cell lines in culture was achieved using Dulbecco's modified Eagle medium (DMEM) supplemented with 10% foetal bovine serum (FBS) and 1% penicillin-streptomycin (P/S), warmed in a water bath set to 37°C and applying 10mL to sterile 15mL tubes. Cryovial suspensions of approximately 1×10^6 cells were diluted with 1mL of DMEM and extracted to the remaining DMEM in the 15mL tubes. The 10mL cell suspensions were centrifuged at 300 xg for 5 minutes at room temperature. The supernatants was aspirated to remove DMSO cryoprotectant. The cells were then re-suspended in 10mL DMEM and transferred to 25cm² cell culture flasks (Corning) and incubated at 37°C/5% CO₂ until reaching confluence. Cells were passaged and re-seeded, according to the following methods, in 75cm² and 175cm² (both Corning) progressively as cultures were expanded.

Human HaCaT keratinocyte cell line, A549 alveolar epithelial cell line and 16HBE14o⁻ bronchial epithelial cells were regularly maintained, using aseptic technique, in Dulbecco's modified Eagle media (DMEM) supplemented with 10% foetal bovine serum (FBS) and 1% Pen-Strep and passaged after reaching approximately 75% confluence. Cells were washed with Dulbecco's phosphate buffered saline (DPBS) several times before being incubated at 37°C/5% CO₂ with 0.25% trypsin-EDTA solution for up to 10 minutes to achieve cell detachment. Detached cells were suspended in DMEM and centrifuged at 300xg for 5 minutes. Supernatants were aspirated and the cell pellets re-suspended in DMEM before performing cell counts via trypan blue exclusion or seeding new culture surfaces.

Trypan blue exclusion cell counts were achieved by combining aliquots of cell suspensions 1:1 with trypan blue stain (Corning) before applying 10µL to the chamber of a Neubauer hemocytometer (Marienfield). Inverted light microscopy was used to count cells in the 1mm² sections of the brightline grid, with the average number of cells being recorded. The number of cells in suspension was calculated as the average cell count multiplied by 2 (dilution factor) and 10⁴ (chamber volume).

Cryogenic storage of cell lines was achieved by re-suspending cell pellets from passage/counting methods in freeze medium (40% DMEM, 50% FBS, 10% DMSO cryoprotectant). Aliquots of cell suspension (approximately 1×10^6 cells) were then applied to individual cryogenic storage vials (Corning) with 1mL/cryovial. The vials were stored in a cryo-container (Corning) at -80°C overnight before being transferred to liquid nitrogen storage long-term.

3.2.3 Functional Peptide Reactivity Assay

Initially a peptide reactivity assay was conducted with methods adapted from Gerberick *et al*⁵ and Aleksic *et al*^{6,26}. Peptide reaction samples were prepared with 2mM peptide stock solution and 100mM test chemical, then made up to 250µL with pH10 buffer for K/R/Y peptides and pH7.4 buffer for C/H peptides to generate a 10:1 sensitizer-to-peptide molar ratio. A sample of equal composition was also prepared, replacing test chemical with DMSO vehicle as a control. Sample tubes were then sealed, vortexed, and incubated at 37°C for 24 hours. Following incubation, technical sample replicates were analysed by LC-MS.

3.2.4 Adjusted peptide reactivity assay

Sample groups of (Ac)FAACAA and (Ac)FAAKAA peptides were prepared in either 50mM pH7.4 phosphate buffer or serum-free DMEM-F12 cell culture medium (+ 1% penicillin-streptomycin) and diluted to 0.2mM. A concentration dilution series was prepared, followed by 1:1000 dilution with respective peptide buffers. Peptide (0.2mM), buffer and test chemical were combined in sample tubes, maintaining a constant peptide concentration of 8µM in each sample. Additional samples of equal composition were prepared as controls, replacing test chemical with sensitizer vehicle control (DMSO) at a final concentration of 0.1%. Sample tubes were then sealed, vortexed, and incubated at 37°C for 24 hours. Following incubation, samples were analysed by HDMS^E LC-MS analysis (3.2.4).

Further to the above, samples of the same composition were acidified post-incubation by addition of TFA to a final concentration of 0.4%, vortexed, and centrifuged at 14,000 xg on a benchtop microcentrifuge for 10 minutes at room temperature. Sample supernatants were applied to a conditioned (acetonitrile) and equilibrated (0.1% TFA in dH₂O) reverse-phase C18 micro-elution plate (Oasis HLBPrime) in a vacuum manifold and de-salted. Peptide samples were eluted with 70% acetonitrile and transferred to lo-bind tubes, and lyophilised *in vacuo*. Dried peptides were re-suspended in buffer A (0.1% formic acid (v/v) 18.2MΩ H₂O) prior to LC-MS analysis by selected ion recording (SIR) reaction monitoring (3.2.6).

3.2.5 HDMS^E LC-MS analysis

Following incubation, 2µg of sample peptide was loaded onto a C18 reverse-phase column (Waters) for nano-LC separation by a NanoAcquity UPLC system (Waters). Samples were firstly loaded onto the reverse-phase trap column at a trapping rate of 5µL/min and washed for 3min with buffer A (0.1% formic acid (v/v) 18.2MΩ H₂O). Following elution, peptides were separated by

the analytical flow column at a flow rate of 0.3 $\mu\text{L}/\text{min}$ using a linear gradient of 3-85% organic phase (buffer B; 0.1% formic acid/acetonitrile) over 55 minutes.

LC-MS analysis of peptide samples was performed via injection into a Waters Synapt G2Si instrument operating in high resolution mode using positive-mode electrospray ionisation. Data was acquired using MassLynx software (Waters) over a mass range of 80-2000 m/z , alternating between low energy (4V) and elevated energy (45V-60V) scanning. Ion mobility separation was achieved at a pulse height of 2 and 650 m/s wave velocity. LockMass correction was performed using [Glu1]-fibrinopeptide B ($[M+2H]^{2+}$, m/z 785) at a concentration of 100 fmol/ μL and rate of 0.25 $\mu\text{L}/\text{min}$. LockMass was sampled every 60 seconds for mass correction.

3.2.6 Selected Ion Recording (SIR) reaction monitoring LC-MS analysis

Dried peptide samples were reconstituted in buffer A (3% acetonitrile in 18.2M H_2O (v/v) 0.1% formic acid) and 1 μg peptide loaded onto a C18 reverse-phase column for nano-LC separation at a flow rate of 0.6 mL/min using a gradient of 5-85% organic phase (buffer B; 0.1% formic acid/acetonitrile) over 8 minutes. LC-MS analysis was performed via injection into a Waters Xevo QToF quadrupole instrument (Waters) using positive mode electrospray ionisation programmed using MassLynx software (Waters). Data was acquired over a 5 minute retention window with a cone voltage of 35V and minimum sample dwell time of 0.018s. Selected Ion recording was programmed for specific single-type adduct m/z (Table 3.1).

3.2.7 Cell culture sample preparation

Samples for optimisation of cell seeding density were prepared under aseptic conditions through serial dilutions of 3.2×10^5 cells in suspension in complete DMEM (supplemented with 10% FBS and 1% P/S) and applied to two 96-well culture-treated microplates per cell line over a gradient of $1 \times 10^6 - 1.95 \times 10^3$ cells/ cm^2 (three for 16HBE14o⁻), with 8 replicates per density. The upper gradient range was later extended to 8.0×10^6 cells per cm^2 for further assessment of 16HBE14o⁻ maximum density (available in supplementary data). The microplates containing 100 μL of cell suspension were incubated in a humidified environment at 37°C/5% CO_2 for 24 hours. After 24 hours, one sample plate per cell line was removed from incubation for analysis of cell proliferation. The DMEM supernatant was aspirated from the other sample plate for each cell line and washed three times with DPBS before replacing the DPBS with serum-free DMEM/F12 (1% P/S, 0.1% DMSO) and incubating for a further 24 hours. Following 24h incubation in serum-free culture medium, the sample plates were removed from incubation for analysis of cell

proliferation. A third sample plate of 16HBE14o⁻ was allowed to remain in incubation with complete DMEM for a further 24 hours (48h total) before also being removed for analysis.

Samples were prepared for exposure to a range of sensitizer concentrations by seeding cells in culture-treated 96-well microplates at the previously determined optimum density for each cell line to reach approximately 75% confluence after a 24-hour incubation period: approximately 6.0×10^5 cells/cm² for HaCaT, 3.0×10^5 cells/cm² for A549, and approximately 9.0×10^5 cells/cm² for 16HBE14o⁻. Cell-free control samples were prepared as 8 replicates without any cells to serve as a negative control for determine cell culture medium background contribution in data analysis. Vehicle-only cell controls were prepared in triplicate with cells at 0.1% DMSO vehicle, serving as a maximum proliferation control. Maximum LDH release control samples were prepared in triplicate with cells for lysis prior to the cytotoxicity assays, serving as a maximum cytotoxicity control. The microplates containing 100μL of cell suspension in DMEM (supplemented with 10% FBS and 1% P/S) were incubated in a humidified environment at 37°C/5% CO₂ for 24 hours.

Sensitizer chemical stock solutions were prepared in sterile-filtered DMSO at 3M DNCB, 1M DPCP, 2M PA, and 3M TDI – deemed to be maximum solubilities in DMSO, except for TDI which was instead limited by relative cost. A serial dilution was performed with each sensitizer chemical in pure DMSO to generate the concentration gradient for analysis, which was subsequently diluted to 0.1% with serum-free DMEM/F12 (supplemented with 1% P/S) immediately prior to cell culture exposure. Following 24-hour incubation, complete DMEM supernatants were aspirated from the sample plates before washing samples three times with DPBS. The DPBS was then aspirated from each well and replaced with the DMEM/F12 carrying different concentrations of sensitizer chemicals in triplicate. The cell samples were then re-covered and returned to the incubator for another 24h incubation period prior to analysis of cell proliferation and cytotoxicity.

3.2.8 Cell proliferation and cytotoxicity assays

Following the incubation period, the cell density-gradient sample microplates were assessed for appropriate confluence via inverted light microscopy. For the sensitizer-treated samples, the microplates were transferred to a fume hood in a sealed container where the lids were briefly removed to safely disperse any vapour that may have been produced during incubation. The lids were then replaced and sealed prior to inverted light microscopy assessing the presence of free nuclei in the samples as a representation of differing cytotoxicity. The microplates were then returned to the fume hood in sealed containers and 10X lysis solution (9% (v/v) Triton® x-100) added to the maximum LDH release control wells at least 45 minutes prior to cytotoxicity analysis.

The CellTiter96® AQueous non-radioactive cell proliferation assay was performed according to the manufacturer recommendations. Cell culture supernatants were removed from the sample plates and either transferred to a fresh 96-well plate for subsequent cytotoxicity analysis (sensitiser-treated samples) or discarded (cell density optimisation samples). The cells were then washed in the sample plates with DPBS three times prior before replacing with 100µL of DMEM/F12 (1% P/S, 0.1% DMSO). Tetrazolium salt (MTS) and phenazine methosulfate (PMS) reagents were thawed and combined in a 20:1 ratio immediately prior to the addition of 20µL MTS/PMS solution to each well of the sample plates at final concentrations of 333µg/mL MTS and 25µM PMS. The plates were then incubated at 37°C/5% CO₂ for 3 hours before measurement of raw end-point absorbance at 490nm with an ELISA plate reader.

The CytoTox96® non-radioactive cytotoxicity assay was also performed for sensitiser-treated samples according to manufacturer recommendations. Aliquots (50µL) of sample cell culture supernatants extracted prior to CellTiter96® analysis were transferred to fresh 96-well flat bottom microplates, whilst original supernatant sample plates were sealed and stored at -20°C. The new supernatant sample plates were then combined 1:1 with CytoTox96® reagent and incubated at room temperature and protected from light. After 30 minutes of incubation, 50µL of stop solution (1M acetic acid) was added to each well. The microplates were then inserted into an ELISA plate reader and raw end-point absorbance recorded at 490nm within 1 hour of applying the stop solution.

3.2.9 Data Analysis – Cell Viability

Mean media background normalisation was calculated for normalising data. The mean and standard deviation was also calculated for sensitiser-treated sample absorbance data following the appropriate data transformations and formatting to generate individual datasets for each sensitiser per cell line. Mean cell proliferation was converted to a percentage of the mean normalised absorbance value of the vehicle-only samples. Normalisation, mean calculation and standard deviation were also calculated for the cytotoxicity data, with mean cytotoxicity for each sensitiser concentration being converted to a percentage of the mean normalised absorbance value of the maximum LDH release samples. Percentage proliferation and cytotoxicity were then plotted and visualised together against sensitiser concentration. All data analyses here were performed with Microsoft Office tools (Microsoft Corporation) and Rstudio packages (RStudio Team 2020).

3.2.10 Data analysis – Peptide Reactivity

Unmodified (control) peptide retention times were identified in ion chromatograms and confirmed with spectral peaks corresponding to the unmodified peptide mass-to-charge ratios. Comparison of chromatograms and associated spectra between control and treated samples allowed identification of new adducts, with structures and mass differences interpreted from theoretical hapteneation reaction mechanism products (Figures 3.1-3.4). Relative ion intensities for adduct peaks were recorded for each sensitizer concentration studied for relative comparison of adduct formation in samples of the same chemical species. All HDMS^E data were acquired and processed using MassLynx software (Waters) and calibrated with enolase solution (Waters) and monitored/corrected by intermittent injection of [Glu1]-fibrinopeptide B ($[M+2H]^{2+}$, m/z 785) and leucine-enkephalin ($[M+H]^+$, m/z 556) lock mass. Blank samples between analytical runs were visually checked to ensure the exclusion of confounding spectral peaks between samples.

3.3 Results

3.3.1 Functional peptide reactivity assay allows confirmation of adduct formation and qualitative selectivity under different reaction conditions

To further the understanding of the selective reactivity of these skin and respiratory sensitiser chemicals (Table 3.1) in *in vitro* reaction environments, the methods of Aleksic *et al*⁶ were adapted here. Qualitative LC-MS assessment of adduct formation with single nucleophile containing peptides (Cys, Lys, His, Arg, or Tyr) was observed following sensitiser exposure. Identified adducts were attributed to one or more of the proposed chemical reaction mechanisms for each sensitiser chemical (Figures 3.1-3.4). Further optimisation followed, in which reactivity was examined under different reaction conditions.

For the majority of samples, formation of the predominant single peptide adduct was generated by each sensitiser chemical with both cysteine- and lysine-containing peptides was clearly evident (Figures 3.5 & 3.6) – whether present or absent – with no observed change in pH. Adduct formation for arginine, histidine and tyrosine were less obvious (data not shown), requiring close manual inspection of the spectra. All untreated and peptide adduct ion peaks appear as singly-charged species, hence each appears at a mass-to-charge ratio (m/z) equal to the species molecular mass $[M+H]^+$. Respiratory sensitiser chemicals showed a greater ion intensity in the MS spectra with lysine-containing peptide compared to modification of cysteine-containing peptides. Indeed, PA and TDI showed non-detectable intensity at the single adduct m/z for cysteine-containing peptide (743 m/z). Observations during experiment optimisation suggested that the proposed tautomeric structure of phthalic anhydride (Figure 3.3) may depend on the proportion of organic solvent, i.e. more frequently observed in less aqueous conditions. The hydrolysed TDI adduct (Δ 148 m/z) was the most frequently observed adduct across all the samples, with no other TDI single adducts being observed. Logically, any double adduct formation with TDI would therefore be comprised of two hydrolysed TDI molecules on the same amino acid residue. This is evident from the peak at 916 m/z with no peaks observed at the m/z for other TDI double adducts (Table 3.1).

A doubly-charged species $[M+2H]^{2+}$ was observed at 594 m/z in the (Ac)FAACAA peptide samples alongside the singly-charged species ($[M+H]^+$, 595 m/z), consistently at the greatest relative ion intensity. Being doubly-charged, this likely represents the formation of a disulphide bridge between the cysteine residue on two individual (Ac)FAACAA peptides. This structural formation likely obscures the reduced cysteine sulfhydryl group from hapteneation. Despite this observation,

cysteine modification was evident with the highly cysteine-reactive DNCB and DPCP chemicals. Interestingly, DPCP showed the lowest peptide adduct ion intensity of all the sensitiser chemicals, despite being classified as the most potent sensitiser based on EC3 in the local lymph node assay (Table 3.1). However, this observation remains purely qualitative as quantitative comparison of ion intensities of different peptide adduct species remains challenging here due to different ionisation efficiencies between the individual chemical species.

The majority of peptide reactivity methods to this point have not included a method of removing the free sensitiser chemical following the 24h incubation (37°C) exposure period. Such methods appear more focused on end-point unmodified peptide depletion. This was believed to result in increasing length of incubation time with free reactants in the MS auto-sampler between the first and last sample prior to analysis injection. For this reason, reverse-phase C18 peptide purification process was incorporated to remove free reactants whilst simultaneously purifying the peptides prior to comparison of the resulting ion chromatograms and MS spectra (Figure 3.7).

3.3.2 Optimisation of the adjusted peptide reactivity assay for analysis of adduct formation at a range of sensitiser concentrations by Selected Ion Recording (SIR) LC-MS

Further to the functional peptide reactivity methods outlined previously, reverse-phase peptide purification was incorporated to remove free reactants and purify the peptides prior to analysis. A targeted approach using Selective Ion Recording (SIR) was developed and employed to improve sensitivity and increase throughput, using a Waters Xevo triple quadrupole mass spectrometer with an on-line LC system. Data generated by the HDMS^E experiments (3.3.1) provided the required information (e.g. specific m/z of adduct ions) to optimise the SIR method. The elution gradient was optimised and adapted, reducing analysis time by 10x (10 min) compared to the previously used HDMS^E methods.

Following initial analysis of 1µg (approximately 2 nanomoles) untreated control peptide samples, substantial differences in ion intensity between the cysteine and lysine containing peptides were observed. To further characterise this difference, a 10-fold serial dilution of each untreated control peptide was performed in either 50mM phosphate buffer or serum-free DMEM/F12 culture medium (0.1% penicillin-streptomycin). Samples were analysed using the SIR method previously described to determine the optimum peptide quantity for sample loading (Figure 3.8). The un-diluted lysine containing peptide sample was omitted to avoid overloading the LC column.

The unmodified cysteine containing peptide (595 m/z) was not observed in either buffer at less than 0.2 nanomoles (10x dilution), whereas the lysine containing peptide (620 m/z) at 2×10^{-3}

nanomoles was readily detected. The results of this dilution series demonstrate a difference in ionisation efficiency rather than a difference in sample peptide concentration. As such, the Base Peak Intensity (BPI) between cysteine and lysine containing peptides are not directly comparable without a shared internal reference peptide. However, quantitative comparisons across the dilution series for the same peptides were performed with the optimum concentration of peptide determined to be 0.2 nanomoles (10x sample dilution) for both (Ac)FAAKAA and (Ac)FAACAA peptides.

The SIR methods here have not yet been adapted to target the doubly-charged species identified in the HDMS^E experiments, the oxidised dimer of (Ac)FAACAA ($[M+H]^+$, 1189 *m/z*; $[M+2H]^{2+}$, 594 *m/z*), in addition to the reduced cysteine (Ac)FAACAA ($[M+H]^+$, 595 *m/z*). Cysteine haptentation is believed to occur only with reduced cysteine amino acid residues, therefore preventing peptide dimerisation. Without free sensitizer chemicals available to haptentate the cysteine containing peptide in control samples, the oxidised dimer would hypothetically be the predominant species observed relative to the singly-charged reduced species. The sensitivity and mass error tolerance of the current SIR methods do not directly distinguish between the two cysteine-containing peptide species at 595 *m/z*. However, the two species can be differentiated by their distinct peak retentions in the ion chromatograms (data not shown).

3.3.3 SIR analysis of adduct formation over a range of sensitizer concentrations reveals points of maximum reactivity

The highest sensitizer concentration at which the maximum adduct ion intensity is achieved when monitored by LC-MS analysis (without unmodified peptide nucleophile depletion) was investigated in both optimum (phosphate buffer) and cell culture (serum-free cell culture medium) reaction conditions. Due to differences in ionisation efficiencies of different chemical species, comparison of the ion intensities/counts at specific concentrations between the different sensitizer-peptide samples is not relevant. However, they do allow quantitative comparison of the reactivity profile trends of the same peptide adduct across the different sensitizer concentrations. It has been noted previously that haptentated adduct peaks are generally observed at a lower ion intensity than unmodified peptide peaks⁸. Therefore this was expected to be observed here as well, particularly where the single polar residue of the model peptides has been covalently modified with a relatively non-polar hapten.

Unmodified peptide depletion was generally observed for (Ac)FAACAA at increasing concentrations of DNCB/DPCP but not with PA/TDI. Additionally, (Ac)FAAKAA unmodified peptide depletion was generally not evident at all, except to a limited extent with the highest

concentrations of PA. PA demonstrated a linear relationship between sensitiser concentration up to 1280 μ M (Figure 3.10) and the (Ac)FAAKAA Δ 148 m/z adduct.

Maximum adduct formation was generally observed in the phosphate buffer reaction environment for each sensitiser single adduct with the purported favoured amino acid (Figure 3.10): DNCB-Cysteine, DPCP-Cysteine, PA-Lysine, TDI-Lysine. Furthermore, the concentration at which each sensitiser chemical reached maximum reactivity with either (Ac)FAACAA and (Ac)FAAKAA also generally reflected their respective EC₃ values (Table 3.1), suggesting a reactivity ranking here of: DPCP>DNCB>PA>TDI. This is also true in general for adduct formation in the cell culture medium reaction system (Figure 3.11). Though notable differences include a more prominent reaction profile for (Ac)FAACAA with PA, and a lack of any measurable (Ac)FAAKAA adduct formation with DNCB. However, it was notable that the ion counts were up to 100-fold lower in cell culture medium compared to the phosphate buffer system.

3.3.4 Optimisation of cell seeding density demonstrates sustained cell viability in serum-free cell culture medium

In order to measure changes in cell viability over a range of sensitiser exposure concentrations, the optimum cell seeding density first needed to be determined. Enzymatic conversion of MTS into soluble formazan demonstrated a maximum absorbance signal at the greatest cell densities for both A549 and 16HBE14o⁻. HaCaT cells were not assayed in this capacity as the optimum seeding densities are already well-established^{9,28,114}. Visual representation of the sigmoidal trend presented by A549 samples (Figure 3.12 A) is provided by inverted light microscopy, providing additional context for the comparison of absorbance to culture confluence.

The maximum absorbance range for A549 samples appeared to be at approximately 3.0 absorbance units (Au), suggesting 100% confluence is achieved between 2.5×10^5 and 1.25×10^5 cells/cm², which is further supported by the observed levels of cell confluence. As a result, 75% confluence is represented at 6.25×10^4 cells/cm² (2.25 Au), with the same being true following a further 24h incubation in DMEM/F12 after the initial 24h incubation in DMEM. Serum-free DMEM/F12 media resulted in an actual increase in 16HBE14o⁻ proliferation, specifically at cell densities above 1.6×10^4 and reaching approximately the same concentration of formazan as cells incubated for 24h in DMEM. Additionally, an overall lower concentration of formazan was identified for 16HBE14o⁻ than A549 (Figure 3.12). However, the maximum absorbance value obtained with an extended density gradient of 16HBE14o⁻ (Appendix Figure 1) did not increase beyond the general maximum of 2.5 Au.

3.3.5 Substantial differences revealed in cell viability following exposure to skin and respiratory sensitisers *in vitro*

Exposure of *in vitro/ex vivo* nucleophile systems to skin and respiratory sensitisers required an optimum exposure dose had to be identified; the optimum concentration would be such that no excessive proliferation or cytotoxicity was observed *in vitro*. Clear cytotoxicity profiles associated with skin sensitisers were demonstrated in HaCaT and 16HBE14o⁻ cells, though a general lack of consistent cytotoxicity profiles were generated for A549 cells (Figure 3.13). Further, the changes in proliferation profiles observed with A549 occurred at double the concentration of DNCB (20µM) compared to the same treatment in HaCaT and 16HBE14o⁻ (10µM). The decline in proliferation profile for cells treated with DPCP was also observed at a different concentration in each cell line; 5µM in HaCaT, 10µM in 16HBE14o⁻, and somewhat less reliably in A549 samples at 20µM. Interestingly, a lack of change in proliferation or cytotoxicity is displayed across all cell lines treated with the respiratory sensitisers PA and TDI. One exception was for PA in A549 cells, but this is rejected as a true positive result due to the lack of any visible change in the cells under inverted light microscopy following 24h incubation with any concentration of phthalic anhydride.

Notable inconsistencies were observed at the intercept of proliferation and cytotoxicity profiles within a number of test conditions, for example the DNCB-treated 16HBE14o⁻. Additionally, large error bars were evident for the proliferation assays including sensitiser treatments, particularly at sub-cytotoxic regions where the average percentage proliferation remained relatively constant. This may be due to degradation in the assay reagents, though re-evaluation of the analysis procedures for potential miscalculations/mis-conversions may be prudent. The optimum concentrations of the skin sensitisers DNCB and DPCP for use with *in vitro* cells are well-documented^{9,28,114}, with the results presented here generally being in good agreement. However, no optimum concentration was clear for PA or TDI due to the lack of proliferation or cytotoxicity changes

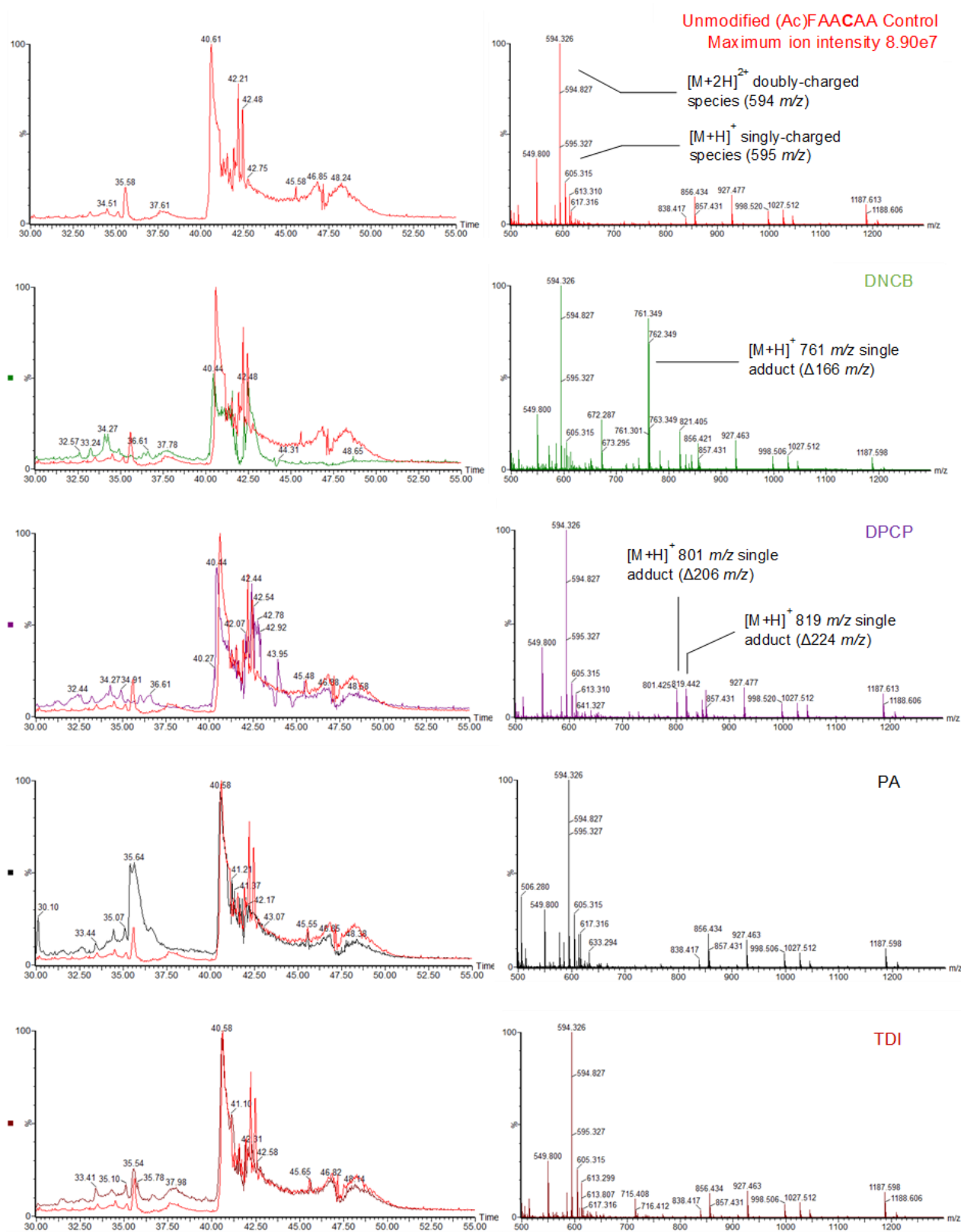


Figure 3.5 Cysteine-containing peptide (Ac)FAACAA adduct identification – LC

chromatograms demonstrating retention times for unmodified peptide related to peptide adduct elution points with each sensitizer chemical (overlaid - left). LC-MS spectra associated with each chromatogram following treatment with each sensitizer chemical (right).

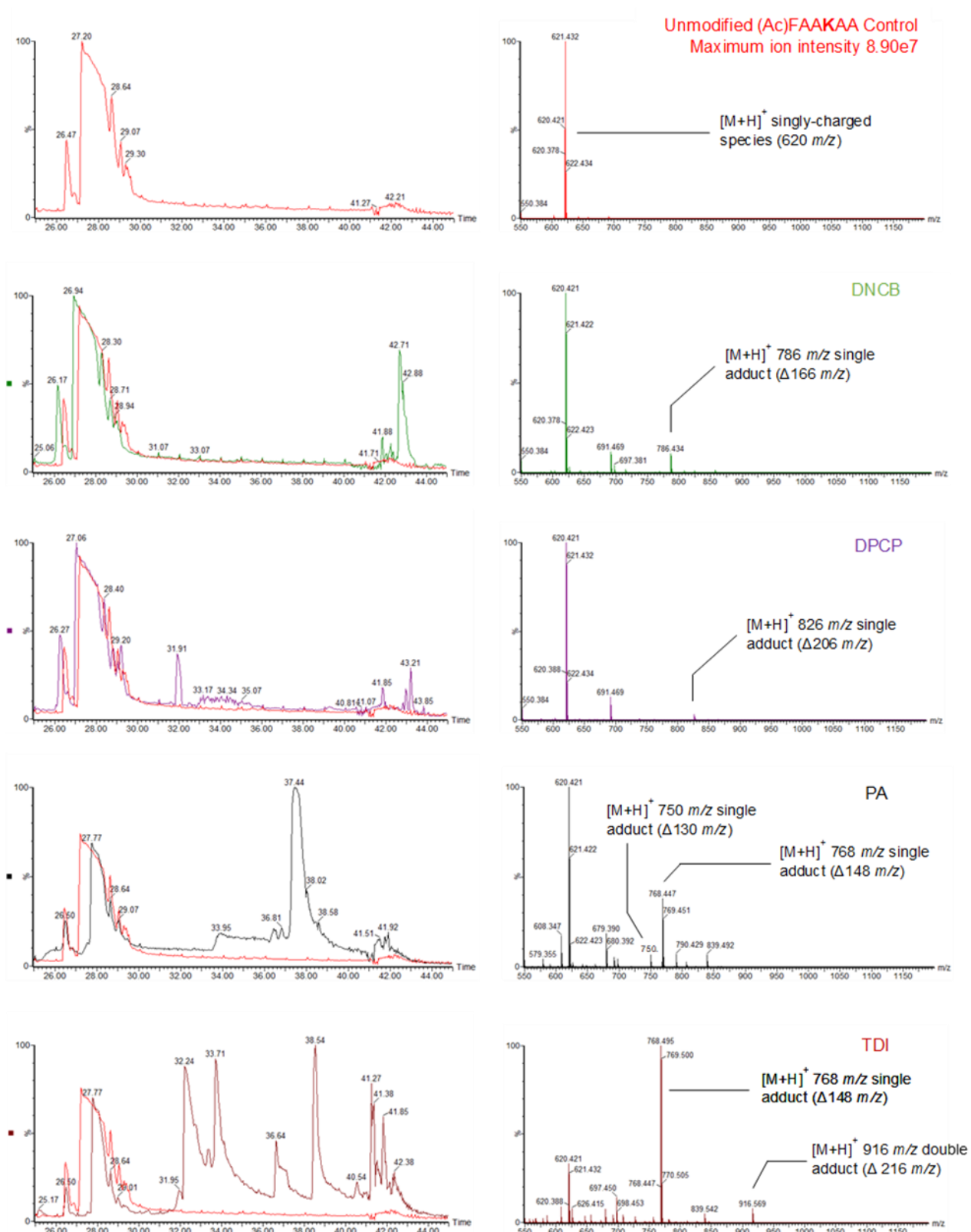


Figure 3.6: Lysine-containing peptide (Ac)FAAKAA adduct identification – LC

chromatograms demonstrating retention times for unmodified peptide related to peptide adduct elution points with each sensitizer chemical (overlaid - left). LC-MS spectra associated with each chromatogram following treatment with each sensitizer chemical (right).

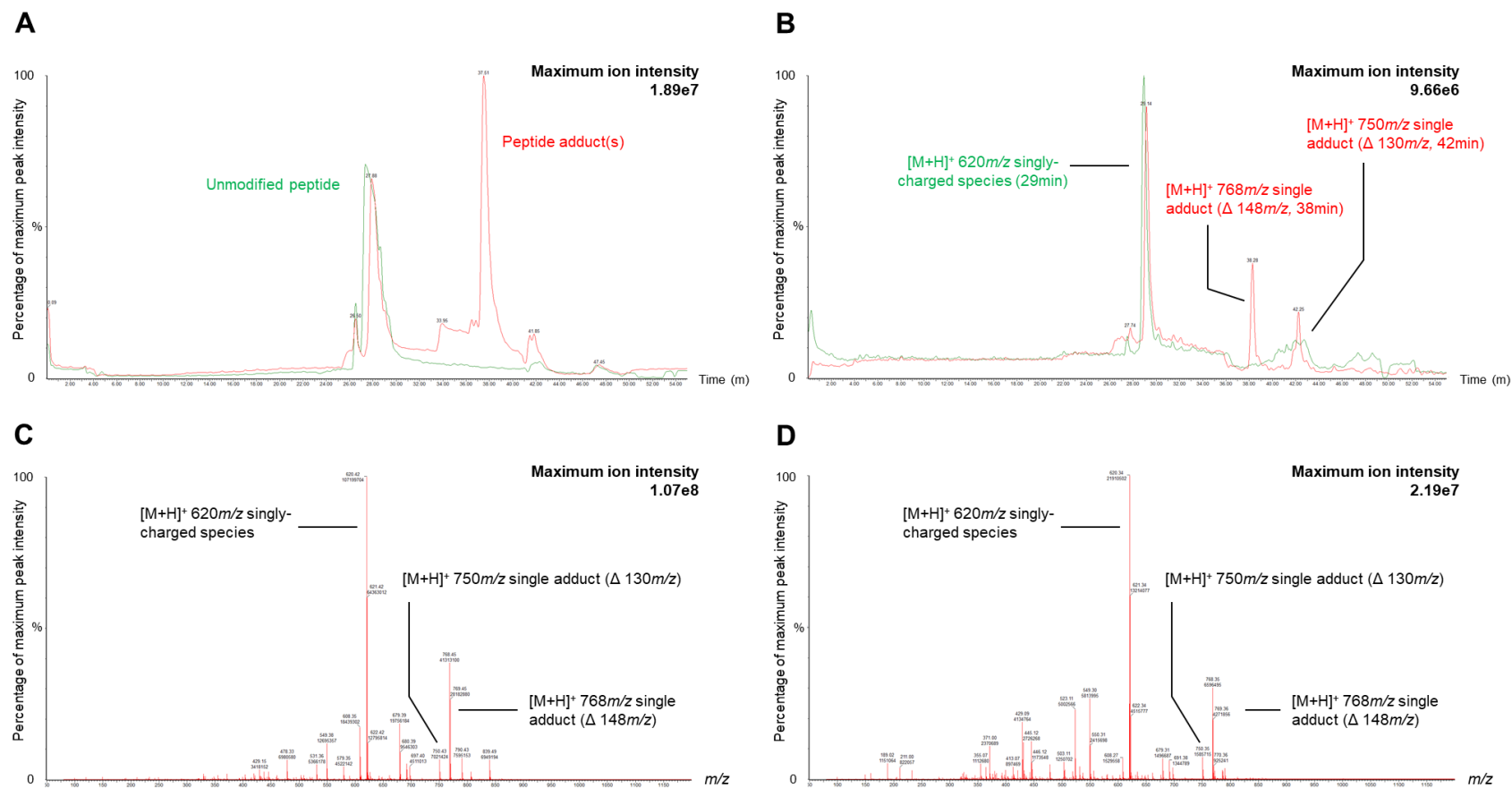


Figure 3.7: Comparison of example ion chromatograms and MS spectra generated by peptide reactivity analysis methods – Ion chromatogram retention times for unmodified (Ac)FAAKAA related to peptide adduct elution points with phthalic anhydride using HDMS^E analysis (overlaid - A) and the associated MS spectra with adduct mass shift annotations (C). Ion chromatogram retention times for unmodified (Ac)FAAKAA related to peptide adduct elution points with phthalic anhydride using adjusted methodology and HDMS^E analysis (overlaid - B) and the associated MS spectra with adduct mass shift annotations (D).

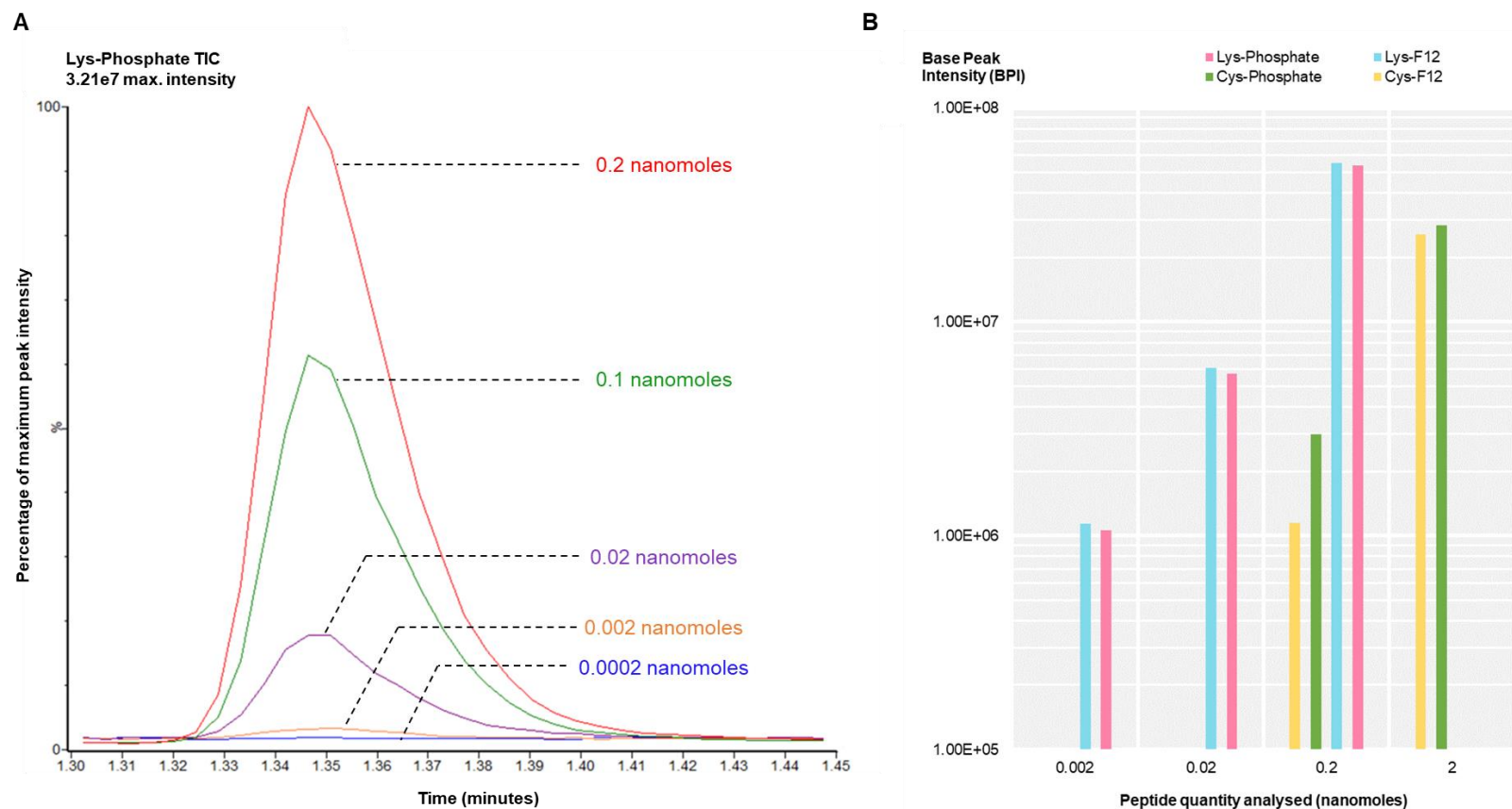


Figure 3.8: SIR LC-MS analysis optimisation – Ion chromatogram at the retention time for unmodified (Ac)FAAKAA peptide from the 50mM pH7.4 phosphate buffer reaction system at a range of loading quantities (overlaid - A). Spectral peak intensities at the mass-to-charge ratio for unmodified (Ac)FAAKAA peptide from both the phosphate buffer and cell culture medium reaction environments at a range of loading quantities (B). The 2 nanomole loading quantity has been omitted here to avoid overloading the LC column.

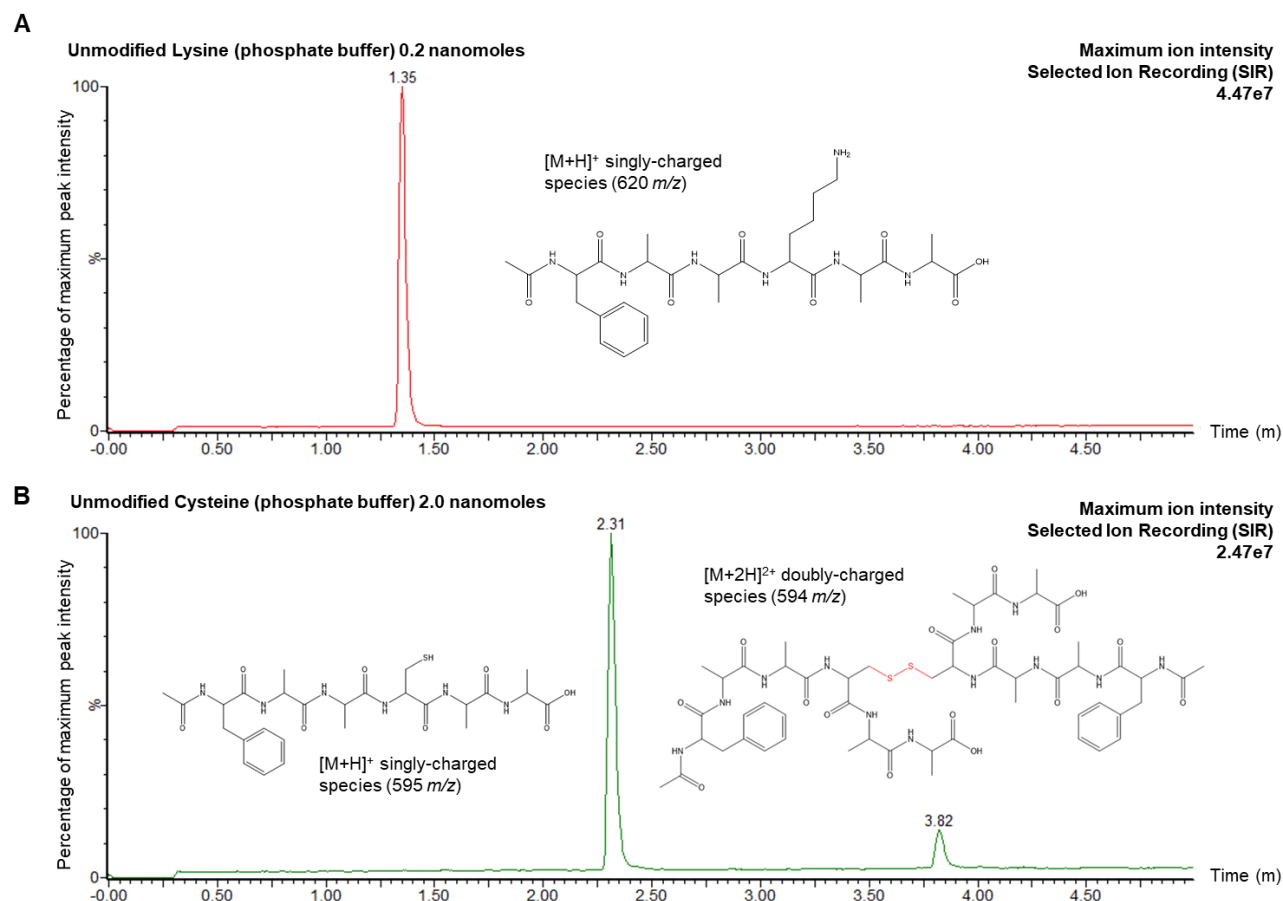


Figure 3.9: Selected ion recording BPI chromatograms for the unmodified cysteine- and lysine-containing control peptides demonstrating the respective LC elution times prior to MS injection. The singly-charged [M+H]⁺ peak at 620 m/z representing (Ac)FAAKAA is shown above (A). The cysteine-containing peptide (Ac)FAACAA spectra shows an elution peak for both a singly-charged [M+H]⁺ 595 m/z species and a doubly-charged [M+2H]²⁺ 594 m/z species (B). The distinct elution peaks reflect the alterations to the experimental design & analysis.

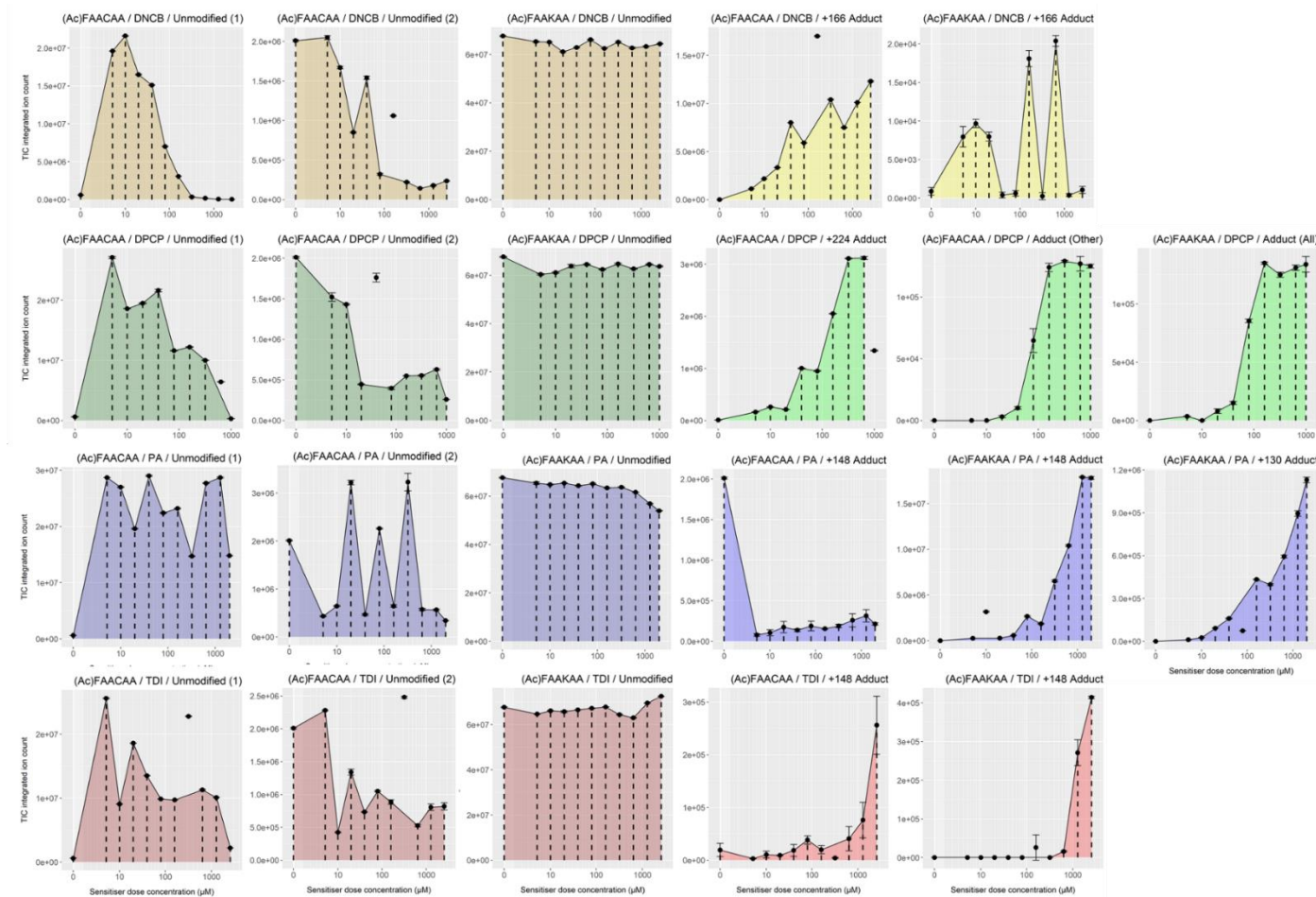


Figure 3.10: SIR integrated ion counts for both unmodified (Ac)FAACAA* and (Ac)FAAKAA and haptenated peptide-adducts at increasing concentrations of each chemical sensitizer in a phosphate buffer reaction environment. *Two profiles for each (Ac)FAACAA sample presenting the singly-charged $[M+H]^+$ species (1) and the doubly-charged $[M+2H]^{2+}$ species (2).

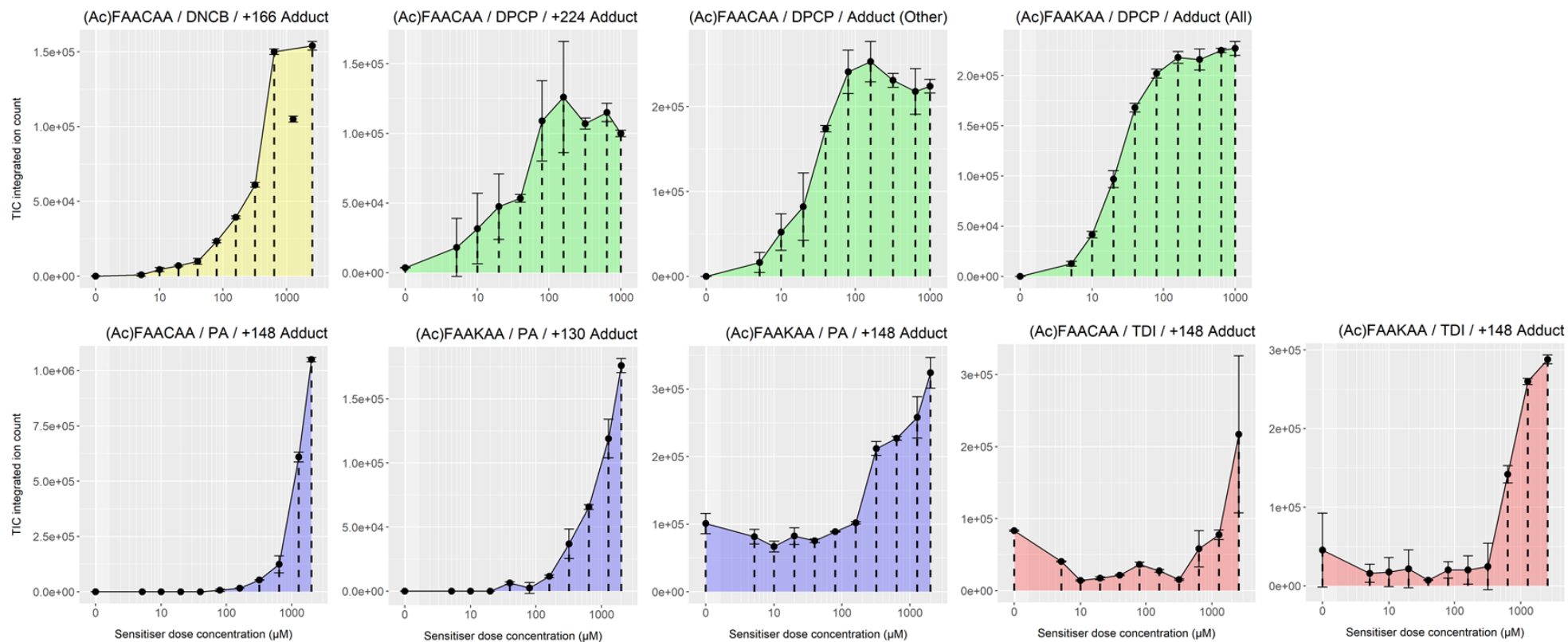


Figure 3.11: SIR integrated ion counts for (Ac)FAACAA* and (Ac)FAAKAA haptenated peptide-adducts at increasing concentrations of each chemical sensitiser in a serum-free cell culture medium reaction environment.

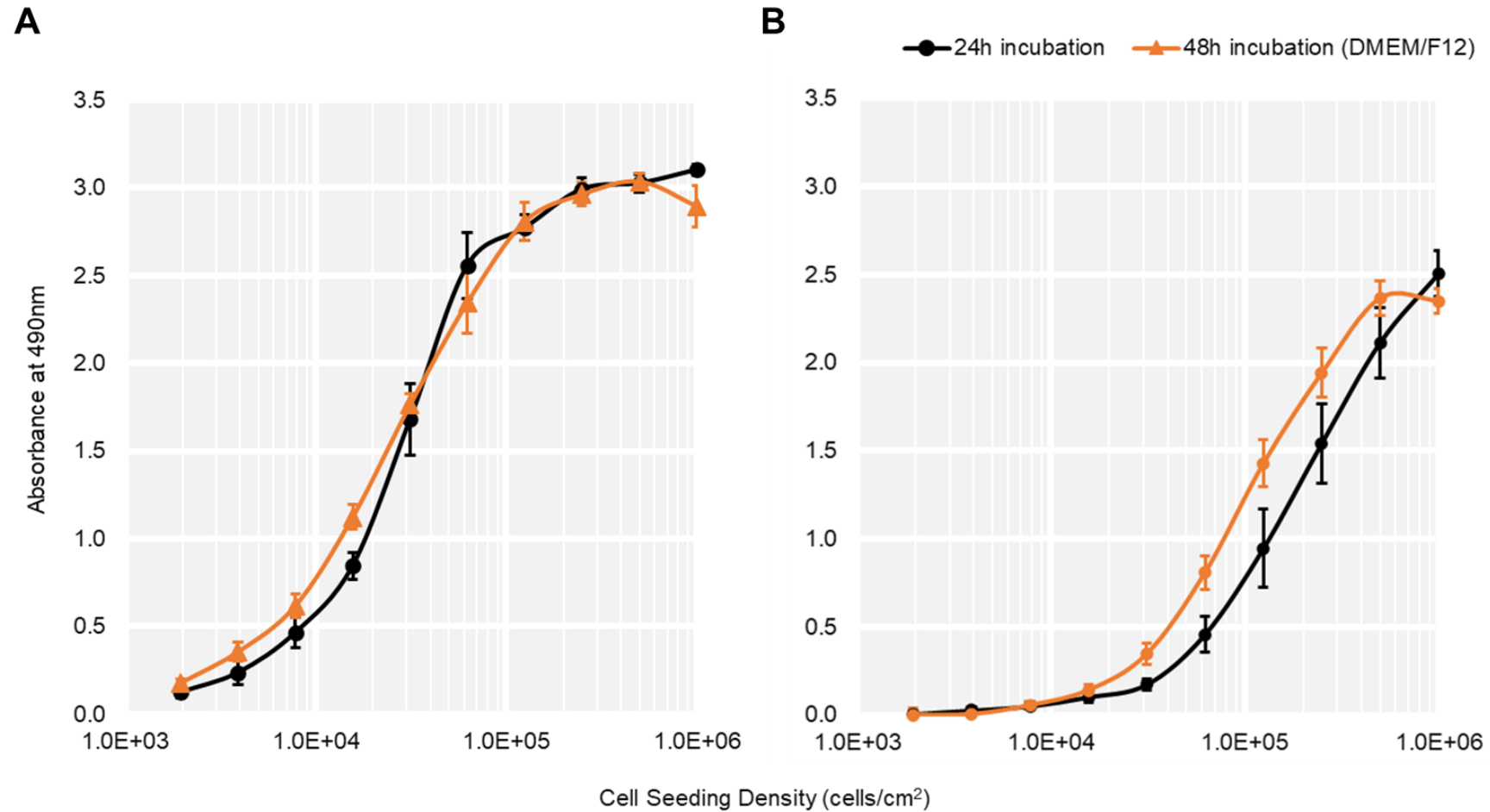


Figure 3.12: Absorbance of soluble formazan produced from MTS/PMS in both A549 (A) and 16HBE14o⁻ (B) cells – The absorbance values are demonstrated as a measure of cell proliferation over a gradient of initial seeding densities following 24h incubation in DMEM followed by a further 24h incubation in serum-free DMEM/F12.



Figure 3.13: Cell viability profiles – Changes in cell proliferation and cytotoxicity for each cell line following 24hr exposure to skin sensitisers DNCB & DPCP and respiratory sensitisers PA & TDI. Results are presented as % proportion of the maximum value, i.e. the proportion of living cells (positive control) or dead cells (negative control).

3.4 Discussion

The experiments here were designed to confirm and characterise hapten reactivity with nucleophiles by LC-MS to inform hapten-peptide post-translational modifications that may form intracellularly. Information from this analysis was used in the investigation of hapten-peptide adduct formation at different concentrations of each chemical sensitiser by a targeted LC-MS method. The aim of this extended methodology was to determine maximum functional reactivity under more physiologically relevant conditions than had previously been used elsewhere. In addition, this reactivity analysis was carried out in a cell culture medium reaction environment to determine the feasibility of adduct formation under such conditions. In line with this, the experiments here optimised cell culture conditions and explored cell viability exposed to the same sensitiser concentrations used in the peptide reactivity methods. The overall aim was to determine the most appropriate dose of each sensitiser chemical for use in more complex cell-based proteomics and immunopeptidomics workflows. This was determined here by a combination of cytotoxic dose cut-offs and maximum peptide-reactive concentrations of chemical sensitisers.

It has been stated that qualitative adduct analyses reveal more information about reactivity that may appear negligible when assessing quantitative % nucleophile depletion alone⁶. The initial qualitative analyses presented here defined the specific reaction mechanisms of each chemical sensitiser forming adducts with each of the nucleophilic amino acid residues; Cys, Lys, His, Arg, Tyr. Despite skin and respiratory sensitisers generally favouring either cysteine or lysine residues respectively^{1,2,16}, qualitative analysis in this chapter showed that both types of sensitiser chemical can modify both cysteine and lysine residues to varying extents^{7,208,235}. This was somewhat evident in the results presented here. Qualitative evaluation with initial peptide reactivity methods (3.3.1) did reveal preferential lysine containing peptide hapteneation with non-detectable (Ac)FAACAA modification by respiratory sensitisers (Figures 3.5 & 3.6), and vice versa with skin sensitisers.

The most intense adduct m/z peak identified in each of the peptide MS spectra corresponded to the expected single adduct for each test chemical; DNCB +166 Da, DPCP +206 Da, PA +148 Da, TDI +148 Da. A number of additional modifications proposed in Table 3.1 based on theoretical reaction mechanisms were also observed. Phthalic anhydride predominantly exhibited the acylation $\Delta 148$ m/z adduct with both cysteine- and lysine-containing peptide (Figures 3.5 & 3.6), but also the imide-like adduct at $\Delta 130$ m/z exclusively with (Ac)FAAKAA resulting from cyclisation that was also recently reported by Khong *et al*²³¹ at time points longer than 8 hours of incubation.

Comparison of the adduct ion intensity profiles between all samples in phosphate buffer (Figure 3.10) with those in serum-free culture medium (Figure 3.11) illustrates suppression of adduct formation at lower sensitiser concentrations in culture medium. Furthermore, the overall ion intensity/count of peptide adducts in these samples was up to 100-fold lower than those observed in phosphate buffer reaction mixtures. This may be due to cell culture medium supplements acting as competing nucleophiles with peptide amino acid residues. Optimisation experiments showed that penicillin-streptomycin at 0.1% did not have an observable impact (data not shown), although this is a possibility with the other essential components of culture media that are present at higher concentrations. For example, the amino acid supplement of the serum-free culture medium is 500 μ M, which is also the apparent point above which adduct m/z intensity greatly increases relative to the rest of the trend. This would suggest haptenation of peptides may occur most favourably once the sensitiser chemical is in excess of the competing amino acids supplement in the reaction mixture.

Double adducts were identified in the HDMS^E results (3.3.1) in a number of cases, reinforcing the theoretically proposed adduct mass and reaction mechanisms. For example, the single hydrolysed adduct resulting from TDI acylation was primarily observed with lysine, but also the hydrolysed double adduct at +296 m/z . Instances of multiple adducts on a single nucleophile (e.g. double adducts) may in part explain why complete peptide saturation was not observed under optimum peptide reactivity conditions (3.3.1). The large excess of sensitiser relative to peptide nucleophile in the most concentrated sensitiser samples was expected to result in saturation of peptide nucleophiles by adduct formation. However, this nucleophile saturation was not observed completely. Double adducts seem less likely to form (if at all) in more complex heterogeneous nucleophile samples, such as peptides/proteins with numerous nucleophilic sites.

As it relates to haptenation in more complex heterogeneous nucleophile samples, such as proteins with numerous nucleophilic residues and steric constraints, double adducts seem unlikely to form compared to single adducts. TDI serves as an example of the convoluting factors that present a challenge in these types of analyses; with multiple reaction mechanisms and adducts possible, inconsistencies in double adduct formation across different reaction conditions, inter-/intra-molecular cross-linking, and partial or complete hydrolysis/oxidation all serving to demonstrate the value of in-depth qualitative analysis of haptenation products prior to quantitative adaptations of the DPRA and other peptide reactivity assays.

Notable absence of adduct formation was observed for PA and TDI with cysteine-containing peptide compared to lysine-containing peptide. This is supported by previous literature evidence suggesting respiratory sensitisers preferentially haptenate lysine residues over cysteine^{4,7,16,208}.

However, this relative lack of cysteine modification may in part be due to the cysteine containing peptide dimers noted previously. The challenges presented by cysteine oxidation and dimerization in reactivity assays have been noted in the literature⁶, but to date there does not appear to be an iteration of a peptide reactivity assay that incorporated a reducing agent (e.g. dithiothreitol) or similar to maintain the reduced state of the cysteine residue sulfhydryl group. However, the presence of reducing agents may potentially interfere with haptenation reactions, which should be investigated first.

The proposed cysteine oxidation mechanism impacts the extent of haptenation by formation of a disulphide bridge, and resulting in removal of the nucleophile availability. Acylation of the cysteine residue by PA and TDI (Figures 3.2 & 3.3) would then no longer be achieved, hence no adduct ion intensity would be observed. Further relative inhibition of cysteine reactivity may be due to polarity. Cysteine is considered the most nucleophilic of the 20 amino acid residues²⁴⁶. However, it is also the only nonpolar residue of the 5 nucleophilic amino acids studied here. This may result in cysteine being relatively less conducive to these analyses than the other residues, for example due to intensified solubility limitations relative to the other amino acids.

The different reaction kinetics between cysteine dimerization and specific haptenation reaction mechanisms may be an important additional factor here, as suggested in similar studies elsewhere²⁰⁸. Cysteine containing peptide control samples demonstrated near-complete oxidation and dimerization with the presence of the doubly-charged species $[M+2H]^{2+}$ following 24h incubation. However, DNCB single adduct formation (Δ 166Da, 761 m/z) was observed at a substantial ion intensity similar to that of the unmodified peptide (595 m/z). Whilst not a quantitative direct comparison, this does suggest preferential haptenation of cysteine hypothetically occurs at a greater rate than oxidation of the cysteine residues. A lack of cysteine preference for a given sensitizer may conversely result in oxidation of cysteine occurring more rapidly than cysteine haptenation. This would result in the nucleophilic sulfhydryl microenvironment being unavailable, thereby preventing the haptenation reaction from proceeding at the requisite reduced cysteine residue.

These additional limitations on the reactivity with cysteine residues is not evident or expected with lysine residues under similar *in chemico* conditions to those presented in peptide reactivity assays here. It therefore seems pragmatic that the methods presented here be adapted in future to maintain the reduced state of cysteine residues, especially for applicability to the reducing conditions of intracellular environments in more complex *in vitro* systems.

Understanding of how pH affects haptenation remains incomplete. Physiological pH7.4 constitutes a less favourable reaction environment for some residues, with a basic pH being more

chemically favourable in certain cases²⁶ (though less physiologically relevant). Haptenation is putatively considered an irreversible covalent reaction^{4,16,36,208}, though it may be possible that extreme changes in pH may partially reverse certain haptenation reaction mechanisms such as acylation. This therefore seems unlikely for DNCB and DPCP, but it would be valuable to investigate any adduct ion intensity loss for PA and TDI following acidification to extremely low pH. This would also potentially give an indication of the level of reversibility (if any) introduced by the reverse-phase peptide purification methods incorporated in the adjusted peptide reactivity assay. Further implications of the routine acidification prior to peptide purification and LC-MS analysis in proteomics experimental workflows could also be determined. The effect of acidification on peptide adducts pre/post-haptenation may also provide interesting insights into the dynamics of haptenation and metabolism in low pH cellular compartments (e.g. endosomal and lysosomal pathways) in *in vitro* haptenation models.

The methods outlined here may be improved in terms of quantitative accuracy of adduct formation by employing a multiple reaction monitoring (MRM) strategy to selectively detect and quantify the peptides based upon the measurement of specified precursor-to-fragment ion transitions (using the shared (Ac)FA fragment of 206 Da), at specific retention times of the peptide or peptide adducts similar to the methods of Alesksic *et al*²⁰⁸. The use of MS/MS information would be particularly valuable for qualitative identification of structural differences of the peptides (e.g. oxidised (Ac)FAACAA dimers). This approach would also further de-convolute the samples by filtering out noise spectra and allowing identification of any instance of test chemical co-elution with a peptide/adduct of interest (e.g. where conformers are generated). However, the structures of the acetylated peptides used here have been elucidated with only a single hapten-reactive site⁶. Therefore, relating hypothetical adduct structures to the *m/z* shift of known peptide structures remains the apparent method of choice here for investigating haptenation.

In conclusion, the functional reactivity methods of Aleksic *et al*²⁰⁸ have been utilised and adapted here primarily to confirm reactivity of the skin sensitisers DNCB and DPCP and the respiratory sensitisers PA and TDI under different reaction conditions. In addition, the results served to identify specific peptide adducts according to a series of theoretical reaction mechanisms. The assay was further adapted to assess peptide reactivity over a range of sensitizer concentrations to identify the maximum reactivity of each chemical sensitizer with single-nucleophile containing peptides under experimental conditions relevant to exposure in living cell culture. Further adaptations to the peptide reactivity assay included solid-phase peptide purification and application of high-throughput, targeted (SIR) LC-MS methods to improve both sensitivity and throughput.

Cell seeding density optimisations demonstrated that serum-free DMEM culture medium (supplemented with F12 nutrient) was sufficient for maintaining cell viability during a secondary 24-hour incubation where sensitiser exposure can be incorporated following the initial 24-hour growth period. The results demonstrated the maximum appropriate dose for the skin sensitisers DNCB and DPCP. These concentrations reflected the published optimum *in vitro* concentrations of DNCB^{9,11,28,213} and DPCP^{10,11}, comparable to *in vivo* sensitising concentrations in humans¹¹⁶. Conversely, this was not observed following exposure to the respiratory sensitisers PA and TDI under these experimental conditions – even after increasing the concentration of sensitiser to the maximum solubility (at 0.1% DMSO vehicle). In these cases, the optimum concentration was deemed to be the greatest possible in the continuous exponential gradient of sensitiser concentrations.

Finally, the results presented here show some agreement with the cysteine/lysine reaction duality present in the literature^{4,7}, with skin sensitisers showing a preference for cysteine-containing peptides and respiratory sensitisers showing a preference for lysine-containing peptides (Figure 3.5 & 3.6). The analyses presented also measure changes in living cell culture viability after exposure to skin and respiratory sensitisers and optimisation of cell seeding density. Further, a dose concentration has been identified for each sensitiser where maximum reactivity was observed in comparison with cell viability at the same dosage. These sensitiser dose concentrations provide valuable information for the design of experiments exposing living cell cultures to chemical sensitisers *in vitro* for downstream proteomics experiments. Crucially, the different concentrations of chemical sensitisers here have been demonstrated as peptide-reactive, yet (in the case of respiratory sensitisers) non-cytotoxic in the same reaction mixture composition.

Chapter 4 Haptenation within the complexity of living human epithelial cell proteomes

4.1 Introduction

Mechanistic *in chemico* evidence for covalent modification of endogenous proteins (haptenation) is numerous and historically predicated upon relatively simple models with limited physiological relevance. Much of the initial understanding was provided by single amino acid nucleophile peptides and model proteins^{26,206–208}. Several considerations were needed to gain a more physiologically relevant understanding of haptenation reactions during sensitisation. These considerations include (but are not limited to) competition for binding sites on different nucleophiles, differences in protein nucleophile expression in cells and tissues, and steric constraints. Whilst useful for initial characterisation of the different haptenation reaction mechanisms and related selectivity, such models are too limited for informing processes in multi-dimensional nucleophile systems such as cell lysates and tissue homogenates.

A wealth of *in vivo* evidence is available from occupational exposure and animal studies^{94,101,102}. However, such investigations lack the mechanistic molecular insight to explain the divergence in adverse immunological outcomes^{1,2} following skin or respiratory sensitiser exposure. This previously presented a substantial knowledge gap, limiting the utility of AOP models in risk assessment. Understanding the proteins specifically haptenated or dysregulated in cells believed to be frequently located at the sites of sensitiser exposure *in vivo* was therefore considered to be crucial.

It follows that peptides presented by the major histocompatibility complex proteins of cells exposed to chemical sensitisers may be representative of the specific proteins/pathways affected. Despite not being the cells that initially migrate and prime naïve T cells, keratinocytes and respiratory epithelial cells are initially exposed to the same sensitiser chemicals/conjugates as professional antigen-presenting cells if not arguably more so due to their great abundance at the proposed sites of exposure. Consequently, keratinocytes appear to be the primary stimulator of circulating memory T cells in the effector phase; acting as an epidermal model for peptide presentation in both the sensitisation phase in which they are relatively less active, and in the effector phase where they exert their most notable effects¹. It is proposed that this may be reflected in alveolar and/or bronchial epithelial cells.

Dual stable isotope labelling^{9,11,27,28} has proved instrumental in investigation and characterisation of haptation in living keratinocytes after treatment with sub-cytotoxic concentrations of skin sensitiser chemicals. As noted by Parkinson *et al*, previous studies using this approach investigated either model proteins, keratinocyte lysates, or skin tissue homogenates often in artificially high and clinically irrelevant concentrations of chemical sensitisers⁹. These previous studies do however represent valuable method development from initial *in chemico* studies, presenting suitable sensitivity of the approach for detection of haptation at very low abundance in complex proteome systems. Furthermore, this approach has yet to be applied to respiratory sensitisers or skin sensitisers in non-skin derived models.

Keratinocytes and bronchoalveolar epithelial cells can induce and co-ordinate inflammatory immune responses through cytokine and chemokine secretion. This has been shown to partly involve excess reactive oxygen species through alteration of antioxidant response pathways, which further contributes to inflammation and cell/tissue damage²⁴². There is a good amount of evidence pointing to DCs as the primary APC influencing T cell induction, though there is also growing evidence for bronchial (and alveolar) epithelial cells in cell signaling and antigen presentation for induction of the immune responses of interest^{19,247}. In light of these observations, the human epithelial cell lines A549 and 16HBE14o⁻ are potentially useful *in vitro* models that address the needs in a number of reports⁵⁹.

The study presented here addresses hypothetical differences in the dynamics and specificity of haptation in alveolar epithelial cells by skin and respiratory sensitizer chemicals. The latest LC-MS proteomics technologies have been utilised in conjunction with the recently developed stable dual isotope labelling methods optimised for the identification of specific haptation events within the context of differential expression in cellular proteomes.

4.2 Methods

4.2.1 Materials & reagents

Cell culture reagents were purchased from Fisher Scientific; Dulbecco's phosphate-buffered saline (DPBS), Dulbecco's modified Eagle medium (DMEM), Corning foetal bovine serum supplement (FBS, 10X), penicillin-streptomycin (P/S, 100X), Dulbecco's modified Eagle medium/Ham's nutrient mixture F12 (DMEM/F12, with L-glutamine, HEPES, no phenol red, no serum), trypsin-EDTA dissociation reagent (0.25%).

The test chemicals here included both skin and respiratory sensitizers, with all solutions being dispensed and prepared in a fume cabinet with nitrile gloves for skin protection. The following

chemical sensitiser were purchased from Sigma-Aldrich; 2,4-dinitrochlorobenzene (DNCB, M_w 202.552 Da, >99% purity), diphenylcyclopropenone (DPCP, M_w 206.244 Da, 98% purity), phthalic anhydride (PA, M_w 148.117 Da, >99% purity), and 2,4-toluene diisocyanate (TDI, M_w 174.159 Da, >98% purity). Sterile-filtered dimethyl sulfoxide (DMSO) was also purchased from Sigma-Aldrich as a sensitiser chemical vehicle. Deuterated DNCB- d_3 (M_w 205.552 Da, >99% purity) and DPCP- d_{10} (M_w 216.244 Da, 97.1% purity) were purchased from CDN isotopes and Quotient BioResearch respectively. Deuterated PA- d_4 (M_w 152.117 Da, >98% purity) and TDI- d_6 (M_w 180.159 Da, >98% purity) were also purchased from CDN isotopes.

Mass spectrometry preparation reagents included; methanol (Optima LC-MS grade), chloroform (Fisher Scientific), 6M urea/50mM Tris-HCl (pH8), dithiothreitol (DTT, Thermo Scientific), iodoacetamide (IAA, Bio-Rad), trypsin/LysC mix (Promega), Trifluoroacetic acid (TFA, Sigma-Aldrich), MS-grade water (Optima), acetonitrile (Optima LC-MS grade), and formic acid (Sigma-Aldrich).

4.2.2 Cell culture

Human A549 alveolar epithelial cell line and 16HBE14o⁻ bronchial epithelial cells were regularly maintained, using aseptic technique, according to methods previously described (chapter 2). Suspensions of detached cells were seeded in 10cm culture dishes as biological replicates, at previously optimised cell/cm² densities (chapter 2), in triplicate and incubated in a humidified environment at 37°C/5% CO₂ for 24 hours in complete DMEM (10% FBS, 1% penicillin-streptomycin). Further technical replicates of A549 control samples were prepared for optimisation of extraction methods and protein quantification in triplicate.

4.2.3 Sensitiser modification of living cell cultures and sample extraction

Stock sensitiser solutions were prepared and combined in 50:50 molar concentration ratio of unlabelled-to-labelled at 3M DNCB/DNCB- d_3 , 1M DPCP/DPCP- d_{10} , 2M PA/PA- d_4 , and 3M TDI/TDI- d_6 in sterile-filtered 100% DMSO. Working concentrations of each 50:50 sensitiser mixture were prepared by dilution of stock solution aliquots with serum-free DMEM/F12 culture medium to a final concentration of 10 μ M DNCB, 5 μ M DPCP, 1280 μ M PA, and 2560 μ M TDI at 0.1% DMSO carrier. These concentrations had previously been optimised and determined sub-cytotoxic (chapter 2), or exhibiting maximum functional reactivity under these experimental conditions where cytotoxicity was not demonstrable (chapter 3). Control DMEM/F12 was also prepared with an equal volume of sterile-filtered 100% DMSO only.

Following 24h incubation of cell cultures in complete DMEM, the culture media was aspirated before washing cells three times with DPBS. The DPBS was then replaced with sensitiser-treated DMEM/F12 and incubated for a further 24 hours at 37°C/5% CO₂. After 24 hours, the culture dishes were transferred to a fume cupboard in sealed containers.

Extraction of adhered cells from culture dishes was achieved for A549 control samples in triplicate either by incubation with 0.25% trypsin-EDTA dissociation reagent or through *in situ* lysis by application of 1mL cell lysis buffer (50mM Tris, 150mM NaCl, 0.1% SDS, EDTA-free protease inhibitor cocktail tablet) followed by scraping and extraction of the cell lysates to individual tubes. Trypsinised cells were centrifuged at 300 xg for 5 minutes at room temperature before aspirating the supernatant and lysing pelleted cells by manual disruption with a pipette in 1mL cell lysis buffer.

Following cell lysate protein quantification method optimisation (section 4.2.4) for the two extraction methods above, the sensitiser-treated cell culture supernatants were extracted and stored at 4°C. The cells were then washed three times with DPBS before scraping in 1mL lysis buffer and extracting the cell lysate to individual tubes. All cell lysates were sonicated with a micro-tip at minimum power setting three times for 5 seconds each with 10 second rests in between. Sonicated cell lysates were centrifuged for clarification at 14,000 xg for 20 minutes at room temperature, with the supernatants being extracted for protein quantitation and the pellets discarded.

4.2.4 Optimisation of cell lysate protein quantification methods

Aliquots of technical replicates of sonicated A549 cell lysates in triplicate, extracted from culture either by trypsin or *in situ* scraping in lysis buffer, were spotted onto Direct Detect® assay-free protein quantitation cards alongside cell lysis buffer as a blank. The dried cards were inserted into the Direct Detect® infrared spectrometer for total protein quantitation by generation of an IR spectrum representative of protein concentration according to the generated calibration curve.

Aliquots were also applied to a Bicinchoninic acid (BCA) assay kit (Thermo Scientific) for determination of protein concentration in the range of protein standards generated at 125-2000µg/mL. The cell lysis buffer was incorporated as the standard control. Samples were prepared in 96-well plates with small volumes of standard control, protein standards, and cell lysates of unknown protein concentration. Compatibility reagent stock solution was reconstituted and added to each sample well. The microplates were covered and mixed on a plate shaker at medium speed prior to incubation at 37°C for 15 minutes. BCA working reagent was added to each sample well after the incubation period and mixed thoroughly before further incubation at

37°C for 30 minutes. Raw end-point absorbance of each plate was measured at 562nm using an ELISA plate reader. Raw absorbance values were normalised to the assay background before determination of protein concentration of cell lysate samples relative to standard curve of protein standards.

4.2.5 Protein digestion and peptide purification

Following optimisation, sensitizer-treated cell lysates were analysed by Direct Detect® and average protein concentration recorded. To 100µg of cell lysate protein, 4 volumes of methanol was added and vortexed before addition of 1 volume of chloroform, vortexing further before finally adding 3 volumes of 18.2MΩ water (MilliQ) with a final vortex. The samples were centrifuged at 14,000 xg for 5 minutes, precipitating the protein content between the organic and inorganic phases. The aqueous phase was removed, followed by the addition of 4 volumes of methanol and a brief vortex to mix. The precipitate was pelleted by centrifugation at 14,000 xg for 5 minutes. The methanol was completely removed and the pellet allowed to air-dry in the dark for up to 20 minutes at room temperature. Dried pellets were re-solubilised in 100µL of 50mM Tris-HCl buffer containing 6M urea. Proteins were reduced with 5mM DTT for 30 minutes at 37°C, alkylated with 15mM for 30 minutes in the dark at room temperature, then digested for 4 hours at 37°C with trypsin/Lys-C at a ratio of 25:1 protein-to-trypsin/LysC. The peptides were then diluted with 750µL of 50mM Tris-HCl (pH8), diluting the urea to <1M, and incubated overnight at 37°C.

Digestion was completed by the addition of TFA to a final concentration of 0.4%. Samples were vortexed, and centrifuged at 14,000 xg on a benchtop microcentrifuge for 10 minutes at room temperature. Sample supernatants were applied to a reverse-phase C18 micro-elution plate (Oasis HLBPrime) conditioned with 100% acetonitrile and equilibrated with 0.1% TFA in dH₂O. After de-salting the samples with 0.1% TFA and MS-grade H₂O (Optima), purified peptide samples were eluted in 70% acetonitrile, transferred to lo-bind tubes, and dried overnight in an evaporator centrifuge.

4.2.6 Mass spectrometry

Dried peptides were re-constituted in buffer A (0.1% formic acid (v/v) dH₂O) prior to MS analysis, with approximately 2µg of peptide sample loaded onto a reverse-phase trap column at a trapping rate of and washed for 5 minutes with buffer A prior to analytical nano-LC separation with a C18 reverse-phase column. Following elution, peptides were separated over a 250 minute gradient at a flow rate of 0.3µL/min using a gradient of 3-80%. Eluted samples were injected directly into a

Thermo Fusion Orbitrap Tribrid (Thermo Scientific) mass spectrometer using electrospray ionisation and data-dependent acquisition in the range of 300-1500 m/z . Full scans were acquired with an orbitrap mass analyser using the Top Speed data-dependent mode, performing an MS scan every 3s cycle, followed by higher-energy collision-induced dissociation (HCD) MS/MS scans with an ion trap mass analyser.

4.2.7 Database searches and data analysis

Raw spectrum files from data-dependent acquisition were analysed using Peaks Studio^{248,249} version X to process data through generation of reduced charge state and de-isotoped precursor and associated product ion peak lists, which were searched against the UniProt human protein sequence database (2020-04-07) and a default contaminants list. Variable modifications were set for all datasets as carbamidomethylation (57.02 Da) of cysteine, N-terminal acetylation (42.01 Da) and methionine oxidation (15.99 Da). Specific, variable single adduct modifications (table 2) of cysteine and lysine were set for each treatment group; DNCB (166.092 Da), DPCP (206.244 Da & 224.259 Da) with 222.243Da for cysteine only, Phthalic anhydride (148.117 Da) with 130.102 Da (lysine only) and 164.116 (cysteine only), and TDI (148.165 & 174.159).

Two missed cleavages with specific trypsin digestion were allowed, with the number of variable modifications allowed per peptide set to the default values. The data was submitted to Peaks® label-free relative quantitation, then filtered according to the recommended default vector ratio quality (A549 – 7; 16HBE – 4) and average abundance (1E5) cut-offs. The filtered data was tested for significance by T-test ($p < 0.05$) and adjusted for multiple comparisons with the Benjamini-Hochberg method for false discovery rate (1% FDR).

Downstream data analyses and visualisation was performed in Peaks Studio, Rstudio, and Microsoft Office tools. Modified peptides were confirmed by filtering for specific haptentation modifications in Peaks Studio and observing a unique signature of 2 peptide isotopes clusters with a fixed $\Delta m/z$ in the MS spectrum, with exact location of haptentation confirmed by manual inspection of the MS/MS fragmentation spectrum of the identified modified precursor. Gene ontology analysis was performed via PANTHER²⁵⁰ for biological process, cellular component, molecular function, and Reactome pathway analysis. Downstream analyses were performed using R^{251,252} and Microsoft Office tools (Microsoft Corporation).

4.3 Results

4.3.1 Assessment of cell culture harvest and protein concentration measurement techniques for optimum protein quantitation prior to mass spectrometry

Two methods of extracting cells from culture were compared for technical replicates of A549 cells according to the measured protein quantitation. Two methods of protein quantitation were also compared here to establish the relative accuracies of the various method combinations.

Incubation of cell culture with 0.25% trypsin-EDTA dissociation reagent is a common approach to harvesting cell cultures. Scraping of cell cultures with cell lysis buffer *in situ* was tested as an alternative method, with the hypothetical benefit of limiting incomplete cell harvest due to incomplete trypsinisation of membrane proteins.

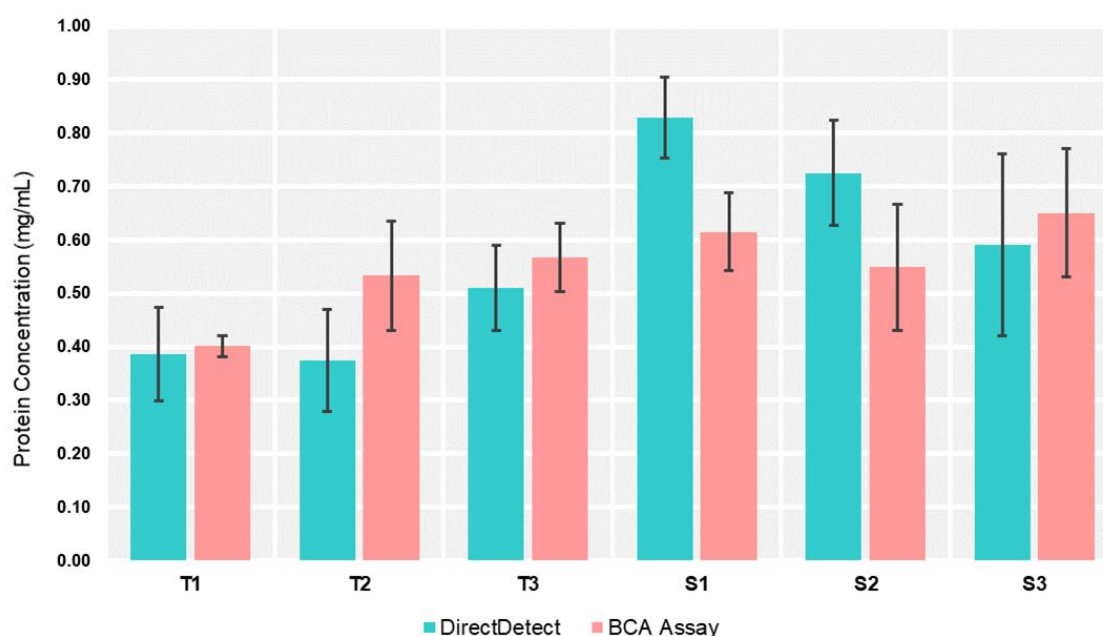


Figure 4.1: Protein concentration for cell lysates derived from trypsin or lysis buffer scraping-based extraction methods. Protein concentrations are presented as mg/mL as determined by both Direct Detect® and BCA assay for trypsinised samples (T1-3) and scraped samples (S1-3).

Following generation of cell protein lysates from both harvest methods, the lysates were measured for protein concentration both by Direct Detect® and by standard BCA assay (Thermo Scientific) (Figure 4.1). In general, the protein concentration appeared greater for scraping compared to trypsin extraction, and remained within the error range between Direct Detect® and BCA assay measurements. On average, the protein concentration derived from scraped samples was greater than the concentration derived from trypsinised samples when measured by BCA. Overall, the cell culture harvest methods generally showed comparable consistency based on

standard deviation, with lysis buffer scraping on average yielding a greater protein concentration than trypsin with the additional benefits mentioned previously.

4.3.2 Cellular proteome response to skin and respiratory chemical sensitisers

The A549 data for biological replicates presented here identified on average: 4827 proteins in the control group, 4934 proteins with DNCB treatment, 4814 proteins with DPCP treatment, 4820 proteins with PA treatment, and 4852 proteins with TDI treatment. Data for biological replicates of treated 16HBE14o⁻ samples identified on average: 4017 proteins in the control group, 4238 proteins with DNCB treatment, 4260 proteins with DPCP treatment, 4254 proteins with PA treatment, and 4361 proteins with TDI treatment (Figure 4.2).

The log₂ ratio of fold change for significantly different proteins for each treatment group were compared to the control, with a comparison of individual sample global proteomes (Figures 4.3 & 4.4). A greater magnitude of differential abundance with respiratory sensitiser compared to skin sensitiser treatment was observed. Additionally, all sensitisers appeared to cause a general increase of protein abundance in the proteome relative to the control (Figure 4.3). This was quite a subtle observation, but the sensitisers exhibiting the greatest change in both cell lines ranked from most to least: TDI – PA – DPCP – DNCB. The general shift in global abundance was more pronounced for 16HBE14o⁻ than A549, with the global protein abundance generally being greater for A549. The A549 data demonstrate a generally stronger agreement between the first and second biological replicates relative to the third in terms of fold change (Figure 4.4, A-D). 16HBE14o⁻ data clustering was uniform across all three replicates (Figure 4.4, E-H).

A large number of statistically significant (1% FDR), differentially expressed proteins (fold change ≥ 1.5) were identified for A549 cells treated with PA and TDI relative to the control. However, this was not observed with the skin sensitisers DNCB and DPCP (Figure 4.5). Treatment with PA resulted in significantly different expression of 301 proteins (6.3% of the proteome), whilst TDI treatment resulted in significantly different expression of 596 proteins (12.3% of the proteome). Contrary to the A549 results, 16HBE14o⁻ demonstrated a greater number of significantly different proteins after DPCP treatment (Figure 4.7), with 1259 proteins (representing 29.6% of the proteome). Treatment of these cells with PA resulted in significantly different expression of 1539 proteins (36.2% of the proteome), and 2158 proteins with TDI treatment (49.5% of the proteome).

Proteins with increased expression across the treatment groups generally included keratins, heat-shock proteins, proteasomal proteins, dynamin, transforming growth factor- β (TGF- β), ubiquitin-related proteins (e.g. E3 ligases), NEDD proteins, ribosomal/RNA proteins, and histone-associated

proteins. Superoxide dismutase, responsible for catalysing the conversion of superoxide radicals to normal molecular oxygen, demonstrated increased expression in all 16HBE14o⁻ samples where a significant cellular response was observed. DAZ-associated protein-1 (DAZAP1), which has previously been demonstrated to be up-regulated in allergen-induced bronchoalveolar lavage (BAL) secretomes²⁵³, was also identified broadly across the treatment groups.

Also showing significantly increased expression across the sample groups was a variety of redox-related redoxin proteins, such as: glutaredoxin, thioredoxin, peroxiredoxin, sulfiredoxin, and nucleoredoxin. Clusterin, which is implicated in oxidative stress and inflammation²⁵⁴, was up-regulated exclusively in A549 cells following respiratory sensitiser exposure. Aldehyde dehydrogenase proteins are important in cellular responses to oxidative/electrophilic stress by metabolising the array of aldehydes generated during lipid peroxidation²⁵⁵, and showed increased expression in all sample groups. Succinate dehydrogenase is similarly important in oxidative stress, playing a role in reactive oxygen species (ROS) homeostasis in cells^{256,257}. Succinate-CoA ligases were found to be up-regulated in all samples exposed to respiratory sensitiser chemicals. Whereas Succinate dehydrogenase subunits were identified exclusively in 16HBE14o⁻ cells treated with respiratory sensitisers. Cadherin proteins were in addition exclusively up-regulated by respiratory sensitisers. Cadherins are transmembrane proteins generally responsible for cell-cell adhesion at adherens junctions and are well-documented regulators of oxidative stress acting upon endogenous antioxidant systems^{258–260}.

Retinal dehydrogenase has been demonstrated to be involved in asthma and development of a T_H2 response^{261,262}, and was significantly up-regulated exclusively by respiratory sensitisers here. The up-regulation of Nedd8-conjugating enzymes following respiratory sensitiser treatments here demonstrates an associated link in the development of specific immune response, given the capacity of neddylation to regulate the response by selective ubiquitin-like activity²⁶³.

PA exposure to A549 cells resulted in significantly increased expression of proteasome maturation protein, Q9Y244 (figure 4.6, A). This molecular chaperone protein facilitates proteasome formation at the ER²⁶⁴, and demonstrated one of the greatest increases in abundance as well as being one of the most highly significant results. A549 cells exposed to TDI showed the greatest significant increase in expression for aminoacylase-1, Q03154 (figure 4.6, B). Aminoacylase catalyses the hydrolysis of N-acetylated amino acids and plays a role in regulating oxidative stress, as well as interacting with sphingosine kinases to increase cell growth²⁶⁵.

Proteins with the greatest significant increase in expression in 16HBE14o⁻ cells exposed to the skin sensitiser DPCP included CD276 antigen and CD166 antigen (figure 4.8, A). CD276 antigen (Q5ZPR3), also referred to as B7 homolog 3, is a single-pass type I membrane protein with the

ability to regulate CD4 and CD8 T-cell responses and selectively induce the production of IFN- γ ²⁶⁶. CD166 antigen (Q13740), also referred to as ALCAM, is also a single-pass type I membrane protein, but is responsible for T-cell activation and mediating attachment of dendritic cells^{267,268}.

Phthalic anhydride exposure to 16HBE14o⁻ cells (figure 4.8, B) resulted in significantly increased expression of NFATC2-interacting protein (Q8NCF5), a protein regulating the transcription of cytokines characteristic of T_H2 immune responses²⁶⁹. Interleukin-1- α (P01583) is an important inflammatory T_H2 cytokine associated with respiratory sensitisation^{123,270}, and was also one of the most up-regulated proteins following treatment of 16HBE14o⁻ cells with TDI (figure 4.8, C). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is a serine/threonine kinase which generally acts as a master kinase for other kinase signaling pathways, was notably up-regulated in 16HBE14o⁻ cells exposed to TDI. PDK1 potentially has a role in influencing cell survival signaling pathways sensitive to oxidative stress, such as regulation of Akt (protein kinase B) and its association with HSP27^{271,272}.

Sequestosome-1 (ubiquitin-binding protein p62) is a classical autophagy receptor important in the mediation of T_H2 cell function and allergic airway inflammation²⁷³ as well as being involved in a number of signal transduction pathways including the Nrf2-Keap1 antioxidant response element pathway²⁷⁴. This protein showed increased expression in both cell lines following TDI treatment.

The majority of significant changes related to increased expression of proteins in the sensitiser-treated samples, though several highly significant results showed decreased protein expression. Significantly decreased expression was identified in all treatment groups for histone H2 and H3 isoforms.

Serum albumin is known to be lysine-rich^{26,27} and was observed here to be significantly down-regulated in the PA-A549, TDI-A549, and PA-16HBE14o⁻ treatment groups by the more lysine-reactive sensitiser chemicals. Although usually an extracellular protein, serum albumin has been noted as being present intracellularly at very low concentrations²⁷⁵⁻²⁷⁷, and may have been identified in the present study via membrane-bound albumin-binding proteins such as calreticulin²⁷⁵. Furthermore, calreticulin as well as other albumin-binding proteins (e.g. GP18, SPARC) were identified across all of the samples here. Respiratory sensitiser exposure also resulted in decreased abundance of histone H3 proteins in A549 cells, whereas skin sensitiser exposure did not, potentially suggesting DNA damage as a differential feature of this cellular response.

Macrophage migration inhibitory factor (MIF) was identified as being significantly decreased in expression exclusively in A549 cells exposed to the respiratory sensitiser chemicals. Studies have

demonstrated the critical role of MIF secretion in T_h2-associated airway inflammation²⁷⁸, particularly in bronchial asthma²⁷⁹. For example, immune responses demonstrating IFN- γ production for macrophage activation are typically characterised as T_h1 responses. T_h2 immune responses are instead characterised by IL-4, IL-5 and IL-10, inhibiting macrophage activation & recruitment, and inducing antibody production²⁸⁰.

4.3.3 Gene ontology

Proteins with significantly different expression between untreated and treated sample groups were subjected to gene ontology (GO) analysis of biological process, cellular component, and molecular function in the PANTHER overrepresentation test, with a Fisher's exact statistical test with false discovery rate (FDR) correction. The results identified GO terms significantly overrepresented for the differentially expressed proteins with <0.5% proteins being unmapped. The results were filtered by the ratio (fold enrichment) of proteins identified in the test data to the proteins in the PANTHER gene ontology human protein reference list. The proteome results were also annotated with the Reactome pathway analysis database, with the same statistical testing and multiple testing correction parameters. A relatively large number of unclassified results in these analyses is due to the expectation of approximately 10% of proteins in the test dataset being unclassified proteins in the Gene Ontology human protein reference list²⁸¹, however the majority of the proteins in the test data could be mapped here.

Table 4.1: Gene ontology and Reactome pathway analysis results – The number of significantly enriched GO terms for biological process, cellular component, and molecular function of significantly differently expressed proteins are shown for each cell line and sensitiser treatment, alongside the number of Reactome pathways identified.

Cell Line	Sensitiser Chemical	Biological Process	Cellular Component	Molecular Function	Reactome Pathways
A549	DNCB	0	0	0	0
A549	DPCP	0	0	0	0
A549	PA	105	60	38	143
A549	TDI	316	166	97	188
16HBE	DNCB	2	2	1	0
16HBE	DPCP	599	253	146	420

16HBE	PA	632	288	183	523
16HBE	TDI	925	369	249	667

Molecular function analysis revealed a number of shared GO terms across the treatment groups (Figures 4.9-4.11), many of which potentially infer intramolecular haptation events. For example, small molecule binding (GO:0036094), protein binding (GO:0005515), and a variety of other molecular binding terms. Generally, a large proportion of GO terms were identified for cell cycle-related processes and translational functions, as well as related proteins such as kinesins, ribosomal proteins, and endoplasmic reticulum proteins. The molecular function gene ontology term, translation initiation factor activity (GO:0031369), is an example of the multitude of these GO terms offering an explanation for the broad increase in protein abundance across all treatment groups. Oxidoreductase molecular function, and similar terms, were identified across the different treatments where a significant GO enrichment could be observed. In-line with the proteome observations of up-regulated oxidative stress-related proteins (section 4.3.2), this further strengthens the evidence for the cellular response to oxidative stress induced by the chemical sensitisers in these cells.

Significantly enriched biological process GO terms in the A549 PA & TDI (Figure 4.9) data were observed at the greatest fold enrichment values predominantly for metabolic processes. Cellular component terms revealed an enrichment of dense body (GO:0097433) and mRNA/RNA cap binding complexes. Molecular function GO terms provided perhaps the most interesting results here, with numerous protein-disulfide enzyme functions, in addition to a variety of oxidoreductase and hydrolase functions showed significant enrichment. Multiple nucleic acid binding molecular function GO terms were also identified. These observations give an overall impression of cellular metabolic responses to oxidative stress following exposure to respiratory sensitisers. A number of organonitrogen-related GO terms were similarly present, suggesting nitrosative stress may also be of interest in this regard.

Gene ontology results for 16HBE14o⁻ samples resulted in a substantial enrichment of metabolic/catabolic and transport biological processes in general, including polyadenylation and ATPase (V-type) complexes (Figure 4.10 & 4.11). Biological process GO terms for regulation of protein neddylation – a process known for selective ubiquitin-like activity and protection of the ubiquitin proteasome system during proteotoxic stress^{263,282} – was a significant feature of DPCP exposure here (Figure 4.10). Proteotoxic stress can occur due to increased protein misfolding and aggregation²⁸³, which offers an explanation for the misfolded protein binding molecular function GO term (GO:0051787) also identified in 16HBE14o⁻ cells exposed to DPCP here (Figure 4.10).

DPCP demonstrated a major significant cellular proteome response, reflected in the number of GO terms returned in this case. In a similar sense to neddylation-related processes, significant enrichment for several protein UFMylation GO terms were identified exclusively in these cells with DPCP treatment. The skin sensitizer DNCB conversely demonstrated a very minor significant cellular proteome response in 16HBE14o⁻ cells (Figure 4.7), which is reflected in the lack of GO terms returned for this data. Indeed, only 1-2 terms were returned across each gene ontology annotation data set, highlighting the structural properties of the significantly different protein IDs (data not shown).

DPCP showed a number of interesting distinctions in gene ontology for 16HBE14o⁻ cell data compared to the respiratory sensitizer PA, particularly in terms of molecular function. The most enriched GO terms highlighted glutathione oxidoreductase activity (GO:0097573) with DPCP, whereas PA exposure showed enrichment for peptidyl-lysine-5-dioxygenase activity (GO:0070815) (Figure 4.10 & 4.11). Proteins enriched for glutathione oxidoreductase activity here represented >60% of the reference proteins for this term, and included thioredoxins and glutaredoxins – redox proteins typically targeting cysteine residues^{284,285}. Proteins enriched for peptidyl-lysine-5-dioxygenase activity here represented 100% of the reference proteins for this term, and included lysine hydroxylases – enzymes typically targeting lysine residues and producing succinate^{286,287}.

Enrichment for adenylate cyclase activator activity (GO:0010856) was observed with both DPCP and PA exposures to 16HBE14o⁻ cells (Figure 4.10 & 4.11). The same set of proteins was found to be enriched in both sample groups and represented 100% of the reference proteins for the term. The majority of enriched proteins were calmodulin isoforms, which have been reported to have roles in regulating cellular functions induced by chemoattractants, production of intracellular ROS and oxidative burst²⁸⁸. TDI exposure in 16HBE14o⁻ cells did not demonstrate this, however the results did present an enrichment for the cellular component GO term oxoglutarate dehydrogenase complex (GO:0045252). Proteins enriched included 2-oxoglutarate dehydrogenases and proteins with alpha-ketoglutarate dehydrogenase activity – generators of superoxide radicals and oxidative stress respectively^{289,290}.

4.3.4 Pathway analysis

Reactome pathway analysis for A549 cells exposed to PA (Figure 4.12) revealed a statistically significant enrichment for proteins involved in the phospho-PLA2 pathway. Phospholipases A₂ (PLA2s) are important enzymes in fatty acid metabolism of membrane phospholipids, as well as playing a role in oxidative and inflammatory signaling pathways²⁹¹. Providing support for the gene ontology results (section 4.3.3), this cell line and treatment also exhibited enrichment for proteins

involved in the MAPK, cell-cell adhesion, and nucleotide biosynthesis pathways. Exposure of A549 cells to TDI highlighted enrichment and significance of Nef-mediated pathways (Figure 4.12). Namely, down-modulation of cell surface receptors such as CD4 and CD8 by recruitment to clathrin adapters. This presents a series of proteins potentially driving down-regulation of T cell-mediated immune responses following exposure to this respiratory sensitiser in more complex biological systems, therefore supporting the divergence in adverse outcome pathway models of skin/respiratory sensitisation^{2,3,229}. TDI exposure also here resulted in an enrichment of several proteins involved in the CLEC7A/inflammasome pathway. Thus identifying potentially causal factors of the allergic airway inflammation and severe asthma development characteristic of CLEC7A pathogenesis²⁹².

Major histocompatibility complex (MHC) protein-related pathways were identified following exposure to each sensitiser chemical. Surprisingly, MHC class II antigen presentation related pathways were enriched by proteins in all samples. MHC class II is generally associated with professional antigen-presenting cells such as dendritic cells than with the epithelial cell lines studied here. However, MHC class II are known to be expressed on the surface of epithelial cells in the lung, albeit without a current understanding of the consequences of this expression for the respiratory adverse outcome pathway²⁹³. Significant enrichment of MHC class I (present in all nucleated cells) antigen processing and presentation related pathways was observed in each of the 16HBE14o⁻ samples only.

Toll-like receptor (TLR) pathways and toll-like receptor cascade pathways were enriched in 16HBE14o⁻ cells, including pathways pertaining to TLRs 3, 4, 5, 9, and 10. Interestingly, these pathways were substantial in protein numbers significantly enriched in samples treated with respiratory sensitisers only. TLRs have well-documented importance in respiratory allergies^{294–296} and are targets of ERK/MAPK signaling pathways – pathways that also showed significant enrichment here. Proteins identified in the TLR-related pathways here included: cathepsins, dynamins, caspases, serine/threonine protein kinases, MAP kinases, nuclear factor kappa B (NF- κ B), and ubiquitin-conjugating enzymes.

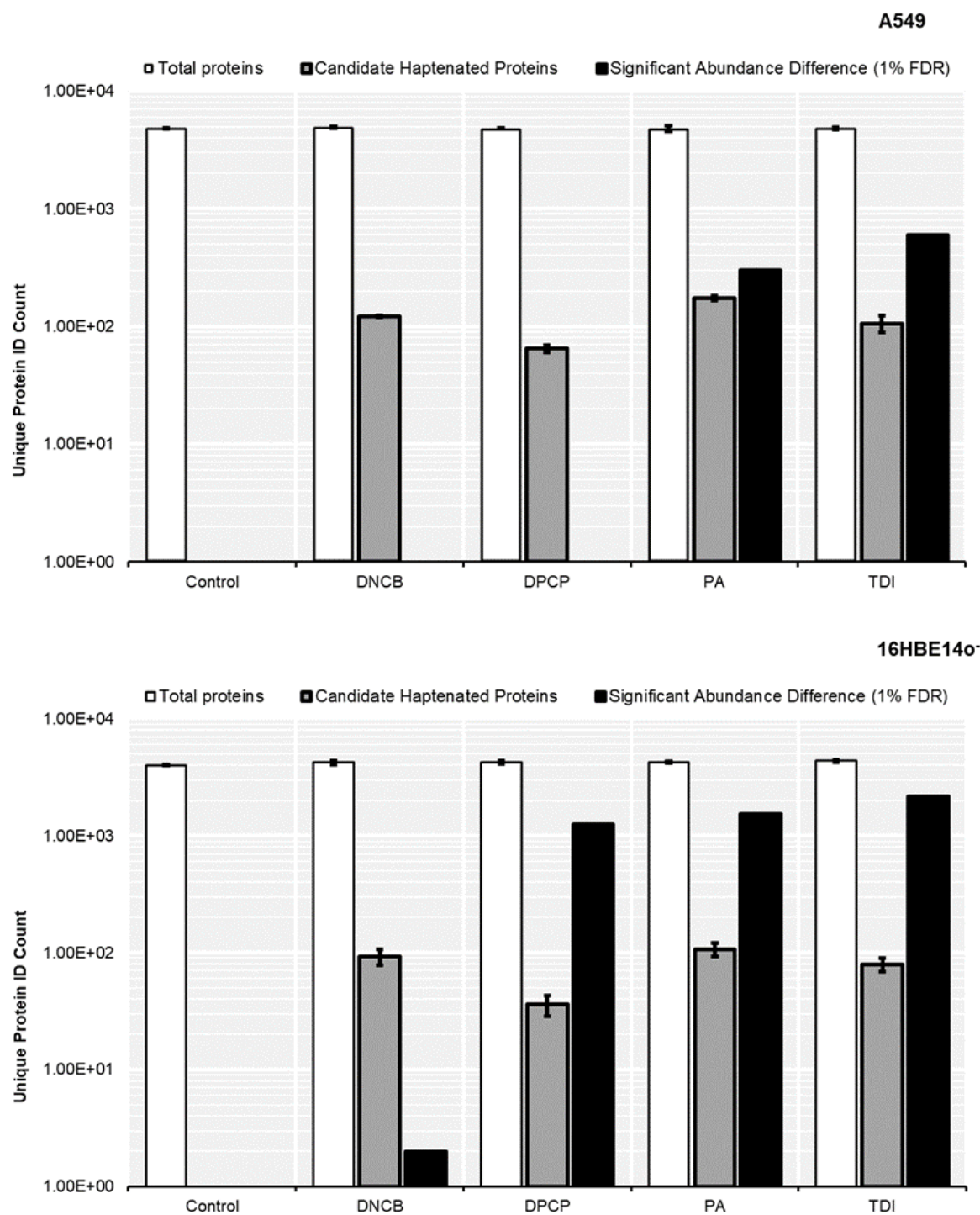


Figure 4.2: The number of total unique proteins, haptenated proteins, and differentially expressed proteins (1% FDR) identified in A549 (top) and 16HBE14o⁻ (bottom) cells – results are presented as unique protein IDs from human proteome database searches for each sensitiser chemical exposure.

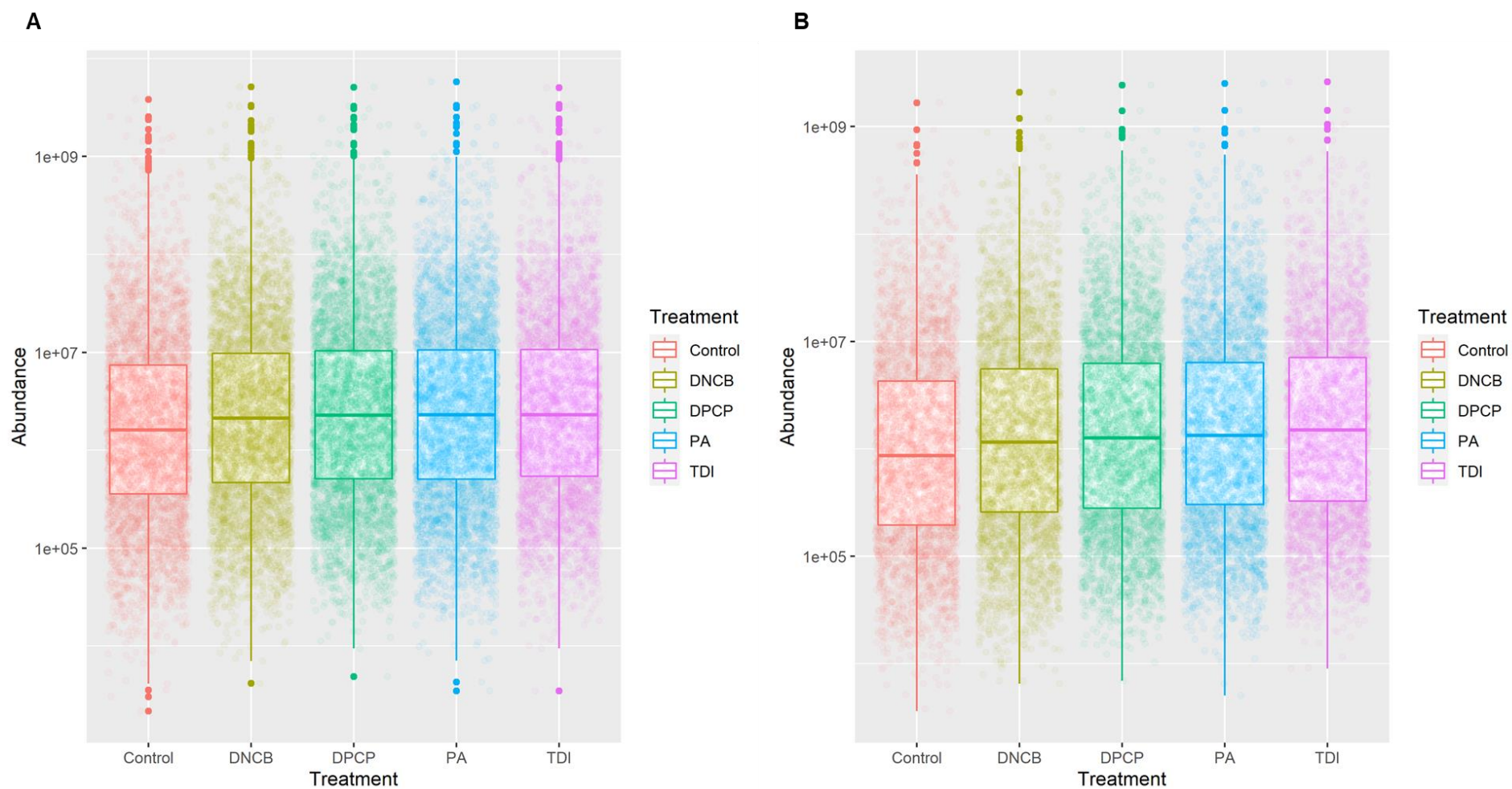


Figure 4.3: The number of proteins identified in the global proteome for A549 (A) and 16HBE14o⁻ (B) cells followed human proteome database searches – results are presented for each sensitizer chemical exposure, showing the relative abundance of each protein identified by LC-MS/MS.

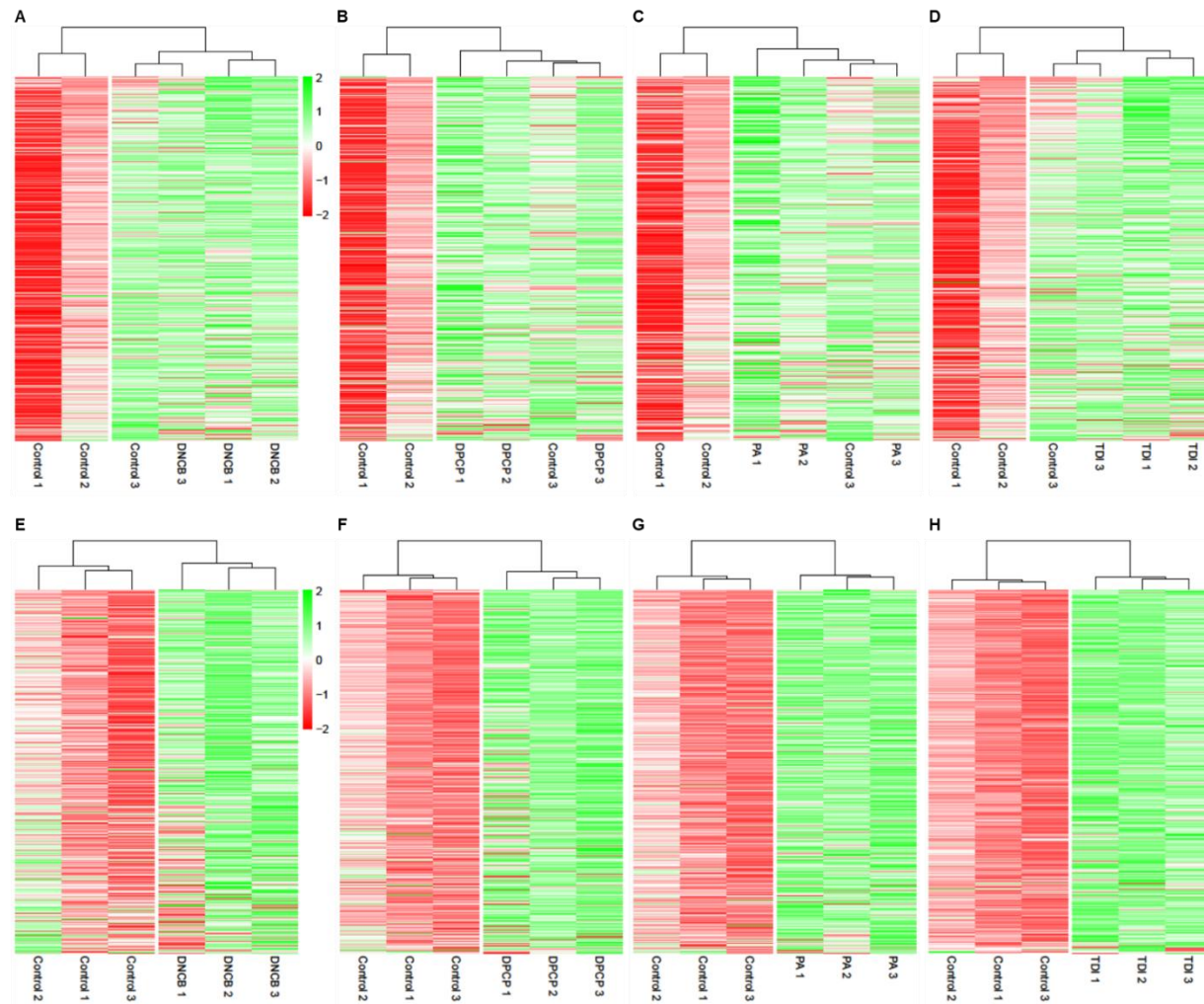


Figure 4.4: Relative fold change in abundance between the control and treatment groups of all proteins identified in the global proteomes – results are presented for each replicate exposure of different sensitisers to A549 cells (A-D) and 16HBE14o⁻ (E-H) following label-free quantitation.

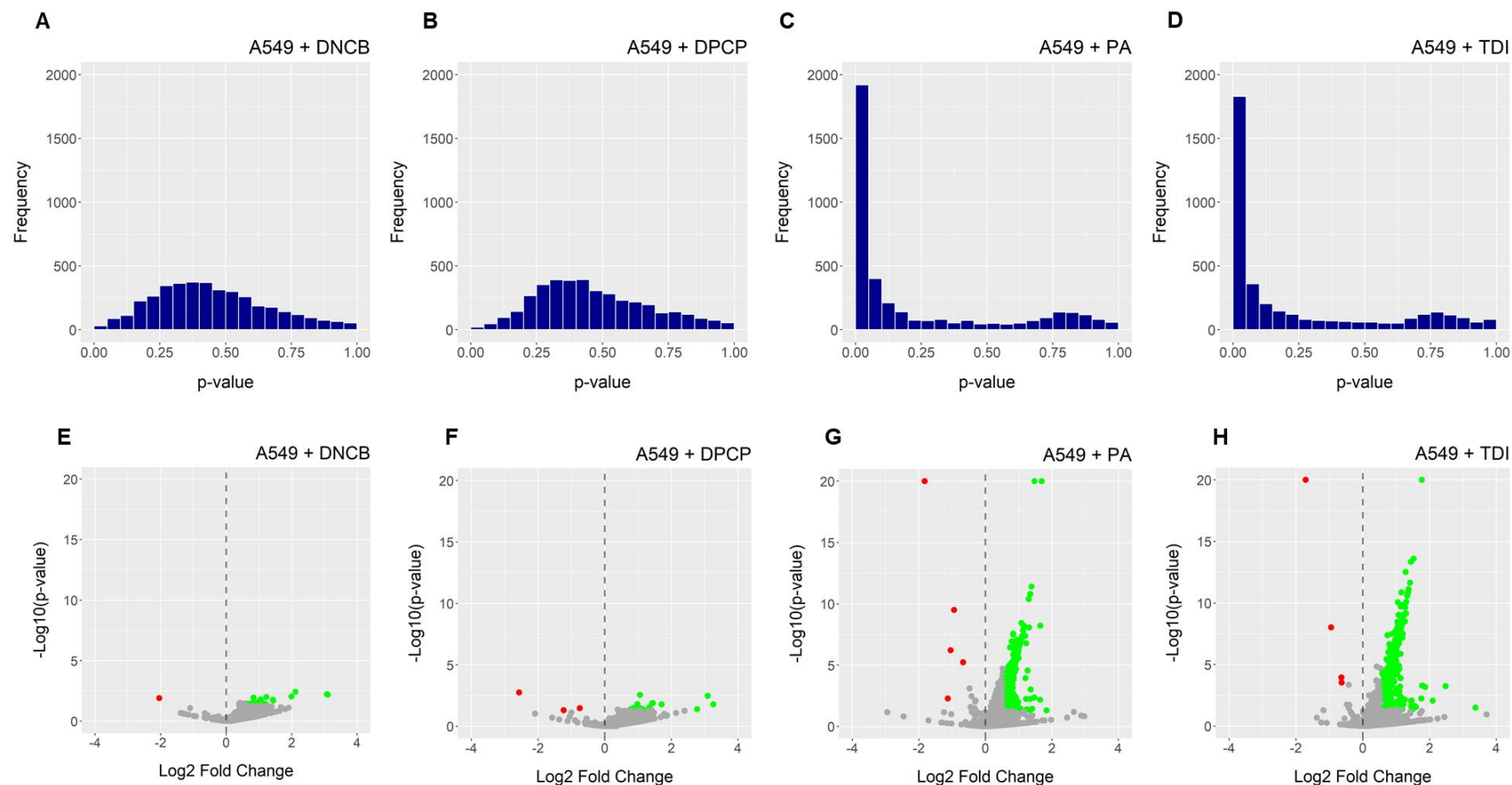


Figure 4.5: Statistical significance of proteins identified in the global A549 proteome following label-free relative quantitation – Histograms of the number of proteins across a range of statistical significance p values are presented for each sensitiser chemical (A-D). Volcano plots for the number of significant proteins ($p < 0.05$) according to log2 fold change are also presented for each sensitiser chemical (E-H).

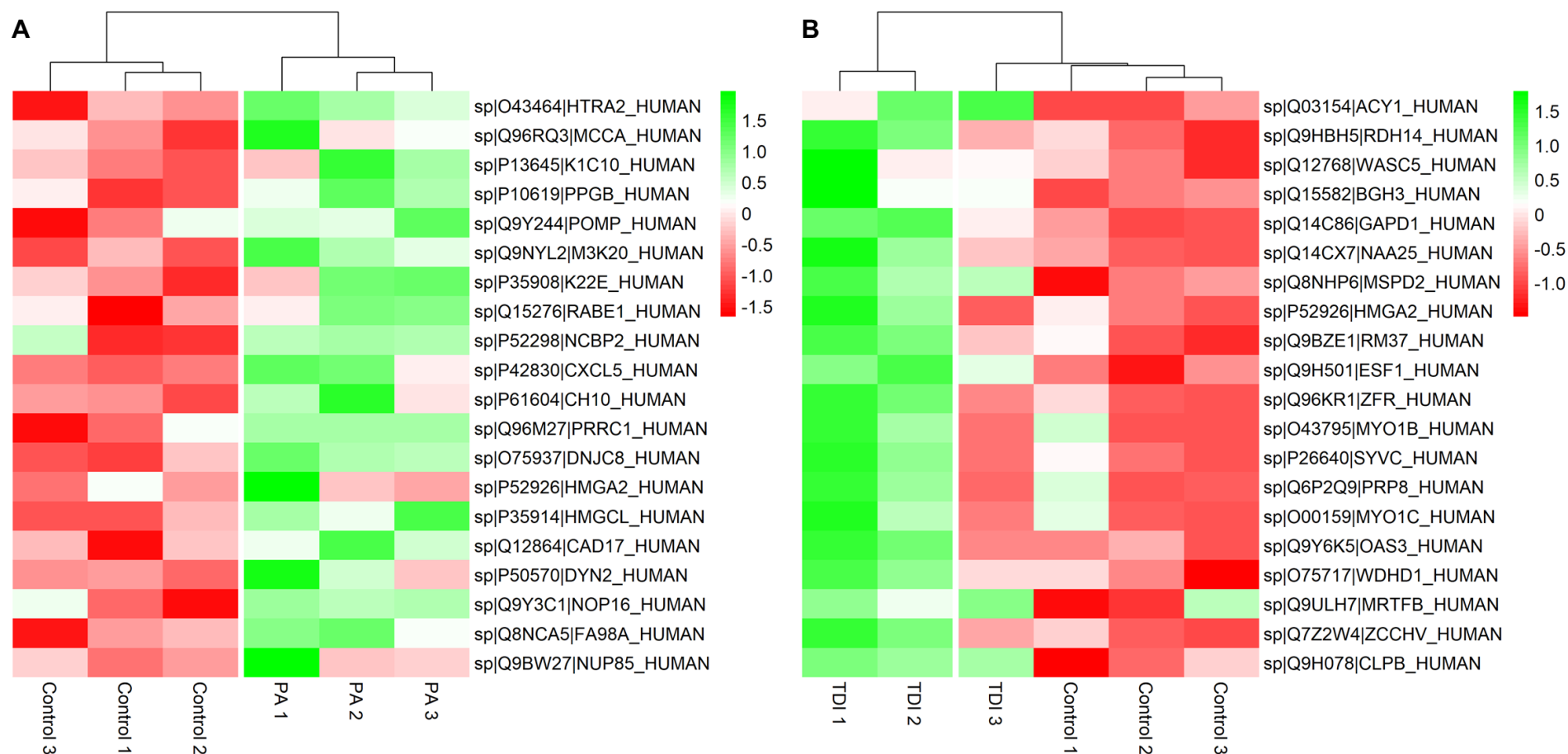


Figure 4.6: Heatmaps of the Top 20 greatest log₂ fold change proteins quantified in the A549 proteome – Statistically significant proteins are presented according to the relative log₂ fold change ratio between the control and sensitiser treatment replicates for PA (A) and TDI (B), clustered in dendrograms according to similarity between sample replicates).

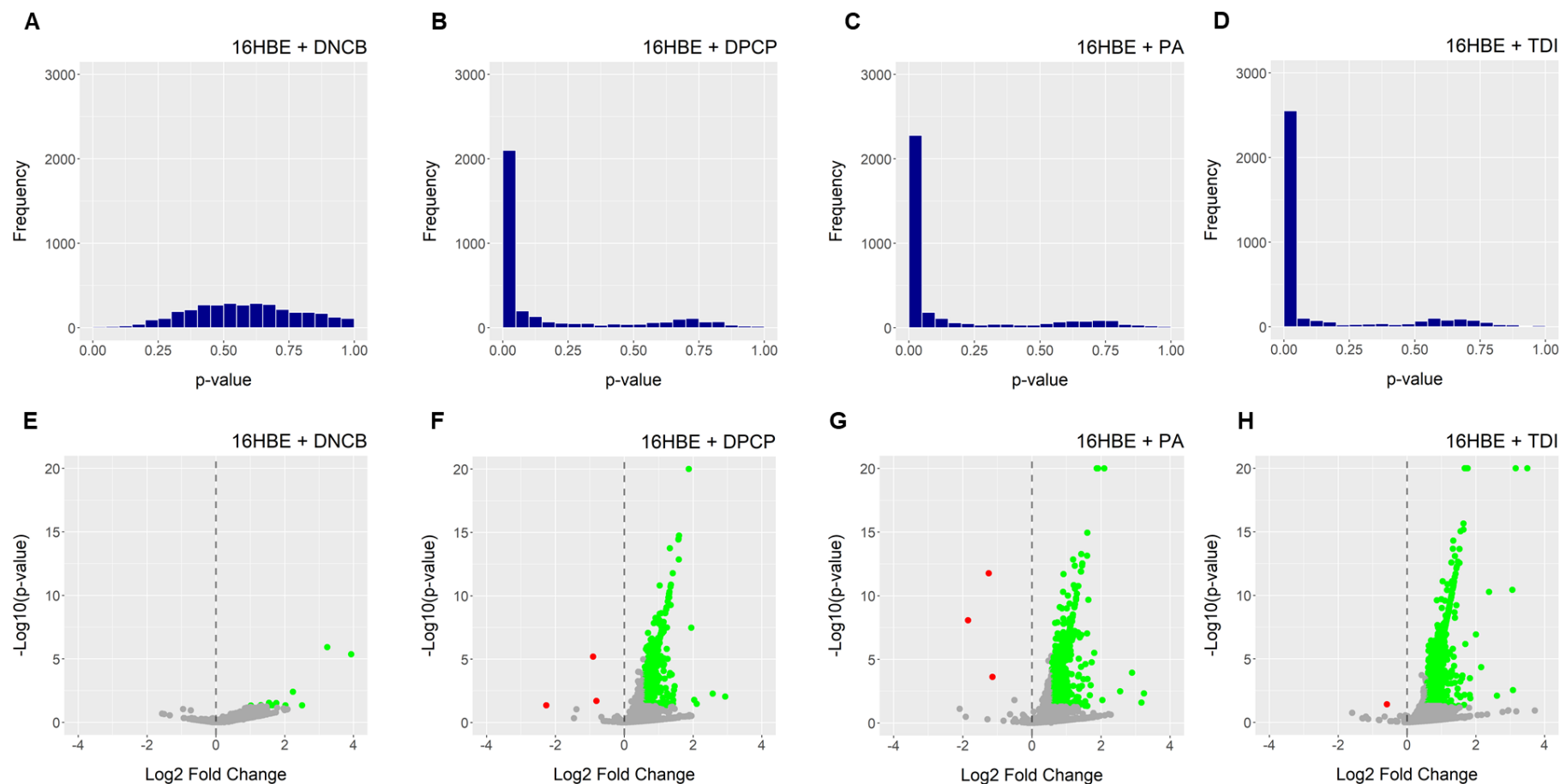


Figure 4.7: Statistical significance of proteins identified in the global 16HBE14o⁻ proteome following label-free relative quantitation – Histograms of the number of proteins across a range of statistical significance p values are presented for each sensitiser chemical (A-D). Volcano plots for the number of significant proteins ($p < 0.05$) according to log₂ fold change are also presented for each sensitiser chemical (E-H).

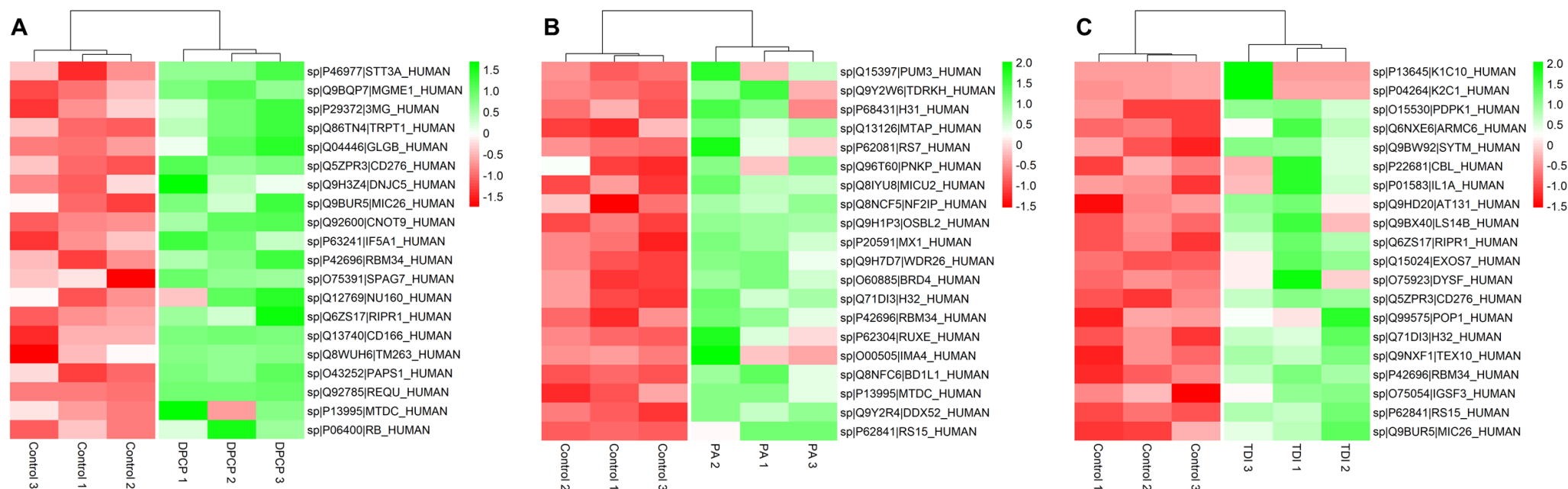


Figure 4.8: Heatmaps of the Top 20 greatest log₂ fold change proteins quantified in the 16HBE14o⁻ proteome – Statistically significant proteins are presented according to the relative log₂ fold change ratio between the control and sensitiser treatment replicates for DPCP (A), PA (B), and TDI (C), clustered in dendrograms according to similarity between sample replicates).

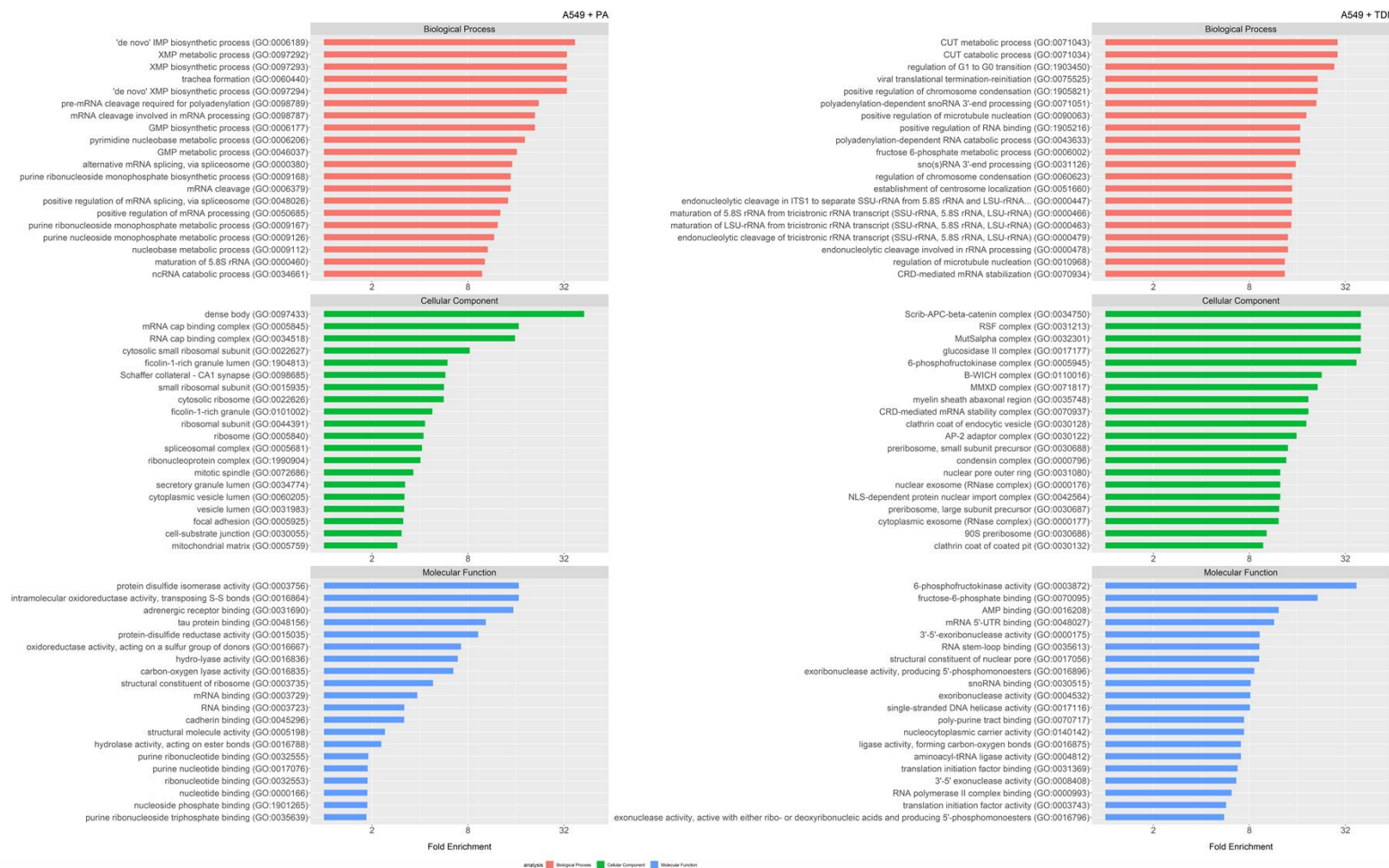


Figure 4.9: Top 20 Gene ontology results for significantly different proteins following PA and TDI exposure to A549 cells – The top 20 greatest fold enrichment and statistically significant (1% FDR) GO terms (biological process, cellular component, and molecular function) in the gene ontology human reference dataset are presented.

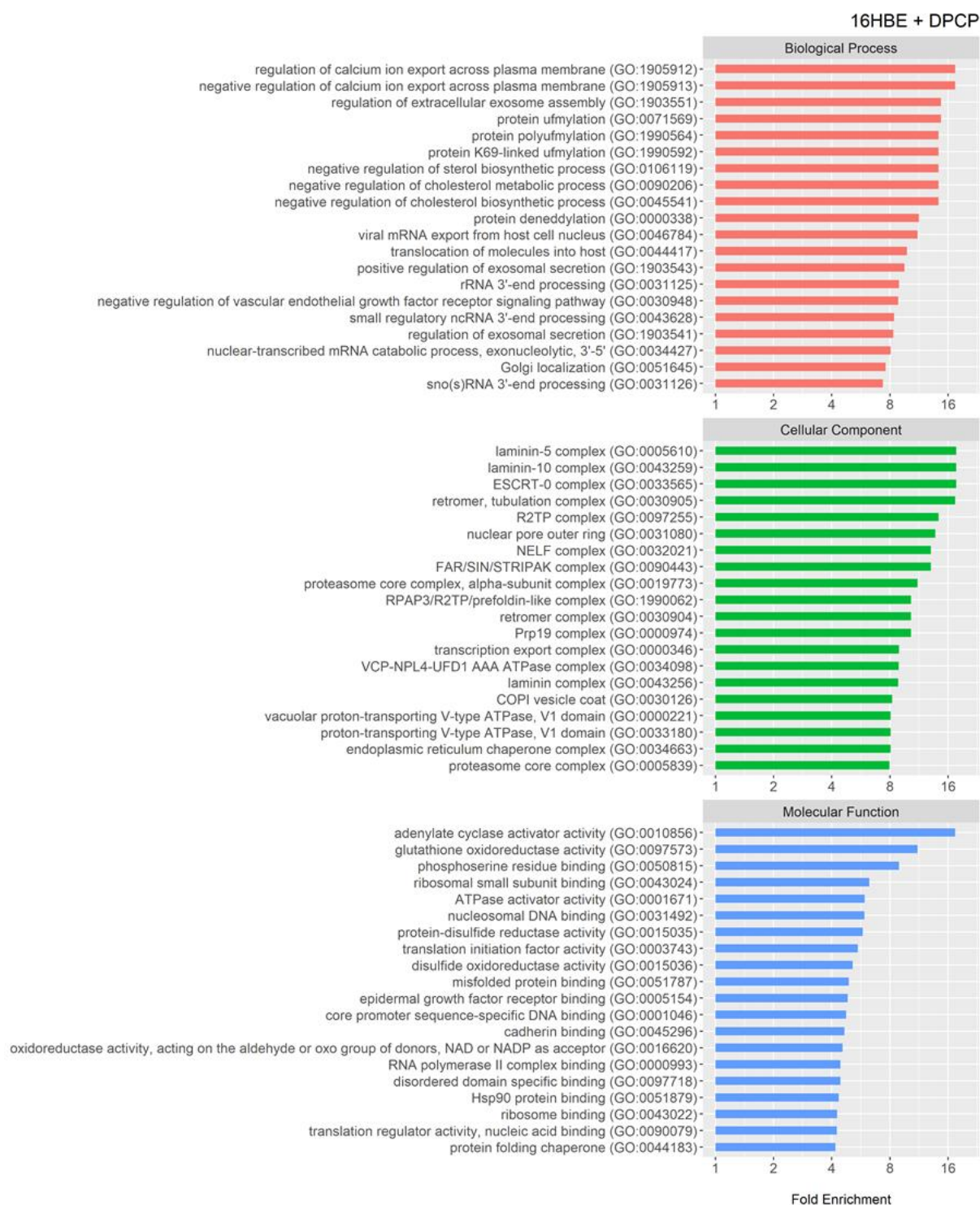


Figure 4.10: Top 20 Gene ontology results for significantly different proteins following DPCP exposure to 16HBE14o⁻ cells – The top 20 greatest fold enrichment and statistically significant (1% FDR) GO terms (biological process, cellular component, and molecular function) in the gene ontology human reference dataset are presented.

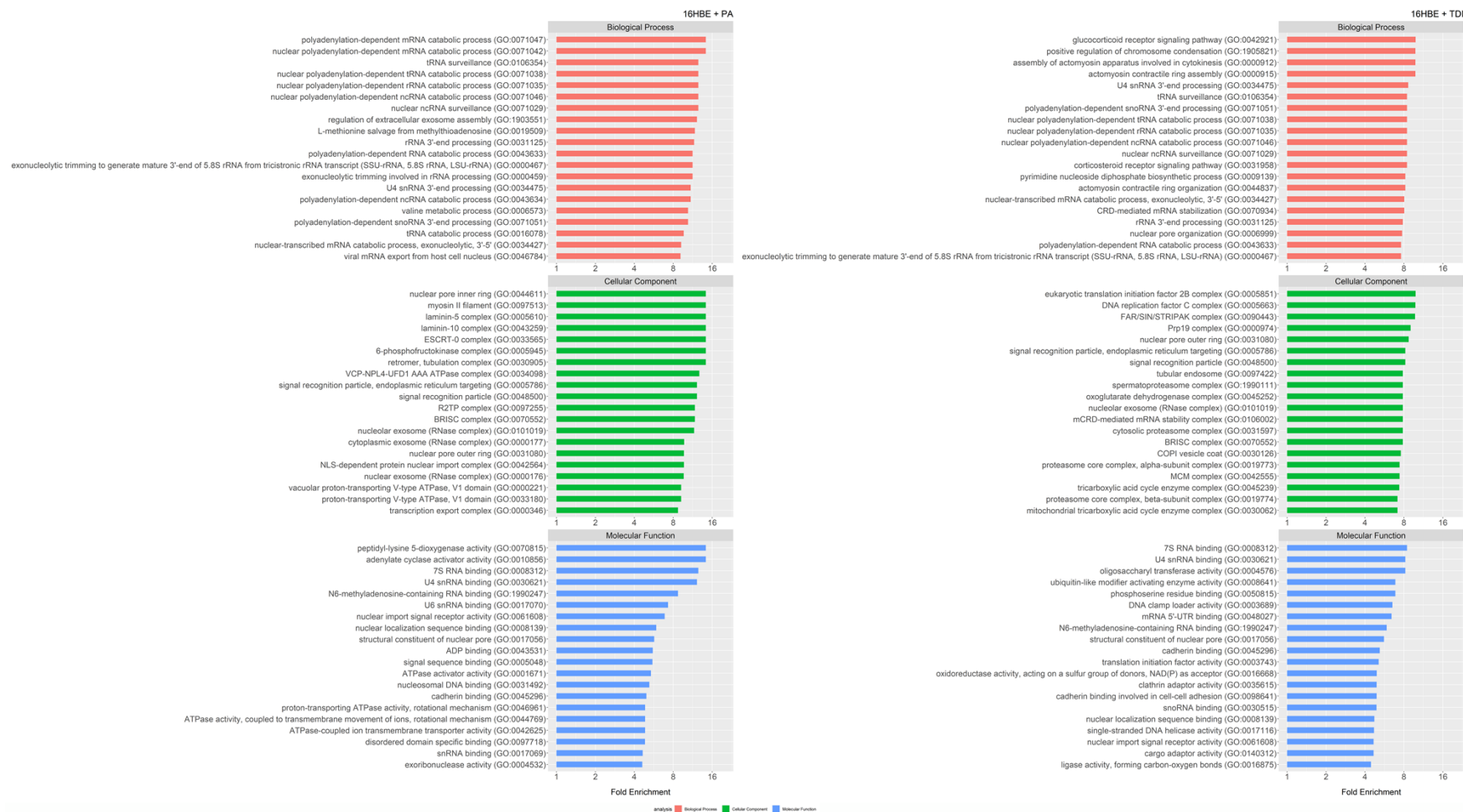


Figure 4.11: Top 20 Gene ontology results for significantly different proteins following PA exposure to A549 and 16HBE140⁻ cells – The top 20 greatest fold enrichment and statistically significant (1% FDR) GO terms (biological process, cellular component, and molecular function) in the gene ontology human reference dataset are presented.

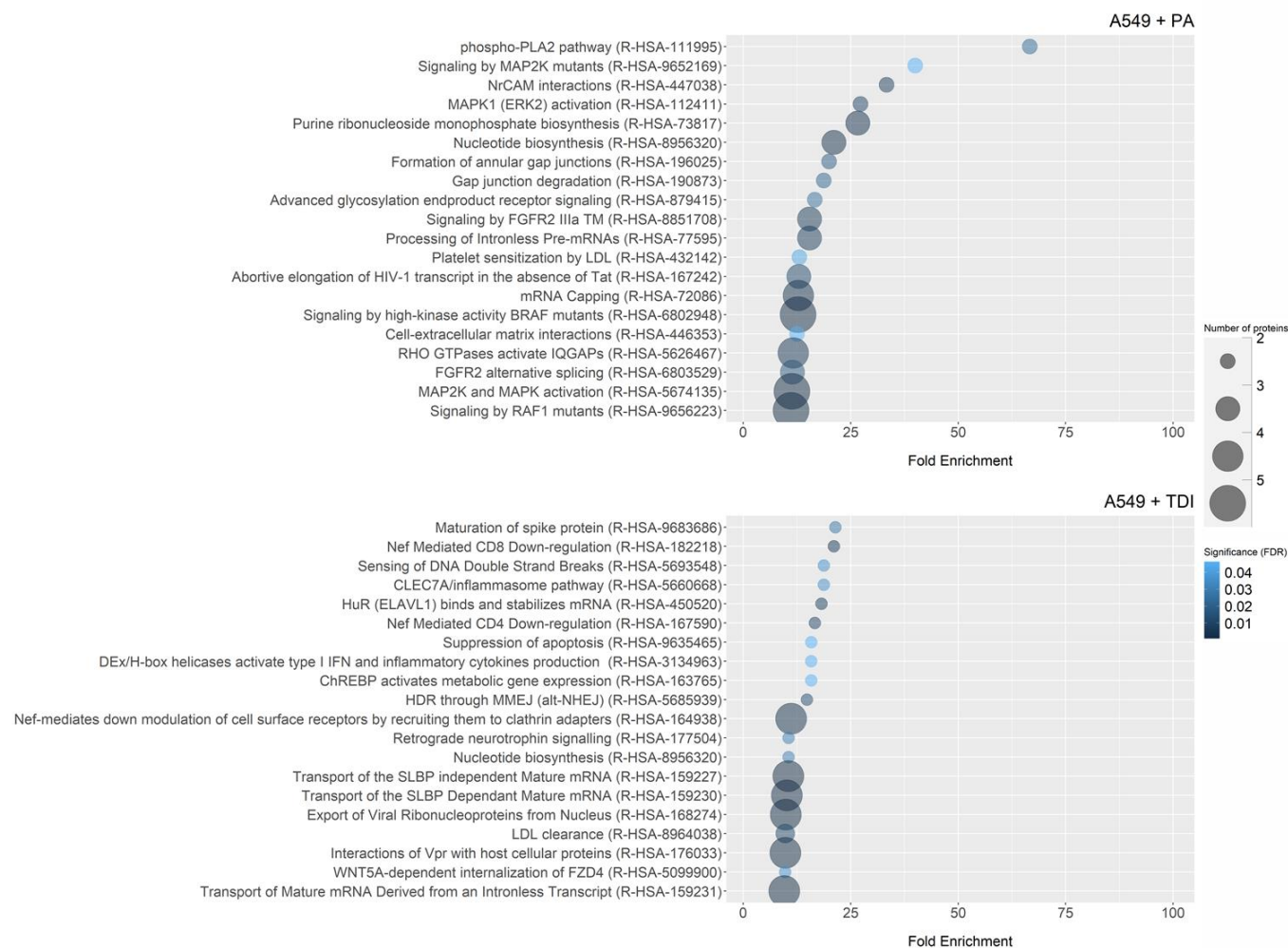


Figure 4.12: Top 20 Reactome pathways enriched for significantly different proteins following PA (top) and TDI (bottom) exposure to A549 cells – The top 20 greatest and statistically significant (1% FDR) fold enrichment pathways in the Reactome reference dataset are presented.

4.3.5 Differential hapten-target proteins elucidated in the haptenome by dual isotope labelling mass spectrometry methods

Stable dual isotope labelling²⁷ was utilised here, in combination with data-dependent LC-MS/MS for the identification of specific haptenated protein candidates as a proportion of the global A549 and 16HBE14o⁻ cellular proteomes. Potentially haptenated proteins were identified according to specific post-translational modification input parameters in Peaks® X Studio with relevant filtering of the total sample protein lists. Haptenated peptides were confirmed qualitatively through observation of a unique signature of 2 peptide isotope clusters with fixed $\Delta m/z$ in the MS spectrum, with exact location of haptenation confirmed by manual inspection of the MS/MS spectrum of the identified modified precursor for confident coverage of *y* and *b* ions (Figures 4.13 & 4.14).

Initial searches for cysteine and lysine modifications by different haptens in the proteome data generated the candidate haptenome prior to validation with MS/MS spectra. The candidate haptenome for A549 cells (Figure 4.2) identified on average: 157 peptides with DNCB, 80 peptides with DPCP, 244 peptides with PA, and 132 peptides with TDI treatment. Repeating the cysteine and lysine modification searches for 16HBE14o⁻ samples (Figure 4.2) identified on average: 112 peptides DNCB, 48 peptides with DPCP, 157 peptides with PA, and 99 peptides with TDI treatment.

Analysing the total number of unique peptides and related proteins in each A549 candidate haptenome presented a total candidate haptenome size of 409 peptides related to 365 proteins with DNCB (7.40% of the proteome), 195 peptides related to 195 proteins with DPCP (4.05% of the proteome), 610 peptides related to 524 proteins with PA (10.87% of the proteome), and 346 peptides related to 318 proteins with TDI (6.55% of the proteome). Analysing the total number of unique peptides and related proteins in each 16HBE14o⁻ candidate haptenome presented a total candidate haptenome size of 289 peptides related to 278 proteins with DNCB (6.56% of the proteome), 111 peptides related to 108 proteins with DPCP (2.54% of the proteome), 354 peptides related to 321 proteins with PA (7.55% of the proteome), and 247 peptides related to 237 proteins with TDI (5.43% of the proteome).

Following validation of MS/MS spectra, A549 haptenomes (Appendix Table 6-9) showed on average: 28 peptides with DNCB, 8 peptides with DPCP, 34 peptides with phthalic anhydride, and 17 peptides with TDI. These validated haptenomes for A549 cells (Figure 4.16) presented a total of 82 distinct peptides associated with 97 unique proteins following DNCB exposure (1.97% of the proteome), 24 distinct peptides related to 24 unique proteins with DPCP (0.50% of the proteome),

100 peptides related to 93 proteins with PA (1.93% of the proteome), and 49 peptides related to 47 proteins with TDI (0.97% of the proteome). Further, the relative total number of cysteine and lysine residues following validation were 87 (DNCB), 24 (DPCP), 106 (PA), and 57 (TDI).

There is a precedence for confirmed modifications appearing in only one or two replicates which was attributed to detection of haptentation at low levels coinciding with sensitivity limitations of the instrumentation and data processing²⁸. The true positive rate of identifying haptentation is essentially a measure of sensitivity. The large number of false positives identified in other haptentation studies^{11,28} is similar to the level observed here, reinforcing the concept of sensitivity limitations in distinguishing between true and false positives. The dual stable isotope labelling method and manual confirmation adds a further level of sensitivity and confidence that serves to lessen the impact of these limitations in identifying confirmed haptentated proteins. Furthermore, the low level of proteome haptentation and candidate peptides in the haptentome mean that the majority of peptides are not replicated between samples. The number of confirmed protein modifications in studies using this stable dual isotope labelling method has generally been demonstrated to be a lower proportion of the proteome (<1%) than the candidate haptentomes presented here^{8,9} – being more in line with the validated haptentome results.

It was observed that the candidate haptentome peptides were identified later in the MS scan (higher MS scan no.) where the concentration of organic solvent is at its greatest in the LC elution gradient. This is logical given haptentation of polar, nucleophilic residues would also increase the hydrophobicity of the peptides, making them less polar and elute later in the gradient. Further to this, the candidate haptentome peptides were general of lower relative abundance compared to the full repertoire of peptides identified in the MS scan. Indeed, there were a substantial number of candidate peptides too low in abundance to be quantified at all. Haptentated peptides following manual MS/MS spectra validation also followed this general trend. However, the identity of the modified amino acid (whether cysteine or lysine) was different to the general lysine preference demonstrated in the candidate haptentome here. Following validation, it was observed that the majority of modified residues in the haptentome were cysteine for skin sensitisers and lysine for respiratory sensitisers.

Of the validated haptentome results for A549 cells exposed to DNCB, several of interest were uniquely identified. Alcohol dehydrogenase class-3 (glutathione dehydrogenase) was modified on a lysine residue that catalyses the oxidation of glutathione whilst also being important in the prevention of DNA damage²⁹⁷. Glutathione is an important antioxidant protein in the AOP protein haptentation models of skin sensitisation. Further, cells putatively produce glutathione to resist

oxidative stress, with increased levels of oxidised glutathione being an indicator of cellular oxidative stress²⁹⁸.

CD44 antigen is a transmembrane glycoprotein with an extracellular matrix hyaluronic acid component crucial in the recruitment of effector and memory T cells^{299,300}. This function of CD44 is characteristic of the cell-mediated hypersensitivity of skin sensitisation. Further, a peptide of the CD44 protein was observed to be haptenated exclusively by DNCB on a lysine residue here. Heat shock proteins were also observed in the DNCB-A549 haptenome here, consistent with the haptenome findings in similar studies on human keratinocytes⁸. Interestingly, HSPs have also been shown to cross-present with MHCI complex proteins responsible for endogenous antigen presentation³⁰¹.

Hypoxia-upregulated 1 gene is a chaperone protein localised to the endoplasmic reticulum and associated frequently with cellular stress³⁰². A peptide for this protein was found to be exclusively haptenated on a lysine residue by phthalic anhydride, along with other PA adduct structures and other redox-related proteins. For example, thioredoxins are important cysteine-targeting antioxidant proteins highlighted in the cellular response to sensitisation here previously, and were present in the A549-PA haptenome here too. Human alpha-enolase (ENOA, Uniprot: P06733) was haptenated on both a cysteine and lysine residue by PA adduct structures of $\Delta 148$ and $\Delta 130$ respectively. ENOA is a cytoplasmic/membrane glycolytic enzyme, which in addition to glycolysis is also important in processes of hypoxia tolerance and allergic response^{303,304}, which also has the potential to stimulate immunoglobulin production in human cells³⁰⁵.

Dual specificity mitogen-activated protein kinase kinase 1 (MAP2K1) is an essential component of the MAP kinase signaling pathway, and showed a significantly increased expression in the A549 proteome following exposure to phthalic anhydride. Additionally, a peptide for this protein was haptenated exclusively by PA on a lysine residue in the A549 haptenome here, further highlighting the importance of this protein in the cellular response to PA exposure. The importance of transmembrane cadherins in the cellular response to respiratory sensitisers has been illustrated here previously, with roles in oxidative stress regulation via endogenous antioxidant systems. Vinculin (P18206) is an actin filament-binding protein which regulates cadherin expression³⁰⁶, and was haptenated exclusively by PA on a lysine residue in the A549 haptenome.

TDI exposure to A549 cells resulted in several distinct peptides for mitochondrial proteins involved in electron transfer and the respiratory chain complex. NADH-ubiquinone oxidoreductase (NDUS1), 3-ketoacyl-CoA thiolase (THIM), and the dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (ODP2) were each exclusively observed in the haptenome modified by TDI on lysine residues.

Generally, a notable proportion of proteins represented in the A549 haptenome with each sensitiser were mitochondrial proteins, including various dehydrogenases, redoxins and other redox-related proteins. Further, a number of these proteins were distinct between the different sensitiser exposure groups. A large proportion of membrane and cytoskeletal proteins were observed throughout the haptenome following exposure to different sensitiser chemicals. As well as being one of the major sites for the ubiquitin-proteasome system, this observation serves to demonstrate the value of the cell culture extraction scraping method used to harvest cells in the methodology here (chapter 3.2.3). A majority of proteins represented in the haptenomes were also cytoplasmic/cytosolic proteins, which is another major site for the ubiquitin-proteasome system. For example, differences in the E3 ubiquitin-protein ligases were also observed in the haptenome following exposure to chemical sensitisers: TRIM47 and UBR4 with DNCB exposure, RNF213 and UBR4 with phthalic anhydride exposure, and ARIH2 – which mediates lysine-linked polyubiquitination³⁰⁷ – with TDI.

Gene ontology cellular component enrichment analysis showed that the majority of proteins represented in the haptenome are localised to the cytoplasm, cytosol, endoplasmic reticulum, and mitochondrion (data not shown). However, an enrichment for 48 proteins in the DNCB haptenome of A549 cells showed a statistically significant (FDR) 1.63-fold enrichment for nuclear localisation. This was not observed with the haptenome proteins for either respiratory sensitiser. Peptidyl-prolyl cis-trans isomerases were observed in the A549 haptenome following respiratory sensitiser exposure, but not skin sensitiser exposure. These proteins potentially have protective roles against oxidative stress in mitochondria. Therefore, they would logically be of further interest in distinguishing between the reactivity of skin and respiratory chemical sensitisers in more complex cellular systems.

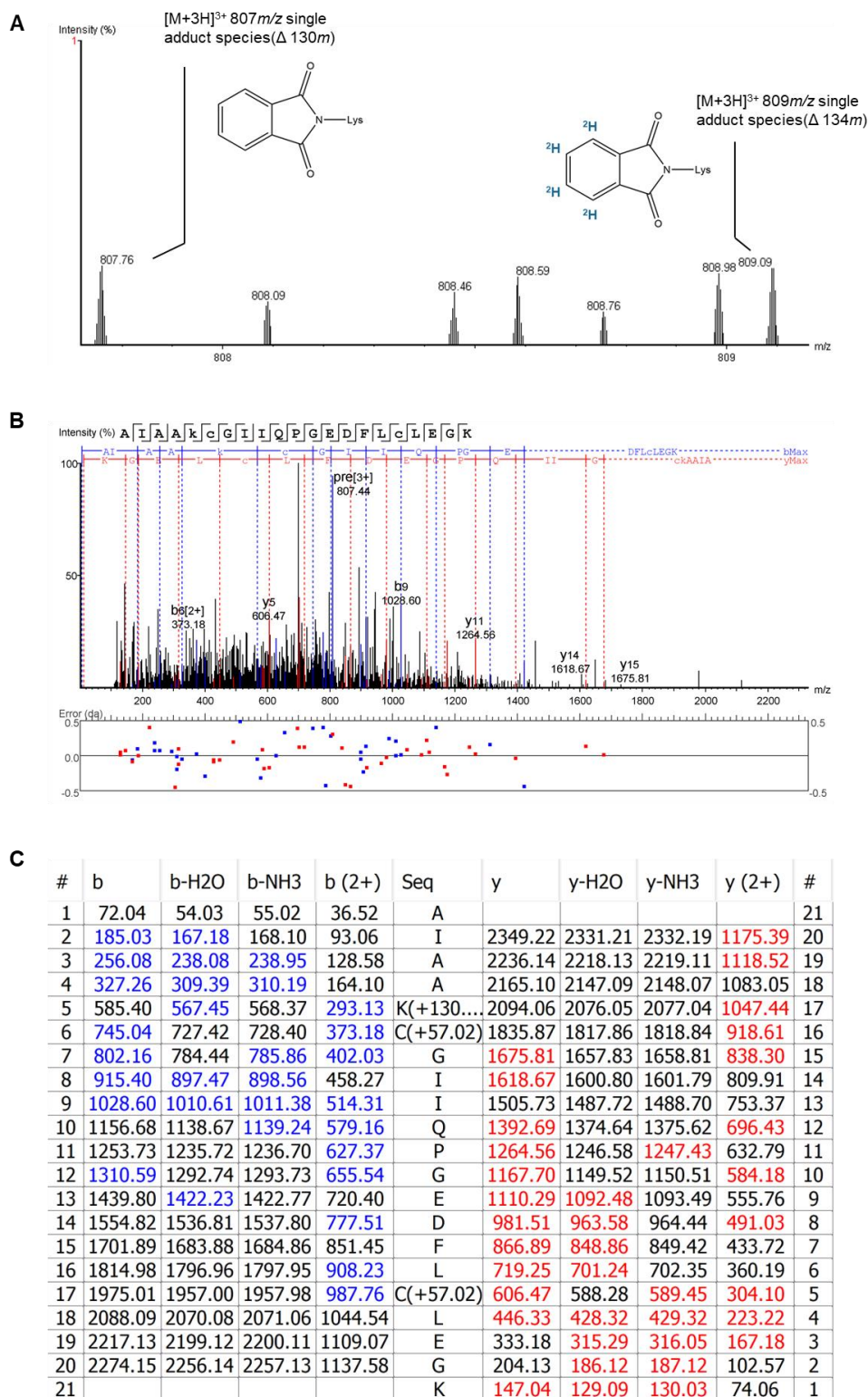


Figure 4.13: Haptenated peptide validation for a single lysine residue haptenation (+130 m/z) of plasma membrane calcium-transporting ATPase 3 (ATP2B3, Uniprot: Q16720) in the A549 haptenome – LC-MS spectrum highlighting the peptide m/z doublet with a single un-deuterated modification and single deuterated modification in the same sample (A). Fragmentation spectrum for the peptide sequence the haptenation was observed on (B). Ion table presenting coverage of the various y and b ions generated by peptide fragmentation for the modified sequence (C).

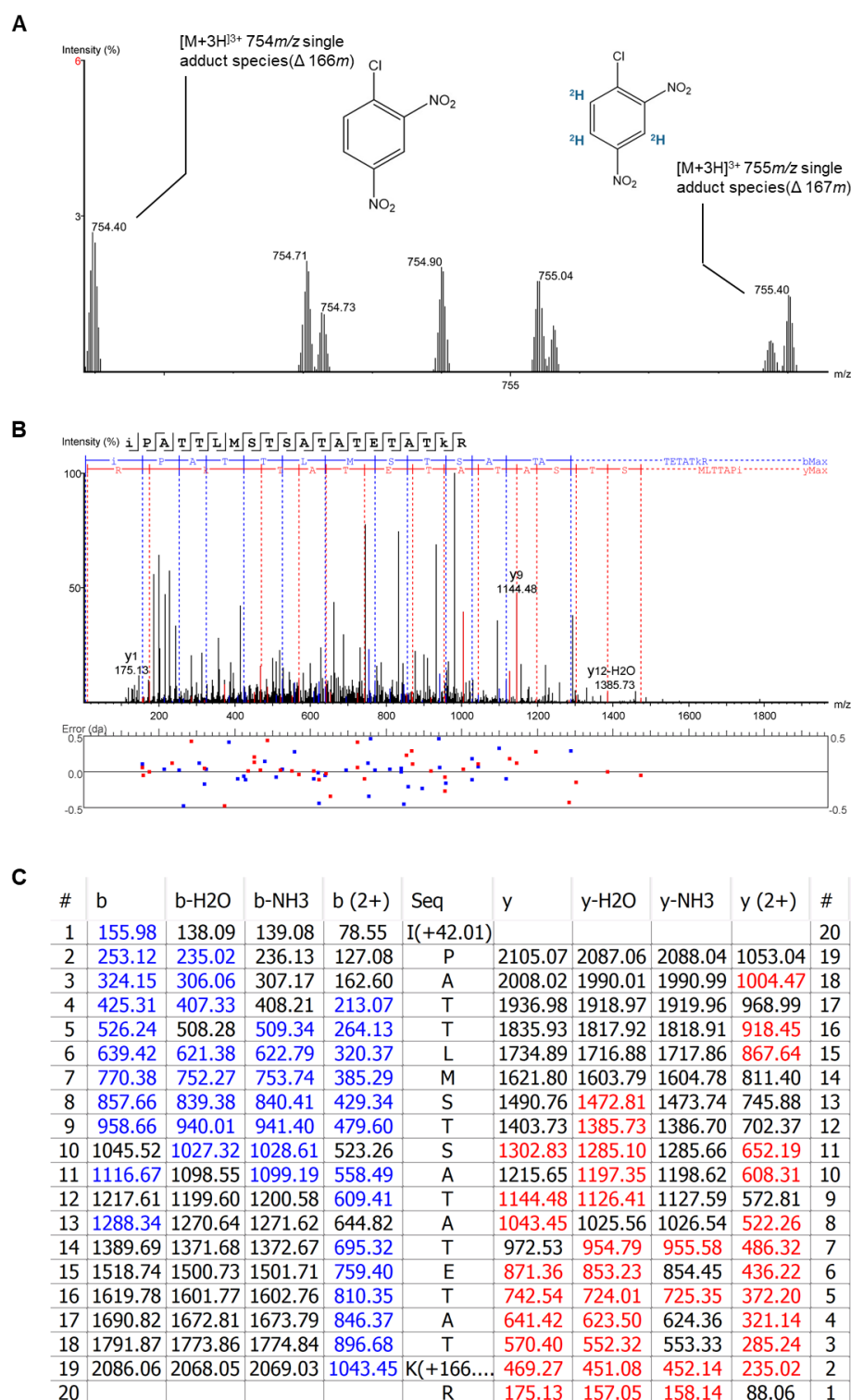


Figure 4.14: Haptenated peptide validation for a single lysine residue haptenation ($\Delta 166$ m/z) of CD44 antigen (CD44, Uniprot: P16070) in the A549 haptenome – LC-MS spectrum highlighting the peptide m/z doublet with a single un-deuterated modification and single deuterated modification in the same sample (A). Fragmentation spectrum for the peptide sequence the haptenation was observed on (B). Ion table presenting coverage of the various y and b ions generated by peptide fragmentation for the modified sequence (C).

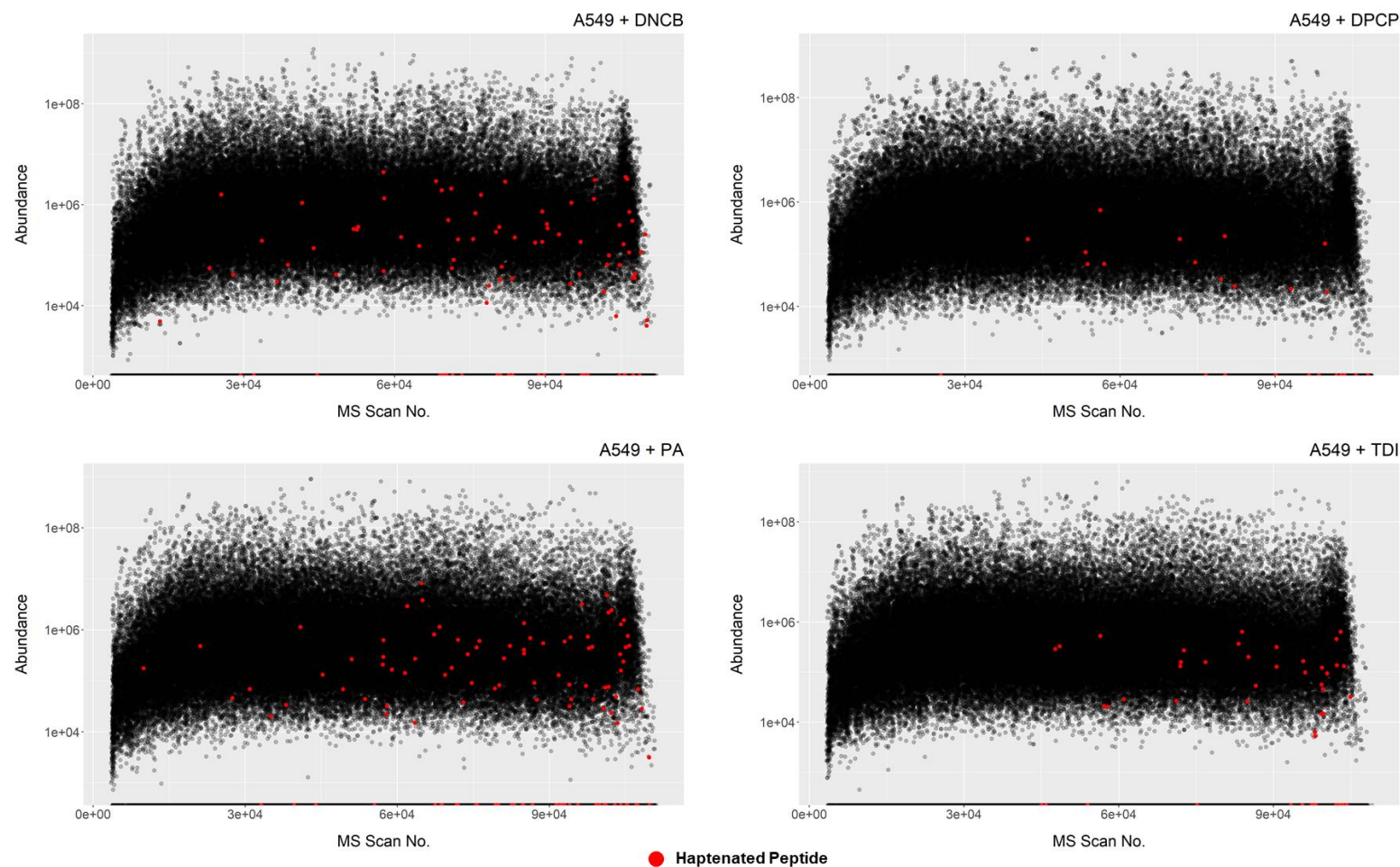


Figure 4.15: A549 validated haptenome – The repertoire of peptides for each sensitiser exposure identified in human proteome database searches are presented according to their relative abundance and position within the total LC-MS separation gradient. Peptides validated with a hapten post-translational modification are highlighted.

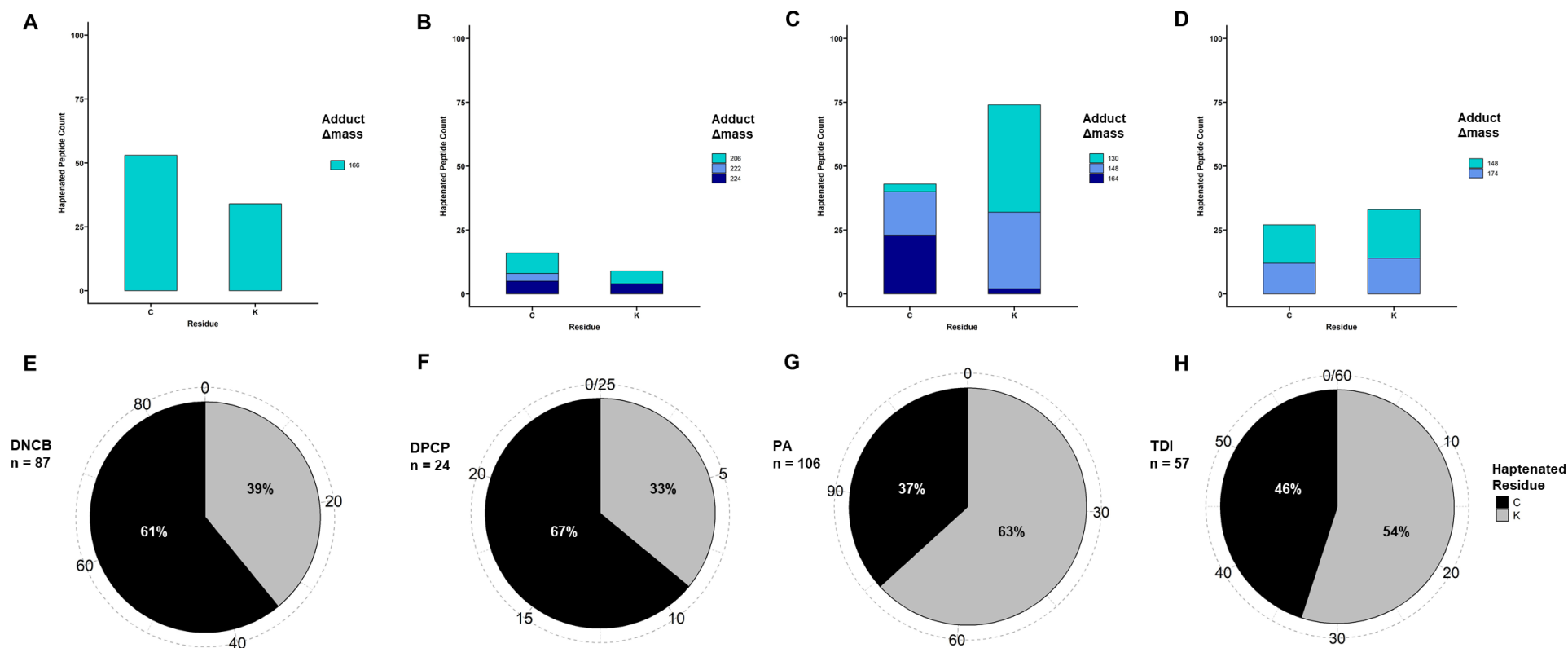


Figure 4.16: Proportions of hapten modifications in the validated haptenome for A549 cells exposed to each chemical sensitiser – The number of cysteine and lysine residues in the global proteome data observed with a hapten post-translational modification, and validated via inspection of MS/MS spectra are presented. The number of each hapten-peptide adduct structure (adduct Δ mass) is presented as a relative proportion of the total haptenated residues following exposure to DNCB (A), DPCP (B), PA (C), and TDI (D). The number of haptenated cysteine residues is presented alongside the number of haptenated lysine residues as relative proportions of the total haptenome for DNCB (E), DPCP (F), PA (G), and TDI (H).

4.4 Discussion

Until recently, *in vitro* data for formation of specific protein conjugates and associated cellular response in keratinocytes represented a significant knowledge/data gap. Understanding was also unsatisfactory for chemical reactions favouring nucleophilic amino acid residues other than cysteine/lysine^{1,31}. These gaps have since been decreased through the work of Aleksic *et al*²⁶ and Parkinson *et al*²⁷, amongst others, in increasingly complex nucleophile systems. This has been extended here to respiratory epithelial cells, with exposure to both skin and respiratory chemical sensitisers.

Distinct differences in proteins and associated functions/pathways are naturally of interest to the further development of adverse outcome pathways of sensitisation. However, the dynamics of haptenation and specific modified proteins with sensitising chemicals in the human cell lines studied here is under-represented in the literature, and hitherto also remained a key knowledge gap as a comparison to keratinocytes. Tandem mass spectrometry was utilised here with deuterium dual isotope labelling methods optimised for the identification of specific, low abundance haptenation events^{8,27} within the context of differential expression in the proteomes of living cells following exposure to different chemical sensitisers.

With the chemical viewpoint of biological systems in studies of this nature, it is apparent that a very large proportion of structures (particularly nucleic acids and proteins) contain electron-rich nucleophilic groups¹⁶. Therefore, it is perhaps unsurprising that a broad array of structures and processes can be disrupted by the electrophilic haptenation action of chemical sensitisers. However, in this context even fairly ubiquitous proteins potentially have important roles in the adverse immunological outcomes of sensitisation. The variety of proteins – both of high and low abundance – demonstrating significant differential expression following skin and respiratory sensitiser exposure demonstrate this. Further, the patterns of biological process, molecular function, cellular component, and Reactome pathways reinforce this.

Proteins identified consistently across the treatment groups here reflect proteins identified by Parkinson *et al* in keratinocytes^{8–10}. For example, keratins, heat-shock proteins, and cytoskeletal proteins. Differential expression of histones were also identified in the analyses here, potentially reflecting the relative importance of histone modification in asthma³⁰⁸ and supporting the observed haptenation of histones in other studies²³¹.

Differences in the uniformity of results across the treatment groups here may in part result from differences in the exposure dosage, sensitisation potential and relative potencies of the various

sensitiser chemicals. The different dynamics in haptentation reaction mechanisms for an individual chemical may also have an influence. These analyses alone cannot completely answer these questions, but instead contribute to the findings of studies designed to address them within the weight-of-evidence of the adverse outcome pathway models. Nevertheless, a number of inferences can be made from the data presented here.

The redox and oxidative stress-related proteins glutaredoxins, thioredoxins, peroxiredoxins, sulfiredoxins, nucleoredoxins, cadherins, and aldehyde dehydrogenases are of particular interest and were shown to significantly increase in protein expression for each cell line. Comparison of the skin sensitiser DPCP and respiratory sensitiser PA revealed an interesting difference in GO molecular function enrichment. The glutathione oxidoreductase activity identified following DPCP exposure at the greatest fold enrichment amongst significantly enriched functions included a variety of proteins from this repertoire. Molecular function enrichment for PA-exposed cells featured peptidyl-lysine-5-dioxygenase activity with several lysine hydroxylase enzymes. This further highlights the role of cellular stress in response to these chemical sensitisers, but also illustrates potential divergence between target residues for the enzyme activity (i.e. cysteine vs lysine). Differences in the formation of reactive oxygen species (ROS) and reactive nitrogen species (RNS) would also be of interest in this capacity. In future it is therefore also worth comparing the induction of oxidative stress, nitrosative stress, and electrophilic stress by skin and respiratory sensitisers exposed to these cells.

Lysine hydroxylase proteins are known to target lysine residues whilst producing succinate^{286,287}, and were found to be significantly enriched in peptidyl-lysine-5-dioxygenase molecular functions. Increased intracellular succinate levels have been linked to oxidative stress in human keratinocytes³⁰⁹. Further evidence for the importance of succinate metabolism has been presented here with the significantly increased expression of succinate CoA ligases exclusively following respiratory sensitiser exposure. Paired with the succinate dehydrogenase differential expression observed with all sensitiser exposures, this may suggest all the chemical sensitisers used here induce oxidative stress but possibly to a greater extent with respiratory sensitisers. A wealth of mitochondrial proteins/pathways were differentially regulated in the context of oxidative stress here. The mitochondrial respiratory chain complex therefore also appears to be of importance to the cellular response to these electrophilic insults.

The range of peroxiredoxin antioxidant proteins with significantly increased expression here suggests detoxification of peroxides are an important feature of the cellular response in this model. Oxidative stress coupled to oxidative degradation of lipid membranes, commonly referred to as lipid peroxidation²⁵⁵, characteristically increases permeability of cell membranes³¹⁰. This

offers some explanation for the variety of membrane proteins and signaling pathways being differentially regulated. These considerations present the hypothesis of sensitiser exposure causing differential membrane permeability to haptens and/or hapten-conjugates via lipid peroxidation. This would logically result in increasing levels of intracellular haptening and associated cellular resistance to this stressor. A threshold between these two processes would likely exist. Additionally, cell membrane permeability would hypothetically provide a route by which endogenous hapten-protein conjugates from initial exposure could subsequently become exogenous antigens for other cells. Further research, in more complex systems, would be needed to further develop these hypotheses for exploring haptening dynamics and divergence of T_h1/T_h2 immune responses. Though the results and analysis here do provoke new hypotheses such as these.

Increased metabolic burden is a likely feature created by the cellular stress responses evident with these cells following sensitiser exposure. It is perhaps unsurprising then that cell survival signaling pathways and nucleic acid-structural/synthesis proteins were identified so extensively in the results presented in this chapter. Cell survival indeed seems to be a common feature throughout these analyses where sensitiser exposure induces a statistically significant cellular response. For example, the MAPK and phospholipase A2 (PLA2) pathways significantly up-regulated following PA exposure (Figure 4.12). DNA damage, proteotoxic stress, and the downstream consequences appeared to be a significant feature of the analyses. Differential expression of histone proteins and increased expression of heat shock proteins (HSPs) was observed, alongside proteins and processes implying increased transcription/translation.

Cells often produce heat shock proteins in response to exposure to stressors, many of which act as chaperones stabilising the folding of newly synthesised proteins and refolding of misfolded or damaged proteins³¹¹. The ubiquitin-proteasome system (UPS), amongst various other functions, is responsible for degradation of structurally aberrant proteins³¹². Additionally, neddylation and UFMylation were significant features observed in the cellular response, which have roles in protecting the UPS from being overwhelmed by misfolded proteins^{263,282}. In relation, serum albumin showed decreased expression in cells exposed to respiratory sensitiser chemicals. The implication is that heavy haptening of lysine-rich serum albumin may occur, followed by induction of degradation and detoxification pathways, similar to those proposed here and in the literature^{8,26,27}.

Protein components of the UPS and associated gene ontologies & pathways were consistently observed in this study, particularly following cell exposure to respiratory sensitisers. The UPS also controls metabolic processes and progression through the cell cycle³¹². Taken together with the

enriched transcriptional/translation proteins, protein degradation features of the analyses, and the demonstrated increase in cell proliferation, there is a clear role for changes in protein turnover following exposure to chemical sensitisers.

Toll-like receptors (TLRs) are a type of pattern recognition receptors which contribute to the detection of exogenous or endogenous danger-associated molecular patterns²⁹⁴, such as haptens or hapten-protein conjugates in this case. TLRs are also known to be expressed as type I transmembrane proteins on the surface of human epithelial cells³¹³. TLRs and their associated signaling pathways have important implications in driving the T_H2 immune response in respiratory allergies^{294–296}. In this study, such pathways were enriched for proteins in 16HBE14o⁻ cells exposed exclusively to respiratory sensitisers. Given the importance of these proteins, the cell culture extraction method optimisation (section 4.3.1) seems particularly valuable here for preservation of membrane proteins.

Macrophage migration inhibitory factor (MIF) is an important pro-inflammatory lymphokine in cell-mediated immunity, which is in turn a feature more strongly associated with models of skin sensitisation than respiratory sensitisation. The significant differential expression of this protein following respiratory sensitiser exposure here is of particular interest as a potential molecular driver/facilitator of the T_H1/T_H2 immunological divergence of sensitisation AOPs^{1–3}.

Further evidence for the down-regulation of T-cell mediated immunity was observed here following respiratory sensitiser exposure. Significant pathway enrichment was observed for proteins with increased expression involved in the negative regulation of CD4 and CD8 related pathways for cells exposed to TDI. Additionally, 16HBE14o⁻ cells exposed to the skin sensitiser DPCP highlighted the increased expression of T-cell antigens CD276 antigen and CD166 antigen. These proteins are evident regulators of T-cell mediated immunity, adding to the evidence for differential expression of molecular drivers of cell-mediated immunity processes. In turn, this provides candidate molecular drivers for the immunological divergence of skin and respiratory sensitisation models.

Prior to validation, the haptenomes presented here (Appendix Figure 3) do not appear to adhere to the purported cysteine/lysine duality. The general preference for lysine in the candidate haptenome results is most likely due to the greater abundance of lysine in the human proteome relative to the other nucleophilic amino acids²⁴⁶. In addition, the analyses here have not yet been extended to nucleophilic amino acids other than cysteine and lysine (His, Tyr, Arg). There remains interest in haptenation of these additional residues, despite being shown to be less reactive with chemical sensitisers⁶. For example, histidine modification of low abundance proteins in reconstructed human skin epidermis²³¹, the reaction of tyrosine with reactive nitrogen species³¹⁴

such as during nitrosative stress, and the multiple possible reaction sites of arginine by virtue of the guanidino group. Furthermore, such residues may be more highly favoured by hapten reaction mechanisms in addition to the primary mechanism.

Haptenated proteins were identified here according to specific modification of cysteine and lysine residues only due to the relative limitations in search space. Investigating haptentation with other nucleophilic residues separately – histidine, arginine and tyrosine – may change the overall profile of potential haptentated proteins. Such analyses may be particularly instrumental for confirmation of true modifications, especially considering the increasing importance of histidine residues in haptentation studies including these sensitiser chemical structures^{9,10,231}. Assessment of the modifications as a proportion of each distinct amino acid would likely be valuable, though naturally would follow database searches with other residues and manual validation of MS/MS spectra. The percentage of available nucleophiles for modification would also be of interest in the context of the results presented here.

The non-stoichiometric hypothesis of haptentation^{8,27} appears to also apply to the results presented in this study (Appendix, Figures 4 & 5). If haptentation was stoichiometric, then logically the observed modifications would occur more frequently at higher relative abundance. The implication is that steric constraints and specific residue availability in the reaction microenvironment determine the extent of haptentation rather than peptide/protein abundance implying that haptentation is a highly specific, relatively rare molecular interaction. Therefore, there is substantial interest in assessing the potential immunogenicity of hapten-protein conjugates in the immunopeptidome (see Chapter 5).

Following haptenome validation, modifications were identified related to a variety of proteins of interest. A range of mitochondrial proteins were observed, particularly in relation to cellular redox regulation and oxidative stress. A substantial number of cell membrane proteins were also represented. This potentially reflects cytoskeletal signaling pathways, but also membrane perturbation due to sensitiser penetration of the cell membrane – an important initial event in the adverse outcome pathways of skin and respiratory sensitisation. Endoplasmic reticulum, cytosol, and cytoskeleton proteins were represented in the haptenomes with implications in the ubiquitin-proteasome degradation system. The consequences of differences in the E3 ubiquitin-protein ligases modified by the different chemical sensitisers remains to be elucidated. However, the haptentation of these proteins and others involved in the ubiquitin-proteasome and similar pathways indicates the haptens/hapten-protein conjugates are reaching these cellular components. This provokes interest in whether the haptens and/or hapten-protein conjugates

localise to specific organelles or cellular compartments. Naturally, investigation of the ubiquitome after exposure to skin and respiratory chemical sensitisers would also be of further interest.

The overall proteome profiles presented here show DPCP exposure being more similar than DNCB to the respiratory sensitiser exposures with 16HBE14o⁻. The propensity of both DPCP and the respiratory sensitiser chemicals to form multiple adducts by several reaction mechanisms would seem to offer some support for more varied residue preference relative to the frequently observed single adduct formation of DNCB. As previously discussed, confirmation of haptenated residues/proteins and further assessment of the other nucleophilic amino acid residues (His, Tyr, Arg) would be prudent in deciphering these processes. For example, the potential importance of histidine modification of low abundance proteins has recently been indicated by Khong *et al*²³¹.

By default, PEAKS X Studio^{249,315} uses the average total ion current (chromatogram peak area) in a sample to calculate the normalisation factor. Normalised abundance is calculated from the raw abundance of proteins divided by the normalisation factor. Therefore, the different control and sensitiser-treatment groups are not subjected to the same protein-level normalization factors. This also does not necessarily scale linearly for greater abundance proteins in one sample group compared to another as it is dependent on the relative intensities of the total ion currents compared to the raw protein abundance within each sample.

Proteins in the sensitiser treated groups show overall increased abundance across the groups compared to the control (likely due to a combination of increased protein turnover, orbitrap instrument under-sampling bias, and increased cell proliferation following sensitiser exposure) and are compared using individual normalisation factors in a ratio relative to the sample with which relative protein quantitation is being compared. This incorporates the relative differences in total ion current (and abundance) into the normalisation between different samples, where samples with greater abundance will show greater total ion currents and therefore a greater individual normalisation value. This normalisation value will then be represented as a proportion of the base comparison sample normalisation value during quantitation within the PEAKS software algorithm (table 4.2).

Table 4.2: Relative normalization factors from PEAKS algorithm output. Normalization factors are shown for each sample in the control and PA-treated A549 groups as an example, expressed as a ratio with the base comparison sample value (Control_01).

Sample	Normalization Factor
Control_01	1
Control_02	0.71669066
Control_03	0.777401924
PA_01	0.591806889
PA_02	0.385063678
PA_03	0.631414294

This results in the sensitiser-treated sample groups generally show a greater protein quantitation than the same proteins in the control groups following relative quantitation with PEAKS software, therefore appearing as a 'skew' towards up-regulation of proteins in the sensitiser treatment groups. This can be further evaluated when comparing the control sample group protein quantitation only to other control sample proteins, which results in no notable skewing. The same is true when comparing relative protein quantitation only within the specific sensitiser-treated groups.

Manual normalisation and relative label-free quantitation methods may be prudent to explore further in future. For example, mean normalisation, median normalisation and quantile normalisation are all common normalisation methods in manual data analysis worth consideration. However, normalisation is often inherently bad at dealing with sample datasets where all values change as it generally renormalises the data and therefore shows no changes. This would then result in the loss of representation of the true difference in raw protein abundance between the treatment and control groups potentially resulting from processes such as increased protein turnover.

The limiting factor for DNCB and DPCP treatment in *in vitro* assays using living cell cultures has been shown as the acute cytotoxicity induced at relatively low micro-molar concentrations. However, this was determined not to be the case for respiratory sensitisers, which exhibited no notable change in proliferation or toxicity profile. Hypothetically, this meant that the respiratory sensitiser concentrations representing the maximum functional reactivity could be used here to achieve the maximum response of cells to exposure. In future, *in vitro* comparison of equal concentrations may prove interesting, but it seems pragmatic to compare the maximum possible response initially. Particularly when considering the relative differences in reactivity, potency, and sensitisation potential.

Literature evidence suggests that most DNCB modification occurs at 8 hours or less, with almost none observed at 24h/48h⁹. These findings may somewhat refute the earlier hypotheses that haptenation is a lengthy process²⁷, and suggests <8h incubation time may be more appropriate for observing haptenated proteins. Recent results from phthalic anhydride exposure in reconstructed human skin epidermis proteins demonstrated maximal reactivity at even the earliest time points, but also formation of additional distinct structures at >8h exposure duration²³¹. Consequently, it could be suggested that the haptenation process initiates a rapid induction of detoxification processes removing haptenated proteins from cells.

Attempts to identify true differences in haptenation may benefit from repeating these living cell haptenation studies with a shorter optimised incubation time. Also, an alternative buffered solution replacing the serum-free culture medium may be useful in lessening the impact of competing nucleophiles originating from cell culture medium supplements (e.g. amino acids). Elucidation of the dynamics of haptenation across skin and respiratory sensitiser chemicals in different systems evidently remains incomplete. Certainly, the relative importance of repeated low dose exposure over time compared to single high dose exposure events remains unclear. On balance, it seems sensible that the precedent of 24h experimental exposure^{8,16,114} at maximum sub-cytotoxic sensitiser concentration initially be maintained where information on the dynamics of haptenation in specific systems is unavailable.

In conclusion, this study aimed to identify initial distinct divergence between skin and respiratory sensitisers in terms of haptenated proteins and differential expression in the proteome, hence the results presented here remain reasonably broad in scope. However, a number of specific proteins and processes of interest have been identified exclusively following either skin or respiratory sensitiser exposure. Relative reactivity/potency (EC3), cell proliferation & cytotoxicity, and cellular proteome response do not appear to directly reflect the number of haptenated peptides or proteins in the haptenome. This suggests a variety of other factors are also involved in determining the relative differences in these features. However, this chapter also demonstrates a putative preference for skin sensitisers favouring cysteine modification and respiratory sensitisers favouring lysine modification within the observed haptenomes.

Results from the cellular proteome response here represent an advancement in the general understanding of the intracellular response to sensitiser chemical electrophilic insults. The role of a range of interconnected cellular processes were identified in a differential capacity following exposure to skin or respiratory chemical sensitisers. Cellular stress (particularly oxidative stress), genotoxicity & proteotoxicity, the ubiquitin proteasome system, and a number of potential

drivers of immunological divergence all appear to be significant features of the difference in cellular response to hapteneration here.

Ultimately, this chapter provides a characterisation of the response to hapteneration in selected alveolar and bronchial epithelial cells following exposure to skin and respiratory chemical sensitisers. These findings also contribute valuable information and parameters for the modelling of skin and respiratory sensitisation in adverse outcome pathways.

Chapter 5 Investigating divergent peptide antigen presentation in the immunopeptidome of human alveolar epithelial cells

5.1 Introduction

Adverse outcome pathways of skin and respiratory sensitisation are centred upon divergent immunological outcomes as the result of two-phase processes of a similar yet distinct nature. These AOPs present an initial sensitisation phase followed by an elicitation phase upon repeated exposures where the respective symptoms of skin and respiratory sensitisation become clinically evident¹⁻³. The more covert sensitisation phase putatively begins with a molecular initiation event (MIE) whereby electrophilic sensitiser chemicals covalently modify (haptenate) endogenous proteins within cells at the site of exposure, with multiple reviews of the specific nature of the reactivity being available^{16,91,108}.

Haptenation of endogenous proteins has been shown to result in secretion of pro-inflammatory cytokines²³⁶ which generally stimulate dendritic cells which internalise and process degraded proteins. Following movement to draining lymph nodes, peptide antigen presentation by dendritic cells results in priming and clonal expansion of divergent population of T_h cells². Cytotoxic T cell mediation has also been observed in skin sensitisation models, whereas a debatable IgE component has been associated with respiratory sensitisation^{1,2}. Immunological stimulation following subsequent repeated exposures to chemical sensitisers is believed to occur by recruitment and activation of hapten-protein conjugate-specific T cell subsets.

A number of advances in understanding of reactivity of skin sensitisers such as DNCB^{16,26,27}, and the dynamics of haptenation in living cell systems^{8,9} and human tissue^{8,231} have been made. However, questions have persisted regarding the cellular response to sensitiser exposure in terms of the specific proteins modified and how this relates to differential regulation of the global proteome and stimulation of other cells of the immune system.

Immunopeptidomics and dual isotope labelling methods have recently emerged as valuable tools for confirming which haptenated endogenous proteins are presented to the immune system as peptide antigens by the membrane proteins major histocompatibility proteins (MHC)^{8,114}. MHC class I is generally present on the surface of all nucleated cells and presents endogenous cytoplasmic peptide antigens of 8-10 amino acids in length in the peptide binding cleft domain.

Conversely, MHC class II is generally restricted to the surface of professional antigen-presenting cells and presents exogenous peptide antigens of 14-18 amino acids³¹⁶ (Figure 5.1).

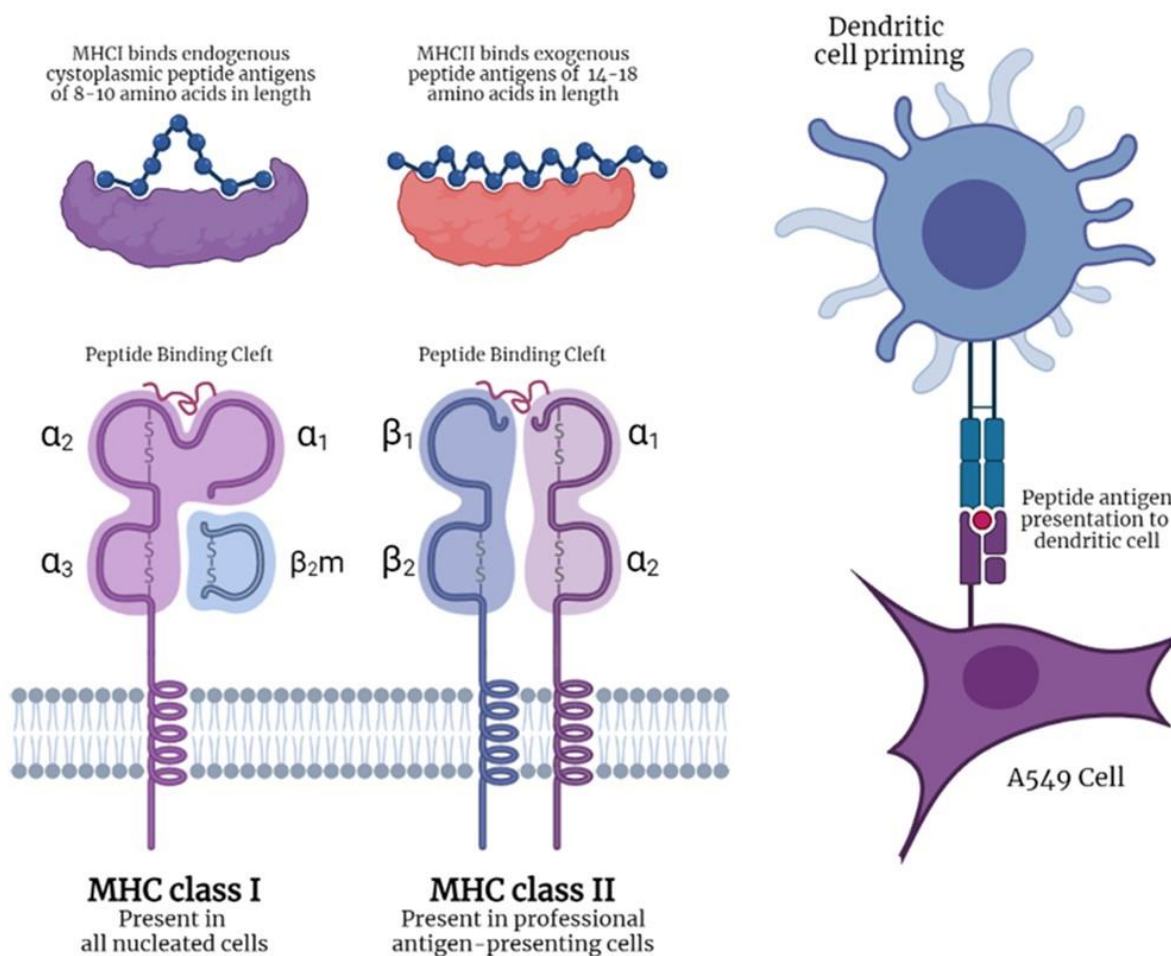


Figure 5.1: Cartoon representation of the differences between MHC class I and II.

Given the uncertainty surrounding the capability of many sensitiser chemicals, particularly respiratory sensitisers, to penetrate cell membranes in an aqueous medium this presented the argument of sensitiser modification of the immunopeptidome without direct interaction with MHCs. Three non-mutually exclusive models have been proposed¹¹⁴; direct presentation of peptide antigens (Figure 5.1), hapten modification of external regions of the MHC protein, and differences in regulation of global proteomes leading to differences reflected in the immunopeptidome. These processes were initially delineated using the skin sensitiser DNCB¹¹, which has frequently been utilised as a model skin sensitiser, partly for its propensity to sensitise immunocompetent individuals^{115,116}. Further complexity was presented with direct modification and conformational change of the peptide binding groove having been observed in immunopeptidomes following sensitisation by pharmacological agents¹¹⁷. The local inflammatory environment has also been demonstrated altering the specific chemistry and length in the immunopeptidome (i.e. the motifs). For example, oxidative stress resulting in generation of

reactive oxygen species capable of influencing antigen processing and the immunopeptidome^{317–319}. However, none of these factors were found to affect the study of Bailey *et al*¹¹⁴ when deciphering the relative importance of the three models of haptentation in the human keratinocyte peptidome following exposure to DNCB. Investigating the processing and presentation of MHC I peptide antigens in keratinocytes exposed to DNCB was further demonstrated to be the predominant route for direct presentation of internalised haptentated conjugates.

To date, immunopeptidomics have exclusively explored skin sensitisation by DNCB with HaCaT keratinocyte MHC class I proteins. The potential divergence and connection of haptentated endogenous proteins, differential cellular proteome regulation, and downstream dendritic cell and T cell evidence from *in vivo* studies demonstrates the interest in comparing immunopeptidomes resulting from skin and respiratory sensitiser exposure. Consequently, stable isotope labelling and immunopeptidomics methods^{8,11} have here been adapted to address this missing comparison by investigating peptide antigen presentation by MHC I of A549 alveolar epithelial cells following exposure to the skin sensitiser DNCB and respiratory sensitiser phthalic anhydride.

5.2 Methods

5.2.1 Cell culture & antibody extraction

A549 alveolar epithelial cells (HLA type: A*25:01, A*30:01, B*18:01, B*44:03, C*12:03, C*16:01, DRB1*07:01, DRB1*11:04, DQB1*02:02, DQB1*03:01, DPB1*03:01, DPB1*06:01) and 16HBE14o bronchial epithelial cells (HLA type: A*01:01, A*32:01, B*18:01, B*51:01, DRB1*07:01, DRB1*11:04, DQB1*03:01, DQB1*03:03, DPB1*04:02) were maintained in Dulbecco's modified Eagle medium (DMEM) supplemented with 4.5g/L glucose, 2mM L-glutamine, 1% penicillin-streptomycin, and 10% FBS according to methods previously described (chapter 2). Cells were incubated at 37°C and 5% CO₂. IVA12 and W6/32 hybridoma cells were maintained in RPMI supplemented with GlutaMAX™, 1% penicillin-streptomycin, and 10% FBS. Confluent cell culture suspensions were washed in DPBS, counted, then resuspended in R-15 medium (1% GlutaMAX™, 15% IgG-depleted FBS, 1% penicillin-streptomycin, 1% MEM non-essential amino acids, 1% sodium pyruvate and 55µM β-mercaptoethanol) before seeding in CELLline bioreactors (Corning). The bioreactor nutrient compartment was filled with 1L of RPMI medium supplemented with 1% GlutaMAX™, 1% penicillin-streptomycin, 1% MEM non-essential amino acids, 1% sodium pyruvate, and 50µM β-mercaptoethanol. Seeded bioreactors were incubated at 37°C/5% CO₂ and

re-seeded weekly after extracting cell compartment supernatant containing anti-MHCI/anti-MHCII monoclonal antibody.

5.2.2 Anti-MHC monoclonal antibody purification

Hybridoma culture supernatants were loaded onto a HiTrap Protein A column (Cytiva) washed with 10 column volumes of 20mM sodium phosphate binding buffer (pH7.4) at 4mL/min buffer before and after binding at 1mL/min in an AKTA Pure fast protein liquid chromatography (FPLC) system using the manufacturer protocols. Elution was achieved with 3 column volumes of 0.1 M citric acid (pH 3) elution buffer at 1mL/min. Eluted antibodies were immediately neutralized with 1 M Tris-HCl (pH 9) prior to buffer exchange into phosphate buffered saline (PBS) using a 50 kDa cut-off Vivaspın® column (Sartorius). Antibodies were stored at -20°C prior to analysis. A supplementary supply of W6/32 monoclonal anti-MHCI antibody was also ordered from SAL Scientific.

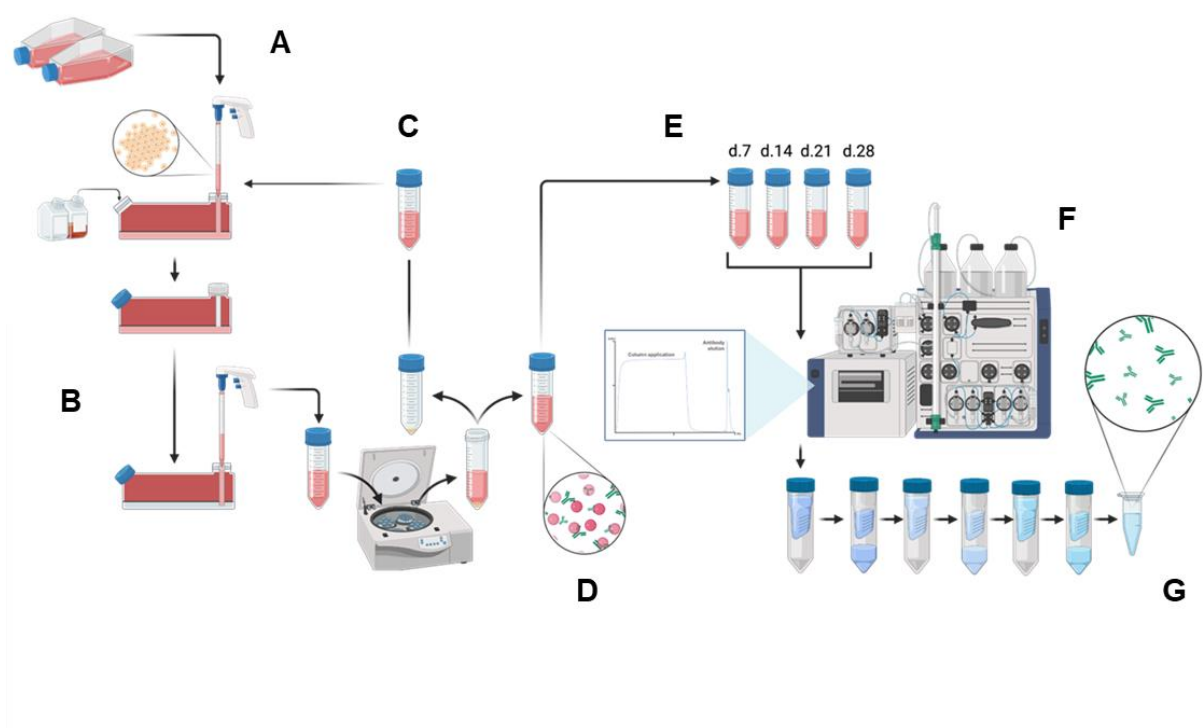


Figure 5.2: Workflow overview for hybridoma cell growth, anti-MHC antibody extraction and purification – Hybridoma cells lines seeded and grown in bioreactors (A) before extraction of cell compartment suspension (B). Hybridoma cell suspensions were centrifuged to pellet the cells which were resuspended and re-seeded in bioreactors for subsequent extractions (C). Hybridoma cell suspension supernatants containing anti-MHC antibodies were transferred to new tubes (D), with the previous steps being repeated to

produce an additional antibody suspension every 7 days for 28 days (E). Antibody suspensions were pooled then applied to protein A FPLC for purification (F). Eluted antibodies were buffer exchanged into PBS and quantified, then stored at -20°C prior to further analysis workflows (G).

5.2.3 Sensitiser exposure methods

A549 cells ($1.0-1.5 \times 10^8$) were exposed to DNCB/DNCB- d_3 and PA/PA- d_4 according to the concentrations and methods previously described (chapter 4) in a series of 175cm² culture flasks. Following 24h incubation cells were washed three times with DPBS and incubated with 0.25% trypsin-EDTA dissociation reagent for up to 10 minutes. Detached cell suspensions were centrifuged at 300 xg for 10 minutes at room temperature. Supernatants were aspirated and cell pellets resuspended in DPBS before repeating the centrifugation. The DPBS supernatant was again aspirated, and the cell pellets snap-frozen and stored at -80°C prior to analysis.

5.2.4 Purification of MHC complexes and peptides

Snap-frozen cell pellets ($1.0-1.5 \times 10^8$ cells) were briefly thawed before the addition of 8mL lysis buffer (0.02M Tris, 0.5% (w/v) IGEPAL, 0.25% (w/v) sodium deoxycholate, 0.15mM NaCl, 1mM EDTA, 0.2mM iodoacetamide supplemented with EDTA-free protease inhibitor cocktail mix) with lysis being aided manually by pipetting. Samples were incubated at 4°C for 30 minutes to solubilise before the resulting lysates were subjected to clarification spins at 2000 xg for 10 minutes at 4°C followed by 60 minutes at 14,000 xg at 4°C. Anti-MHCI monoclonal antibody (2mg) covalently conjugated to protein A Sepharose (Repligen) was added to clarified supernatants for all sample replicates and incubated with constant agitation for 2h at 4°C. The resulting complexes were pelleted by centrifugation at 400 xg for 5 minutes at 4°C. The process was repeated on the sample supernatant with anti-MHCII monoclonal antibody for a separate, single replicate of A549 and 16HBE14o⁻ cells only (figure 5.3).

The captured MHC protein complexes bound to antibody-conjugated Sepharose beads were resuspended in lysis buffer and applied to a 96-well filter plate (NunC), with binding achieved by gravity flow. The filter plate wells were then washed with 2 column volumes of lysis buffer. The filter plate was then subjected to sequential stringency washes with 2 column volumes of low (isotonic, 0.15M NaCl) TBS, high (hypertonic, 0.4M NaCl) TBS, and 20mM Tris-HCl (pH 8.0) before elution with 10% acetic acid. The eluates were then dried under vacuum.

Dried eluates were resuspended in 0.1% TFA/1% acetonitrile and applied to a reverse-phase C18 micro-elution plate (Oasis HLBPrime) conditioned with 100% acetonitrile and equilibrated with

0.1% TFA in dH₂O. The bound peptides were de-salted with 0.1% TFA and MS-grade H₂O (Optima). The peptide samples were eluted with a step gradient of 2.5%-30% acetonitrile in 0.1% TFA solution, with fractions being pooled as odd and even fractions and dried under vacuum. Dried peptide fractions were resuspended in 25µL buffer A (0.1% formic acid) and separated into 4 samples (2 odd, 2 even) for mass spectrometry.

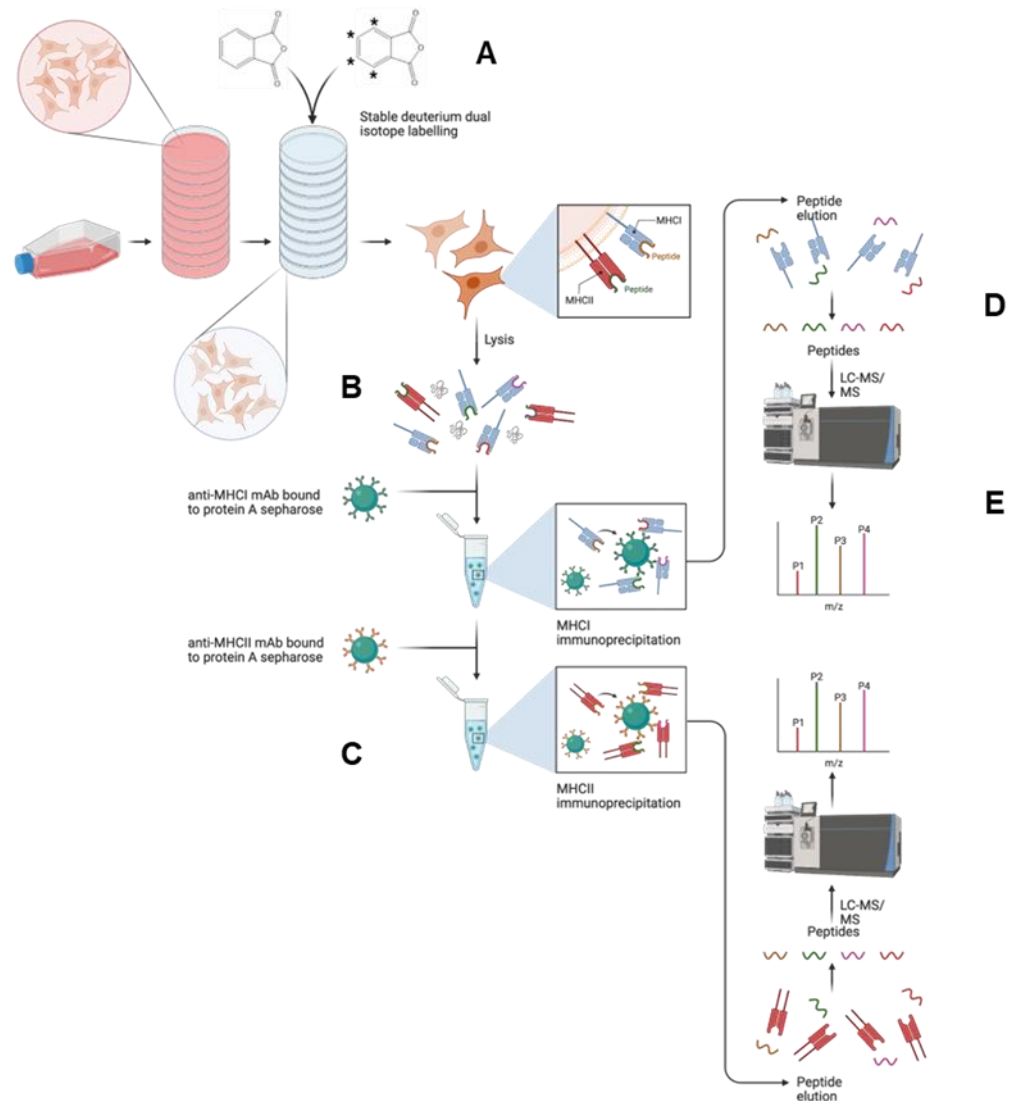


Figure 5.3: Immunopeptidomics sample analysis workflow overview: A549 cells separately exposed to DNCB or phthalic anhydride for 24 hours in serum-free culture medium (A). Harvested cells were then subjected to immunoprecipitation using anti-MHC class I monoclonal antibodies to obtain the MHC class I-peptide complexes in solution (B). Subsequent immunoprecipitation for MHC class II can optionally then follow the MHC class I using the same sample incubated with anti-MHC class II monoclonal antibodies instead – this was only done for comparison of untreated A549 and 16BE14o- cell samples here (C). MHC-peptide complexes were then eluted, with the separated immunopeptides being further purified and separated into 12 fractions using an acetonitrile gradient, then pooled into odd and even fractions for analysis (D). The

immunopeptide sample fractions were then transferred to tandem mass spectrometry for orbitrap mass analysis (E).

5.2.5 LC-MS/MS analysis of MHCI/MHCII peptides

Peptides were separated by an Ultimate 3000 RSLC nano system (Thermo Scientific) using a PepMap C18 EASY-Spray LC column, 2 μm particle size, 75 μm x 75 cm column (Thermo Scientific) in buffer A (0.1% formic acid) and coupled online to an Orbitrap Fusion Tribrid Mass Spectrometer (Thermo Fisher Scientific) with a nanoelectrospray ion source. Peptides were eluted with a linear gradient of 3%-30% buffer B (acetonitrile w/ 0.1% formic acid) at a flow rate of 300 nL/min over 110 min. Full scans were acquired in the Orbitrap mass analyser using the Top Speed data dependent mode to perform an MS scan in 3s cycles. This was followed by high energy collision-induced dissociation (HCD) MS/MS scans. The MS spectra were acquired at resolution of 120,000 at 300 m/z, RF lens 60% and an automatic gain control ion target value of 4.0e5 for a maximum of 100ms. The MS/MS resolution was 30,000 at 100 m/z. Higher-energy collisional dissociation (HCD) fragmentation was induced at an energy setting of 28 for peptides with a charge state of 2-4, whereas singly charged peptides were fragmented at an energy setting of 32 at lower priority. Fragments were analysed in the Orbitrap at 30,000 resolution. Fragmented m/z values were dynamically excluded for 30s.

5.2.6 Data Analysis

Raw spectrum files from data-dependent acquisition were analysed using Peaks Studio^{248,249} version X to process data through generation of reduced charge state and de-isotoped precursor and associated product ion peak lists. The data was searched against the UniProt human protein sequence database (2020-04-07) and a default contaminants list. The parent mass error tolerance was set for a 5 ppm parent mass error tolerance and 0.03 Da fragment mass error tolerance. Variable modifications were set for carbamidomethylation (57.02 Da) of cysteine, DNCB single adduct formation (166.092 Da) with cysteine and lysine, and phthalic anhydride adducts (130.102 Da, 148.117 Da, and 164.116 Da) with cysteine and lysine. A maximum of 3 variable modifications were allowed. The false discovery rate (FDR) was estimated with decoy-fusion database²⁴⁹ searching and the results filtered for 1% FDR. Downstream data analysis and visualisation was performed in R^{251,252}.

PEAKS database search results for each sample replicate were filtered for the variables necessary for further analysis, namely: peptide sequence, mass, length, m/z , retention time, peak area, sample fraction number, MS scan number, and protein database accession. The data was further

filtered for distinct peptide sequences and the number per sample replicate counted. The results were then compared to the total number of peptides in each replicate to give an indication of what proportion of unique sequences were reproducible between replicates. The results were then plotted using the ggVennDiagram R package³²⁰.

Results were further separated according to the length of individual peptide amino acid sequences for each of: <6mer, 7mer, 8mer, 9mer, 10mer, 11mer, 12mer, 13mer, 14mer, 15mer, and >16mer. The total number of peptides for each length was used to calculate the frequency distribution of data for each defined length and plotted in frequency polygons using the ggplot2 R package^{251,321}. The protein accession data for each distinct peptide was exported for gene ontology enrichment analysis²⁵⁰. MHC class I data was filtered for peptides of either 9 or 10 amino acids in length. The relative frequency of each specific amino acid residue at positions 1-9 or 1-10 for each peptide was plotted in sequence logo plots using the ggplot2 R package^{251,321}.

5.3 Results

5.3.1 Improvement and optimisation of anti-MHC monoclonal antibody purification and quantification by Fast Protein Liquid Chromatography

W6/32 and IVA12 hybridoma cells were grown in bioreactors for secretion of anti-MHC I monoclonal antibody (mAb) and anti-MHC II monoclonal antibody. These antibodies were necessary for the extraction of peptide-bound MHC protein complexes for characterisation of the immunopeptidome of alveolar epithelial cells exposed to chemical sensitisers. Following Hybridoma growth and anti-MHC monoclonal antibody extraction, mAb purification and quantitation was achieved with a protein A column online to an FPLC system (Figure 5.2). The methodology demonstrated advantages in purification speed and real-time quantitation estimation at a specific elution point (Figure 5.3). Further, the workflow presented provided lower costs relative to commercial antibody production. These aspects were of particular utility in the presented study due to the large amount of sample material required for experimental analysis (see 5.2.3 – 5.2.4).

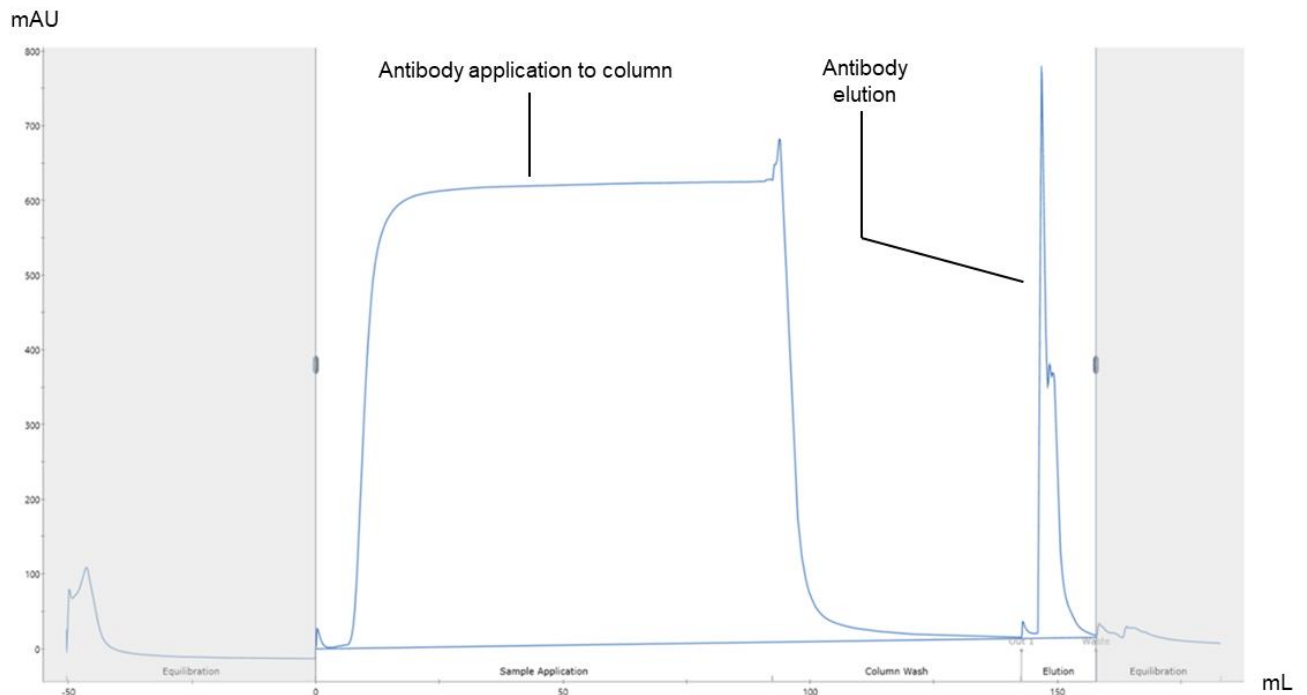


Figure 5.4: Example UV chromatogram generated during sample binding and elution of anti-MHCI antibody in protein A FPLC system. Elution signal (mAU) is presented at 150mL as an indication of antibody concentration, achieved via the FPLC instrument UV detector measuring absorbance of UV light by the sample solution during elution with default absorbance parameters.

5.3.2 No discernible induction of altered peptidomes with DNCB or phthalic anhydride exposure

From 4 biological replicates of A549 cells a total of 5944 immunopeptides were identified across the control and treatment groups with an average of 427 peptides in control samples (1706 total), 469 peptides in DNCB exposure samples (1875 total), and 591 peptides in phthalic anhydride exposure samples (2363 total). The total number of unique peptides observed in the immunopeptidome coverage within each group (Figure 5.4) demonstrated 857 unique control peptides, with 740 and 886 unique peptides observed in cells exposed to DNCB and PA respectively (Tables 5.1-5.3).

Exposure to DNCB resulted in identification of a lower number of distinct peptides than for the control cells, consistent with DNCB exposure to human keratinocytes in similar experiments¹¹. Similarly, there was no evidence for reduced cell quantities following DNCB treatment here either (see Chapter 3, Figure 3.13). Conversely, phthalic anhydride exposure resulted in identification of more distinct peptides than the control here. Further, there was evidence for increased abundance in the proteome in general (Figures 4.3 & 4.6).

It is understood that the biochemical and geometric properties of the peptide-binding cleft of MHC proteins determine the peptide-binding motif, according to amino acid preference at each position within a peptide³²² as well as the length³²³ (i.e. 9mers and 10mers). Neither DNCB or phthalic anhydride exposure noticeably altered the MHC-peptide binding motifs (Figure 5.6 & 5.7) or the length distribution of observed immunopeptides (Figure 5.5). Additionally, gene ontology classification of the proteins represented in the peptidome did not show any clear difference in cellular component GO enrichment (Figure 5.8).

5.3.3 Minimal evidence for haptenated peptides in the class I immunopeptidome

Dual isotope labelling methods of LC-MS/MS using a 50:50 molar ratio of un-deuterated and deuterated chemical haptens^{11,27,28} have been adapted and used here to eliminate false positive identification of DNCB and PA modified peptides in the immunopeptidome. Haptenated peptides were confirmed by observation of a pair of peaks in the MS spectra separated by a fixed shift in m/z provided by deuterium atoms (DNCB-d3 and PA-d4). As demonstrated here (Figure 5.9 & 5.10), PA-modified peptide (Δ 148.11 Da) with an m/z of 1026.60 ionised with a +2 charge (z) would be observed as a peak at 515.30 m/z , representing the un-deuterated modified peptide. Confirmation of haptenation would be achievable where an additional peak of approximately equal ion intensity was observed at 517.31 m/z equalling the mass difference provided by the

deuterium atoms, e.g. $4.024 (\Delta m) / 2 (z) = 2.012 \Delta m/z$. This process was repeated for each candidate peptide where a PTM was observed in the PEAKS search results, and further confirmed by examination of the MS/MS spectra for satisfactory coverage of *y* and *b* ions.

Of the 5944 peptides across the sample replicates, one potential phthalic anhydride modification of a lysine residue ($\Delta 130m/z$) was observed for sentrin-specific protease 2 (SEN2, Uniprot: Q9HC62) in two replicates (Figure 5.9 & 5.10) – albeit without satisfactory MS spectra to accompany the MS/MS spectra. SEN2 is a protease catalysing essential functions of the SUMO pathway with nuclear localisation and export signal motifs^{324,325}.

5.3.4 Comparison of class I and class II peptidomes between alveolar epithelial cells and bronchial epithelial cells

Previous results have suggested exposure to respiratory sensitisers increases expression of proteins related to MHC II pathways – pathways putatively restricted to professional antigen-presenting cells³¹⁶. Further, it has been shown that under certain conditions both keratinocytes and bronchoalveolar epithelial cells express detectable levels of MHC II^{11,293}. However, before extending the post-sensitiser exposure immunopeptidome analysis here to MHC II it seemed sensible to explore the number of immunopeptides presented by MHC II relative to MHC I in the native immunopeptidome. To this end, individual replicates of both A549 alveolar epithelial cells and 16HBE14o⁻ bronchial epithelial cells were subjected to the immunopeptidomics analysis workflow primarily for comparison of the number of peptides observed for MHC I and MHC II.

A total of 5042 peptides were identified in the 4 samples, with 1021 and 510 associated with MHC I and MHC II in A549 cells respectively. Additionally, 3181 peptides were associated with MHC I in 16HBE14o⁻ cells relative to 330 associated with MHC II (figure 5.11, B). The majority of peptides observed in the immunopeptidome associated with MHC I for both cell lines were of 8-10 amino acids in length – characteristic of MHC I-derived peptides. However, this majority was not reflected in the MHC II-derived immunopeptidome for immunopeptides of 14-18 amino acids in length (figure 5.11, A).

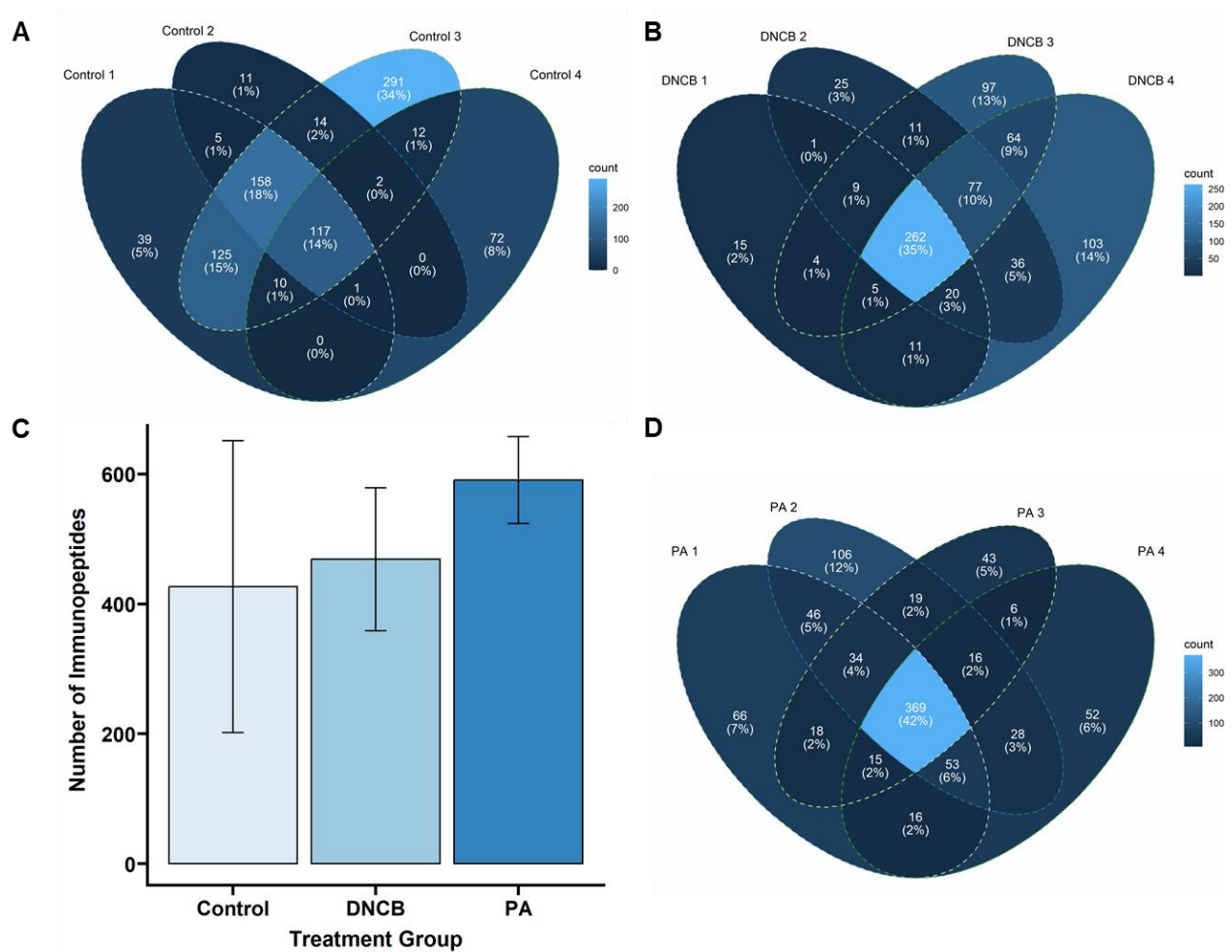


Figure 5.5: Immunopeptide identification – Venn diagram intersections of distinct MHC-I peptides for 4 biological replicates of control A549 cells (A) and A549 cells exposed to either DNCB (B) or phthalic anhydride (D). The mean number of peptides identified in each exposure group are also presented (C).

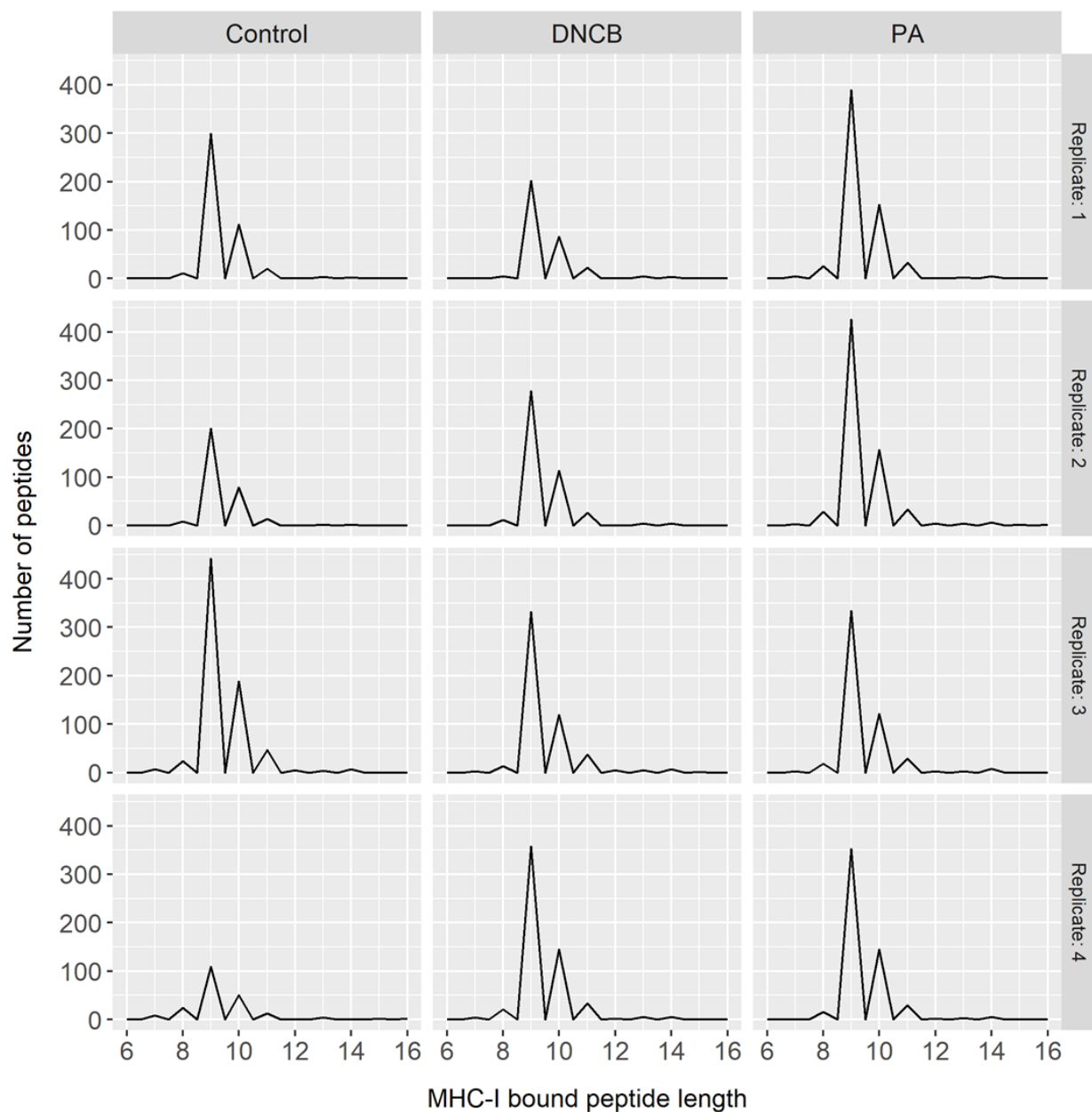


Figure 5.6: A549 MHC-I-bound immunopeptide length distribution frequency polygons – peptides of 6 amino acids to 16 amino acids in length (6mer-16mer) observed in the peptidome of control cells and cells exposed to DNCB and phthalic anhydride.

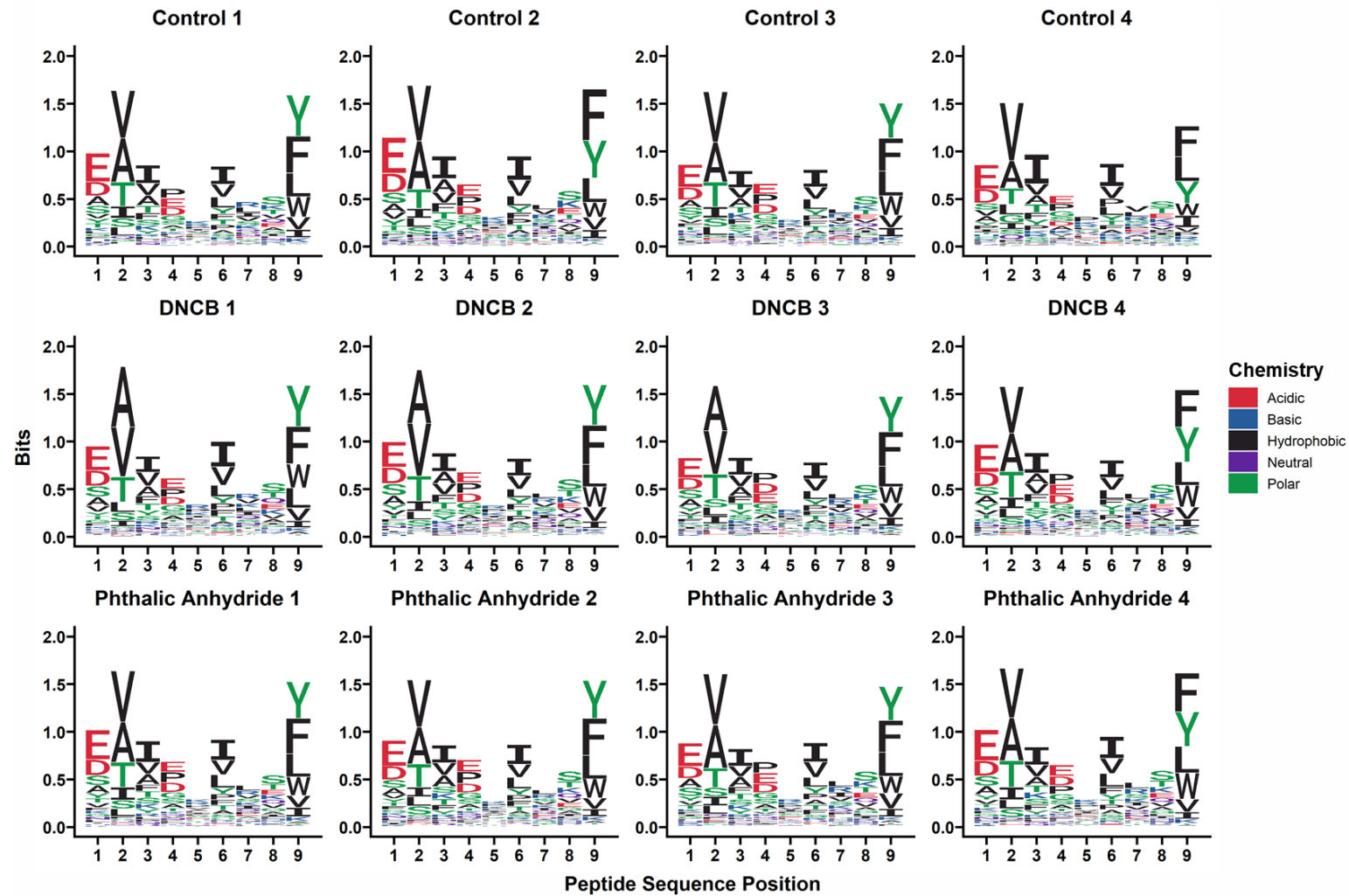


Figure 5.7: Peptide sequence (9mer) motif analysis of the natural HLA class I immunopeptidome (HLA-A*25:01, A*30:01, B*18:01, B*44:03, C*12:03, C*16:01) in A549 cells exposed to DNCB and phthalic anhydride. Anchor residues (mainly hydrophobic) are apparent predominantly at position 2 and the C terminus.

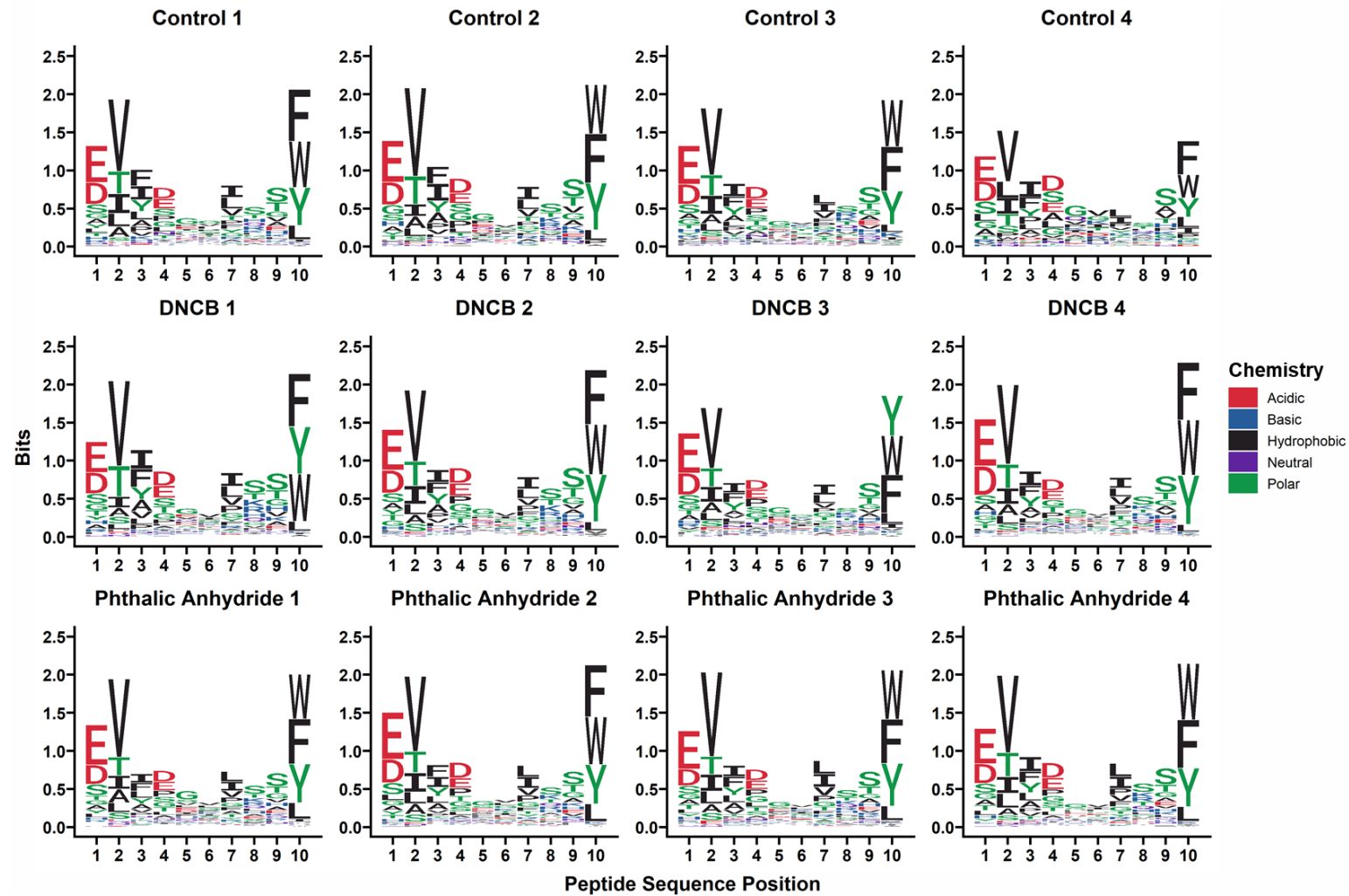


Figure 5.8: Peptide sequence (10mer) motif analysis of the natural HLA class I immunopeptidome (HLA-A*25:01, A*30:01, B*18:01, B*44:03, C*12:03, C*16:01) in A549 cells exposed to DNCB and phthalic anhydride. Anchor residues (mainly hydrophobic) are apparent predominantly at position 2 and the C terminus.

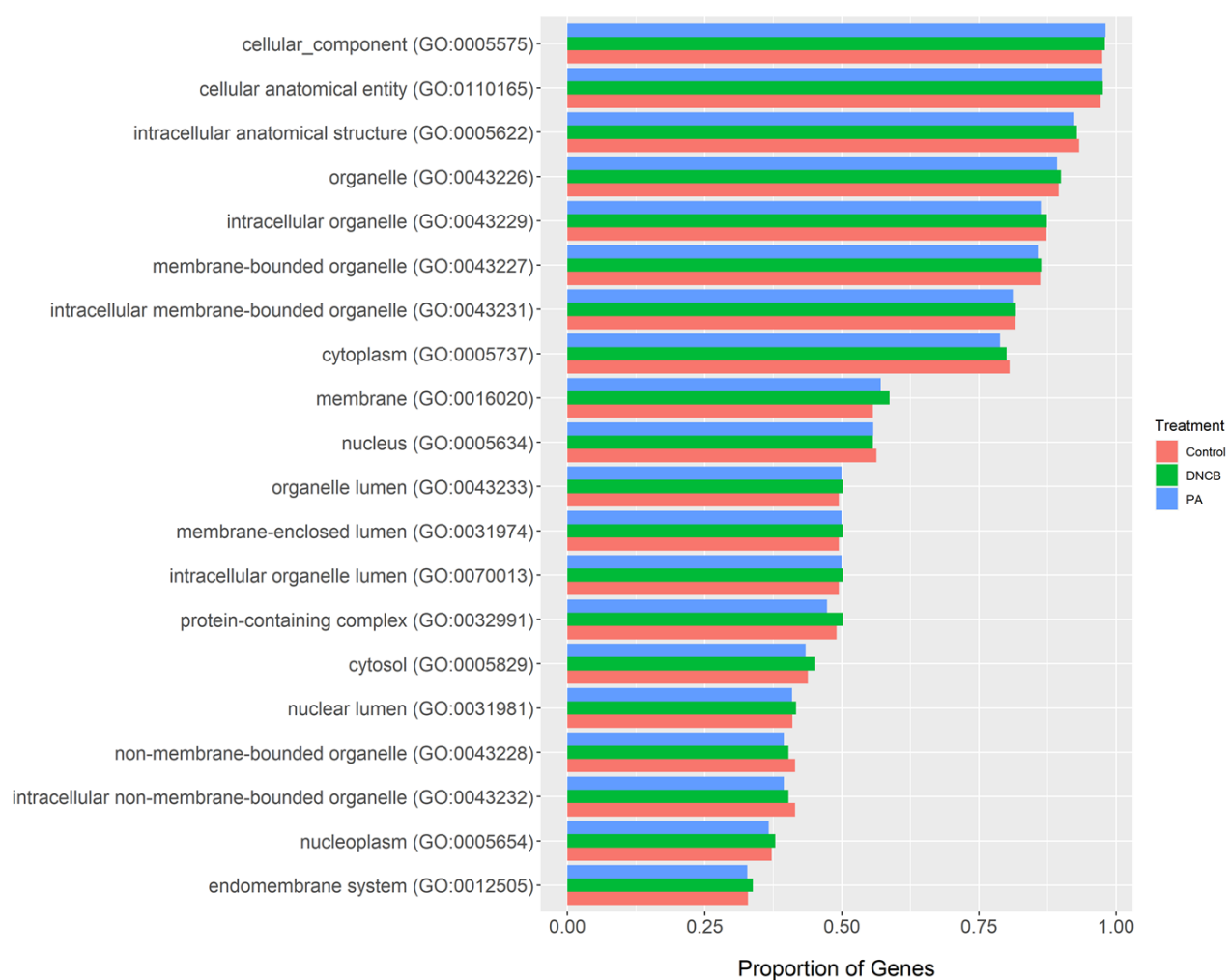


Figure 5.9: Cell component gene ontology classification – PANTHER²⁵⁰ gene ontology analysis for genes derived from the peptidome of 4 biological replicates of control A549 cells, and A549 cells exposed to either DNCB or phthalic anhydride.

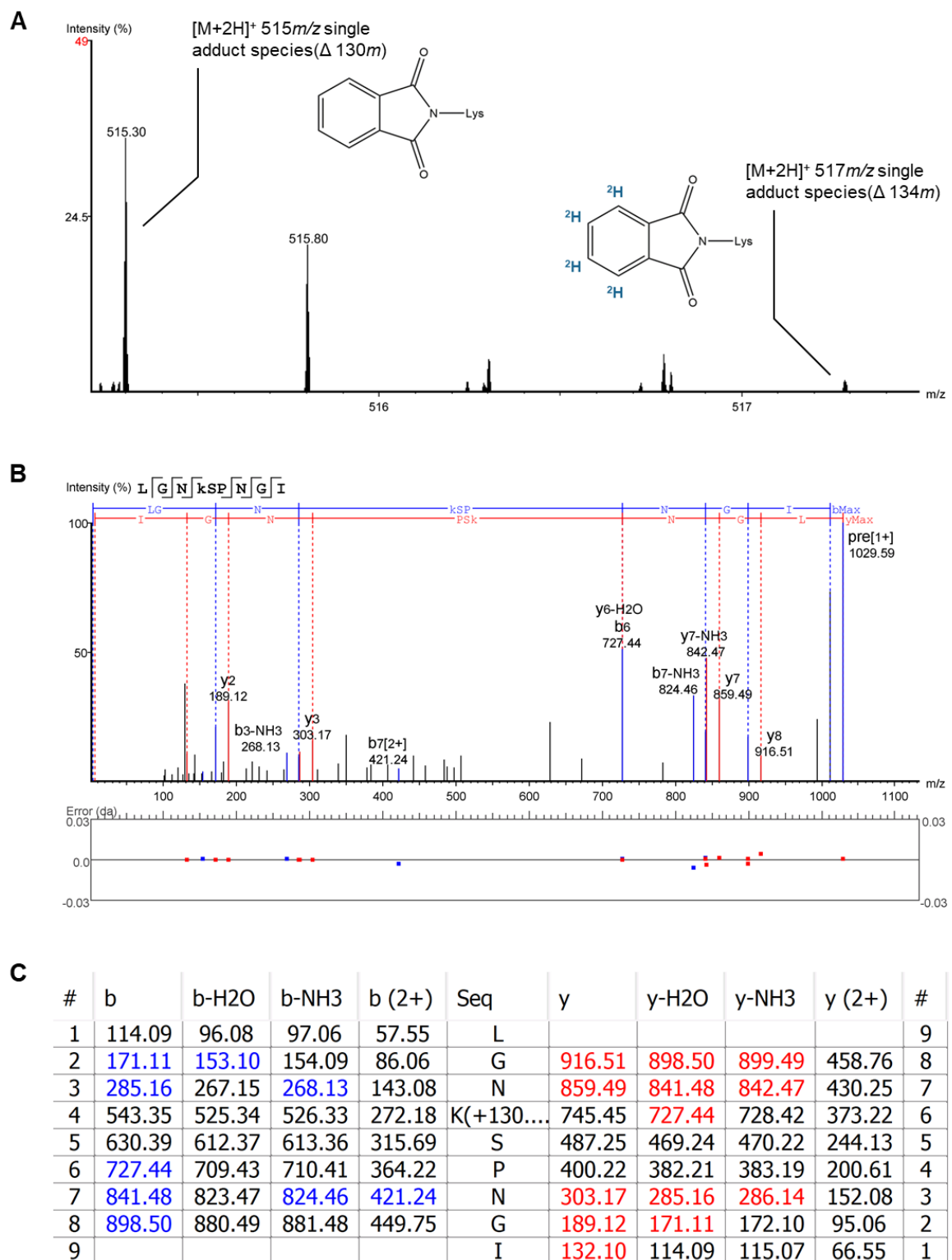


Figure 5.10: Haptened immunopeptide validation for a single lysine residue PA
haptation (+130 m/z) of sentrin-specific protease 2 (SEN2, Uniprot: Q9HC62) in the
A549 class I immunopeptidome – LC-MS spectrum highlighting the peptide m/z doublet
with a single un-deuterated modification and single deuterated modification in the same
sample (A). Fragmentation spectrum for the peptide sequence the haptation was
observed on (B). Ion table presenting coverage of the y and b ions generated by peptide
fragmentation for the modified sequence (C).

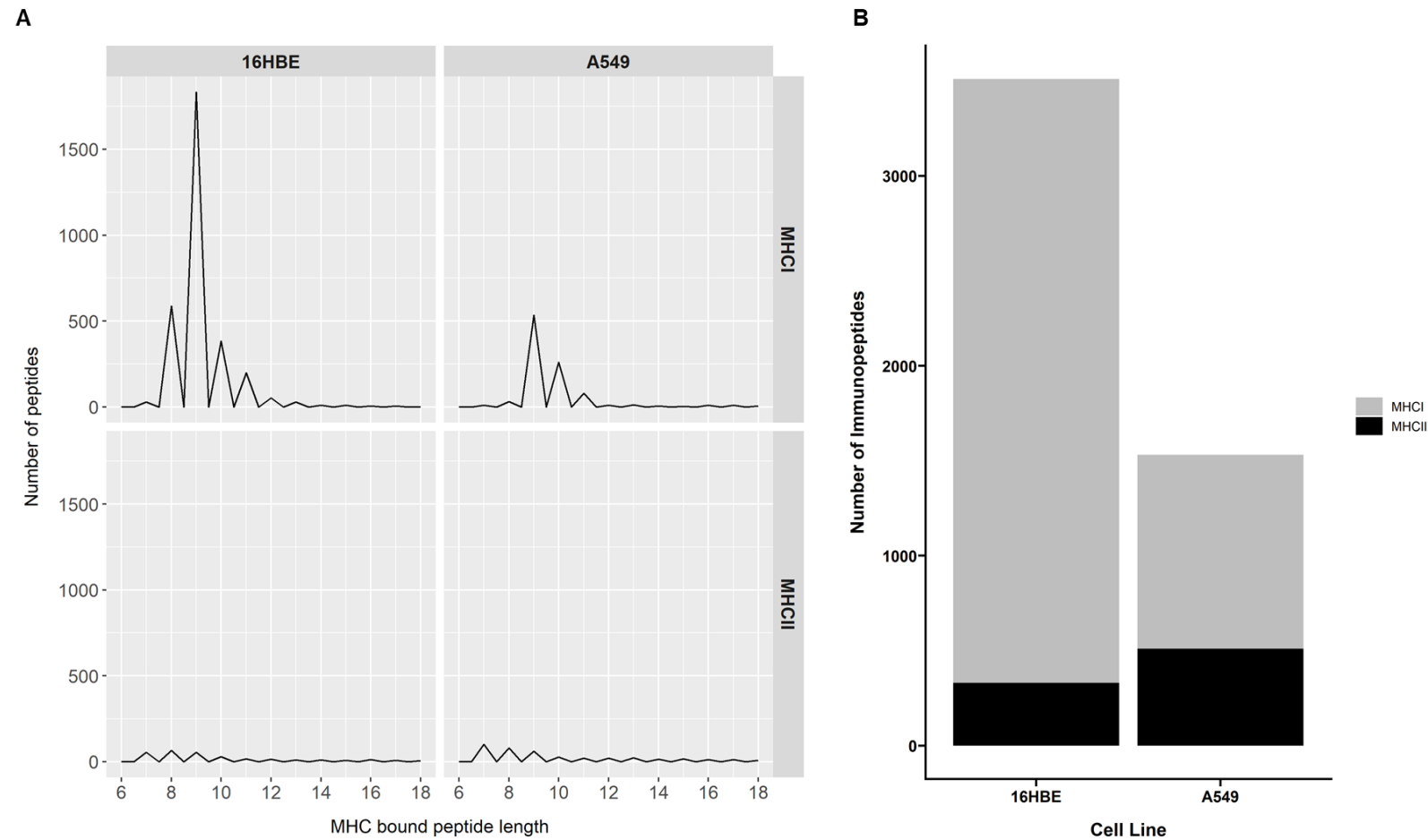


Figure 5.12: Comparison of class I and II immunopeptides between A549 & 16HBE14o⁻ untreated cells – Frequency polygons for peptides of 6 amino acids to 18 amino acids in length (6mer-18mer) observed in the class I and II peptidomes of control cells (A). The total number of immunopeptides for both MHC complexes is shown for each cell line (B).

5.4 Discussion

Previous chapters here demonstrated specific peptide reactivity of skin and respiratory sensitisers with the nucleophilic cysteine and lysine amino acid residues. Further, the specific hapten chemical reactivity was characterised within the complexity of respiratory epithelial cell proteomes. These results highlighted the importance of understanding and determining the potential immunogenicity of intracellular hapten-protein conjugates. This study sought to characterise the effects of phthalic anhydride exposure on the immunopeptidome of alveolar epithelial cells in the context of respiratory sensitisation. The potent skin sensitiser DNCB was included for comparison with PA, in light of the previous knowledge of the specificity and dynamics of DNCB haptenation^{9,28} and effects on the immunopeptidome of keratinocytes¹¹. No changes in the amino acid motif or in the typical MHC I length distribution were observed. Additionally, the only haptenated immunopeptides observed in any sample were two instances of $\Delta 130$ *m/z* modification by PA of an immunopeptide involved in the cellular SUMO proteasomal pathway.

MHCI-derived peptide length distributions presented predominantly 9mers and 10mers in each of the control, DNCB and PA sample groups. Amino acid compositions of the peptide motifs highlighted the reproducibility between samples as well as the lack of alteration induced by either chemical sensitiser. These considerations taken together provide confidence the MHC I-derived immunopeptidome presents true immunopeptides. Further to this, the average number of immunopeptides observed for each sample group was consistent with the magnitude of overall proteome abundance shifts induced by each chemical sensitiser (Figure 4.3, A).

The polygenic MHC class I heavy chain locus encodes HLA-A, HLA-B, and HLA-C, with each gene also being polymorphic³²⁶. Indeed, there are over 200 HLA-A, 500 HLA-B, and 100 HLA-C variants³²⁷. MHC class I proteins bind a diverse array of peptides sharing similar structural features – most notably a particular amino acid residue at certain positions within peptide sequences of 8-10 residues in length^{112,328}. Polymorphisms in the MHC class I genes result in differences in the specific structure of the peptide binding cleft and consequently differences in specificity of immunopeptide binding^{111,329}. A hallmark of the interaction between peptide ligands and MHC class I molecule is the existence of anchors. The anchor residues, typically found at position 2 and the and C-terminus of a peptide, form extensive networks of hydrogen bonds with the MHC class I molecule and contribute the most to binding energy^{330,331}. A preference is noted in the literature for F/W/Y/L residues at position 9 for HLA-A*25:01³³² and HLA-A*26:01³³³ with a large proportion of hydrophobic residues at the position 2 anchor point. The class I immunopeptide motifs

presented in this chapter (figure 5.7 & 5.8) predominantly resemble HLA-A*25:01 motifs^{333,334}. These results are supported by A549 and 16HBE14o⁻ phenotyping by next generation sequencing from peripheral blood samples for the Nicholas *et al*³³³ study, with further literature evidence for the HLA phenotypes available elsewhere^{335–339}. Overall, it is clear that the residues conserved at certain points in the immunopeptide motif are important for interaction MHC I proteins based on the biochemical properties of the peptide-binding groove.

The total number of immunopeptides observed was overall much lower than expected (approximately 10-fold) based on results from similar experiments performed in our laboratory^{11,333}. It is possible that differences in native expression of the MHC I protein in A549 cells under the specific experimental conditions used here may be partially responsible, though this seems unlikely to have been the only factor. It is worth noting that the immunopeptidomics workflow for the MHC I/MHC II immunopeptidome comparison (chapter 5.3.4) used a different batch of anti-MHC antibodies and separate cell samples to the sensitiser-exposed cells (chapter 5.3.2 & 5.3.3). It seems likely that antibody binding efficiency is the primary cause of the relatively low number of peptides identified in the sensitiser-exposed samples.

However, the MHC-derived immunopeptides identified in the MHC I/ MHC II comparison (see 5.3.4) were obtained as a single biological replicate only. Additionally, the number of MHC I-derived immunopeptides in this comparison still remain approximately 5-fold to 6-fold lower than expected based on similar studies in our laboratory^{11,333}. For these reasons, the antibody binding efficiency cannot alone be attributed to the lower number of identified immunopeptides than expected. Despite these differences in quantitative comparison between experiments within this study and with similar studies^{11,333}, it should be noted that the utility of immunopeptidomics is predominantly in qualitative analysis, as comparison of quantitative analyses still remains challenging³⁴⁰.

The low number of candidate haptenated peptides observed here is consistent with previous haptenation immunopeptidomics studies in human cells¹¹. Such studies did identify a low number of DNCB-modified immunopeptides (<10) relative to the lack of any DNCB-modified peptides in this study. Despite this, these observations were made from human skin keratinocytes with a potent skin sensitiser in immunopeptidomes of much greater peptide numbers. It is unsurprising then that no modifications were observed with DNCB in the smaller immunopeptidomes in this study. Although, a decreased total number of peptides identified in DNCB-exposed cell samples relative to the control cells was observed by Bailey *et al*¹¹, which was also observed with DNCB-exposed cells in this study. Similarly, no decrease in cell viability was observed in either study. It seems logical that the up-regulation of intracellular detoxification proteins and pathways

identified both here (chapter 4) and elsewhere in the literature combined with the precedence of 24-hour exposure durations throughout the relevant literature^{9,10,28}, could partially explain the lack of observed haptenated peptides in the study presented in this chapter.

Haptenation of sentrin-specific protease 2 (SEN2, Uniprot: Q9HC62) on lysine residues by PA was identified here in two sample replicates (Figure 5.9 & 5.10). This was the only haptenation event observed in this study. SEN2 is a protease catalysing essential functions of the SUMO pathway with nuclear localisation and export signal motifs^{324,325}. SUMOylation involves the covalent attachment of small ubiquitin-like modifier proteins to lysine residues in specific target proteins by an enzymatic cascade similar to the ubiquitination pathway³⁴¹. This process has recently emerged as an important regulator of oxidative stress and hypoxic response pathways³⁴². Additionally, the interplay of SUMOylation and immune signaling/development pathways with the potential to shape specificity and recognition of immune responses has recently been outlined^{343,344}. Taken together, these represent pathways and responses that may be of interest in distinguishing between adverse immunological outcome pathway models of skin and respiratory sensitisation¹⁻³.

Whilst interesting, these SEN2 modifications did not however display particularly satisfactory MS spectra alongside MS/MS spectra for confirmation of haptenation by deuterium dual isotope labeling (Figures 5.9 & 5.10). Whilst the coverage of *y* and *b* ions was good, the relative intensities of the un-deuterated and deuterated adduct peaks in the LC-MS spectra did not confirm the 50:50 ratio expected in these analyses for a true haptenation event (Figure 5.9, A; Figure 5.10, A). If confidence in this result was greater, it would be pragmatic to perform additional experiments or assays to determine potential immunogenicity of the haptenated peptide antigen. Not all peptides presented by MHC complexes are inherently immunogenic and antigenic peptides of interest should be further screened for T-cell recognition with supporting methodologies³⁴⁵. For example, *in silico* predictive structural models or cytokine-based assays (e.g. ELISpot) such as those employed by Bailey *et al* for studying DNCB-modified peptide immunogenicity¹¹.

In the comparison between MHC I/MHC II-derived peptides, a substantial number of MHC I-derived 9 mer and 10 mer peptides were identified in untreated A549 and 16HBE14o⁻ cells. Conversely, a lack of observed 14 mer-18 mer peptides for either cell line in this study infers a low level of native MHCII expression in these cells. These results are expected given the native expression of MHCII in these non-professional antigen presenting cells (APCs) is known to be low in allotyping^{316,333}. Pathway analysis from global proteomics experiments on A549 and 16HBE14o⁻ cells exposed to respiratory sensitisers (chapter 4) demonstrated enrichment for MHCII antigen presentation. This leads to the hypothesis that respiratory sensitiser exposure may induce MHCII

antigen presentation to a greater degree than skin sensitisers. This would seem to be unlikely in light of allotyping results with A549 cells, but remains an area to be potentially investigated. This avenue of investigation was not pursued due to cost and time limitations.

The methodology of immunopectidomics workflows used previously has been streamlined here (chapter 5.3.1). The workflow could benefit though from a number of alterations specifically tailored for studying the relationship between haptenation, antigen presentation and immunogenicity. For example, A549 exposure to phthalic anhydride was selected as the experimental condition based on the largest number of candidate haptenated peptides revealed in the global proteomic experiments (Appendix, section A.2.7). Therefore presenting this condition as the most likely to yield haptenated immunopectides in the immunopectidome. However, it could be argued that 16HBE14o⁻ cells are a better model based on the greater number of MHC I peptides observed here and the greater magnitude of cellular response to respiratory sensitiser exposure (chapter 4.3.2). For reasons stated previously, this does not necessarily mean a greater number of haptenated peptides would be observed. However, without the cost and time limitations associated with this study, this would be a valuable extension to the immunopectidome analyses in this chapter.

Another proposed extension to the methodology presented here is the principle of exposing professional antigen presenting cell lines to heavily haptenated epithelial cell lysates, similar to the methods of Nicholas *et al*³³³. This would benefit from a greater possible exposure concentration of sensitiser chemicals in which the initial cell viability of epithelial cells would not be a limitation of the experiment as it has been to this point. This would mean initially exposed non-APCs cells could be stressed to a point beyond efficient resistance mechanisms and pathways without affecting the APC facilitators of the downstream immunological responses. Comparison of the divergent cytokine profile associated with the adverse outcomes of skin and respiratory sensitisation (Figure 1.3) may be more relevant in such a reaction model system, particularly where T cell co-culture could be incorporated for confirmation of T_h1/T_h2 cytokine secretion profiles with skin or respiratory chemical sensitisers respectively.

In conclusion, the results presented here do not provide compelling support for hapten-protein conjugates identified previously (chapter 4) forming peptide antigens on MHCI complexes under these experimental conditions. However, a level of methodological insight has been provided for improving the efficiency of immunopectidomics workflows and development of more complex methods studying haptenation by respiratory sensitiser chemicals.

Chapter 6 Final Discussion & Further Research

Adverse outcome pathway (AOP) models of sensitisation to low molecular weight organic chemicals have previously demonstrated the series of key events leading to divergent immunological outcomes following initial protein nucleophile haptenation¹⁻³ and potential points of divergence are apparent between skin and respiratory AOP models. Major routes yet to be explored to-date included the differential haptenation of endogenous protein nucleophiles, the associated cellular proteome response, and potential differences in the nature of peptide antigen presentation following exposure to skin or respiratory sensitizer chemicals.

The overall aim of this research project was to capitalise upon recent advancements in mass spectrometry methods specifically designed for the investigation of haptenation events and the associated responses in initial phases of skin sensitisation^{8,27,114}. In this thesis, these approaches were extended to investigating respiratory sensitisation in a series of experiments designed for characterisation of the haptenome, proteome and immunopeptidome. The overarching hypothesis being that differences between human cells exposed to skin or respiratory chemical sensitizers would be apparent from one or more of these perspectives.

The weight-of-evidence based approach employed by the AOPs points to the importance of studying haptenation in living human cells. This is reflected in the precedence of skin sensitisation characterisation predominantly being centred on human keratinocytes^{9-11,27,28}. As such, the experiments in this project were centred on human alveolar and bronchial epithelial cells as parallel models to keratinocytes. Further to this, alveolar epithelial cells share similarities with keratinocytes in the relative proportion (>90%) in lung tissue and skin tissue respectively^{239,243}.

DNCB is a well-studied, classical skin sensitizer used in several studies similar to those presented as part of this project^{8,9,11}. Additionally, the DNCB reaction mechanism is relatively simple compared to other sensitizer chemicals (Figures 3.1-3.4), exclusively forming a single adduct. For these reasons, DNCB was selected for analyses in this thesis. DPCP is a highly reactive chemical skin sensitizer which has more recently been included in cellular haptenation studies¹⁰ and also included here for comparison. Phthalic anhydride and 2,4-TDI each represent one of the two major classes of respiratory sensitizer chemicals – acid anhydrides and diisocyanates²³⁴ – and were selected as model respiratory chemical sensitizers in this study.

Initial experiments in this project involved determination of dose concentrations for each sensitizer chemical. Previous studies demonstrated the importance of the sensitizer dose being as high as possible whilst remaining sub-cytotoxic^{9-11,28}. In this study concentration dose was

optimised to provide the maximum cellular response to exposure and maximum level of haptenation without inducing apoptosis. Standardised cell-based assays for cell proliferation and cytotoxicity were combined to generate cell viability profiles for the different cell lines following exposure to a range of sensitiser concentrations. The most notable observation was the complete lack of change in viability for any cell line exposed to respiratory sensitisers compared to the distinct profiles observed following exposure to skin sensitiser chemicals. This raised the question whether the respiratory sensitisers were reactive but non-cytotoxic even at the maximum concentrations, or whether they were simply non-reactive under such conditions (e.g. due to insolubility). This question was addressed through peptide functional reactivity LC-MS analysis of nucleophilic amino acid residue haptenation.

The direct peptide reactivity assay (DPRA) was originally developed as a screening assay for identification of skin sensitiser chemicals and associated reactivity profiles by nucleophile depletion³⁴⁶. The utility of the assay was further demonstrated with the incorporation of LC-MS methods for specific adduct formation^{26,208} and later also peptide depletion for respiratory sensitiser chemicals⁷. Analysis initially confirmed the reactivity of each sensitiser chemical with peptides containing a single, variable amino acid residue. The results further supported the peptide adduct structures derived from theoretical reaction chemistry (Table 3.1).

It was noted previously that functional peptide reactivity assays to-date have not included methodology for maintaining the sulfhydryl group of free cysteines. This hypothetically prevents hapten reactivity with cysteine residues due to dimerization of cysteine-containing peptides by oxidation. As a result, it could be suggested that cysteine-containing peptide depletion may be overstated in the literature whereas cysteine adduct formation may be under-reported. Incorporating a reducing agent, such as dithiothreitol, would likely prevent this peptide dimerization as well as better reflecting the internal reducing environment of living cells for improved comparison. The reducing potential of such an agent could also be investigated in excess for the potential ability to reverse the haptenation reaction of different hapten-peptide structures.

Further adaptations were incorporated in the experiments presented in this thesis, investigating peptide reactivity under different reaction conditions more reminiscent of cell culture reaction environments. Following these optimisations, hapten-peptide adduct formation for peptides containing either a single cysteine or lysine residue were analysed over a range of chemical sensitiser concentrations using a high-throughput targeted LC-MS method developed as part of this research. The results presented in chapter 3 show agreement with the cysteine/lysine reaction duality present in the literature^{4,7}, with skin sensitisers showing a preference in adduct

formation for cysteine-containing peptides and respiratory sensitisers showing a preference for lysine-containing peptides. The insight provided by these initial experiments provided valuable information for the design of the experiments presented in chapter 4 and 5 exposing living cell cultures to chemical sensitisers *in vitro*.

Stable deuterium dual isotope labelling methods have been established as the method of choice for identification and analysis of low abundance haptenated cellular proteins in human keratinocytes^{27,28}. This methodology was here applied to haptenome characterisation in alveolar and bronchial epithelial cells exposed to equimolar concentrations of deuterated/un-deuterated chemical sensitisers. Peptides exhibiting the unique spectral signature required for inclusion in the haptenome were generally of relatively low abundance and more hydrophobic in nature (Appendix Figures 4 & 5). These observations are similar to the findings of Parkinson *et al*, offering support for the non-stoichiometric hypothesis of haptenation in living cell culture *in vitro*²⁸.

This comparison between skin and respiratory sensitiser hapten reactivity was supported by data-dependent LC-MS/MS analysis and label-free quantitation methods. Statistically significant changes in the global proteome of alveolar and bronchial epithelial cells revealed roles for a range of interconnected cellular processes following exposure to skin or respiratory chemical sensitisers. Cellular stress (particularly oxidative stress), genotoxicity & proteotoxicity, the ubiquitin proteasome system, and several potential drivers of T_h1/T_h2 immunological divergence all appear to be significant features of the difference in cellular response to haptenation. Further, a significant cellular response was observed following exposure to the maximum reactive dose of each respiratory sensitiser chemical, but not with the skin sensitisers, DNCB and DPCP. Indeed, alveolar epithelial cells showed no statistically significant difference in proteome abundance of any protein with either skin sensitiser. Bronchial epithelial cells did exhibit a significant shift with DPCP, but at a lesser magnitude than the respiratory sensitiser chemicals.

The significantly increased expression of detoxification pathways identified in these results suggest that the haptenation process may be efficient in inducing detoxification processes for the removal of haptenated proteins from cells. This offers an explanation for the relatively low level of haptenation observed consistently both here and elsewhere in the literature where 24-hour exposure durations are the precedent. As a result, it may be advisable to further explore these experiments in multiple short exposures. Additionally, a different culture medium with less competing nucleophiles than serum-free culture medium would be logical. These adaptations would hypothetically create the most favourable environment for hapten delivery to cells and observable haptenation of intracellular protein. It is also worth noting that the ratio of nucleophile to hapten electrophile in peptide reactivity assays is fundamentally reversed relative

to the ratio of protein nucleophile to hapten electrophile in living cell culture systems. Therefore, the level of haptenation observed is perhaps expectedly low in line with observations from peptide reactivity assays.

Regardless, a variety of specific proteins and processes of interest have been identified exclusively following either skin or respiratory sensitiser exposure here, representing an advancement in the understanding of intracellular responses to sensitiser chemical electrophilic insults. Relative hapten reactivity, potency (EC₃), cell viability, and cellular proteome response did not appear to directly reflect the number of haptenated peptides or proteins in the haptenome. This suggests a variety of other factors are also involved in determining the relative differences in these features^{1,2}, such as steric constraints in the reaction microenvironment. However, the preference demonstrated *in chemico* for skin sensitisers favouring cysteine modification and respiratory sensitisers favouring lysine modification in peptide reactivity assays was reflected in the *in vitro* haptenome results here (see 4.3.5).

Previous chapters here investigated the specific peptide reactivity of skin and respiratory sensitiser chemicals with specific amino acid nucleophiles under different conditions. Further, the specific hapten chemical reactivity was characterised within the complexity of living respiratory epithelial cell proteomes. These results highlighted interest in determining the potential immunogenicity of different intracellular hapten-protein conjugates. In addition, differences in the number of haptenated peptide antigens or the number/identity of un-modified peptides presented in the immunopeptidome was also of interest.

The importance and utility of immunopeptidomics analysis of MHC-presented peptide antigens has recently been demonstrated for HaCaT keratinocyte exposure to skin sensitiser chemicals¹¹⁴. As with living cell haptenation experiments, a comparison to sensitiser treatment of lung-derived cells was presently unavailable. The previously discussed dual isotope labelling method of Parkinson *et al*²⁷ alongside the immunopeptidomics methods of Bailey *et al*¹¹⁴ were applied to provide this hitherto absent comparison.

Hybridoma cells were grown for the secretion of anti-MHC I monoclonal antibodies. These antibodies were necessary for the extraction of peptide-bound MHC protein complexes for characterisation of the immunopeptidome of alveolar epithelial cells exposed to chemical sensitisers, DNCB and PA. Following Hybridoma growth and anti-MHC monoclonal antibody extraction, mAb purification and quantitation was achieved with a protein A column online to an FPLC system (Figure 5.2). The methodology was utilised for increased mAb purification speed and real-time quantitation estimation. This was particularly useful given the substantial quantities of antibody required for this study where the purchasing cost would potentially be prohibitive.

Methodology of anti-MHC monoclonal antibody growth, purification, and quantification was initially streamlined (chapter 5.3.1). A549 exposure to phthalic anhydride was selected as the experimental condition based on showing the largest number of candidate haptenated peptides revealed in the global proteomic experiments (Appendix, section A.2.7). Therefore, presenting this condition as the most likely to yield haptenated immunopeptides in the immunopeptidome. DNCB was included as a direct comparison to the keratinocyte-based experiments performed by Bailey *et al*¹¹ with the expectation the number of haptenated proteins would be similarly low following DNCB exposure here. Given the significant cellular response of these cells to phthalic anhydride (and not DNCB) in global proteomics experiments, it was hypothesised this would provide similar or even greater levels of haptenation relative to DNCB. Ideally a number of these haptenated peptides would be matched to haptenated or significantly up-regulated proteins in the global proteomics results. However, the results did not provide convincing support for any immunopeptides related to haptenated proteins previously identified (see 4.3.5) forming peptide antigens on MHC-I complexes under these experimental conditions. Whilst a number of alterations to the experimental design and workflow have since been proposed, e.g. a different cell line or different batch of antibody with greater efficacy, it is yet to be determined whether this would result in more haptenated immunopeptides identified.

To summarise the experimental results here, cell proliferation appeared to be induced by each sensitizer chemical, though seemingly to a greater extent with respiratory sensitizers (Figures 3.13 & 4.3). Interestingly, even very low concentrations of skin sensitizer chemicals here were shown to be cytotoxic whereas respiratory sensitizers were not. This raised questions surrounding the relative potency and sensitization potential of the different sensitizers under these specific reaction conditions. Such complexities remain somewhat beyond the scope of the experiments presented here, so the maximum functional reactivity under these conditions was investigated instead. Skin sensitizer chemicals did appear to reach proportional maximum reactivity at lower exposure concentrations than respiratory sensitizers with the favoured amino acid nucleophile. Though a number of other factors like availability of different amino acid nucleophiles in different heterogeneous reaction environments make the importance of this observation incompletely clear. The global proteome presented significantly and substantially more profound alterations following exposure to respiratory sensitizers relative to skin sensitizers. The A549 alveolar epithelial cell immunopeptidome however showed no evidence of being altered following exposure to either a skin (DNCB) or respiratory (PA) sensitizer.

6.1.1 Future Experiments

Based on the results presented in this series of experiments, several further hypotheses have been generated. Different routes of detoxification and cellular stress pathways were identified as being differentially induced between skin and respiratory sensitiser exposure in the global proteomics results. This paired with the relatively low level of haptentation observed in the proteome and immunopeptidome at 24-hour timepoints highlights differences in detoxification and cellular stress – particularly oxidative stress – which offers an interesting area for further investigation. It has recently been demonstrated elsewhere that the maximum level of protein haptentation *in vitro* may occur at time points much below 24 hours^{9,10,231}. These observations further strengthen the rationale for comparing haptentation at additional, shorter time points under similar conditions. Similarly, the relative importance and differences between chronic low hapten dosage exposure and acute single high dose exposure represent another comparison worth further investigation. The differences in cell proliferation and protein abundance following exposure to skin or respiratory sensitisers provokes interest in studying differences in protein turnover. This is reinforced by the differences in ubiquitin and proteasome related proteins and processes significantly enriched differentially following skin or respiratory sensitiser chemical exposure here.

A number of different methodologies, of varying complexities, have been proposed that might aid in studying these newly generated hypotheses. Exposure of cell cultures to aerosol-based respiratory sensitisers in air-liquid interface *in vitro* 3D models, such as MucilAir^{TM 347}, represents a progression in model complexity that could be employed following the results presented here. Such models were not included as part of this project as it was determined the dynamics and response to respiratory sensitisers needed to be understood in a more fundamental context initially – particularly for comparison to skin sensitisers. In a similar sense, studying haptentation in *ex vivo* lung tissue would be of considerable interest, particularly as a comparison to skin tissue studies of a similar nature²⁸.

As noted in previous chapters, the exposure of professional antigen presenting cell lines to heavily haptentated cell lysates³³³, or co-culture of sensitised epithelial cells with professional antigen-presenting cell lines would be useful progressions on the experiments here. This would provide the benefit of greater possible exposure concentrations of sensitiser chemicals, accounting for the differences in nucleophile:electrophile ratio throughout the literature between *in chemico* and *in vitro* experimental designs. This would also provide a more appropriate system in which to compare differences in cytokine secretion associated with skin or respiratory sensitisation adverse outcomes. These methodologies would further connect the upstream adverse outcome pathway

evidence with the downstream divergent T cell proliferation of the AOPs. With this in mind, synthetic analogues of peptides validated in the haptenome would have utility in the challenge of T_h1/T_h2 sub-populations of T cells, simulating repeated sensitiser exposure in the latter phases of skin and respiratory sensitisation.

In conclusion, this research project characterised the haptenome, proteome, and immunopeptidome based on the specific reactivity of select skin and respiratory chemical sensitisers. The results presented here have allowed progression of the initial hypotheses regarding interplay between these aspects. Furthermore, the data represent a contribution to the weight-of-evidence approach to the adverse outcome pathways as well as generation of new hypotheses for further research in this area.

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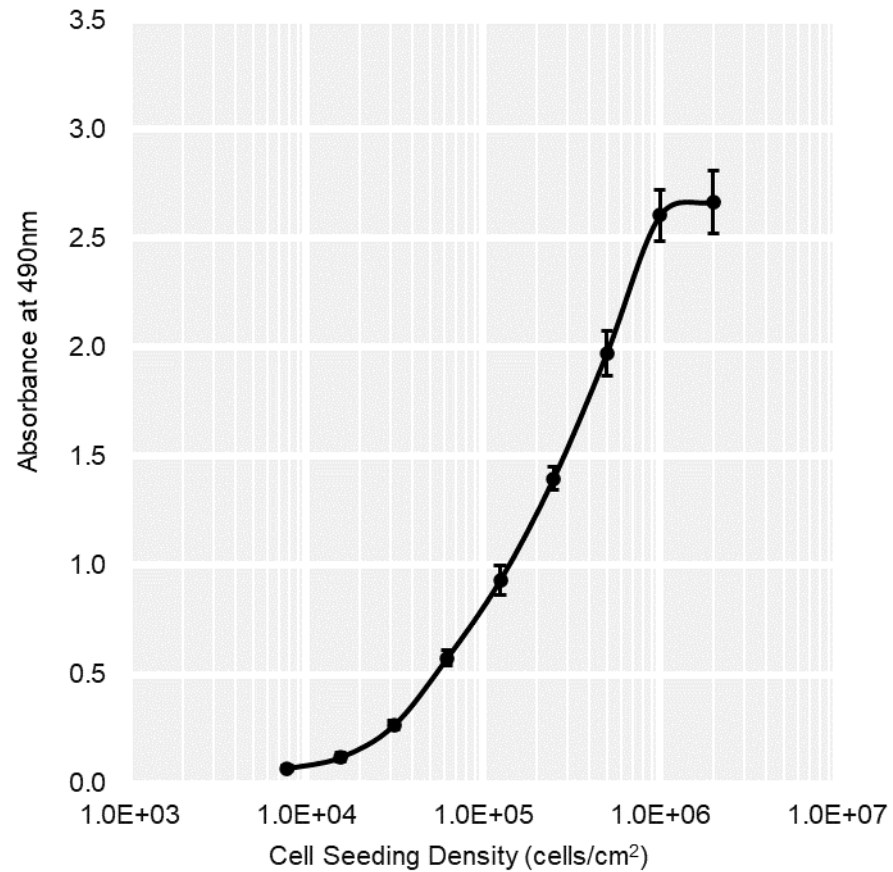
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Appendix A

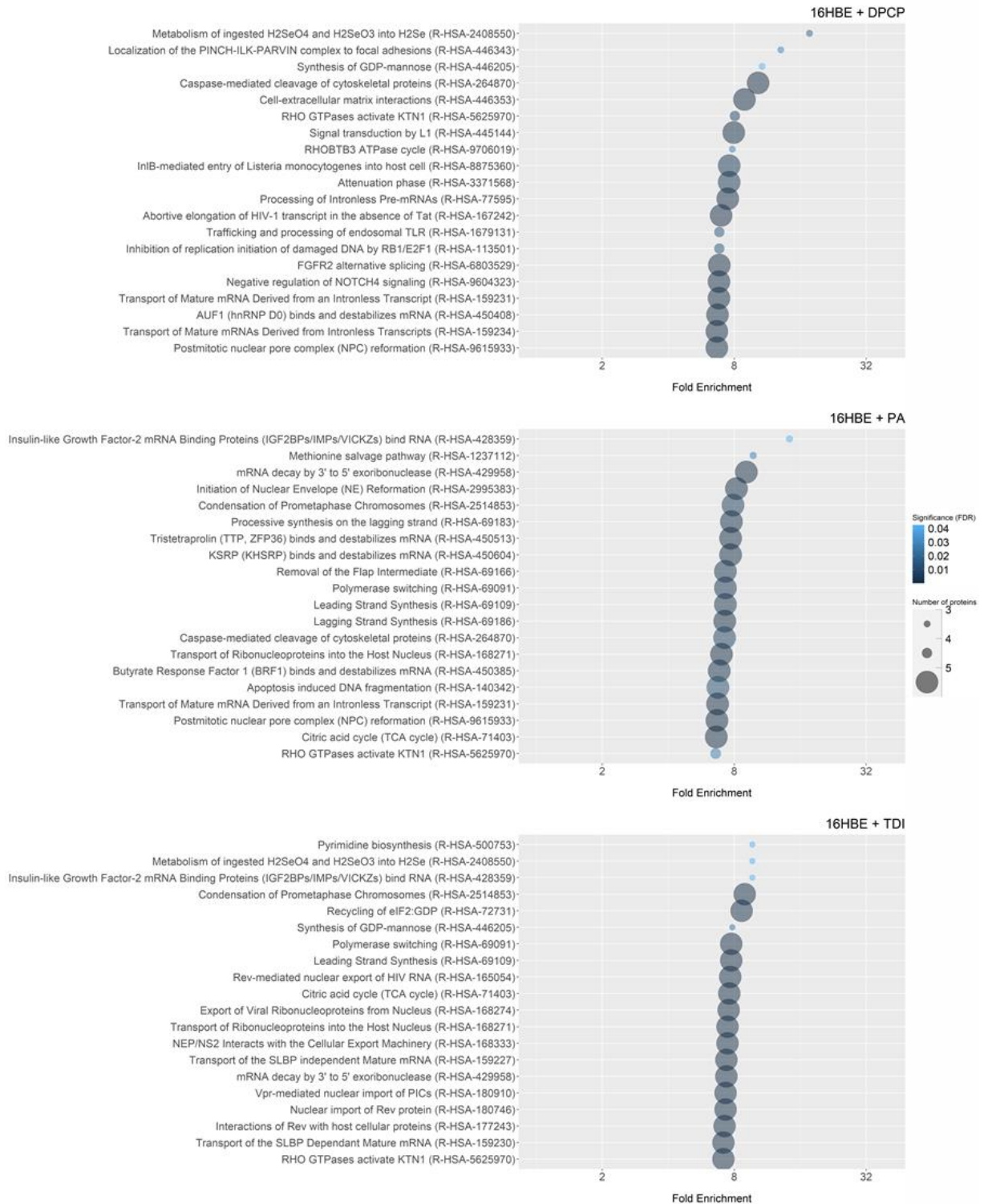
A.1 Supplementary data for chapter 3



Appendix figure 1: Absorbance of soluble formazan produced from MTS/PMS over an extended cell density gradient of 16HBE14o⁻ cells – The absorbance is demonstrated as a measure of cell proliferation over a gradient of initial seeding densities following 24h incubation in complete DMEM.

A.2 Supplementary data for chapter 4

A.2.1 Gene ontology & pathway analysis



Appendix figure 2: Top 20 Reactome pathways enriched for significantly different proteins following DPCP, PA and TDI exposure to 16HBE14o⁻ cells – The top 20 greatest and statistically significant (1% FDR) fold enrichment pathways in the Reactome reference dataset are presented.

A.2.2 Significant proteome changes in A549 cells following exposure to PA

Accession	Uniprot ID	Description	Log2 Fold Change	P value (FDR)
O43464	HTRA2_HUMAN	Serine protease HTRA2 mitochondrial OS=Homo sapiens OX=9606 GN=HTRA2 PE=1 SV=2	1.69453	1.31E-17
Q96RQ3	MCCA_HUMAN	Methylcrotonoyl-CoA carboxylase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=MCCC1 PE=1 SV=3	1.649814	2.35E-06
P13645	K1C10_HUMAN	Keratin type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6	1.478586	1.31E-17
P10619	PPGB_HUMAN	Lysosomal protective protein OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=2	1.387023	3.87E-09
Q9Y244	POMP_HUMAN	Proteasome maturation protein OS=Homo sapiens OX=9606 GN=POMP PE=1 SV=1	1.350578	1.24E-08
Q9NYL2	M3K20_HUMAN	Mitogen-activated protein kinase kinase kinase 20 OS=Homo sapiens OX=9606 GN=MAP3K20 PE=1 SV=3	1.317079	2.60E-06
P35908	K22E_HUMAN	Keratin type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2	1.299161	2.72E-08
Q15276	RABE1_HUMAN	Rab GTPase-binding effector protein 1 OS=Homo sapiens OX=9606 GN=RABEP1 PE=1 SV=2	1.273945	0.001309
P52298	NCBP2_HUMAN	Nuclear cap-binding protein subunit 2 OS=Homo sapiens OX=9606 GN=NCBP2 PE=1 SV=1	1.228468	2.78E-05
P42830	CXCL5_HUMAN	C-X-C motif chemokine 5 OS=Homo sapiens OX=9606 GN=CXCL5 PE=1 SV=1	1.204277	0.003502
P61604	CH10_HUMAN	10 kDa heat shock protein mitochondrial OS=Homo sapiens OX=9606 GN=HSP1 PE=1 SV=2	1.198491	9.76E-06
Q96M27	PRRC1_HUMAN	Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 PE=1 SV=1	1.158504	2.42E-06
O75937	DNJC8_HUMAN	DnaJ homolog subfamily C member 8 OS=Homo sapiens OX=9606 GN=DNAJC8 PE=1 SV=2	1.157417	2.35E-06
P52926	HMG2_HUMAN	High mobility group protein HMGI-C OS=Homo sapiens OX=9606 GN=HMG2 PE=1 SV=1	1.15586	2.60E-06
P35914	HMGCL_HUMAN	Hydroxymethylglutaryl-CoA lyase mitochondrial OS=Homo sapiens OX=9606 GN=HMGCL PE=1 SV=2	1.131502	4.25E-06
Q12864	CAD17_HUMAN	Cadherin-17 OS=Homo sapiens OX=9606 GN=CDH17 PE=2 SV=3	1.100594	9.83E-06
P50570	DYN2_HUMAN	Dynamin-2 OS=Homo sapiens OX=9606 GN=DNM2 PE=1 SV=2	1.087463	1.79E-06
Q9Y3C1	NOP16_HUMAN	Nucleolar protein 16 OS=Homo sapiens OX=9606 GN=NOP16 PE=1 SV=2	1.071018	1.72E-05
Q8NCA5	FA98A_HUMAN	Protein FAM98A OS=Homo sapiens OX=9606 GN=FAM98A PE=1 SV=2	1.067236	1.77E-05
Q9BW27	NUP85_HUMAN	Nuclear pore complex protein Nup85 OS=Homo sapiens OX=9606 GN=NUP85 PE=1 SV=1	1.060349	1.98E-05
Q9C0B1	FTO_HUMAN	Alpha-ketoglutarate-dependent dioxygenase FTO OS=Homo sapiens OX=9606 GN=FTO PE=1 SV=3	1.043279	3.06E-05
Q13188	STK3_HUMAN	Serine/threonine-protein kinase 3 OS=Homo sapiens OX=9606 GN=STK3 PE=1 SV=2	1.036269	3.36E-05
Q92917	GPKOW_HUMAN	G-patch domain and KOW motifs-containing protein OS=Homo sapiens OX=9606 GN=GPKOW PE=1 SV=2	1.028111	3.63E-05
P82909	RT36_HUMAN	28S ribosomal protein S36 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS36 PE=1 SV=2	1.026472	3.89E-05
O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1	1.002179	6.11E-05
Q9NRY4	RHG35_HUMAN	Rho GTPase-activating protein 35 OS=Homo sapiens OX=9606 GN=ARHGAP35 PE=1 SV=3	1.000444	6.18E-05
Q9NZ09	UBAP1_HUMAN	Ubiquitin-associated protein 1 OS=Homo sapiens OX=9606 GN=UBAP1 PE=1 SV=1	0.999418	6.18E-05
Q9H1E3	NUCKS_HUMAN	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens OX=9606 GN=NUCKS1 PE=1 SV=1	0.998631	2.29E-04
Q02252	MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 PE=1 SV=2	0.992083	7.11E-05
Q96DX5	ASB9_HUMAN	Ankyrin repeat and SOCS box protein 9 OS=Homo sapiens OX=9606 GN=ASB9 PE=1 SV=1	0.98669	7.50E-05
Q13685	AAMP_HUMAN	Angio-associated migratory cell protein OS=Homo sapiens OX=9606 GN=AAMP PE=1 SV=2	0.985603	8.15E-05
P51690	ARSL_HUMAN	Arylsulfatase L OS=Homo sapiens OX=9606 GN=ARSL PE=1 SV=2	0.971285	1.07E-04
Q8N2K0	ABD12_HUMAN	Lysophosphatidylserine lipase ABHD12 OS=Homo sapiens OX=9606 GN=ABHD12 PE=1 SV=2	0.947303	1.72E-05
Q5VWZ2	LYPL1_HUMAN	Lysophospholipase-like protein 1 OS=Homo sapiens OX=9606 GN=LYPLAL1 PE=1 SV=3	0.936497	2.29E-04

O95479	G6PE_HUMAN	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens OX=9606 GN=H6PD PE=1 SV=2	0.935665	2.33E-04
P42285	MTREX_HUMAN	Exosome RNA helicase MTR4 OS=Homo sapiens OX=9606 GN=MTREX PE=1 SV=3	0.930262	4.54E-05
Q4KMQ2	ANO6_HUMAN	Anoctamin-6 OS=Homo sapiens OX=9606 GN=ANO6 PE=1 SV=2	0.929967	2.73E-04
Q9HCU5	PREB_HUMAN	Prolactin regulatory element-binding protein OS=Homo sapiens OX=9606 GN=PREB PE=1 SV=2	0.927456	2.80E-04
Q9HC84	MUC5B_HUMAN	Mucin-5B OS=Homo sapiens OX=9606 GN=MUC5B PE=1 SV=3	0.922878	3.14E-04
Q86SX6	GLRX5_HUMAN	Glutaredoxin-related protein 5 mitochondrial OS=Homo sapiens OX=9606 GN=GLRX5 PE=1 SV=2	0.920397	0.001029
P32969	RL9_HUMAN	60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1	0.91983	8.74E-05
P62847	RS24_HUMAN	40S ribosomal protein S24 OS=Homo sapiens OX=9606 GN=RPS24 PE=1 SV=1	0.909872	5.31E-05
Q96KR1	ZFR_HUMAN	Zinc finger RNA-binding protein OS=Homo sapiens OX=9606 GN=ZFR PE=1 SV=2	0.908233	3.89E-04
O14745	NHRF1_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens OX=9606 GN=SLC9A3R1 PE=1 SV=4	0.906736	3.70E-05
P31327	CPSM_HUMAN	Carbamoyl-phosphate synthase [ammonia] mitochondrial OS=Homo sapiens OX=9606 GN=CPS1 PE=1 SV=2	0.906048	2.38E-04
Q3YEC7	RABL6_HUMAN	Rab-like protein 6 OS=Homo sapiens OX=9606 GN=RABL6 PE=1 SV=2	0.903726	4.35E-04
Q6PUV4	CPLX2_HUMAN	Complexin-2 OS=Homo sapiens OX=9606 GN=CPLX2 PE=2 SV=2	0.902852	4.35E-04
Q9ULD2	MTUS1_HUMAN	Microtubule-associated tumor suppressor 1 OS=Homo sapiens OX=9606 GN=MTUS1 PE=1 SV=2	0.895231	5.03E-04
Q9Y2X7	GIT1_HUMAN	ARF GTPase-activating protein GIT1 OS=Homo sapiens OX=9606 GN=GIT1 PE=1 SV=2	0.889856	3.14E-04
P62995	TRA2B_HUMAN	Transformer-2 protein homolog beta OS=Homo sapiens OX=9606 GN=TRA2B PE=1 SV=1	0.884328	6.12E-04
Q5GLZ8	HERC4_HUMAN	Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens OX=9606 GN=HERC4 PE=1 SV=1	0.883355	6.08E-04
Q09161	NCBP1_HUMAN	Nuclear cap-binding protein subunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1	0.882922	0.001658
Q9BU61	NDUF3_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens OX=9606 GN=NDUFAF3 PE=1 SV=1	0.878009	6.48E-04
Q12959	DLG1_HUMAN	Disks large homolog 1 OS=Homo sapiens OX=9606 GN=DLG1 PE=1 SV=2	0.876201	5.31E-05
Q8TAG9	EXOC6_HUMAN	Exocyst complex component 6 OS=Homo sapiens OX=9606 GN=EXOC6 PE=1 SV=3	0.874201	6.11E-05
Q14CX7	NAA25_HUMAN	N-alpha-acetyltransferase 25 NatB auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA25 PE=1 SV=1	0.863295	8.44E-04
O95671	ASML_HUMAN	Probable bifunctional dTTP/UTP pyrophosphatase/methyltransferase protein OS=Homo sapiens OX=9606 GN=ASMTL PE=1 SV=3	0.860692	8.83E-04
Q99447	PCY2_HUMAN	Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens OX=9606 GN=PCYT2 PE=1 SV=1	0.859536	8.83E-04
P62266	RS23_HUMAN	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3	0.852443	9.91E-04
O75886	STAM2_HUMAN	Signal transducing adapter molecule 2 OS=Homo sapiens OX=9606 GN=STAM2 PE=1 SV=1	0.85002	0.001051
P11279	LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens OX=9606 GN=LAMP1 PE=1 SV=3	0.84833	0.003259
Q8N9T8	KRI1_HUMAN	Protein KRI1 homolog OS=Homo sapiens OX=9606 GN=KRI1 PE=1 SV=3	0.845861	0.004088
Q9BZE1	RM37_HUMAN	39S ribosomal protein L37 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL37 PE=1 SV=2	0.844519	3.14E-04
P49916	DNLI3_HUMAN	DNA ligase 3 OS=Homo sapiens OX=9606 GN=LIG3 PE=1 SV=2	0.838448	0.001658
Q9BQ52	RN22_HUMAN	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens OX=9606 GN=ELAC2 PE=1 SV=2	0.83603	8.12E-06
Q9H6Z4	RANB3_HUMAN	Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=1	0.834704	7.14E-06
P20839	IMDH1_HUMAN	Inosine-5'-monophosphate dehydrogenase 1 OS=Homo sapiens OX=9606 GN=IMPDH1 PE=1 SV=2	0.834018	1.30E-04
Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 OS=Homo sapiens OX=9606 GN=DPP7 PE=1 SV=3	0.830075	7.40E-04
Q71UM5	RS27L_HUMAN	40S ribosomal protein S27-like OS=Homo sapiens OX=9606 GN=RPS27L PE=1 SV=3	0.826762	0.009538
Q16513	PKN2_HUMAN	Serine/threonine-protein kinase N2 OS=Homo sapiens OX=9606 GN=PKN2 PE=1 SV=1	0.826447	0.001658
Q96H79	ZCCHL_HUMAN	Zinc finger CCCH-type antiviral protein 1-like OS=Homo sapiens OX=9606 GN=ZC3HAV1L PE=1 SV=2	0.824563	0.001658

Q93050	VPP1_HUMAN	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens OX=9606 GN=ATP6V0A1 PE=1 SV=3	0.816605	0.00669
Q9BQE3	TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1	0.812537	0.002087
Q96JM3	CHAP1_HUMAN	Chromosome alignment-maintaining phosphoprotein 1 OS=Homo sapiens OX=9606 GN=CHAMP1 PE=1 SV=2	0.804586	0.002274
P29992	GNA11_HUMAN	Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens OX=9606 GN=GNA11 PE=1 SV=2	0.80336	0.002326
Q29RF7	PDS5A_HUMAN	Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens OX=9606 GN=PDS5A PE=1 SV=1	0.801458	0.002374
P05387	RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1	0.799931	0.001627
P83916	CBX1_HUMAN	Chromobox protein homolog 1 OS=Homo sapiens OX=9606 GN=CBX1 PE=1 SV=1	0.799013	5.96E-04
Q9UEE9	CFDP1_HUMAN	Craniofacial development protein 1 OS=Homo sapiens OX=9606 GN=CFDP1 PE=1 SV=1	0.798159	0.002136
P39023	RL3_HUMAN	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2	0.796992	0.001983
P29218	IMPA1_HUMAN	Inositol monophosphatase 1 OS=Homo sapiens OX=9606 GN=IMPA1 PE=1 SV=1	0.795723	8.66E-04
P52594	AGFG1_HUMAN	Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=AGFG1 PE=1 SV=2	0.794036	6.84E-04
Q9Y4E1	WAC2C_HUMAN	WASH complex subunit 2C OS=Homo sapiens OX=9606 GN=WASHC2C PE=1 SV=4	0.792204	1.98E-05
P10746	HEM4_HUMAN	Uroporphyrinogen-III synthase OS=Homo sapiens OX=9606 GN=UROS PE=1 SV=1	0.79195	0.002598
Q00535	CDK5_HUMAN	Cyclin-dependent-like kinase 5 OS=Homo sapiens OX=9606 GN=CDK5 PE=1 SV=3	0.791691	0.001277
P41236	IPP2_HUMAN	Protein phosphatase inhibitor 2 OS=Homo sapiens OX=9606 GN=PPP1R2 PE=1 SV=2	0.79102	0.00708
Q6NXS1	IPP2B_HUMAN	Protein phosphatase inhibitor 2 family member B OS=Homo sapiens OX=9606 GN=PPP1R2B PE=1 SV=2	0.79102	0.00708
P49006	MRP_HUMAN	MARCKS-related protein OS=Homo sapiens OX=9606 GN=MARCKSL1 PE=1 SV=2	0.790329	0.003767
P19388	RPAB1_HUMAN	DNA-directed RNA polymerases I II and III subunit RPABC1 OS=Homo sapiens OX=9606 GN=POLR2E PE=1 SV=4	0.789526	0.002744
Q9BQP7	MGME1_HUMAN	Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens OX=9606 GN=MGME1 PE=1 SV=1	0.789125	0.002752
Q07021	C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein mitochondrial OS=Homo sapiens OX=9606 GN=C1QBP PE=1 SV=1	0.784365	0.002744
O00165	HAX1_HUMAN	HCLS1-associated protein X-1 OS=Homo sapiens OX=9606 GN=HAX1 PE=1 SV=2	0.782769	0.002904
Q9UQ13	SHOC2_HUMAN	Leucine-rich repeat protein SHOC-2 OS=Homo sapiens OX=9606 GN=SHOC2 PE=1 SV=2	0.782551	0.002968
Q12972	PP1R8_HUMAN	Nuclear inhibitor of protein phosphatase 1 OS=Homo sapiens OX=9606 GN=PPP1R8 PE=1 SV=2	0.782246	0.002978
P68871	HBB_HUMAN	Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2	0.781414	0.003104
Q5TFE4	NT5D1_HUMAN	5'-nucleotidase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NT5DC1 PE=1 SV=1	0.780687	4.53E-04
Q6L8Q7	PDE12_HUMAN	2' 5'-phosphodiesterase 12 OS=Homo sapiens OX=9606 GN=PDE12 PE=1 SV=2	0.777308	0.004568
P19525	E2AK2_HUMAN	Interferon-induced double-stranded RNA-activated protein kinase OS=Homo sapiens OX=9606 GN=EIF2AK2 PE=1 SV=2	0.775332	0.001333
Q13523	PRP4B_HUMAN	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3	0.77424	5.71E-04
Q658Y4	F91A1_HUMAN	Protein FAM91A1 OS=Homo sapiens OX=9606 GN=FAM91A1 PE=1 SV=3	0.773491	0.003271
Q8IXB1	DJC10_HUMAN	DnaJ homolog subfamily C member 10 OS=Homo sapiens OX=9606 GN=DNAJC10 PE=1 SV=2	0.773307	6.08E-04
Q8ND56	LS14A_HUMAN	Protein LSM14 homolog A OS=Homo sapiens OX=9606 GN=LSM14A PE=1 SV=3	0.771767	0.003104
P69905	HBA_HUMAN	Hemoglobin subunit alpha OS=Homo sapiens OX=9606 GN=HBA1 PE=1 SV=2	0.771376	0.003448
Q8WVJ2	NUDC2_HUMAN	NudC domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NUDCD2 PE=1 SV=1	0.7695	0.003862
Q8TB96	TIP_HUMAN	T-cell immunomodulatory protein OS=Homo sapiens OX=9606 GN=ITFG1 PE=1 SV=1	0.768597	0.00356
P98088	MUC5A_HUMAN	Mucin-5AC OS=Homo sapiens OX=9606 GN=MUC5AC PE=1 SV=4	0.763515	0.002274
P47712	PA24A_HUMAN	Cytosolic phospholipase A2 OS=Homo sapiens OX=9606 GN=PLA2G4A PE=1 SV=2	0.762052	0.005574
P55265	DSRAD_HUMAN	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=4	0.761265	0.005616

Q14257	RCN2_HUMAN	Reticulocalbin-2 OS=Homo sapiens OX=9606 GN=RCN2 PE=1 SV=1	0.761097	0.002904
Q9BT22	ALG1_HUMAN	Chitobiosyldiphosphodolichol beta-mannosyltransferase OS=Homo sapiens OX=9606 GN=ALG1 PE=1 SV=2	0.760173	0.003958
Q9BVG8	KIFC3_HUMAN	Kinesin-like protein KIFC3 OS=Homo sapiens OX=9606 GN=KIFC3 PE=1 SV=4	0.758138	0.001029
Q12979	ABR_HUMAN	Active breakpoint cluster region-related protein OS=Homo sapiens OX=9606 GN=ABR PE=1 SV=2	0.754624	0.002727
P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 OS=Homo sapiens OX=9606 GN=PTPN6 PE=1 SV=1	0.753445	0.004393
P55081	MFAP1_HUMAN	Microfibrillar-associated protein 1 OS=Homo sapiens OX=9606 GN=MFAP1 PE=1 SV=2	0.75269	0.00395
O00425	IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP3 PE=1 SV=2	0.752587	0.007324
Q9H6V9	LDAH_HUMAN	Lipid droplet-associated hydrolase OS=Homo sapiens OX=9606 GN=LDAH PE=1 SV=1	0.751698	0.004342
P35219	CAH8_HUMAN	Carbonic anhydrase-related protein OS=Homo sapiens OX=9606 GN=CA8 PE=1 SV=3	0.751516	0.004551
P27216	ANX13_HUMAN	Annexin A13 OS=Homo sapiens OX=9606 GN=ANXA13 PE=1 SV=3	0.751283	0.005574
Q9Y2Z4	SYYM_HUMAN	Tyrosine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=YARS2 PE=1 SV=2	0.748461	0.003701
Q6P9B6	MEAK7_HUMAN	MTOR-associated protein MEAK7 OS=Homo sapiens OX=9606 GN=MEAK7 PE=1 SV=2	0.74717	0.009739
Q9UDT6	CLIP2_HUMAN	CAP-Gly domain-containing linker protein 2 OS=Homo sapiens OX=9606 GN=CLIP2 PE=1 SV=1	0.746988	0.001844
Q96DZ1	ERLEC_HUMAN	Endoplasmic reticulum lectin 1 OS=Homo sapiens OX=9606 GN=ERLEC1 PE=1 SV=1	0.746829	0.004631
Q5SWX8	ODR4_HUMAN	Protein odr-4 homolog OS=Homo sapiens OX=9606 GN=ODR4 PE=1 SV=1	0.746482	0.004574
Q96RE7	NACC1_HUMAN	Nucleus accumbens-associated protein 1 OS=Homo sapiens OX=9606 GN=NACC1 PE=1 SV=1	0.744576	0.004947
Q96K76	UBP47_HUMAN	Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens OX=9606 GN=USP47 PE=1 SV=3	0.744168	0.00455
Q06124	PTN11_HUMAN	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 PE=1 SV=3	0.742316	5.96E-04
P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI2 PE=1 SV=3	0.740702	0.008648
Q92599	SEPT8_HUMAN	Septin-8 OS=Homo sapiens OX=9606 GN=SEPTIN8 PE=1 SV=4	0.74	0.006409
Q92878	RAD50_HUMAN	DNA repair protein RAD50 OS=Homo sapiens OX=9606 GN=RAD50 PE=1 SV=1	0.739319	4.54E-05
Q13510	ASAH1_HUMAN	Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=5	0.738606	0.005123
Q9UNP9	PPIE_HUMAN	Peptidyl-prolyl cis-trans isomerase E OS=Homo sapiens OX=9606 GN=PPIE PE=1 SV=1	0.737825	0.00521
Q5VTR2	BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens OX=9606 GN=RNFB20 PE=1 SV=2	0.737609	0.002136
Q32P44	EMAL3_HUMAN	Echinoderm microtubule-associated protein-like 3 OS=Homo sapiens OX=9606 GN=EML3 PE=1 SV=1	0.736966	0.005145
P30876	RPB2_HUMAN	DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=1	0.736966	0.005574
P10909	CLUS_HUMAN	Clusterin OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1	0.735758	0.005417
P08708	RS17_HUMAN	40S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=2	0.734279	0.005972
Q92541	RTF1_HUMAN	RNA polymerase-associated protein RTF1 homolog OS=Homo sapiens OX=9606 GN=RTF1 PE=1 SV=4	0.734276	0.005449
Q53HC9	EIPR1_HUMAN	EARP and GARP complex-interacting protein 1 OS=Homo sapiens OX=9606 GN=EIPR1 PE=1 SV=2	0.733659	0.005574
P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 OS=Homo sapiens OX=9606 GN=CAPZA1 PE=1 SV=3	0.733449	0.002884
P17252	KPCA_HUMAN	Protein kinase C alpha type OS=Homo sapiens OX=9606 GN=PRKCA PE=1 SV=4	0.732441	0.002526
O15067	PUR4_HUMAN	Phosphoribosylformylglycinamide synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1 SV=4	0.732202	0.006912
Q9HB40	RISC_HUMAN	Retinoid-inducible serine carboxypeptidase OS=Homo sapiens OX=9606 GN=SCPEP1 PE=1 SV=1	0.731252	0.005574
P35222	CTNB1_HUMAN	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1	0.730869	0.002274
Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=2	0.730525	0.002744
P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNP2 PE=1 SV=1	0.730092	0.005724
Q5TAQ9	DCAF8_HUMAN	DDB1- and CUL4-associated factor 8 OS=Homo sapiens OX=9606 GN=DCAF8 PE=1 SV=1	0.72924	0.005715

Q9Y221	NIP7_HUMAN	60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens OX=9606 GN=NIP7 PE=1 SV=1	0.72849	0.005875
P33240	CSTF2_HUMAN	Cleavage stimulation factor subunit 2 OS=Homo sapiens OX=9606 GN=CSTF2 PE=1 SV=1	0.724464	0.008362
Q9H993	ARMT1_HUMAN	Damage-control phosphatase ARMT1 OS=Homo sapiens OX=9606 GN=ARMT1 PE=1 SV=1	0.723053	0.006227
P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=3	0.72289	0.006662
Q8WW12	PCNP_HUMAN	PEST proteolytic signal-containing nuclear protein OS=Homo sapiens OX=9606 GN=PCNP PE=1 SV=2	0.722043	0.00395
P32121	ARRB2_HUMAN	Beta-arrestin-2 OS=Homo sapiens OX=9606 GN=ARRB2 PE=1 SV=2	0.721887	0.00626
Q9GZS1	RPA49_HUMAN	DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens OX=9606 GN=POLR1E PE=1 SV=3	0.72163	0.006216
Q92643	GPI8_HUMAN	GPI-anchor transamidase OS=Homo sapiens OX=9606 GN=PIGK PE=1 SV=2	0.720561	0.006298
Q9UDY8	MALT1_HUMAN	Mucosa-associated lymphoid tissue lymphoma translocation protein 1 OS=Homo sapiens OX=9606 GN=MALT1 PE=1 SV=1	0.720506	0.004088
P06737	PYGL_HUMAN	Glycogen phosphorylase liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4	0.720355	0.002526
P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=2	0.718261	0.00626
Q02241	KIF23_HUMAN	Kinesin-like protein KIF23 OS=Homo sapiens OX=9606 GN=KIF23 PE=1 SV=3	0.716359	0.006541
O43617	TPPC3_HUMAN	Trafficking protein particle complex subunit 3 OS=Homo sapiens OX=9606 GN=TRAPPC3 PE=1 SV=1	0.716107	0.00669
O43852	CALU_HUMAN	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	0.713627	0.009072
P63261	ACTG_HUMAN	Actin cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1	0.713273	0.006634
O43148	MCES_HUMAN	mRNA cap guanine-N7 methyltransferase OS=Homo sapiens OX=9606 GN=RNMT PE=1 SV=1	0.712905	0.00708
Q9Y613	FHOD1_HUMAN	FH1/FH2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FHOD1 PE=1 SV=3	0.712614	0.00356
Q9NRF8	PYRG2_HUMAN	CTP synthase 2 OS=Homo sapiens OX=9606 GN=CTPS2 PE=1 SV=1	0.712377	0.00669
Q96EE3	SEH1_HUMAN	Nucleoporin SEH1 OS=Homo sapiens OX=9606 GN=SEH1L PE=1 SV=3	0.711829	0.006752
Q13616	CUL1_HUMAN	Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=2	0.709605	0.006978
Q6DKK2	TTC19_HUMAN	Tetratricopeptide repeat protein 19 mitochondrial OS=Homo sapiens OX=9606 GN=TTC19 PE=1 SV=4	0.708621	0.006752
Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SND1 PE=1 SV=1	0.70818	0.003958
Q9UNE7	CHIP_HUMAN	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens OX=9606 GN=STUB1 PE=1 SV=2	0.706066	0.006662
P60709	ACTB_HUMAN	Actin cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1	0.705363	0.007169
Q86SJ2	AMGO2_HUMAN	Amphoterin-induced protein 2 OS=Homo sapiens OX=9606 GN=AMIGO2 PE=1 SV=1	0.705309	0.007169
P46934	NEDD4_HUMAN	E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens OX=9606 GN=NEDD4 PE=1 SV=4	0.703992	0.007169
Q6P5R6	RL22L_HUMAN	60S ribosomal protein L22-like 1 OS=Homo sapiens OX=9606 GN=RPL22L1 PE=1 SV=2	0.703965	0.007169
Q9NUI1	DECR2_HUMAN	Peroxisomal 2 4-dienoyl-CoA reductase OS=Homo sapiens OX=9606 GN=DECR2 PE=1 SV=1	0.703282	0.007327
P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 OS=Homo sapiens OX=9606 GN=MAPK1 PE=1 SV=3	0.703189	7.07E-04
O00541	PESC_HUMAN	Pescadillo homolog OS=Homo sapiens OX=9606 GN=PES1 PE=1 SV=1	0.703101	8.44E-04
P84095	RHOG_HUMAN	Rho-related GTP-binding protein RhoG OS=Homo sapiens OX=9606 GN=RHOG PE=1 SV=1	0.702656	0.002028
Q13451	FKBP5_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens OX=9606 GN=FKBP5 PE=1 SV=2	0.702614	0.005506
Q8TDN6	BRX1_HUMAN	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRX1 PE=1 SV=2	0.702231	0.006736
Q96EM0	T3HPD_HUMAN	Trans-3-hydroxy-L-proline dehydratase OS=Homo sapiens OX=9606 GN=L3HYPDH PE=1 SV=2	0.701036	0.007421
Q9NR50	EI2BG_HUMAN	Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens OX=9606 GN=EIF2B3 PE=1 SV=1	0.70044	0.007551
Q13148	TADBP_HUMAN	TAR DNA-binding protein 43 OS=Homo sapiens OX=9606 GN=TARDBP PE=1 SV=1	0.699855	0.006912
P49407	ARRB1_HUMAN	Beta-arrestin-1 OS=Homo sapiens OX=9606 GN=ARRB1 PE=1 SV=2	0.699569	0.007676
Q9Y376	CAB39_HUMAN	Calcium-binding protein 39 OS=Homo sapiens OX=9606 GN=CAB39 PE=1 SV=1	0.698619	0.006298

P08047	SP1_HUMAN	Transcription factor Sp1 OS=Homo sapiens OX=9606 GN=SP1 PE=1 SV=3	0.697601	0.007676
Q15750	TAB1_HUMAN	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens OX=9606 GN=TAB1 PE=1 SV=1	0.697485	0.007681
Q2NL82	TSR1_HUMAN	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens OX=9606 GN=TSR1 PE=1 SV=1	0.697082	0.00434
Q969X5	ERGI1_HUMAN	Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens OX=9606 GN=ERGIC1 PE=1 SV=1	0.694089	0.006238
P04350	TBB4A_HUMAN	Tubulin beta-4A chain OS=Homo sapiens OX=9606 GN=TUBB4A PE=1 SV=2	0.693897	0.008356
Q9NQG5	RPR1B_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens OX=9606 GN=RPRD1B PE=1 SV=1	0.693573	0.001623
Q4G0N4	NAKD2_HUMAN	NAD kinase 2 mitochondrial OS=Homo sapiens OX=9606 GN=NAKD2 PE=1 SV=2	0.691654	0.006878
Q13724	MOGS_HUMAN	Mannosyl-oligosaccharide glucosidase OS=Homo sapiens OX=9606 GN=MOGS PE=1 SV=5	0.690419	0.008356
P19338	NUCL_HUMAN	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	0.690128	0.00983
Q6UN15	FIP1_HUMAN	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens OX=9606 GN=FIP1L1 PE=1 SV=1	0.689876	0.007418
Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=2	0.688979	0.007551
P84085	ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=2	0.688056	0.008667
P82933	RT09_HUMAN	28S ribosomal protein S9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS9 PE=1 SV=2	0.687722	0.005866
Q9HCD5	NCOA5_HUMAN	Nuclear receptor coactivator 5 OS=Homo sapiens OX=9606 GN=NCOA5 PE=1 SV=2	0.687691	0.008667
Q15643	TRIPB_HUMAN	Thyroid receptor-interacting protein 11 OS=Homo sapiens OX=9606 GN=TRIP11 PE=1 SV=3	0.686892	0.008735
P07237	PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=3	0.686517	0.004476
P49023	PAXI_HUMAN	Paxillin OS=Homo sapiens OX=9606 GN=PXN PE=1 SV=3	0.686442	8.44E-04
Q7Z7H8	RM10_HUMAN	39S ribosomal protein L10 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL10 PE=1 SV=3	0.685982	0.008981
O60462	NRP2_HUMAN	Neuropilin-2 OS=Homo sapiens OX=9606 GN=NRP2 PE=1 SV=3	0.685242	0.009072
Q5ZPR3	CD276_HUMAN	CD276 antigen OS=Homo sapiens OX=9606 GN=CD276 PE=1 SV=1	0.682539	0.009193
Q9NX40	OCAD1_HUMAN	OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCAD1 PE=1 SV=1	0.682096	0.008667
P54803	GALC_HUMAN	Galactocerebrosidase OS=Homo sapiens OX=9606 GN=GALC PE=1 SV=3	0.680721	0.009072
Q6ZRP7	QSOX2_HUMAN	Sulfhydryl oxidase 2 OS=Homo sapiens OX=9606 GN=QSOX2 PE=1 SV=3	0.680236	0.009072
Q92734	TFG_HUMAN	Protein TFG OS=Homo sapiens OX=9606 GN=TFG PE=1 SV=2	0.680045	0.008259
Q8WZA0	LZIC_HUMAN	Protein LZIC OS=Homo sapiens OX=9606 GN=LZIC PE=1 SV=1	0.679772	0.009937
Q9UKY7	CDV3_HUMAN	Protein CDV3 homolog OS=Homo sapiens OX=9606 GN=CDV3 PE=1 SV=1	0.679734	0.008667
Q96CP6	ASTRA_HUMAN	Protein Aster-A OS=Homo sapiens OX=9606 GN=GRAMD1A PE=1 SV=2	0.678072	0.003524
Q99538	LGMN_HUMAN	Legumain OS=Homo sapiens OX=9606 GN=LGMN PE=1 SV=1	0.678072	0.009418
Q8NBQ5	DHB11_HUMAN	Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens OX=9606 GN=HSD17B11 PE=1 SV=3	0.677031	0.00669
Q13247	SRSF6_HUMAN	Serine/arginine-rich splicing factor 6 OS=Homo sapiens OX=9606 GN=SRSF6 PE=1 SV=2	0.67673	0.007172
P49411	EFTU_HUMAN	Elongation factor Tu mitochondrial OS=Homo sapiens OX=9606 GN=TUFM PE=1 SV=2	0.676323	0.009937
Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	0.676281	0.009795
Q00653	NFKB2_HUMAN	Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens OX=9606 GN=NFKB2 PE=1 SV=4	0.675998	0.006565
C9JLW8	MCR11_HUMAN	Mapk-regulated corepressor-interacting protein 1 OS=Homo sapiens OX=9606 GN=MCRIP1 PE=1 SV=1	0.674845	0.009937
Q13228	SBP1_HUMAN	Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=2	0.673936	0.006752
Q13409	DC112_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC112 PE=1 SV=3	0.673584	0.005574
O14936	CSKP_HUMAN	Peripheral plasma membrane protein CASK OS=Homo sapiens OX=9606 GN=CASK PE=1 SV=3	0.673033	0.005608
Q9BRT3	MIEN1_HUMAN	Migration and invasion enhancer 1 OS=Homo sapiens OX=9606 GN=MIEN1 PE=1 SV=1	0.669921	0.006736
P21589	5NTD_HUMAN	5'-nucleotidase OS=Homo sapiens OX=9606 GN=NT5E PE=1 SV=1	0.668794	0.002207

Q14764	MVP_HUMAN	Major vault protein OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=4	0.667913	0.008667
Q15435	PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1	0.667833	0.004041
Q96EP5	DAZP1_HUMAN	DAZ-associated protein 1 OS=Homo sapiens OX=9606 GN=DAZAP1 PE=1 SV=1	0.667149	0.009072
Q93009	UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens OX=9606 GN=USP7 PE=1 SV=2	0.666124	0.004571
P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=3	0.665336	0.002893
Q06203	PUR1_HUMAN	Amidophosphoribosyltransferase OS=Homo sapiens OX=9606 GN=PPAT PE=1 SV=1	0.661812	0.009616
Q9NTX5	ECHD1_HUMAN	Ethylmalonyl-CoA decarboxylase OS=Homo sapiens OX=9606 GN=ECHDC1 PE=1 SV=2	0.660182	0.006397
Q01780	EXOSX_HUMAN	Exosome component 10 OS=Homo sapiens OX=9606 GN=EXOSC10 PE=1 SV=2	0.654312	0.002463
O00159	MYO1C_HUMAN	Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4	0.654197	0.009923
Q9Y277	VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606 GN=VDAC3 PE=1 SV=1	0.652682	0.009193
Q86X55	CARM1_HUMAN	Histone-arginine methyltransferase CARM1 OS=Homo sapiens OX=9606 GN=CARM1 PE=1 SV=3	0.651067	0.008484
Q96G03	PGM2_HUMAN	Phosphoglucomutase-2 OS=Homo sapiens OX=9606 GN=PGM2 PE=1 SV=4	0.650175	0.007664
Q99798	ACON_HUMAN	Aconitate hydratase mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=2	0.647885	0.003448
Q15036	SNX17_HUMAN	Sorting nexin-17 OS=Homo sapiens OX=9606 GN=SNX17 PE=1 SV=1	0.647567	0.004979
Q14137	BOP1_HUMAN	Ribosome biogenesis protein BOP1 OS=Homo sapiens OX=9606 GN=BOP1 PE=1 SV=2	0.646452	0.004342
P83111	LACTB_HUMAN	Serine beta-lactamase-like protein LACTB mitochondrial OS=Homo sapiens OX=9606 GN=LACTB PE=1 SV=2	0.646451	0.007551
Q9BTD8	RBM42_HUMAN	RNA-binding protein 42 OS=Homo sapiens OX=9606 GN=RBM42 PE=1 SV=1	0.645127	0.009072
P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR2A PE=1 SV=2	0.644717	0.006608
Q10471	GALT2_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens OX=9606 GN=GALNT2 PE=1 SV=1	0.644607	0.007347
Q9H8Y8	GORS2_HUMAN	Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2 PE=1 SV=3	0.644305	0.007676
Q9UBC2	EP15R_HUMAN	Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens OX=9606 GN=EPS15L1 PE=1 SV=1	0.643975	0.001941
Q16204	CCDC6_HUMAN	Coiled-coil domain-containing protein 6 OS=Homo sapiens OX=9606 GN=CCDC6 PE=1 SV=2	0.642106	0.009193
Q9Y2L1	RRP44_HUMAN	Exosome complex exonuclease RRP44 OS=Homo sapiens OX=9606 GN=DIS3 PE=1 SV=2	0.639376	0.002274
Q9BUJ2	HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=2	0.636873	0.006552
P42224	STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens OX=9606 GN=STAT1 PE=1 SV=2	0.634084	0.003259
Q13144	EI2BE_HUMAN	Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens OX=9606 GN=EIF2B5 PE=1 SV=3	0.63299	0.009072
P28070	PSB4_HUMAN	Proteasome subunit beta type-4 OS=Homo sapiens OX=9606 GN=PSMB4 PE=1 SV=4	0.631485	0.005145
Q9Y5S9	RBM8A_HUMAN	RNA-binding protein 8A OS=Homo sapiens OX=9606 GN=RBM8A PE=1 SV=1	0.63067	0.008973
Q8NBS9	TXND5_HUMAN	Thioredoxin domain-containing protein 5 OS=Homo sapiens OX=9606 GN=TXNDC5 PE=1 SV=2	0.62977	0.009193
O14744	ANM5_HUMAN	Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=4	0.627398	0.006216
P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=3	0.626236	0.002526
Q96RP9	EFGM_HUMAN	Elongation factor G mitochondrial OS=Homo sapiens OX=9606 GN=GFM1 PE=1 SV=2	0.623891	0.009081
P17480	UBF1_HUMAN	Nucleolar transcription factor 1 OS=Homo sapiens OX=9606 GN=UBTF PE=1 SV=1	0.622443	0.004568
Q8TC07	TBC15_HUMAN	TBC1 domain family member 15 OS=Homo sapiens OX=9606 GN=TBC1D15 PE=1 SV=2	0.622299	0.003448
Q96AQ6	PBIP1_HUMAN	Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens OX=9606 GN=PBXIP1 PE=1 SV=1	0.622195	0.004568
Q9UNZ2	NSF1C_HUMAN	NSF1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=2	0.620138	0.006634
Q92823	NRCAM_HUMAN	Neuronal cell adhesion molecule OS=Homo sapiens OX=9606 GN=NRCAM PE=1 SV=3	0.619802	0.009072

Q9UHR5	S30BP_HUMAN	SAP30-binding protein OS=Homo sapiens OX=9606 GN=SAP30BP PE=1 SV=1	0.619547	0.009072
Q15642	CIP4_HUMAN	Cdc42-interacting protein 4 OS=Homo sapiens OX=9606 GN=TRIP10 PE=1 SV=3	0.618341	0.004568
Q86XP3	DDX42_HUMAN	ATP-dependent RNA helicase DDX42 OS=Homo sapiens OX=9606 GN=DDX42 PE=1 SV=1	0.613469	0.009175
Q01813	PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase platelet type OS=Homo sapiens OX=9606 GN=PFKP PE=1 SV=2	0.610229	0.008321
P23246	SFPQ_HUMAN	Splicing factor proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2	0.608979	0.009407
O60488	ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens OX=9606 GN=ACSL4 PE=1 SV=2	0.605721	0.003742
Q13085	ACACA_HUMAN	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACACA PE=1 SV=2	0.604694	0.009072
Q9BPX3	CND3_HUMAN	Condensin complex subunit 3 OS=Homo sapiens OX=9606 GN=NCAPG PE=1 SV=1	0.603897	0.009072
O75607	NPM3_HUMAN	Nucleoplasmin-3 OS=Homo sapiens OX=9606 GN=NPM3 PE=1 SV=3	0.60014	0.009072
O95861	BPNT1_HUMAN	3'(2') 5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1	0.598637	0.008742
Q93062	RBPM5_HUMAN	RNA-binding protein with multiple splicing OS=Homo sapiens OX=9606 GN=RBPM5 PE=1 SV=1	0.59394	0.007572
Q9NTK5	OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=2	0.591487	0.008356
Q14203	DCTN1_HUMAN	Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=1 SV=3	0.589555	0.005216
P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=2	0.589093	0.004875
Q9UNW1	MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens OX=9606 GN=MINPP1 PE=1 SV=1	0.584114	0.004568
Q9NRN7	ADPPT_HUMAN	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase OS=Homo sapiens OX=9606 GN=AASDHPPT PE=1 SV=2	0.580525	0.002207
P36507	MP2K2_HUMAN	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens OX=9606 GN=MAP2K2 PE=1 SV=1	-0.66551	4.23E-04
P68431	H31_HUMAN	Histone H3.1 OS=Homo sapiens OX=9606 GN=H3C1 PE=1 SV=2	-0.94011	1.79E-07
Q71DI3	H32_HUMAN	Histone H3.2 OS=Homo sapiens OX=9606 GN=HIST2H3A PE=1 SV=3	-1.04111	6.18E-05
P14174	MIF_HUMAN	Macrophage migration inhibitory factor OS=Homo sapiens OX=9606 GN=MIF PE=1 SV=4	-1.82062	1.31E-17

Appendix Table 1: A549 global proteome changes following phthalic anhydride exposure

– Proteins with a significant difference in abundance are presented according to descending log2 fold change.

A.2.3 Significant proteome changes in A549 cells following exposure to TDI

Accession	Uniprot ID	Description	Log2 Fold Change	P value (FDR)
Q03154	ACY1_HUMAN	Aminoacylase-1 OS=Homo sapiens OX=9606 GN=ACY1 PE=1 SV=1	2.480432	0.004941
Q9HBH5	RDH14_HUMAN	Retinol dehydrogenase 14 OS=Homo sapiens OX=9606 GN=RDH14 PE=1 SV=1	1.872977	0.005421
Q12768	WASC5_HUMAN	WASH complex subunit 5 OS=Homo sapiens OX=9606 GN=WASHC5 PE=1 SV=1	1.776371	0.00462
Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens OX=9606 GN=TGFBI PE=1 SV=1	1.765845	1.94E-17
Q14C86	GAPD1_HUMAN	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=GAPVD1 PE=1 SV=2	1.523085	3.21E-11
Q14CX7	NAA25_HUMAN	N-alpha-acetyltransferase 25 NatB auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA25 PE=1 SV=1	1.443931	4.43E-11
Q8NHP6	MSPD2_HUMAN	Motile sperm domain-containing protein 2 OS=Homo sapiens OX=9606 GN=MOSPD2 PE=1 SV=1	1.415037	1.43E-09
P52926	HMGA2_HUMAN	High mobility group protein HMGI-C OS=Homo sapiens OX=9606 GN=HMGA2 PE=1 SV=1	1.373739	4.16E-09
Q9BZE1	RM37_HUMAN	39S ribosomal protein L37 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL37 PE=1 SV=2	1.3615	5.05E-09
Q9H501	ESF1_HUMAN	ESF1 homolog OS=Homo sapiens OX=9606 GN=ESF1 PE=1 SV=1	1.348717	6.28E-09
Q96KR1	ZFR_HUMAN	Zinc finger RNA-binding protein OS=Homo sapiens OX=9606 GN=ZFR PE=1 SV=2	1.334974	9.09E-09
O43795	MYO1B_HUMAN	Unconventional myosin-Ib OS=Homo sapiens OX=9606 GN=MYO1B PE=1 SV=3	1.301049	2.62E-08
P26640	SYVC_HUMAN	Valine--tRNA ligase OS=Homo sapiens OX=9606 GN=VAR51 PE=1 SV=4	1.297388	1.58E-07
Q6P2Q9	PRP8_HUMAN	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens OX=9606 GN=PRPF8 PE=1 SV=2	1.280852	2.36E-10
O00159	MYO1C_HUMAN	Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4	1.274749	5.40E-08
Q9Y6K5	OAS3_HUMAN	2'-5'-oligoadenylate synthase 3 OS=Homo sapiens OX=9606 GN=OAS3 PE=1 SV=3	1.265046	4.71E-07
O75717	WDHD1_HUMAN	WD repeat and HMG-box DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=WDHD1 PE=1 SV=1	1.227941	1.89E-07
Q9ULH7	MRTFB_HUMAN	Myocardin-related transcription factor B OS=Homo sapiens OX=9606 GN=MRTFB PE=1 SV=3	1.217892	2.11E-07
Q7Z2W4	ZCCHV_HUMAN	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens OX=9606 GN=ZC3HAV1 PE=1 SV=3	1.201634	2.78E-06
Q9H078	CLPB_HUMAN	Caseinolytic peptidase B protein homolog OS=Homo sapiens OX=9606 GN=CLPB PE=1 SV=1	1.196463	3.65E-07
O94776	MTA2_HUMAN	Metastasis-associated protein MTA2 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	1.192727	3.90E-07
Q29RF7	PDS5A_HUMAN	Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens OX=9606 GN=PDS5A PE=1 SV=1	1.188901	4.56E-06
Q9H2V7	SPNS1_HUMAN	Protein spinster homolog 1 OS=Homo sapiens OX=9606 GN=SPNS1 PE=1 SV=1	1.186272	4.71E-07
Q3YEC7	RABL6_HUMAN	Rab-like protein 6 OS=Homo sapiens OX=9606 GN=RABL6 PE=1 SV=2	1.17818	5.13E-07
Q5T4S7	UBR4_HUMAN	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens OX=9606 GN=UBR4 PE=1 SV=1	1.166951	6.62E-07
P50570	DYN2_HUMAN	Dynamin-2 OS=Homo sapiens OX=9606 GN=DNM2 PE=1 SV=2	1.16315	4.06E-08
Q9NZM1	MYOF_HUMAN	Myoferlin OS=Homo sapiens OX=9606 GN=MYOF PE=1 SV=1	1.159774	5.89E-09
O43395	PRPF3_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens OX=9606 GN=PRPF3 PE=1 SV=2	1.156959	1.00E-06
Q92917	GPLOW_HUMAN	G-patch domain and KOW motifs-containing protein OS=Homo sapiens OX=9606 GN=GPLOW PE=1 SV=2	1.152003	4.90E-07
P82909	RT36_HUMAN	28S ribosomal protein S36 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS36 PE=1 SV=2	1.14665	1.14E-06
P55265	DSRAD_HUMAN	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=4	1.138336	4.92E-08
Q9BZE4	NOG1_HUMAN	Nucleolar GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP4 PE=1 SV=3	1.13832	2.11E-07
Q13162	PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapiens OX=9606 GN=PRDX4 PE=1 SV=1	1.137083	4.76E-06
Q02543	RL18A_HUMAN	60S ribosomal protein L18a OS=Homo sapiens OX=9606 GN=RPL18A PE=1 SV=2	1.135214	1.38E-06
Q92530	PSMF1_HUMAN	Proteasome inhibitor PI31 subunit OS=Homo sapiens OX=9606 GN=PSMF1 PE=1 SV=2	1.135057	5.04E-05

Q9NRL3	STRN4_HUMAN	Striatin-4 OS=Homo sapiens OX=9606 GN=STRN4 PE=1 SV=2	1.133131	0.001809
P42696	RBM34_HUMAN	RNA-binding protein 34 OS=Homo sapiens OX=9606 GN=RBM34 PE=1 SV=2	1.132776	1.52E-06
A5YKK6	CNOT1_HUMAN	CCR4-NOT transcription complex subunit 1 OS=Homo sapiens OX=9606 GN=CNOT1 PE=1 SV=2	1.131783	1.62E-06
Q96S66	CLCC1_HUMAN	Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 PE=1 SV=1	1.129497	1.62E-06
Q9BW27	NUP85_HUMAN	Nuclear pore complex protein Nup85 OS=Homo sapiens OX=9606 GN=NUP85 PE=1 SV=1	1.117891	2.11E-06
Q2NL82	TSR1_HUMAN	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens OX=9606 GN=TSR1 PE=1 SV=1	1.116482	1.23E-06
Q8NEW0	ZNT7_HUMAN	Zinc transporter 7 OS=Homo sapiens OX=9606 GN=SLC30A7 PE=2 SV=1	1.114311	0.005203
P39060	COIA1_HUMAN	Collagen alpha-1(XVIII) chain OS=Homo sapiens OX=9606 GN=COL18A1 PE=1 SV=5	1.102128	2.89E-06
Q96RQ3	MCCA_HUMAN	Methylcrotonoyl-CoA carboxylase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=MCCC1 PE=1 SV=3	1.101538	3.03E-06
Q13501	SQSTM_HUMAN	Sequestosome-1 OS=Homo sapiens OX=9606 GN=SQSTM1 PE=1 SV=1	1.100357	3.03E-06
Q9Y2P8	RCL1_HUMAN	RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens OX=9606 GN=RCL1 PE=1 SV=3	1.099231	3.18E-06
Q9Y3T9	NOC2L_HUMAN	Nucleolar complex protein 2 homolog OS=Homo sapiens OX=9606 GN=NOC2L PE=1 SV=4	1.09635	0.009376
Q96B23	CR025_HUMAN	Uncharacterized protein C18orf25 OS=Homo sapiens OX=9606 GN=C18orf25 PE=1 SV=3	1.095405	5.41E-04
Q13523	PRP4B_HUMAN	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3	1.089597	2.04E-07
Q92604	LGAT1_HUMAN	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1 OS=Homo sapiens OX=9606 GN=LPGAT1 PE=1 SV=1	1.089039	3.79E-06
Q06587	RING1_HUMAN	E3 ubiquitin-protein ligase RING1 OS=Homo sapiens OX=9606 GN=RING1 PE=1 SV=2	1.08757	3.79E-06
Q02241	KIF23_HUMAN	Kinesin-like protein KIF23 OS=Homo sapiens OX=9606 GN=KIF23 PE=1 SV=3	1.085651	1.05E-05
O15027	SC16A_HUMAN	Protein transport protein Sec16A OS=Homo sapiens OX=9606 GN=SEC16A PE=1 SV=4	1.085521	2.53E-06
O15042	SR140_HUMAN	U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens OX=9606 GN=U2SURP PE=1 SV=2	1.084889	3.79E-06
Q8IX12	CCAR1_HUMAN	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens OX=9606 GN=CCAR1 PE=1 SV=2	1.083351	3.35E-04
Q9BVJ6	UT14A_HUMAN	U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens OX=9606 GN=UTP14A PE=1 SV=1	1.078218	8.86E-06
P13645	K1C10_HUMAN	Keratin type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6	1.074621	1.89E-07
Q6NUM9	RETST_HUMAN	All-trans-retinol 13 14-reductase OS=Homo sapiens OX=9606 GN=RETSAT PE=1 SV=2	1.069841	5.72E-06
O14497	ARI1A_HUMAN	AT-rich interactive domain-containing protein 1A OS=Homo sapiens OX=9606 GN=ARID1A PE=1 SV=3	1.061756	6.93E-06
Q93050	VPP1_HUMAN	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens OX=9606 GN=ATP6V0A1 PE=1 SV=3	1.058973	7.28E-06
Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A OS=Homo sapiens OX=9606 GN=SMC1A PE=1 SV=2	1.057809	7.71E-06
P30876	RPB2_HUMAN	DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=1	1.054448	7.90E-06
Q13085	ACACA_HUMAN	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACACA PE=1 SV=2	1.053599	2.65E-08
Q8TDN6	BRX1_HUMAN	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRX1 PE=1 SV=2	1.04587	6.30E-06
Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=2	1.044297	3.30E-06
Q96QD8	S38A2_HUMAN	Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens OX=9606 GN=SLC38A2 PE=1 SV=2	1.041742	1.05E-05
Q6WCQ1	MPRIIP_HUMAN	Myosin phosphatase Rho-interacting protein OS=Homo sapiens OX=9606 GN=MPRIIP PE=1 SV=3	1.041506	6.27E-04
Q96DB5	RMD1_HUMAN	Regulator of microtubule dynamics protein 1 OS=Homo sapiens OX=9606 GN=RMDN1 PE=1 SV=1	1.041286	9.80E-06
Q14137	BOP1_HUMAN	Ribosome biogenesis protein BOP1 OS=Homo sapiens OX=9606 GN=BOP1 PE=1 SV=2	1.041151	3.30E-06
Q9BQG0	MBB1A_HUMAN	Myb-binding protein 1A OS=Homo sapiens OX=9606 GN=MYBBP1A PE=1 SV=2	1.040679	1.04E-06
Q6UB35	C1TM_HUMAN	Monofunctional C1-tetrahydrofolate synthase mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD1L PE=1 SV=1	1.037583	4.84E-07
P46934	NEDD4_HUMAN	E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens OX=9606 GN=NEDD4 PE=1 SV=4	1.033705	1.25E-05

P62266	RS23_HUMAN	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3	1.031709	0.001016
Q9B7Y7	HGH1_HUMAN	Protein HGH1 homolog OS=Homo sapiens OX=9606 GN=HGH1 PE=1 SV=1	1.030609	9.32E-06
P11388	TOP2A_HUMAN	DNA topoisomerase 2-alpha OS=Homo sapiens OX=9606 GN=TOP2A PE=1 SV=3	1.024151	4.09E-05
Q5VYK3	ECM29_HUMAN	Proteasome adapter and scaffold protein ECM29 OS=Homo sapiens OX=9606 GN=ECPAS PE=1 SV=2	1.023771	1.57E-05
P10619	PPGB_HUMAN	Lysosomal protective protein OS=Homo sapiens OX=9606 GN=CTSA PE=1 SV=2	1.020038	1.68E-05
O76021	RL1D1_HUMAN	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RSL1D1 PE=1 SV=3	1.014539	1.30E-05
P35219	CAH8_HUMAN	Carbonic anhydrase-related protein OS=Homo sapiens OX=9606 GN=CA8 PE=1 SV=3	1.013291	0.006658
P68871	HBB_HUMAN	Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2	1.010793	2.13E-05
Q96PK6	RBM14_HUMAN	RNA-binding protein 14 OS=Homo sapiens OX=9606 GN=RBM14 PE=1 SV=2	1.010508	6.82E-05
P11279	LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens OX=9606 GN=LAMP1 PE=1 SV=3	1.00955	2.09E-05
Q6L8Q7	PDE12_HUMAN	2' 5'-phosphodiesterase 12 OS=Homo sapiens OX=9606 GN=PDE12 PE=1 SV=2	1.003584	1.63E-04
Q86SX6	GLRX5_HUMAN	Glutaredoxin-related protein 5 mitochondrial OS=Homo sapiens OX=9606 GN=GLRX5 PE=1 SV=2	1.001984	0.007438
Q9BUQ8	DDX23_HUMAN	Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens OX=9606 GN=DDX23 PE=1 SV=3	0.997053	1.92E-06
P78316	NOP14_HUMAN	Nucleolar protein 14 OS=Homo sapiens OX=9606 GN=NOP14 PE=1 SV=3	0.99665	2.80E-05
P38432	COIL_HUMAN	Coilin OS=Homo sapiens OX=9606 GN=COIL PE=1 SV=1	0.996515	2.28E-05
Q9BYG3	MK67I_HUMAN	MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens OX=9606 GN=NIFK PE=1 SV=1	0.994183	1.31E-05
Q15149	PLEC_HUMAN	Plectin OS=Homo sapiens OX=9606 GN=PLEC PE=1 SV=3	0.989293	1.68E-06
P52732	KIF11_HUMAN	Kinesin-like protein KIF11 OS=Homo sapiens OX=9606 GN=KIF11 PE=1 SV=2	0.988629	3.26E-05
O43159	RRP8_HUMAN	Ribosomal RNA-processing protein 8 OS=Homo sapiens OX=9606 GN=RRP8 PE=1 SV=2	0.988474	3.22E-05
P28290	ITPID2_HUMAN	Protein ITPRID2 OS=Homo sapiens OX=9606 GN=ITPID2 PE=1 SV=3	0.98683	3.38E-05
Q96GQ7	DDX27_HUMAN	Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens OX=9606 GN=DDX27 PE=1 SV=2	0.984893	7.74E-05
Q16763	UBE2S_HUMAN	Ubiquitin-conjugating enzyme E2 5 OS=Homo sapiens OX=9606 GN=UBE2S PE=1 SV=2	0.978821	4.12E-05
Q13685	AAMP_HUMAN	Angio-associated migratory cell protein OS=Homo sapiens OX=9606 GN=AAMP PE=1 SV=2	0.978636	3.97E-05
P80723	BASP1_HUMAN	Brain acid soluble protein 1 OS=Homo sapiens OX=9606 GN=BASP1 PE=1 SV=2	0.977571	3.74E-05
Q4J6C6	PPCEL_HUMAN	Prolyl endopeptidase-like OS=Homo sapiens OX=9606 GN=PREPL PE=1 SV=1	0.973069	4.34E-05
O00571	DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=3	0.970656	6.93E-06
O15371	EIF3D_HUMAN	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens OX=9606 GN=EIF3D PE=1 SV=1	0.968633	2.39E-05
Q02880	TOP2B_HUMAN	DNA topoisomerase 2-beta OS=Homo sapiens OX=9606 GN=TOP2B PE=1 SV=3	0.96668	6.47E-06
Q9NXF1	TEX10_HUMAN	Testis-expressed protein 10 OS=Homo sapiens OX=9606 GN=TEX10 PE=1 SV=2	0.965727	5.42E-05
Q8TED0	UTP15_HUMAN	U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens OX=9606 GN=UTP15 PE=1 SV=3	0.96563	8.75E-06
Q9H0D6	XRN2_HUMAN	5'-3' exoribonuclease 2 OS=Homo sapiens OX=9606 GN=XRN2 PE=1 SV=1	0.964873	5.73E-04
P27708	PYR1_HUMAN	CAD protein OS=Homo sapiens OX=9606 GN=CAD PE=1 SV=3	0.964815	7.28E-06
P56945	BCAR1_HUMAN	Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens OX=9606 GN=BCAR1 PE=1 SV=2	0.954949	6.32E-05
P41252	SYIC_HUMAN	Isoleucine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=IARS1 PE=1 SV=2	0.954739	6.57E-04
Q6PKG0	LARP1_HUMAN	La-related protein 1 OS=Homo sapiens OX=9606 GN=LARP1 PE=1 SV=2	0.952105	2.40E-05
Q86TI2	DPP9_HUMAN	Dipeptidyl peptidase 9 OS=Homo sapiens OX=9606 GN=DPP9 PE=1 SV=3	0.948865	7.56E-05
P62995	TRA2B_HUMAN	Transformer-2 protein homolog beta OS=Homo sapiens OX=9606 GN=TRA2B PE=1 SV=1	0.947763	8.11E-05
P49327	FAS_HUMAN	Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3	0.947666	0.0027

Q9UKY7	CDV3_HUMAN	Protein CDV3 homolog OS=Homo sapiens OX=9606 GN=CDV3 PE=1 SV=1	0.945167	3.96E-05
Q8N9T8	KRI1_HUMAN	Protein KRI1 homolog OS=Homo sapiens OX=9606 GN=KRI1 PE=1 SV=3	0.942558	8.63E-05
Q12965	MYO1E_HUMAN	Unconventional myosin-le OS=Homo sapiens OX=9606 GN=MYO1E PE=1 SV=2	0.940743	5.54E-04
P28370	SMCA1_HUMAN	Probable global transcription activator SNF2L1 OS=Homo sapiens OX=9606 GN=SMARCA1 PE=1 SV=2	0.939141	8.43E-05
Q14739	LBR_HUMAN	Delta(14)-sterol reductase LBR OS=Homo sapiens OX=9606 GN=LBR PE=1 SV=2	0.934246	1.04E-04
Q09161	NCBP1_HUMAN	Nuclear cap-binding protein subunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1	0.934217	2.99E-05
Q9NYU2	UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens OX=9606 GN=UGGT1 PE=1 SV=3	0.933318	8.92E-04
Q9BU61	NDUF3_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens OX=9606 GN=NDUFAF3 PE=1 SV=1	0.932682	1.40E-04
Q96M27	PRRC1_HUMAN	Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 PE=1 SV=1	0.93253	1.04E-04
Q709C8	VP13C_HUMAN	Vacuolar protein sorting-associated protein 13C OS=Homo sapiens OX=9606 GN=VPS13C PE=1 SV=1	0.932236	1.04E-04
Q6PJ7	ZC3HE_HUMAN	Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens OX=9606 GN=ZC3H14 PE=1 SV=1	0.931828	1.05E-04
O00541	PESC_HUMAN	Pescadillo homolog OS=Homo sapiens OX=9606 GN=PES1 PE=1 SV=1	0.925615	4.48E-05
Q96T76	MMS19_HUMAN	MMS19 nucleotide excision repair protein homolog OS=Homo sapiens OX=9606 GN=MMS19 PE=1 SV=2	0.924939	1.19E-04
Q8IY81	SPB1_HUMAN	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 OS=Homo sapiens OX=9606 GN=FTSJ3 PE=1 SV=2	0.921753	6.21E-04
P36578	RL4_HUMAN	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5	0.920512	2.72E-04
O95674	CDS2_HUMAN	Phosphatidate cytidyltransferase 2 OS=Homo sapiens OX=9606 GN=CDS2 PE=1 SV=1	0.918923	0.00266
Q9Y613	FHOD1_HUMAN	FH1/FH2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FHOD1 PE=1 SV=3	0.915326	1.42E-04
Q14152	EIF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens OX=9606 GN=EIF3A PE=1 SV=1	0.914345	0.001339
P42285	MTREX_HUMAN	Exosome RNA helicase MTR4 OS=Homo sapiens OX=9606 GN=MTREX PE=1 SV=3	0.91168	2.67E-05
P84095	RHOG_HUMAN	Rho-related GTP-binding protein RhoG OS=Homo sapiens OX=9606 GN=RHOG PE=1 SV=1	0.91142	1.30E-05
Q86WR0	CCD25_HUMAN	Coiled-coil domain-containing protein 25 OS=Homo sapiens OX=9606 GN=CCDC25 PE=1 SV=2	0.910185	1.69E-04
P35908	K22E_HUMAN	Keratin type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2	0.908801	2.52E-04
Q8NE71	ABCF1_HUMAN	ATP-binding cassette sub-family F member 1 OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 SV=2	0.906774	1.42E-04
P10909	CLUS_HUMAN	Clusterin OS=Homo sapiens OX=9606 GN=CLU PE=1 SV=1	0.906488	1.28E-04
O75643	U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens OX=9606 GN=SNRNP200 PE=1 SV=2	0.906133	4.39E-04
Q14160	SCRIB_HUMAN	Protein scribble homolog OS=Homo sapiens OX=9606 GN=SCRIB PE=1 SV=4	0.902799	1.91E-04
Q9UKK3	PARP4_HUMAN	Protein mono-ADP-ribosyltransferase PARP4 OS=Homo sapiens OX=9606 GN=PARP4 PE=1 SV=3	0.902153	3.51E-04
Q9Y6H1	CHCH2_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CHCHD2 PE=1 SV=1	0.901116	1.96E-04
P17252	KPCA_HUMAN	Protein kinase C alpha type OS=Homo sapiens OX=9606 GN=PRKCA PE=1 SV=4	0.898432	7.74E-05
Q9BQE3	TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1	0.898429	2.17E-05
Q8N0Z6	TTC5_HUMAN	Tetratricopeptide repeat protein 5 OS=Homo sapiens OX=9606 GN=TTC5 PE=1 SV=2	0.897459	2.12E-04
Q15437	SC23B_HUMAN	Protein transport protein Sec23B OS=Homo sapiens OX=9606 GN=SEC23B PE=1 SV=2	0.896455	5.29E-05
Q8IVT2	MISP_HUMAN	Mitotic interactor and substrate of PLK1 OS=Homo sapiens OX=9606 GN=MISP PE=1 SV=1	0.892664	0.00291
P12236	ADT3_HUMAN	ADP/ATP translocase 3 OS=Homo sapiens OX=9606 GN=SLC25A6 PE=1 SV=4	0.888283	2.52E-04
Q9BQ67	GRWD1_HUMAN	Glutamate-rich WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=GRWD1 PE=1 SV=1	0.887593	5.66E-04
Q7L576	CYFP1_HUMAN	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1	0.886141	1.04E-04
Q96EI5	TCAL4_HUMAN	Transcription elongation factor A protein-like 4 OS=Homo sapiens OX=9606 GN=TCEAL4 PE=1 SV=2	0.884178	2.77E-04

Q9BPX3	CND3_HUMAN	Condensin complex subunit 3 OS=Homo sapiens OX=9606 GN=NCAPG PE=1 SV=1	0.881451	2.79E-06
Q05397	FAK1_HUMAN	Focal adhesion kinase 1 OS=Homo sapiens OX=9606 GN=PTK2 PE=1 SV=2	0.880478	2.94E-04
Q13895	BYST_HUMAN	Bystin OS=Homo sapiens OX=9606 GN=BYSL PE=1 SV=3	0.878603	3.38E-05
Q10471	GALT2_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens OX=9606 GN=GALNT2 PE=1 SV=1	0.878234	0.003741
O14972	VP26C_HUMAN	Vacuolar protein sorting-associated protein 26C OS=Homo sapiens OX=9606 GN=VPS26C PE=1 SV=1	0.87668	3.10E-04
P32969	RL9_HUMAN	60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1	0.873577	2.31E-04
P52701	MSH6_HUMAN	DNA mismatch repair protein Msh6 OS=Homo sapiens OX=9606 GN=MSH6 PE=1 SV=2	0.873283	6.79E-04
O00560	SDCB1_HUMAN	Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1	0.867306	5.41E-04
P83916	CBX1_HUMAN	Chromobox protein homolog 1 OS=Homo sapiens OX=9606 GN=CBX1 PE=1 SV=1	0.865909	3.91E-04
Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SND1 PE=1 SV=1	0.864912	7.95E-04
Q96FQ6	S10AG_HUMAN	Protein S100-A16 OS=Homo sapiens OX=9606 GN=S100A16 PE=1 SV=1	0.864889	0.004334
Q9Y6Y8	S23IP_HUMAN	SEC23-interacting protein OS=Homo sapiens OX=9606 GN=SEC23IP PE=1 SV=1	0.864588	0.002998
Q13617	CUL2_HUMAN	Cullin-2 OS=Homo sapiens OX=9606 GN=CUL2 PE=1 SV=2	0.863008	5.00E-04
Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=OGDH PE=1 SV=3	0.860862	0.001708
O43747	AP1G1_HUMAN	AP-1 complex subunit gamma-1 OS=Homo sapiens OX=9606 GN=AP1G1 PE=1 SV=5	0.859219	0.001803
O75746	CMC1_HUMAN	Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens OX=9606 GN=SLC25A12 PE=1 SV=2	0.858049	2.52E-04
Q03701	CEBPZ_HUMAN	CCAAT/enhancer-binding protein zeta OS=Homo sapiens OX=9606 GN=CEBPZ PE=1 SV=3	0.855837	4.91E-04
Q6ZRP7	QSOX2_HUMAN	Sulfhydryl oxidase 2 OS=Homo sapiens OX=9606 GN=QSOX2 PE=1 SV=3	0.855776	2.77E-04
P57088	TMM33_HUMAN	Transmembrane protein 33 OS=Homo sapiens OX=9606 GN=TMEM33 PE=1 SV=2	0.855166	4.65E-04
Q99447	PCY2_HUMAN	Ethanolamine-phosphate cytidyltransferase OS=Homo sapiens OX=9606 GN=PCYT2 PE=1 SV=1	0.853	3.90E-04
P52594	AGFG1_HUMAN	Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=AGFG1 PE=1 SV=2	0.851262	2.29E-04
P49916	DNLI3_HUMAN	DNA ligase 3 OS=Homo sapiens OX=9606 GN=LIG3 PE=1 SV=2	0.849216	4.97E-04
P54886	P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens OX=9606 GN=ALDH18A1 PE=1 SV=2	0.846655	5.54E-04
Q9H7D7	WDR26_HUMAN	WD repeat-containing protein 26 OS=Homo sapiens OX=9606 GN=WDR26 PE=1 SV=3	0.844224	5.54E-04
Q8N2K0	ABD12_HUMAN	Lysophosphatidylserine lipase ABHD12 OS=Homo sapiens OX=9606 GN=ABHD12 PE=1 SV=2	0.842402	2.33E-04
O43143	DHX15_HUMAN	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens OX=9606 GN=DHX15 PE=1 SV=2	0.84236	8.09E-04
P27635	RL10_HUMAN	60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=4	0.839393	8.70E-04
Q9Y5M8	SRPRB_HUMAN	Signal recognition particle receptor subunit beta OS=Homo sapiens OX=9606 GN=SRPRB PE=1 SV=3	0.837671	6.17E-04
O94808	GFPT2_HUMAN	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 OS=Homo sapiens OX=9606 GN=GFPT2 PE=1 SV=3	0.835847	5.23E-04
P20839	IMDH1_HUMAN	Inosine-5'-monophosphate dehydrogenase 1 OS=Homo sapiens OX=9606 GN=IMPDH1 PE=1 SV=2	0.835805	6.12E-04
Q9NTJ3	SMC4_HUMAN	Structural maintenance of chromosomes protein 4 OS=Homo sapiens OX=9606 GN=SMC4 PE=1 SV=2	0.833642	0.001689
P61916	NPC2_HUMAN	NPC intracellular cholesterol transporter 2 OS=Homo sapiens OX=9606 GN=NPC2 PE=1 SV=1	0.831594	6.57E-04
P35222	CTNB1_HUMAN	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1	0.830932	3.99E-04
O14936	CSKP_HUMAN	Peripheral plasma membrane protein CASK OS=Homo sapiens OX=9606 GN=CASK PE=1 SV=3	0.829907	3.08E-04
Q5ZPR3	CD276_HUMAN	CD276 antigen OS=Homo sapiens OX=9606 GN=CD276 PE=1 SV=1	0.828721	6.94E-04
P04150	GCR_HUMAN	Glucocorticoid receptor OS=Homo sapiens OX=9606 GN=NR3C1 PE=1 SV=1	0.828365	8.43E-05
Q9UIA9	XPO7_HUMAN	Exportin-7 OS=Homo sapiens OX=9606 GN=XPO7 PE=1 SV=3	0.825971	0.001734
Q15021	CND1_HUMAN	Condensin complex subunit 1 OS=Homo sapiens OX=9606 GN=NCAPD2 PE=1 SV=3	0.824051	0.001436

Q9BQ52	RNZ2_HUMAN	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens OX=9606 GN=ELAC2 PE=1 SV=2	0.823626	2.09E-05
Q7Z6Z7	HUWE1_HUMAN	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens OX=9606 GN=HUWE1 PE=1 SV=3	0.823623	1.32E-04
E9PAV3	NACAM_HUMAN	Nascent polypeptide-associated complex subunit alpha muscle-specific form OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1	0.821936	8.47E-04
Q92643	GPI8_HUMAN	GPI-anchor transamidase OS=Homo sapiens OX=9606 GN=PIGK PE=1 SV=2	0.818803	8.38E-04
Q14694	UBP10_HUMAN	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens OX=9606 GN=USP10 PE=1 SV=2	0.817743	7.43E-04
P19525	E2AK2_HUMAN	Interferon-induced double-stranded RNA-activated protein kinase OS=Homo sapiens OX=9606 GN=EIF2AK2 PE=1 SV=2	0.816751	0.002583
Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=2	0.816136	6.17E-04
P33993	MCM7_HUMAN	DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=1 SV=4	0.815767	0.004151
Q14690	RRP5_HUMAN	Protein RRP5 homolog OS=Homo sapiens OX=9606 GN=PDCD11 PE=1 SV=3	0.813509	0.002832
Q01780	EXOSX_HUMAN	Exosome component 10 OS=Homo sapiens OX=9606 GN=EXOSC10 PE=1 SV=2	0.813497	4.01E-04
Q96MG7	NSE3_HUMAN	Non-structural maintenance of chromosomes element 3 homolog OS=Homo sapiens OX=9606 GN=NSMCE3 PE=1 SV=1	0.813311	9.04E-04
Q96RP9	EFGM_HUMAN	Elongation factor G mitochondrial OS=Homo sapiens OX=9606 GN=GFM1 PE=1 SV=2	0.81263	1.77E-04
Q9NUM4	T106B_HUMAN	Transmembrane protein 106B OS=Homo sapiens OX=9606 GN=TMEM106B PE=1 SV=2	0.812127	8.96E-04
P62829	RL23_HUMAN	60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1	0.809829	8.35E-04
Q9UBU9	NXF1_HUMAN	Nuclear RNA export factor 1 OS=Homo sapiens OX=9606 GN=NXF1 PE=1 SV=1	0.809816	6.17E-04
Q969X6	UTP4_HUMAN	U3 small nucleolar RNA-associated protein 4 homolog OS=Homo sapiens OX=9606 GN=UTP4 PE=1 SV=1	0.809532	9.48E-04
P39023	RL3_HUMAN	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2	0.80903	0.00151
P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens OX=9606 GN=PRKDC PE=1 SV=3	0.808519	0.004505
Q12769	NU160_HUMAN	Nuclear pore complex protein Nup160 OS=Homo sapiens OX=9606 GN=NUP160 PE=1 SV=3	0.80654	9.99E-04
Q15904	VAS1_HUMAN	V-type proton ATPase subunit S1 OS=Homo sapiens OX=9606 GN=ATP6AP1 PE=1 SV=2	0.806239	9.54E-04
Q04206	TF65_HUMAN	Transcription factor p65 OS=Homo sapiens OX=9606 GN=RELA PE=1 SV=2	0.806128	0.001028
Q96J84	KIRR1_HUMAN	Kin of IRRE-like protein 1 OS=Homo sapiens OX=9606 GN=KIRREL1 PE=1 SV=2	0.805033	9.99E-04
P48960	CD97_HUMAN	CD97 antigen OS=Homo sapiens OX=9606 GN=CD97 PE=1 SV=4	0.804888	0.001011
P61962	DCAF7_HUMAN	DDB1- and CUL4-associated factor 7 OS=Homo sapiens OX=9606 GN=DCAF7 PE=1 SV=1	0.804415	9.99E-04
P23246	SFPQ_HUMAN	Splicing factor proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2	0.804106	2.34E-04
Q00653	NFKB2_HUMAN	Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens OX=9606 GN=NFKB2 PE=1 SV=4	0.802439	0.001045
Q9UQ13	SHOC2_HUMAN	Leucine-rich repeat protein SHOC-2 OS=Homo sapiens OX=9606 GN=SHOC2 PE=1 SV=2	0.801883	0.00104
Q9BXK5	B2L13_HUMAN	Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1	0.801312	4.23E-04
Q9UG63	ABCF2_HUMAN	ATP-binding cassette sub-family F member 2 OS=Homo sapiens OX=9606 GN=ABCF2 PE=1 SV=2	0.80023	5.05E-04
Q92878	RAD50_HUMAN	DNA repair protein RAD50 OS=Homo sapiens OX=9606 GN=RAD50 PE=1 SV=1	0.798817	0.001454
P40818	UBP8_HUMAN	Ubiquitin carboxyl-terminal hydrolase 8 OS=Homo sapiens OX=9606 GN=USP8 PE=1 SV=1	0.798488	0.001072
O15067	PUR4_HUMAN	Phosphoribosylformylglycinamide synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1 SV=4	0.798476	7.24E-04
P30260	CDC27_HUMAN	Cell division cycle protein 27 homolog OS=Homo sapiens OX=9606 GN=CDC27 PE=1 SV=2	0.798152	6.04E-04
Q07021	C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein mitochondrial OS=Homo sapiens OX=9606 GN=C1QBP PE=1 SV=1	0.797785	2.77E-04
Q96HS1	PGAM5_HUMAN	Serine/threonine-protein phosphatase PGAM5 mitochondrial OS=Homo sapiens OX=9606 GN=PGAM5 PE=1 SV=2	0.797776	0.001823
Q9GZP4	PITH1_HUMAN	PITH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PITHD1 PE=1 SV=1	0.797007	0.001141
Q96SU4	OSBL9_HUMAN	Oxysterol-binding protein-related protein 9 OS=Homo sapiens OX=9606 GN=OSBPL9 PE=1 SV=2	0.796562	0.001163

O75533	SF3B1_HUMAN	Splicing factor 3B subunit 1 OS=Homo sapiens OX=9606 GN=SF3B1 PE=1 SV=3	0.796144	0.00136
P53618	COPB_HUMAN	Coatomer subunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3	0.795242	0.002167
Q9NQ84	GPC5C_HUMAN	G-protein coupled receptor family C group 5 member C OS=Homo sapiens OX=9606 GN=GPRC5C PE=1 SV=2	0.792975	0.00151
Q8TC12	RDH11_HUMAN	Retinol dehydrogenase 11 OS=Homo sapiens OX=9606 GN=RDH11 PE=1 SV=2	0.792904	0.0012
Q9UBC2	EP15R_HUMAN	Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens OX=9606 GN=EPS15L1 PE=1 SV=1	0.792167	1.18E-05
Q9Y5Q9	TF3C3_HUMAN	General transcription factor 3C polypeptide 3 OS=Homo sapiens OX=9606 GN=GTF3C3 PE=1 SV=1	0.789936	0.001252
P49756	RBM25_HUMAN	RNA-binding protein 25 OS=Homo sapiens OX=9606 GN=RBM25 PE=1 SV=3	0.789012	0.005744
Q96JQ2	CLMN_HUMAN	Calmin OS=Homo sapiens OX=9606 GN=CLMN PE=1 SV=1	0.78784	0.001339
O15118	NPC1_HUMAN	NPC intracellular cholesterol transporter 1 OS=Homo sapiens OX=9606 GN=NPC1 PE=1 SV=2	0.785416	0.001698
Q93009	UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens OX=9606 GN=USP7 PE=1 SV=2	0.785272	3.93E-04
Q9NR50	EI2BG_HUMAN	Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens OX=9606 GN=EIF2B3 PE=1 SV=1	0.78477	0.001361
Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP] mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=4	0.780111	5.96E-04
Q6P9B6	MEAK7_HUMAN	MTOR-associated protein MEAK7 OS=Homo sapiens OX=9606 GN=MEAK7 PE=1 SV=2	0.779545	0.001499
P40938	RFC3_HUMAN	Replication factor C subunit 3 OS=Homo sapiens OX=9606 GN=RFC3 PE=1 SV=2	0.778991	7.24E-04
O95817	BAG3_HUMAN	BAG family molecular chaperone regulator 3 OS=Homo sapiens OX=9606 GN=BAG3 PE=1 SV=3	0.778766	5.54E-04
Q9ULA0	DNPEP_HUMAN	Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1	0.778328	0.001514
Q96T23	RSF1_HUMAN	Remodeling and spacing factor 1 OS=Homo sapiens OX=9606 GN=RSF1 PE=1 SV=2	0.778002	0.00151
Q16850	CP51A_HUMAN	Lanosterol 14-alpha demethylase OS=Homo sapiens OX=9606 GN=CYP51A1 PE=1 SV=3	0.777402	0.001541
Q5VWZ2	LYPL1_HUMAN	Lysophospholipase-like protein 1 OS=Homo sapiens OX=9606 GN=LYPLAL1 PE=1 SV=3	0.777189	0.001436
P29218	IMPA1_HUMAN	Inositol monophosphatase 1 OS=Homo sapiens OX=9606 GN=IMPA1 PE=1 SV=1	0.776035	3.91E-04
Q9Y3C1	NOP16_HUMAN	Nucleolar protein 16 OS=Homo sapiens OX=9606 GN=NOP16 PE=1 SV=2	0.775454	0.00151
Q9NQ75	EXOS3_HUMAN	Exosome complex component RRP40 OS=Homo sapiens OX=9606 GN=EXOSC3 PE=1 SV=3	0.77433	0.002632
Q9NZI8	IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=1 SV=2	0.773977	8.35E-04
Q13155	AIMP2_HUMAN	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens OX=9606 GN=AIMP2 PE=1 SV=2	0.773554	0.001596
Q99700	ATX2_HUMAN	Ataxin-2 OS=Homo sapiens OX=9606 GN=ATXN2 PE=1 SV=2	0.77288	0.002922
O95453	PARN_HUMAN	Poly(A)-specific ribonuclease PARN OS=Homo sapiens OX=9606 GN=PARN PE=1 SV=1	0.772278	0.003511
O00425	IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP3 PE=1 SV=2	0.77126	0.001016
Q9NZB2	F120A_HUMAN	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A PE=1 SV=2	0.770838	0.002988
Q99805	TM9S2_HUMAN	Transmembrane 9 superfamily member 2 OS=Homo sapiens OX=9606 GN=TM9SF2 PE=1 SV=1	0.769046	0.001591
P05121	PAI1_HUMAN	Plasminogen activator inhibitor 1 OS=Homo sapiens OX=9606 GN=SERPINE1 PE=1 SV=1	0.768574	0.001725
Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6	0.768189	0.003733
Q9BTW9	TBCD_HUMAN	Tubulin-specific chaperone D OS=Homo sapiens OX=9606 GN=TBCD PE=1 SV=2	0.768024	0.003511
P0DPB6	RPAC2_HUMAN	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Homo sapiens OX=9606 GN=POLR1D PE=1 SV=1	0.767858	0.001809
O94973	AP2A2_HUMAN	AP-2 complex subunit alpha-2 OS=Homo sapiens OX=9606 GN=AP2A2 PE=1 SV=2	0.767008	0.001013
Q14684	RRP1B_HUMAN	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens OX=9606 GN=RRP1B PE=1 SV=3	0.76686	0.001719
Q9ULV4	COR1C_HUMAN	Coronin-1C OS=Homo sapiens OX=9606 GN=CORO1C PE=1 SV=1	0.766234	0.001463
Q9NXV6	CARF_HUMAN	CDKN2A-interacting protein OS=Homo sapiens OX=9606 GN=CDKN2AIP PE=1 SV=3	0.766226	0.001717
Q9NUI1	DECR2_HUMAN	Peroxisomal 2 4-dienoyl-CoA reductase OS=Homo sapiens OX=9606 GN=DECR2 PE=1 SV=1	0.764622	0.001831

Q9Y6I3	EPN1_HUMAN	Epsin-1 OS=Homo sapiens OX=9606 GN=EPN1 PE=1 SV=2	0.764311	3.97E-05
Q5VTR2	BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens OX=9606 GN=RNF20 PE=1 SV=2	0.762809	0.003277
P31350	RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens OX=9606 GN=RRM2 PE=1 SV=1	0.762788	0.002533
O15321	TM9S1_HUMAN	Transmembrane 9 superfamily member 1 OS=Homo sapiens OX=9606 GN=TM9SF1 PE=2 SV=2	0.762719	0.001848
Q96P16	RPR1A_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1A OS=Homo sapiens OX=9606 GN=RPRD1A PE=1 SV=1	0.762057	0.001929
Q13148	TADBP_HUMAN	TAR DNA-binding protein 43 OS=Homo sapiens OX=9606 GN=TARDBP PE=1 SV=1	0.759915	0.002096
Q2TB90	HKDC1_HUMAN	Hexokinase HKDC1 OS=Homo sapiens OX=9606 GN=HKDC1 PE=1 SV=3	0.758819	0.003374
Q8NI36	WDR36_HUMAN	WD repeat-containing protein 36 OS=Homo sapiens OX=9606 GN=WDR36 PE=1 SV=1	0.757111	0.001289
Q8N9N8	EIF1A_HUMAN	Probable RNA-binding protein EIF1AD OS=Homo sapiens OX=9606 GN=EIF1AD PE=1 SV=1	0.75641	0.00215
P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=2	0.755142	0.001252
Q12979	ABR_HUMAN	Active breakpoint cluster region-related protein OS=Homo sapiens OX=9606 GN=ABR PE=1 SV=2	0.754976	6.75E-04
Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A OS=Homo sapiens OX=9606 GN=DHX9 PE=1 SV=4	0.754503	9.48E-04
Q9H4L4	SEN3_HUMAN	Sentrin-specific protease 3 OS=Homo sapiens OX=9606 GN=SEN3 PE=1 SV=2	0.75361	0.00219
Q9H6V9	LDAH_HUMAN	Lipid droplet-associated hydrolase OS=Homo sapiens OX=9606 GN=LDAH PE=1 SV=1	0.75303	0.002096
P15924	DESP_HUMAN	Desmoplakin OS=Homo sapiens OX=9606 GN=DSP PE=1 SV=3	0.752407	0.00151
Q8WZA9	IRGQ_HUMAN	Immunity-related GTPase family Q protein OS=Homo sapiens OX=9606 GN=IRGQ PE=1 SV=1	0.751344	0.001689
P16144	ITB4_HUMAN	Integrin beta-4 OS=Homo sapiens OX=9606 GN=ITGB4 PE=1 SV=5	0.749698	0.004007
P17858	PFKAL_HUMAN	ATP-dependent 6-phosphofructokinase liver type OS=Homo sapiens OX=9606 GN=PFKL PE=1 SV=6	0.748827	0.002318
Q9UBF2	COPG2_HUMAN	Coatmer subunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 PE=1 SV=1	0.748428	6.76E-04
Q6DKJ4	NXN_HUMAN	Nucleoredoxin OS=Homo sapiens OX=9606 GN=NXN PE=1 SV=2	0.747692	9.99E-04
Q9NVJ2	ARL8B_HUMAN	ADP-ribosylation factor-like protein 8B OS=Homo sapiens OX=9606 GN=ARL8B PE=1 SV=1	0.746574	0.002331
Q9NQX3	GEPH_HUMAN	Gephyrin OS=Homo sapiens OX=9606 GN=GPHN PE=1 SV=1	0.746311	0.002401
P48739	PIPNB_HUMAN	Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens OX=9606 GN=PITPNB PE=1 SV=2	0.745995	0.002483
Q9BQ75	CMS1_HUMAN	Protein CMSS1 OS=Homo sapiens OX=9606 GN=CMSS1 PE=1 SV=2	0.745455	0.00234
Q9NQG5	RPR1B_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens OX=9606 GN=RPRD1B PE=1 SV=1	0.744717	1.41E-04
Q8N5I4	DHRX_HUMAN	Dehydrogenase/reductase SDR family member on chromosome X OS=Homo sapiens OX=9606 GN=DHRX PE=1 SV=2	0.744698	0.002533
Q9NY93	DDX56_HUMAN	Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens OX=9606 GN=DDX56 PE=1 SV=1	0.7442	0.002522
P28288	ABCD3_HUMAN	ATP-binding cassette sub-family D member 3 OS=Homo sapiens OX=9606 GN=ABCD3 PE=1 SV=1	0.744072	0.003126
O95573	ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens OX=9606 GN=ACSL3 PE=1 SV=3	0.743816	8.09E-04
Q63HN8	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens OX=9606 GN=RNF213 PE=1 SV=3	0.743479	0.005716
Q9UDY8	MALT1_HUMAN	Mucosa-associated lymphoid tissue lymphoma translocation protein 1 OS=Homo sapiens OX=9606 GN=MALT1 PE=1 SV=1	0.742682	0.001252
Q6DKI1	RL7L_HUMAN	60S ribosomal protein L7-like 1 OS=Homo sapiens OX=9606 GN=RPL7L1 PE=1 SV=2	0.742278	9.22E-04
Q14151	SAFB2_HUMAN	Scaffold attachment factor B2 OS=Homo sapiens OX=9606 GN=SAFB2 PE=1 SV=1	0.741804	0.002572
Q9Y2A7	NCKP1_HUMAN	Nck-associated protein 1 OS=Homo sapiens OX=9606 GN=NCKAP1 PE=1 SV=1	0.741099	3.19E-06
Q96D46	NMD3_HUMAN	60S ribosomal export protein NMD3 OS=Homo sapiens OX=9606 GN=NMD3 PE=1 SV=1	0.740976	0.002685
P08243	ASNS_HUMAN	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=ASNS PE=1 SV=4	0.740876	0.002602
Q9Y5A9	YTHD2_HUMAN	YTH domain-containing family protein 2 OS=Homo sapiens OX=9606 GN=YTHDF2 PE=1 SV=2	0.740744	0.002515
P47895	AL1A3_HUMAN	Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens OX=9606 GN=ALDH1A3 PE=1 SV=2	0.739914	0.002532
Q96CV9	OPTN_HUMAN	Optineurin OS=Homo sapiens OX=9606 GN=OPTN PE=1 SV=3	0.739786	0.002622

P40429	RL13A_HUMAN	60S ribosomal protein L13a OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2	0.739055	0.002671
Q8N983	RM43_HUMAN	39S ribosomal protein L43 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL43 PE=1 SV=1	0.738991	0.002742
C9JLW8	MCRI1_HUMAN	Mapk-regulated corepressor-interacting protein 1 OS=Homo sapiens OX=9606 GN=MCRI1 PE=1 SV=1	0.738875	0.002612
Q15036	SNX17_HUMAN	Sorting nexin-17 OS=Homo sapiens OX=9606 GN=SNX17 PE=1 SV=1	0.738409	0.002602
P21399	ACOC_HUMAN	Cytoplasmic aconitate hydratase OS=Homo sapiens OX=9606 GN=ACO1 PE=1 SV=3	0.738037	0.002122
Q92599	SEPT8_HUMAN	Septin-8 OS=Homo sapiens OX=9606 GN=SEPTIN8 PE=1 SV=4	0.736966	0.003336
Q8N3D4	EH1L1_HUMAN	EH domain-binding protein 1-like protein 1 OS=Homo sapiens OX=9606 GN=EHP1L1 PE=1 SV=2	0.736361	0.001463
P62847	RS24_HUMAN	40S ribosomal protein S24 OS=Homo sapiens OX=9606 GN=RPS24 PE=1 SV=1	0.736099	0.002974
Q9H788	SH24A_HUMAN	SH2 domain-containing protein 4A OS=Homo sapiens OX=9606 GN=SH2D4A PE=1 SV=1	0.735612	0.002715
P53396	ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens OX=9606 GN=ACLY PE=1 SV=3	0.735146	0.001186
P49757	NUMB_HUMAN	Protein numb homolog OS=Homo sapiens OX=9606 GN=NUMB PE=1 SV=2	0.734646	0.002685
Q9UDT6	CLIP2_HUMAN	CAP-Gly domain-containing linker protein 2 OS=Homo sapiens OX=9606 GN=CLIP2 PE=1 SV=1	0.734646	0.002696
Q02878	RL6_HUMAN	60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3	0.733978	0.006532
P53597	SUCA_HUMAN	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=SUCLG1 PE=1 SV=4	0.73301	0.002343
Q9P289	STK26_HUMAN	Serine/threonine-protein kinase 26 OS=Homo sapiens OX=9606 GN=STK26 PE=1 SV=2	0.732834	0.002832
Q13724	MOGS_HUMAN	Mannosyl-oligosaccharide glucosidase OS=Homo sapiens OX=9606 GN=MOGS PE=1 SV=5	0.732724	0.002847
Q9Y2Z4	SYYM_HUMAN	Tyrosine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=YARS2 PE=1 SV=2	0.73245	0.003078
O14530	TXND9_HUMAN	Thioredoxin domain-containing protein 9 OS=Homo sapiens OX=9606 GN=TXNDC9 PE=1 SV=2	0.73168	0.002847
Q8WUX9	CHMP7_HUMAN	Charged multivesicular body protein 7 OS=Homo sapiens OX=9606 GN=CHMP7 PE=1 SV=1	0.731328	0.002832
O95782	AP2A1_HUMAN	AP-2 complex subunit alpha-1 OS=Homo sapiens OX=9606 GN=AP2A1 PE=1 SV=3	0.730813	0.001186
Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein mitochondrial OS=Homo sapiens OX=9606 GN=SSBP1 PE=1 SV=1	0.730187	0.002583
Q8TAG9	EXOC6_HUMAN	Exocyst complex component 6 OS=Homo sapiens OX=9606 GN=EXOC6 PE=1 SV=3	0.729947	0.0029
O14925	TIM23_HUMAN	Mitochondrial import inner membrane translocase subunit Tim23 OS=Homo sapiens OX=9606 GN=TIMM23 PE=1 SV=1	0.728943	0.002983
Q8NCA5	FA98A_HUMAN	Protein FAM98A OS=Homo sapiens OX=9606 GN=FAM98A PE=1 SV=2	0.728932	0.002847
P48449	ERG7_HUMAN	Lanosterol synthase OS=Homo sapiens OX=9606 GN=LSS PE=1 SV=1	0.728786	5.05E-04
Q9H6Y2	WDR55_HUMAN	WD repeat-containing protein 55 OS=Homo sapiens OX=9606 GN=WDR55 PE=1 SV=2	0.728296	0.002952
Q13144	EI2BE_HUMAN	Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens OX=9606 GN=EIF2B5 PE=1 SV=3	0.728259	0.002952
P30838	AL3A1_HUMAN	Aldehyde dehydrogenase dimeric NADP-preferring OS=Homo sapiens OX=9606 GN=ALDH3A1 PE=1 SV=3	0.727654	0.001764
P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNPH2 PE=1 SV=1	0.727198	0.001809
Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase mitochondrial OS=Homo sapiens OX=9606 GN=SQOR PE=1 SV=1	0.727159	0.004872
Q9UGP4	LIMD1_HUMAN	LIM domain-containing protein 1 OS=Homo sapiens OX=9606 GN=LIMD1 PE=1 SV=1	0.726841	0.005252
Q96PZ0	PUS7_HUMAN	Pseudouridylate synthase 7 homolog OS=Homo sapiens OX=9606 GN=PUS7 PE=1 SV=2	0.726705	0.002852
Q8N4X5	AF1L2_HUMAN	Actin filament-associated protein 1-like 2 OS=Homo sapiens OX=9606 GN=AFAP1L2 PE=1 SV=1	0.72654	0.003078
Q9UHB9	SRP68_HUMAN	Signal recognition particle subunit SRP68 OS=Homo sapiens OX=9606 GN=SRP68 PE=1 SV=2	0.724152	8.38E-04
P43034	LIS1_HUMAN	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens OX=9606 GN=PAFAH1B1 PE=1 SV=2	0.722724	7.76E-04
Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9 mitochondrial OS=Homo sapiens OX=9606 GN=ACOT9 PE=1 SV=2	0.721108	0.003417
Q10567	AP1B1_HUMAN	AP-1 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP1B1 PE=1 SV=2	0.720435	0.005475

P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=3	0.719273	0.001163
P41214	EIF2D_HUMAN	Eukaryotic translation initiation factor 2D OS=Homo sapiens OX=9606 GN=EIF2D PE=1 SV=3	0.718177	0.003446
Q96L92	SNX27_HUMAN	Sorting nexin-27 OS=Homo sapiens OX=9606 GN=SNX27 PE=1 SV=2	0.717959	0.003432
Q06787	FMR1_HUMAN	Synaptic functional regulator FMR1 OS=Homo sapiens OX=9606 GN=FMR1 PE=1 SV=1	0.717631	0.003395
Q4G0J3	LARP7_HUMAN	La-related protein 7 OS=Homo sapiens OX=9606 GN=LARP7 PE=1 SV=1	0.715543	0.00406
Q9UI12	VATH_HUMAN	V-type proton ATPase subunit H OS=Homo sapiens OX=9606 GN=ATP6V1H PE=1 SV=1	0.712927	0.003733
Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=3	0.712291	0.002983
Q99613	EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens OX=9606 GN=EIF3C PE=1 SV=1	0.712162	0.001274
P13611	CSPG2_HUMAN	Versican core protein OS=Homo sapiens OX=9606 GN=VCAN PE=1 SV=3	0.711795	0.003748
O00139	KIF2A_HUMAN	Kinesin-like protein KIF2A OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=3	0.711443	0.001458
Q14008	CKAP5_HUMAN	Cytoskeleton-associated protein 5 OS=Homo sapiens OX=9606 GN=CKAP5 PE=1 SV=3	0.711392	0.001825
Q15007	FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP OS=Homo sapiens OX=9606 GN=WTAP PE=1 SV=2	0.71115	0.003868
Q8WVC0	LEO1_HUMAN	RNA polymerase-associated protein LEO1 OS=Homo sapiens OX=9606 GN=LEO1 PE=1 SV=1	0.710657	0.00386
Q9Y2L1	RRP44_HUMAN	Exosome complex exonuclease RRP44 OS=Homo sapiens OX=9606 GN=DIS3 PE=1 SV=2	0.709808	0.00406
P61764	STXB1_HUMAN	Syntaxin-binding protein 1 OS=Homo sapiens OX=9606 GN=STXB1 PE=1 SV=1	0.709382	0.003912
P49590	SYHM_HUMAN	Histidine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=HARS2 PE=1 SV=1	0.709323	0.007744
Q9HCU5	PREB_HUMAN	Prolactin regulatory element-binding protein OS=Homo sapiens OX=9606 GN=PREB PE=1 SV=2	0.70866	1.21E-04
P07099	HYEP_HUMAN	Epoxide hydrolase 1 OS=Homo sapiens OX=9606 GN=EPHX1 PE=1 SV=1	0.707957	0.003748
P15291	B4GT1_HUMAN	Beta-1 4-galactosyltransferase 1 OS=Homo sapiens OX=9606 GN=B4GALT1 PE=1 SV=5	0.706843	0.003937
O15160	RPAC1_HUMAN	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens OX=9606 GN=POLR1C PE=1 SV=1	0.706358	0.005502
P62873	GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens OX=9606 GN=GNB1 PE=1 SV=3	0.704676	0.00136
P22692	IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens OX=9606 GN=IGFBP4 PE=1 SV=2	0.704449	0.004007
O60313	OPA1_HUMAN	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=3	0.704239	0.004124
P82675	RT05_HUMAN	28S ribosomal protein S5 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS5 PE=1 SV=2	0.704078	0.004078
P31153	METK2_HUMAN	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens OX=9606 GN=MAT2A PE=1 SV=1	0.703247	0.001498
P10620	MGST1_HUMAN	Microsomal glutathione S-transferase 1 OS=Homo sapiens OX=9606 GN=MGST1 PE=1 SV=1	0.702815	0.00392
P05141	ADT2_HUMAN	ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC25A5 PE=1 SV=7	0.702294	0.004941
Q9GZS1	RPA49_HUMAN	DNA-directed RNA polymerase I subunit RPA49 OS=Homo sapiens OX=9606 GN=POLR1E PE=1 SV=3	0.701812	0.004169
O60934	NBN_HUMAN	Nibrin OS=Homo sapiens OX=9606 GN=NBN PE=1 SV=1	0.701732	0.004227
P47914	RL29_HUMAN	60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=1 SV=2	0.701401	0.004124
O95299	NDUAA_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFA10 PE=1 SV=1	0.700912	0.004188
Q9HD20	AT131_HUMAN	Manganese-transporting ATPase 13A1 OS=Homo sapiens OX=9606 GN=ATP13A1 PE=1 SV=2	0.700237	0.001533
Q9Y570	PPME1_HUMAN	Protein phosphatase methylesterase 1 OS=Homo sapiens OX=9606 GN=PPME1 PE=1 SV=3	0.700202	0.002583
P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=2	0.699804	0.001842
Q99436	PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens OX=9606 GN=PSMB7 PE=1 SV=1	0.698766	8.76E-04
Q8TCS8	PNPT1_HUMAN	Polyribonucleotide nucleotidyltransferase 1 mitochondrial OS=Homo sapiens OX=9606 GN=PNPT1 PE=1 SV=2	0.69837	0.006512

P42224	STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens OX=9606 GN=STAT1 PE=1 SV=2	0.698035	0.001252
Q4G0N4	NAKD2_HUMAN	NAD kinase 2 mitochondrial OS=Homo sapiens OX=9606 GN=NAKD2 PE=1 SV=2	0.697896	0.004599
Q9H9P8	L2HDH_HUMAN	L-2-hydroxyglutarate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=L2HGDH PE=1 SV=3	0.697341	0.004424
Q8N1F7	NUP93_HUMAN	Nuclear pore complex protein Nup93 OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=2	0.696487	0.002974
Q96K76	UBP47_HUMAN	Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens OX=9606 GN=USP47 PE=1 SV=3	0.695681	0.004685
Q9UEW8	STK39_HUMAN	STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens OX=9606 GN=STK39 PE=1 SV=3	0.695007	0.004589
P53992	SEC24C_HUMAN	Protein transport protein Sec24C OS=Homo sapiens OX=9606 GN=SEC24C PE=1 SV=3	0.694997	0.0029
Q96DZ1	ERLEC_HUMAN	Endoplasmic reticulum lectin 1 OS=Homo sapiens OX=9606 GN=ERLEC1 PE=1 SV=1	0.694643	0.002994
Q9H3K6	BOLA2_HUMAN	Bola-like protein 2 OS=Homo sapiens OX=9606 GN=BOLA2 PE=1 SV=1	0.694613	0.002815
P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR2A PE=1 SV=2	0.694505	0.002309
P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI2 PE=1 SV=3	0.693715	0.00653
Q15427	SF3B4_HUMAN	Splicing factor 3B subunit 4 OS=Homo sapiens OX=9606 GN=SF3B4 PE=1 SV=1	0.693339	0.004674
Q9BSC4	NOL10_HUMAN	Nucleolar protein 10 OS=Homo sapiens OX=9606 GN=NOL10 PE=1 SV=1	0.692565	0.004652
Q06124	PTN11_HUMAN	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 PE=1 SV=3	0.692447	0.002779
Q9UBM7	DHCR7_HUMAN	7-dehydrocholesterol reductase OS=Homo sapiens OX=9606 GN=DHCR7 PE=1 SV=1	0.691185	0.005129
P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 OS=Homo sapiens OX=9606 GN=MAPK1 PE=1 SV=3	0.690537	0.00406
O43617	TPPC3_HUMAN	Trafficking protein particle complex subunit 3 OS=Homo sapiens OX=9606 GN=TRAPPC3 PE=1 SV=1	0.690197	0.005045
O15231	ZN185_HUMAN	Zinc finger protein 185 OS=Homo sapiens OX=9606 GN=ZNF185 PE=1 SV=3	0.690186	0.004827
O00567	NOP56_HUMAN	Nucleolar protein 56 OS=Homo sapiens OX=9606 GN=NOP56 PE=1 SV=4	0.689596	0.002401
P35270	SPRE_HUMAN	Sepiapterin reductase OS=Homo sapiens OX=9606 GN=SPR PE=1 SV=1	0.689323	0.004872
P05387	RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1	0.688852	0.005449
A0AVT1	UBA6_HUMAN	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens OX=9606 GN=UBA6 PE=1 SV=1	0.688692	0.003467
P19338	NUCL_HUMAN	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	0.687974	0.005291
Q96P11	NSUN5_HUMAN	Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens OX=9606 GN=NSUN5 PE=1 SV=2	0.687741	0.005105
P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=5	0.687483	0.005407
P62753	RS6_HUMAN	40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1	0.687346	0.00508
O60264	SMCA5_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 SV=1	0.687134	0.003174
O43776	SYNC_HUMAN	Asparagine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=NARS1 PE=1 SV=1	0.68634	0.002522
Q8WZ82	OVCA2_HUMAN	Esterase OVCA2 OS=Homo sapiens OX=9606 GN=OVCA2 PE=1 SV=1	0.685841	0.005165
P50416	CPT1A_HUMAN	Carnitine O-palmitoyltransferase 1 liver isoform OS=Homo sapiens OX=9606 GN=CPT1A PE=1 SV=2	0.685787	0.00501
P08195	4F2_HUMAN	4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=3	0.685755	0.002974
Q9NWH9	SLTM_HUMAN	SAFB-like transcription modulator OS=Homo sapiens OX=9606 GN=SLTM PE=1 SV=2	0.685536	0.004246
P04183	KITH_HUMAN	Thymidine kinase cytosolic OS=Homo sapiens OX=9606 GN=TK1 PE=1 SV=2	0.685041	0.005104
Q14498	RBM39_HUMAN	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2	0.684189	0.003091
O14828	SCAM3_HUMAN	Secretory carrier-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=SCAMP3 PE=1 SV=3	0.683634	0.006111
Q9UID3	VPS51_HUMAN	Vacuolar protein sorting-associated protein 51 homolog OS=Homo sapiens OX=9606 GN=VPS51 PE=1 SV=2	0.683276	0.005341

Q9NX02	NALP2_HUMAN	NACHT LRR and PYD domains-containing protein 2 OS=Homo sapiens OX=9606 GN=NLRP2 PE=1 SV=1	0.682626	0.004631
Q9BRR6	ADPGK_HUMAN	ADP-dependent glucokinase OS=Homo sapiens OX=9606 GN=ADPGK PE=1 SV=1	0.682447	0.009787
Q5JRX3	PREP_HUMAN	Presequence protease mitochondrial OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=3	0.682353	0.005203
Q14257	RCN2_HUMAN	Reticulocalbin-2 OS=Homo sapiens OX=9606 GN=RCN2 PE=1 SV=1	0.682178	0.005068
P26373	RL13_HUMAN	60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RPL13 PE=1 SV=4	0.6819	0.006037
Q9NXR7	BABA2_HUMAN	BRISC and BRCA1-A complex member 2 OS=Homo sapiens OX=9606 GN=BABAM2 PE=1 SV=2	0.681639	0.005504
Q9BZF1	OSBL8_HUMAN	Oxysterol-binding protein-related protein 8 OS=Homo sapiens OX=9606 GN=OSBPL8 PE=1 SV=3	0.681538	0.005434
O43813	LANC1_HUMAN	Glutathione S-transferase LANCL1 OS=Homo sapiens OX=9606 GN=LANCL1 PE=1 SV=1	0.681377	0.005407
Q86Y56	DAAF5_HUMAN	Dynein assembly factor 5 axonemal OS=Homo sapiens OX=9606 GN=DNAAF5 PE=1 SV=4	0.680891	0.005663
Q969S3	ZN622_HUMAN	Zinc finger protein 622 OS=Homo sapiens OX=9606 GN=ZNF622 PE=1 SV=1	0.68001	0.005607
O14744	ANM5_HUMAN	Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=4	0.679593	0.00151
P22033	MUTA_HUMAN	Methylmalonyl-CoA mutase mitochondrial OS=Homo sapiens OX=9606 GN=MMUT PE=1 SV=4	0.676311	0.005759
O60256	KPRB_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens OX=9606 GN=PRPSAP2 PE=1 SV=1	0.67614	0.005489
O43684	BUB3_HUMAN	Mitotic checkpoint protein BUB3 OS=Homo sapiens OX=9606 GN=BUB3 PE=1 SV=1	0.675757	0.008416
Q9H9B1	EHMT1_HUMAN	Histone-lysine N-methyltransferase EHMT1 OS=Homo sapiens OX=9606 GN=EHMT1 PE=1 SV=4	0.67575	0.005813
P02786	TFR1_HUMAN	Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2	0.674861	0.004424
Q9Y697	NFS1_HUMAN	Cysteine desulfurase mitochondrial OS=Homo sapiens OX=9606 GN=NFS1 PE=1 SV=3	0.673469	0.006067
P60033	CD81_HUMAN	CD81 antigen OS=Homo sapiens OX=9606 GN=CD81 PE=1 SV=1	0.673071	0.006034
Q15836	VAMP3_HUMAN	Vesicle-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=VAMP3 PE=1 SV=3	0.672147	0.007441
P56182	RRP1_HUMAN	Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens OX=9606 GN=RRP1 PE=1 SV=1	0.671893	0.006289
Q9BVG8	KIFC3_HUMAN	Kinesin-like protein KIFC3 OS=Homo sapiens OX=9606 GN=KIFC3 PE=1 SV=4	0.671529	7.48E-04
P09132	SRP19_HUMAN	Signal recognition particle 19 kDa protein OS=Homo sapiens OX=9606 GN=SRP19 PE=1 SV=3	0.670876	0.006206
P63096	GNAI1_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens OX=9606 GN=GNAI1 PE=1 SV=2	0.670386	0.006176
Q14653	IRF3_HUMAN	Interferon regulatory factor 3 OS=Homo sapiens OX=9606 GN=IRF3 PE=1 SV=1	0.670072	0.006176
Q9Y678	COPG1_HUMAN	Coatamer subunit gamma-1 OS=Homo sapiens OX=9606 GN=COPG1 PE=1 SV=1	0.670024	0.001962
P35250	RFC2_HUMAN	Replication factor C subunit 2 OS=Homo sapiens OX=9606 GN=RFC2 PE=1 SV=3	0.669971	0.002832
Q9NPF4	OSGEP_HUMAN	Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens OX=9606 GN=OSGEP PE=1 SV=1	0.669096	0.006285
P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(i)/G(s)/G(t) subunit beta-2 OS=Homo sapiens OX=9606 GN=GNB2 PE=1 SV=3	0.668318	0.006289
P11586	C1TC_HUMAN	C-1-tetrahydrofolate synthase cytoplasmic OS=Homo sapiens OX=9606 GN=MTHFD1 PE=1 SV=3	0.668307	0.00716
Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3	0.668104	0.004007
Q6UX04	CWC27_HUMAN	Spliceosome-associated protein CWC27 homolog OS=Homo sapiens OX=9606 GN=CWC27 PE=1 SV=1	0.667709	0.006425
Q13868	EXOS2_HUMAN	Exosome complex component RRP4 OS=Homo sapiens OX=9606 GN=EXOSC2 PE=1 SV=2	0.667514	0.002964
O43852	CALU_HUMAN	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	0.666427	0.006285
O43670	ZN207_HUMAN	BUB3-interacting and GLEBS motif-containing protein ZNF207 OS=Homo sapiens OX=9606 GN=ZNF207 PE=1 SV=1	0.666092	0.006491
Q8WUM0	NU133_HUMAN	Nuclear pore complex protein Nup133 OS=Homo sapiens OX=9606 GN=NUP133 PE=1 SV=2	0.665756	0.004827
Q9UNW1	MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens OX=9606 GN=MINPP1 PE=1 SV=1	0.665519	7.43E-04
P49366	DHYS_HUMAN	Deoxyhypusine synthase OS=Homo sapiens OX=9606 GN=DHPS PE=1 SV=1	0.663924	0.006745
Q9NR30	DDX21_HUMAN	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5	0.663818	0.008366

Q01813	PFKP_HUMAN	ATP-dependent 6-phosphofructokinase platelet type OS=Homo sapiens OX=9606 GN=PFKP PE=1 SV=2	0.663464	0.001659
Q9BYN0	SRXN1_HUMAN	Sulfiredoxin-1 OS=Homo sapiens OX=9606 GN=SRXN1 PE=1 SV=2	0.663464	0.006745
Q92544	TM9S4_HUMAN	Transmembrane 9 superfamily member 4 OS=Homo sapiens OX=9606 GN=TM9SF4 PE=1 SV=2	0.663329	0.006637
O00762	UBE2C_HUMAN	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens OX=9606 GN=UBE2C PE=1 SV=1	0.662992	0.006978
Q8IZ83	A16A1_HUMAN	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens OX=9606 GN=ALDH16A1 PE=1 SV=2	0.662344	0.009787
Q3ZCQ8	TIM50_HUMAN	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens OX=9606 GN=TIMM50 PE=1 SV=2	0.662116	0.006892
Q9Y277	VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606 GN=VDAC3 PE=1 SV=1	0.661099	0.005407
P33992	MCM5_HUMAN	DNA replication licensing factor MCM5 OS=Homo sapiens OX=9606 GN=MCM5 PE=1 SV=5	0.661017	0.005165
O60763	USO1_HUMAN	General vesicular transport factor p115 OS=Homo sapiens OX=9606 GN=USO1 PE=1 SV=2	0.660574	0.00774
Q9BSJ8	ESYT1_HUMAN	Extended synaptotagmin-1 OS=Homo sapiens OX=9606 GN=ESYT1 PE=1 SV=1	0.658409	0.007859
O75694	NU155_HUMAN	Nuclear pore complex protein Nup155 OS=Homo sapiens OX=9606 GN=NUP155 PE=1 SV=1	0.658393	0.001265
O76071	CIAO1_HUMAN	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens OX=9606 GN=CIAO1 PE=1 SV=1	0.657712	0.006489
Q5GLZ8	HERC4_HUMAN	Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens OX=9606 GN=HERC4 PE=1 SV=1	0.657258	0.007447
O96008	TOM40_HUMAN	Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens OX=9606 GN=TOMM40 PE=1 SV=1	0.656959	0.009589
Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2	0.655846	0.007808
P62917	RL8_HUMAN	60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=2	0.655398	0.009884
O43818	U3IP2_HUMAN	U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens OX=9606 GN=RRP9 PE=1 SV=1	0.65539	0.007447
P06737	PYGL_HUMAN	Glycogen phosphorylase liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4	0.654778	0.007179
Q96JM3	CHAP1_HUMAN	Chromosome alignment-maintaining phosphoprotein 1 OS=Homo sapiens OX=9606 GN=CHAMP1 PE=1 SV=2	0.653887	0.007805
P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=3	0.653885	0.005203
P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1	0.653527	0.006637
P0DMV9	HS71B_HUMAN	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1	0.653527	0.006637
P07814	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens OX=9606 GN=EPRS1 PE=1 SV=5	0.653371	0.002602
P46776	RL27A_HUMAN	60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=2	0.651763	0.008602
Q9NW13	RBM28_HUMAN	RNA-binding protein 28 OS=Homo sapiens OX=9606 GN=RBM28 PE=1 SV=3	0.650889	0.00783
Q8TEX9	IPO4_HUMAN	Importin-4 OS=Homo sapiens OX=9606 GN=IPO4 PE=1 SV=2	0.650098	0.001553
Q9UL25	RAB21_HUMAN	Ras-related protein Rab-21 OS=Homo sapiens OX=9606 GN=RAB21 PE=1 SV=3	0.649676	0.005407
P60981	DEST_HUMAN	Dextrin OS=Homo sapiens OX=9606 GN=DSTN PE=1 SV=3	0.648312	0.0083
Q96A65	EXOC4_HUMAN	Exocyst complex component 4 OS=Homo sapiens OX=9606 GN=EXOC4 PE=1 SV=1	0.648308	0.004169
O43172	PRP4_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens OX=9606 GN=PRPF4 PE=1 SV=2	0.646984	0.007648
Q9UJ83	HACL1_HUMAN	2-hydroxyacyl-CoA lyase 1 OS=Homo sapiens OX=9606 GN=HACL1 PE=1 SV=2	0.646743	0.008416
Q9H814	PHAX_HUMAN	Phosphorylated adapter RNA export protein OS=Homo sapiens OX=9606 GN=PHAX PE=1 SV=1	0.646566	0.008103
P63261	ACTG_HUMAN	Actin cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1	0.645935	0.008369
Q14738	2A5D_HUMAN	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens OX=9606 GN=PPP2R5D PE=1 SV=1	0.645133	0.008479
Q8NBQ5	DHB11_HUMAN	Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens OX=9606 GN=HSD17B11 PE=1 SV=3	0.644657	0.008616
P55060	XPO2_HUMAN	Exportin-2 OS=Homo sapiens OX=9606 GN=CSE1L PE=1 SV=3	0.643856	0.002983
Q9Y3E5	PTH2_HUMAN	Peptidyl-tRNA hydrolase 2 mitochondrial OS=Homo sapiens OX=9606 GN=PTRH2 PE=1 SV=1	0.642954	0.008369

Q9Y394	DHRS7_HUMAN	Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 PE=1 SV=1	0.641175	0.009078
Q7L014	DDX46_HUMAN	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens OX=9606 GN=DDX46 PE=1 SV=2	0.640838	0.008964
P08237	PFKAM_HUMAN	ATP-dependent 6-phosphofructokinase muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=2	0.64052	0.006142
Q96CW1	AP2M1_HUMAN	AP-2 complex subunit mu OS=Homo sapiens OX=9606 GN=AP2M1 PE=1 SV=2	0.640458	0.006285
Q9P2R3	ANFY1_HUMAN	Rabankyrin-5 OS=Homo sapiens OX=9606 GN=ANKFY1 PE=1 SV=2	0.640053	0.002742
O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR PE=1 SV=1	0.639922	0.004547
O75818	RPP40_HUMAN	Ribonuclease P protein subunit p40 OS=Homo sapiens OX=9606 GN=RPP40 PE=1 SV=3	0.639683	0.006959
Q13641	TPBG_HUMAN	Trophoblast glycoprotein OS=Homo sapiens OX=9606 GN=TPBG PE=1 SV=1	0.639228	0.009036
O75153	CLU_HUMAN	Clustered mitochondria protein homolog OS=Homo sapiens OX=9606 GN=CLUH PE=1 SV=2	0.639221	0.003453
Q9UNE7	CHIP_HUMAN	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens OX=9606 GN=STUB1 PE=1 SV=2	0.637729	0.005608
Q9Y5Q8	TF3C5_HUMAN	General transcription factor 3C polypeptide 5 OS=Homo sapiens OX=9606 GN=GTF3C5 PE=1 SV=2	0.637725	0.009787
Q8WW12	PCNP_HUMAN	PEST proteolytic signal-containing nuclear protein OS=Homo sapiens OX=9606 GN=PCNP PE=1 SV=2	0.637555	0.008892
O60684	IMA7_HUMAN	Importin subunit alpha-7 OS=Homo sapiens OX=9606 GN=KPNA6 PE=1 SV=1	0.637327	0.009787
Q92520	FAM3C_HUMAN	Protein FAM3C OS=Homo sapiens OX=9606 GN=FAM3C PE=1 SV=1	0.636037	0.009734
Q9H3Q1	BORG4_HUMAN	Cdc42 effector protein 4 OS=Homo sapiens OX=9606 GN=CDC42EP4 PE=1 SV=1	0.635523	0.007248
P49257	LMAN1_HUMAN	Protein ERGIC-53 OS=Homo sapiens OX=9606 GN=LMAN1 PE=1 SV=2	0.635182	0.009787
O43252	PAPS1_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens OX=9606 GN=PAPSS1 PE=1 SV=2	0.635003	8.90E-04
Q9UNZ2	NSF1C_HUMAN	NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=2	0.634716	0.004344
P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=3	0.634673	0.008611
A1L0T0	ILVBL_HUMAN	Acetolactate synthase-like protein OS=Homo sapiens OX=9606 GN=ILVBL PE=1 SV=2	0.634252	9.48E-04
Q0VDF9	HSP7E_HUMAN	Heat shock 70 kDa protein 14 OS=Homo sapiens OX=9606 GN=HSPA14 PE=1 SV=1	0.634129	0.003467
P35580	MYH10_HUMAN	Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3	0.63408	8.70E-04
Q68CZ2	TENS3_HUMAN	Tensin-3 OS=Homo sapiens OX=9606 GN=TNS3 PE=1 SV=2	0.634019	0.00632
Q86Y39	NDUAB_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens OX=9606 GN=NDUFA11 PE=1 SV=3	0.633872	0.007575
Q96T51	RUFY1_HUMAN	RUN and FYVE domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RUFY1 PE=1 SV=2	0.633689	0.006037
P43246	MSH2_HUMAN	DNA mismatch repair protein Msh2 OS=Homo sapiens OX=9606 GN=MSH2 PE=1 SV=1	0.630959	0.002249
P52292	IMA1_HUMAN	Importin subunit alpha-1 OS=Homo sapiens OX=9606 GN=KPNA2 PE=1 SV=1	0.629817	0.002029
Q06210	GFPT1_HUMAN	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens OX=9606 GN=GFPT1 PE=1 SV=3	0.629462	0.001155
Q9NSE4	SYIM_HUMAN	Isoleucine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=IARS2 PE=1 SV=2	0.629219	0.002905
Q08380	LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1	0.628906	0.007783
P09874	PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4	0.628865	0.005868
Q7Z3B4	NUP54_HUMAN	Nucleoporin p54 OS=Homo sapiens OX=9606 GN=NUP54 PE=1 SV=2	0.628479	0.00136
Q9Y295	DRG1_HUMAN	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=DRG1 PE=1 SV=1	0.628455	0.006144
P50991	TCPD_HUMAN	T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4	0.627306	0.003482
Q14790	CASP8_HUMAN	Caspase-8 OS=Homo sapiens OX=9606 GN=CASP8 PE=1 SV=1	0.625576	0.006637
Q10570	CPSF1_HUMAN	Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens OX=9606 GN=CPSF1 PE=1 SV=2	0.624961	0.007852
Q5QJE6	TDIF2_HUMAN	Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens OX=9606 GN=DNTTIP2 PE=1 SV=2	0.624903	0.001016
Q13310	PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1	0.622347	0.007972

Q9BWU0	NADAP_HUMAN	Kanadaplin OS=Homo sapiens OX=9606 GN=SLC4A1AP PE=1 SV=1	0.621368	0.008258
Q8WWI1	LMO7_HUMAN	LIM domain only protein 7 OS=Homo sapiens OX=9606 GN=LMO7 PE=1 SV=3	0.619067	0.004106
Q16643	DREB_HUMAN	Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4	0.61891	0.002876
P17655	CAN2_HUMAN	Calpain-2 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN2 PE=1 SV=6	0.618654	0.004434
P11166	GTR1_HUMAN	Solute carrier family 2 facilitated glucose transporter member 1 OS=Homo sapiens OX=9606 GN=SLC2A1 PE=1 SV=2	0.617643	0.00937
O43237	DC1L2_HUMAN	Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1L2 PE=1 SV=1	0.617075	0.008035
P11908	PRPS2_HUMAN	Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens OX=9606 GN=PRPS2 PE=1 SV=2	0.615763	0.006655
Q00535	CDK5_HUMAN	Cyclin-dependent-like kinase 5 OS=Homo sapiens OX=9606 GN=CDK5 PE=1 SV=3	0.611859	0.00899
P22830	HEMH_HUMAN	Ferrochelatase mitochondrial OS=Homo sapiens OX=9606 GN=FECH PE=1 SV=2	0.611824	0.007575
P39687	AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32A PE=1 SV=1	0.61138	0.004294
Q9BX79	STRA6_HUMAN	Receptor for retinol uptake STRA6 OS=Homo sapiens OX=9606 GN=STRA6 PE=1 SV=1	0.610372	0.006142
Q9Y262	EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1	0.608257	0.002998
Q6P1J9	CDC73_HUMAN	Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1	0.607655	0.004424
Q12874	SF3A3_HUMAN	Splicing factor 3A subunit 3 OS=Homo sapiens OX=9606 GN=SF3A3 PE=1 SV=1	0.606508	0.006512
O00203	AP3B1_HUMAN	AP-3 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP3B1 PE=1 SV=3	0.606065	0.009295
Q9BUJ2	HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=2	0.604479	0.003511
O95208	EPN2_HUMAN	Epsin-2 OS=Homo sapiens OX=9606 GN=EPN2 PE=1 SV=3	0.604455	0.004151
P49591	SYSC_HUMAN	Serine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=SARS1 PE=1 SV=3	0.604252	0.005661
P17812	PYRG1_HUMAN	CTP synthase 1 OS=Homo sapiens OX=9606 GN=CTPS1 PE=1 SV=2	0.603143	0.004941
P00387	NB5R3_HUMAN	NADH-cytochrome b5 reductase 3 OS=Homo sapiens OX=9606 GN=CYB5R3 PE=1 SV=3	0.602873	0.008918
Q13564	ULA1_HUMAN	NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens OX=9606 GN=NAE1 PE=1 SV=1	0.601654	0.008369
P35658	NU214_HUMAN	Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=2	0.59988	8.76E-04
P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3 PE=1 SV=2	0.59958	0.008304
P18031	PTN1_HUMAN	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens OX=9606 GN=PTPN1 PE=1 SV=1	0.599525	0.008369
Q12959	DLG1_HUMAN	Disks large homolog 1 OS=Homo sapiens OX=9606 GN=DLG1 PE=1 SV=2	0.599179	0.002602
P11216	PYGB_HUMAN	Glycogen phosphorylase brain form OS=Homo sapiens OX=9606 GN=PYGB PE=1 SV=5	0.597943	0.008039
Q9BT09	CNPY3_HUMAN	Protein canopy homolog 3 OS=Homo sapiens OX=9606 GN=CNPY3 PE=1 SV=1	0.593202	0.006745
Q15008	PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens OX=9606 GN=PSMD6 PE=1 SV=1	0.592032	0.006442
P51003	PAPOA_HUMAN	Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOLA PE=1 SV=4	0.589368	0.002715
O14745	NHRF1_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens OX=9606 GN=SLC9A3R1 PE=1 SV=4	0.588018	0.009403
Q8N4Q1	MIA40_HUMAN	Mitochondrial intermembrane space import and assembly protein 40 OS=Homo sapiens OX=9606 GN=CHCHD4 PE=1 SV=1	0.585526	0.006512
Q14203	DCTN1_HUMAN	Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=1 SV=3	0.585215	0.004
Q15942	ZYX_HUMAN	Zyxin OS=Homo sapiens OX=9606 GN=ZYX PE=1 SV=1	0.583505	9.95E-04
Q01105	SET_HUMAN	Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=3	-0.63198	0.003011
P02768	ALBU_HUMAN	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2	-0.63988	0.001627
Q71DI3	H32_HUMAN	Histone H3.2 OS=Homo sapiens OX=9606 GN=HIST2H3A PE=1 SV=3	-0.94869	1.11E-06
P14174	MIF_HUMAN	Macrophage migration inhibitory factor OS=Homo sapiens OX=9606 GN=MIF PE=1 SV=4	-1.70851	1.94E-17

Appendix Table 2: A549 global proteome changes following TDI exposure – Proteins with a significant difference in abundance are presented according to descending log2 fold change.

A.2.4 Significant proteome changes in 16HE140⁻ cells following exposure to DPCP

Accession	Uniprot ID	Description	Log2 Fold Change	P value (FDR)
Q9BQP7	MGME1_HUMAN	Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens OX=9606 GN=MGME1 PE=1 SV=1	1.878533	3.39E-17
P29372	3MG_HUMAN	DNA-3-methyladenine glycosylase OS=Homo sapiens OX=9606 GN=MPG PE=1 SV=3	1.592117	3.01E-12
Q04446	GLGB_HUMAN	1 4-alpha-glucan-branching enzyme OS=Homo sapiens OX=9606 GN=GBE1 PE=1 SV=3	1.577717	3.01E-12
Q5ZPR3	CD276_HUMAN	CD276 antigen OS=Homo sapiens OX=9606 GN=CD276 PE=1 SV=1	1.572151	3.01E-12
Q13740	CD166_HUMAN	CD166 antigen OS=Homo sapiens OX=9606 GN=ALCAM PE=1 SV=2	1.323238	1.22E-11
Q86TN4	TRPT1_HUMAN	tRNA 2'-phosphotransferase 1 OS=Homo sapiens OX=9606 GN=TRPT1 PE=1 SV=2	1.583217	7.56E-11
Q92600	CNOT9_HUMAN	CCR4-NOT transcription complex subunit 9 OS=Homo sapiens OX=9606 GN=CNOT9 PE=1 SV=1	1.412429	7.86E-10
P42696	RBM34_HUMAN	RNA-binding protein 34 OS=Homo sapiens OX=9606 GN=RBM34 PE=1 SV=2	1.35393	5.55E-09
Q15418	KS6A1_HUMAN	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1 SV=2	1.028302	5.73E-09
Q12769	NU160_HUMAN	Nuclear pore complex protein Nup160 OS=Homo sapiens OX=9606 GN=NUP160 PE=1 SV=3	1.342674	6.65E-09
O43252	PAPS1_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens OX=9606 GN=PAPSS1 PE=1 SV=2	1.313366	1.49E-08
Q92785	REQU_HUMAN	Zinc finger protein ubi-d4 OS=Homo sapiens OX=9606 GN=DPF2 PE=1 SV=2	1.305639	1.83E-08
P06400	RB_HUMAN	Retinoblastoma-associated protein OS=Homo sapiens OX=9606 GN=RB1 PE=1 SV=2	1.30375	1.83E-08
Q6L8Q7	PDE12_HUMAN	2' 5'-phosphodiesterase 12 OS=Homo sapiens OX=9606 GN=PDE12 PE=1 SV=2	1.303304	1.83E-08
P13995	MTDC_HUMAN	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD2 PE=1 SV=2	1.305598	2.95E-08
Q9UBU9	NXF1_HUMAN	Nuclear RNA export factor 1 OS=Homo sapiens OX=9606 GN=NXF1 PE=1 SV=1	1.282822	2.95E-08
Q96SU4	OSBL9_HUMAN	Oxysterol-binding protein-related protein 9 OS=Homo sapiens OX=9606 GN=OSBPL9 PE=1 SV=2	1.262807	5.65E-08
O75391	SPAG7_HUMAN	Sperm-associated antigen 7 OS=Homo sapiens OX=9606 GN=SPAG7 PE=1 SV=2	1.349017	9.98E-08
O76071	CIAO1_HUMAN	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens OX=9606 GN=CIAO1 PE=1 SV=1	1.22715	1.41E-07
Q9Y5A9	YTHD2_HUMAN	YTH domain-containing family protein 2 OS=Homo sapiens OX=9606 GN=YTHDF2 PE=1 SV=2	1.227715	1.41E-07
Q969V3	NCLN_HUMAN	Nicalin OS=Homo sapiens OX=9606 GN=NCLN PE=1 SV=2	1.220867	1.84E-07
Q8WX92	NELFB_HUMAN	Negative elongation factor B OS=Homo sapiens OX=9606 GN=NELFB PE=1 SV=1	1.214534	1.86E-07
Q9Y613	FHOD1_HUMAN	FH1/FH2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FBOD1 PE=1 SV=3	1.195091	3.20E-07
P78318	IGBP1_HUMAN	Immunoglobulin-binding protein 1 OS=Homo sapiens OX=9606 GN=IGBP1 PE=1 SV=1	1.078497	3.20E-07
P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 OS=Homo sapiens OX=9606 GN=PTPN6 PE=1 SV=1	1.193363	3.20E-07
P08237	PFKAM_HUMAN	ATP-dependent 6-phosphofructokinase muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=2	1.029777	3.42E-07
Q96KG9	SCYL1_HUMAN	N-terminal kinase-like protein OS=Homo sapiens OX=9606 GN=SCYL1 PE=1 SV=1	0.906891	6.95E-07
Q7KZ85	SPT6H_HUMAN	Transcription elongation factor SPT6 OS=Homo sapiens OX=9606 GN=SPT6H PE=1 SV=2	1.012441	9.15E-07
Q9UBV2	SEL1L_HUMAN	Protein sel-1 homolog 1 OS=Homo sapiens OX=9606 GN=SEL1L PE=1 SV=3	1.05153	1.31E-06
Q9Y314	NOSIP_HUMAN	Nitric oxide synthase-interacting protein OS=Homo sapiens OX=9606 GN=NOSIP PE=1 SV=1	1.142565	1.31E-06
Q8NFH4	NUP37_HUMAN	Nucleoporin Nup37 OS=Homo sapiens OX=9606 GN=NUP37 PE=1 SV=1	1.133625	1.39E-06
Q8IXB1	DJC10_HUMAN	DnaJ homolog subfamily C member 10 OS=Homo sapiens OX=9606 GN=DNAJC10 PE=1 SV=2	0.860495	1.46E-06
Q6IQ22	RAB12_HUMAN	Ras-related protein Rab-12 OS=Homo sapiens OX=9606 GN=RAB12 PE=1 SV=3	1.133337	1.46E-06
Q8IYB8	SUV3_HUMAN	ATP-dependent RNA helicase SUPV3L1 mitochondrial OS=Homo sapiens OX=9606 GN=SUPV3L1 PE=1 SV=1	1.132326	1.46E-06

P00390	GSHR_HUMAN	Glutathione reductase mitochondrial OS=Homo sapiens OX=9606 GN=GSR PE=1 SV=2	1.00489	1.49E-06
P33527	MRP1_HUMAN	Multidrug resistance-associated protein 1 OS=Homo sapiens OX=9606 GN=ABCC1 PE=1 SV=3	1.12919	1.57E-06
P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNPH2 PE=1 SV=1	1.122796	1.58E-06
P20591	MX1_HUMAN	Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens OX=9606 GN=MX1 PE=1 SV=4	1.123744	1.58E-06
O00754	MA2B1_HUMAN	Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=3	1.114869	2.03E-06
O14656	TOR1A_HUMAN	Torsin-1A OS=Homo sapiens OX=9606 GN=TOR1A PE=1 SV=1	1.109506	2.38E-06
P05187	PPB1_HUMAN	Alkaline phosphatase placental type OS=Homo sapiens OX=9606 GN=ALPP PE=1 SV=2	1.108763	2.38E-06
P62841	RS15_HUMAN	40S ribosomal protein S15 OS=Homo sapiens OX=9606 GN=RPS15 PE=1 SV=2	1.082647	2.38E-06
Q14244	MAP7_HUMAN	Enscosin OS=Homo sapiens OX=9606 GN=MAP7 PE=1 SV=1	1.108196	2.38E-06
Q9H7D7	WDR26_HUMAN	WD repeat-containing protein 26 OS=Homo sapiens OX=9606 GN=WDR26 PE=1 SV=3	1.105566	2.43E-06
P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=2	1.244443	2.43E-06
P46977	STT3A_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens OX=9606 GN=STT3A PE=1 SV=2	1.951302	2.44E-06
O75190	DNJB6_HUMAN	DnaJ homolog subfamily B member 6 OS=Homo sapiens OX=9606 GN=DNAJB6 PE=1 SV=2	1.096416	3.13E-06
Q9Y2D5	AKAP2_HUMAN	A-kinase anchor protein 2 OS=Homo sapiens OX=9606 GN=AKAP2 PE=1 SV=3	1.088913	3.82E-06
Q9UKS6	PACN3_HUMAN	Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens OX=9606 GN=PACSIN3 PE=1 SV=2	1.081665	4.31E-06
Q13501	SQSTM_HUMAN	Sequestosome-1 OS=Homo sapiens OX=9606 GN=SQSTM1 PE=1 SV=1	1.14293	4.65E-06
Q9BQ52	RNZ2_HUMAN	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens OX=9606 GN=ELAC2 PE=1 SV=2	0.688871	5.61E-06
Q658Y4	F91A1_HUMAN	Protein FAM91A1 OS=Homo sapiens OX=9606 GN=FAM91A1 PE=1 SV=3	1.071495	5.67E-06
Q16881	TRXR1_HUMAN	Thioredoxin reductase 1 cytoplasmic OS=Homo sapiens OX=9606 GN=TXNRD1 PE=1 SV=3	1.109993	5.76E-06
Q9Y4W2	LAS1L_HUMAN	Ribosomal biogenesis protein LAS1L OS=Homo sapiens OX=9606 GN=LAS1L PE=1 SV=2	1.063194	6.56E-06
Q13547	HDAC1_HUMAN	Histone deacetylase 1 OS=Homo sapiens OX=9606 GN=HDAC1 PE=1 SV=1	1.060803	7.03E-06
Q02127	PYRD_HUMAN	Dihydroorotate dehydrogenase (quinone) mitochondrial OS=Homo sapiens OX=9606 GN=DHODH PE=1 SV=3	1.057732	7.35E-06
Q8TAE8	G45IP_HUMAN	Growth arrest and DNA damage-inducible proteins-interacting protein 1 OS=Homo sapiens OX=9606 GN=GADD45GIP1 PE=1 SV=1	1.05672	7.49E-06
Q8IXM3	RM41_HUMAN	39S ribosomal protein L41 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL41 PE=1 SV=1	1.055819	8.02E-06
Q13421	MSLN_HUMAN	Mesothelin OS=Homo sapiens OX=9606 GN=MSLN PE=1 SV=2	1.04456	9.57E-06
O15042	SR140_HUMAN	U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens OX=9606 GN=U2SURP PE=1 SV=2	1.042135	1.08E-05
P15291	B4GT1_HUMAN	Beta-1 4-galactosyltransferase 1 OS=Homo sapiens OX=9606 GN=B4GALT1 PE=1 SV=5	1.038349	1.11E-05
P50443	S26A2_HUMAN	Sulfate transporter OS=Homo sapiens OX=9606 GN=SLC26A2 PE=1 SV=2	1.038706	1.15E-05
Q9NVI7	ATD3A_HUMAN	ATPase family AAA domain-containing protein 3A OS=Homo sapiens OX=9606 GN=ATAD3A PE=1 SV=2	1.035104	1.15E-05
P35237	SPB6_HUMAN	Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=3	0.984579	1.15E-05
O94776	MTA2_HUMAN	Metastasis-associated protein MTA2 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	0.799036	1.25E-05
P28070	PSB4_HUMAN	Proteasome subunit beta type-4 OS=Homo sapiens OX=9606 GN=PSMB4 PE=1 SV=4	0.992062	1.37E-05
O75746	CMC1_HUMAN	Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens OX=9606 GN=SLC25A12 PE=1 SV=2	0.770491	1.46E-05
Q99627	CSN8_HUMAN	COP9 signalosome complex subunit 8 OS=Homo sapiens OX=9606 GN=COPS8 PE=1 SV=1	1.018262	1.70E-05
P29590	PML_HUMAN	Protein PML OS=Homo sapiens OX=9606 GN=PML PE=1 SV=3	0.788496	1.70E-05
Q9BRT3	MIEN1_HUMAN	Migration and invasion enhancer 1 OS=Homo sapiens OX=9606 GN=MIEN1 PE=1 SV=1	1.017978	1.70E-05
P46976	GLYG_HUMAN	Glycogenin-1 OS=Homo sapiens OX=9606 GN=GYG1 PE=1 SV=4	1.014873	1.70E-05
P15144	AMPN_HUMAN	Aminopeptidase N OS=Homo sapiens OX=9606 GN=ANPEP PE=1 SV=4	1.015745	1.80E-05

Q9BV38	WDR18_HUMAN	WD repeat-containing protein 18 OS=Homo sapiens OX=9606 GN=WDR18 PE=1 SV=2	1.014666	1.80E-05
O15446	RPA34_HUMAN	DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens OX=9606 GN=CD3EAP PE=1 SV=1	1.015061	1.81E-05
Q9Y4W6	AFG32_HUMAN	AFG3-like protein 2 OS=Homo sapiens OX=9606 GN=AFG3L2 PE=1 SV=2	0.901207	1.81E-05
P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E OS=Homo sapiens OX=9606 GN=SNRPE PE=1 SV=1	0.95335	1.84E-05
O95163	ELP1_HUMAN	Elongator complex protein 1 OS=Homo sapiens OX=9606 GN=ELP1 PE=1 SV=3	1.01841	1.84E-05
O43148	MCES_HUMAN	mRNA cap guanine-N7 methyltransferase OS=Homo sapiens OX=9606 GN=RNMT PE=1 SV=1	1.011047	1.93E-05
Q96AC1	FERM2_HUMAN	Fermitin family homolog 2 OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1	1.008082	1.94E-05
P49914	MTHFS_HUMAN	5-formyltetrahydrofolate cyclo-ligase OS=Homo sapiens OX=9606 GN=MTHFS PE=1 SV=2	1.00601	1.98E-05
Q9H7Z7	PGES2_HUMAN	Prostaglandin E synthase 2 OS=Homo sapiens OX=9606 GN=PTGES2 PE=1 SV=1	1.00875	2.01E-05
Q6P587	FAHD1_HUMAN	Acylpyruvase FAHD1 mitochondrial OS=Homo sapiens OX=9606 GN=FAHD1 PE=1 SV=2	1.002504	2.01E-05
O00499	BIN1_HUMAN	Myc box-dependent-interacting protein 1 OS=Homo sapiens OX=9606 GN=BIN1 PE=1 SV=1	0.85377	2.01E-05
Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2 OS=Homo sapiens OX=9606 GN=SPCS2 PE=1 SV=3	0.913262	2.10E-05
Q93052	LPP_HUMAN	Lipoma-preferred partner OS=Homo sapiens OX=9606 GN=LPP PE=1 SV=1	1.029101	2.12E-05
P17676	CEBPB_HUMAN	CCAAT/enhancer-binding protein beta OS=Homo sapiens OX=9606 GN=CEBPB PE=1 SV=2	0.998346	2.36E-05
Q96RE7	NACC1_HUMAN	Nucleus accumbens-associated protein 1 OS=Homo sapiens OX=9606 GN=NACC1 PE=1 SV=1	0.99482	2.46E-05
O95817	BAG3_HUMAN	BAG family molecular chaperone regulator 3 OS=Homo sapiens OX=9606 GN=BAG3 PE=1 SV=3	0.995225	2.58E-05
O95372	LYPA2_HUMAN	Acyl-protein thioesterase 2 OS=Homo sapiens OX=9606 GN=LYPLA2 PE=1 SV=1	0.990052	2.58E-05
Q9Y3D9	RT23_HUMAN	28S ribosomal protein S23 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS23 PE=1 SV=2	0.992223	2.58E-05
P62633	CNBP_HUMAN	Cellular nucleic acid-binding protein OS=Homo sapiens OX=9606 GN=CNBP PE=1 SV=1	0.993532	2.60E-05
P56537	IF6_HUMAN	Eukaryotic translation initiation factor 6 OS=Homo sapiens OX=9606 GN=EIF6 PE=1 SV=1	0.986137	2.84E-05
Q9Y333	LSM2_HUMAN	U6 snRNA-associated Sm-like protein LSM2 OS=Homo sapiens OX=9606 GN=LSM2 PE=1 SV=1	0.987791	2.91E-05
Q6DD88	ATLA3_HUMAN	Atlastin-3 OS=Homo sapiens OX=9606 GN=ATL3 PE=1 SV=1	0.715886	3.08E-05
P68431	H31_HUMAN	Histone H3.1 OS=Homo sapiens OX=9606 GN=H3C1 PE=1 SV=2	0.734587	3.08E-05
Q4V328	GRAP1_HUMAN	GRIP1-associated protein 1 OS=Homo sapiens OX=9606 GN=GRIPAP1 PE=1 SV=2	0.980034	3.29E-05
Q9NP61	ARFG3_HUMAN	ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens OX=9606 GN=ARFGAP3 PE=1 SV=1	0.781207	3.29E-05
Q8WVQ1	CANT1_HUMAN	Soluble calcium-activated nucleotidase 1 OS=Homo sapiens OX=9606 GN=CANT1 PE=1 SV=1	0.976007	3.67E-05
Q6P1J9	CDC73_HUMAN	Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1	0.931716	3.75E-05
P35606	COPB2_HUMAN	Coatamer subunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2	0.654308	3.75E-05
Q9P2R3	ANFY1_HUMAN	Rabankyrin-5 OS=Homo sapiens OX=9606 GN=ANKFY1 PE=1 SV=2	0.73682	3.82E-05
Q96H20	SNF8_HUMAN	Vacuolar-sorting protein SNF8 OS=Homo sapiens OX=9606 GN=SNF8 PE=1 SV=1	0.971525	3.88E-05
P84243	H33_HUMAN	Histone H3.3 OS=Homo sapiens OX=9606 GN=H3-3A PE=1 SV=2	0.971242	3.88E-05
Q14192	FHL2_HUMAN	Four and a half LIM domains protein 2 OS=Homo sapiens OX=9606 GN=FHL2 PE=1 SV=3	0.829184	4.17E-05
P82933	RT09_HUMAN	28S ribosomal protein S9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS9 PE=1 SV=2	0.966487	4.17E-05
O75351	VPS4B_HUMAN	Vacuolar protein sorting-associated protein 4B OS=Homo sapiens OX=9606 GN=VPS4B PE=1 SV=2	0.967066	4.45E-05
Q9BZK7	TBL1R_HUMAN	F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens OX=9606 GN=TBL1XR1 PE=1 SV=1	0.924602	4.45E-05
O14776	TCRG1_HUMAN	Transcription elongation regulator 1 OS=Homo sapiens OX=9606 GN=TCERG1 PE=1 SV=2	1.234838	4.99E-05
P08133	ANXA6_HUMAN	Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3	0.63422	5.11E-05
P45985	MP2K4_HUMAN	Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens OX=9606 GN=MAP2K4 PE=1 SV=1	0.958895	5.19E-05

Q7Z3T8	ZFY16_HUMAN	Zinc finger FYVE domain-containing protein 16 OS=Homo sapiens OX=9606 GN=ZFYVE16 PE=1 SV=3	0.955212	5.41E-05
Q9BSJ2	GCP2_HUMAN	Gamma-tubulin complex component 2 OS=Homo sapiens OX=9606 GN=TUBGCP2 PE=1 SV=2	0.821763	5.98E-05
Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens OX=9606 GN=TGFB1 PE=1 SV=1	0.990695	5.98E-05
Q9NXF1	TEX10_HUMAN	Testis-expressed protein 10 OS=Homo sapiens OX=9606 GN=TEX10 PE=1 SV=2	0.950206	6.39E-05
Q9UIV1	CNOT7_HUMAN	CCR4-NOT transcription complex subunit 7 OS=Homo sapiens OX=9606 GN=CNOT7 PE=1 SV=3	0.946426	6.50E-05
Q8ND56	LS14A_HUMAN	Protein LSM14 homolog A OS=Homo sapiens OX=9606 GN=LSM14A PE=1 SV=3	0.943416	6.79E-05
P43304	GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=GPDM2 PE=1 SV=3	0.6822	6.92E-05
O00566	MPP10_HUMAN	U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens OX=9606 GN=MPHOSPH10 PE=1 SV=2	0.943505	7.15E-05
Q9BVL2	NUP58_HUMAN	Nucleoporin p58/p45 OS=Homo sapiens OX=9606 GN=NUP58 PE=1 SV=1	0.940818	7.15E-05
Q8WU90	ZC3HF_HUMAN	Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens OX=9606 GN=ZC3H15 PE=1 SV=1	0.943846	7.20E-05
Q96JJ7	TMX3_HUMAN	Protein disulfide-isomerase TMX3 OS=Homo sapiens OX=9606 GN=TMX3 PE=1 SV=2	0.921776	7.25E-05
P52948	NUP98_HUMAN	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens OX=9606 GN=NUP98 PE=1 SV=4	0.938652	7.25E-05
Q9UFC0	LRWD1_HUMAN	Leucine-rich repeat and WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=LRWD1 PE=1 SV=2	0.940997	7.31E-05
Q06546	GABPA_HUMAN	GA-binding protein alpha chain OS=Homo sapiens OX=9606 GN=GABPA PE=1 SV=1	0.939337	7.38E-05
Q06265	EXOS9_HUMAN	Exosome complex component RRP45 OS=Homo sapiens OX=9606 GN=EXOSC9 PE=1 SV=3	0.937229	7.51E-05
Q9NP81	SYSM_HUMAN	Serine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=SARS2 PE=1 SV=1	0.849409	8.09E-05
Q0JRZ9	FCHO2_HUMAN	F-BAR domain only protein 2 OS=Homo sapiens OX=9606 GN=FCHO2 PE=1 SV=2	0.933363	8.37E-05
P61201	CSN2_HUMAN	COP9 signalosome complex subunit 2 OS=Homo sapiens OX=9606 GN=COPS2 PE=1 SV=1	0.872816	9.17E-05
O60825	F262_HUMAN	6-phosphofructo-2-kinase/fructose-2 6-bisphosphatase 2 OS=Homo sapiens OX=9606 GN=PFKFB2 PE=1 SV=2	0.928726	9.70E-05
Q96EP5	DAZP1_HUMAN	DAZ-associated protein 1 OS=Homo sapiens OX=9606 GN=DAZAP1 PE=1 SV=1	0.928146	9.74E-05
O14530	TXND9_HUMAN	Thioredoxin domain-containing protein 9 OS=Homo sapiens OX=9606 GN=TXNDC9 PE=1 SV=2	0.92267	1.07E-04
Q96S52	PIGS_HUMAN	GPI transamidase component PIG-S OS=Homo sapiens OX=9606 GN=PIGS PE=1 SV=3	0.919961	1.10E-04
Q96BJ3	AIDA_HUMAN	Axin interactor dorsalization-associated protein OS=Homo sapiens OX=9606 GN=AIDA PE=1 SV=1	0.916966	1.19E-04
Q9H6T3	RPAP3_HUMAN	RNA polymerase II-associated protein 3 OS=Homo sapiens OX=9606 GN=RPAP3 PE=1 SV=2	0.817185	1.25E-04
O15067	PUR4_HUMAN	Phosphoribosylformylglycinamide synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1 SV=4	0.911762	1.26E-04
P62834	RAP1A_HUMAN	Ras-related protein Rap-1A OS=Homo sapiens OX=9606 GN=RAP1A PE=1 SV=1	0.911296	1.26E-04
P36543	VATE1_HUMAN	V-type proton ATPase subunit E 1 OS=Homo sapiens OX=9606 GN=ATP6V1E1 PE=1 SV=1	0.911593	1.26E-04
P49247	RPIA_HUMAN	Ribose-5-phosphate isomerase OS=Homo sapiens OX=9606 GN=RPIA PE=1 SV=3	0.912784	1.26E-04
Q92769	HDAC2_HUMAN	Histone deacetylase 2 OS=Homo sapiens OX=9606 GN=HDAC2 PE=1 SV=2	0.91184	1.26E-04
P36551	HEM6_HUMAN	Oxygen-dependent coproporphyrinogen-III oxidase mitochondrial OS=Homo sapiens OX=9606 GN=CPOX PE=1 SV=3	0.930282	1.30E-04
Q9BW60	ELOV1_HUMAN	Elongation of very long chain fatty acids protein 1 OS=Homo sapiens OX=9606 GN=ELOVL1 PE=1 SV=1	0.907213	0.000131
Q96E11	RRFM_HUMAN	Ribosome-recycling factor mitochondrial OS=Homo sapiens OX=9606 GN=MRRF PE=1 SV=1	0.911526	0.000131
P46199	IF2M_HUMAN	Translation initiation factor IF-2 mitochondrial OS=Homo sapiens OX=9606 GN=MTIF2 PE=1 SV=2	0.911228	1.32E-04
Q9NY27	PP4R2_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PPP4R2 PE=1 SV=3	1.060379	1.32E-04
P08047	SP1_HUMAN	Transcription factor Sp1 OS=Homo sapiens OX=9606 GN=SP1 PE=1 SV=3	0.907543	1.32E-04
P35914	HMGCL_HUMAN	Hydroxymethylglutaryl-CoA lyase mitochondrial OS=Homo sapiens OX=9606 GN=HMGCL PE=1 SV=2	0.905942	1.35E-04
Q96TA1	NIBA2_HUMAN	Protein Niban 2 OS=Homo sapiens OX=9606 GN=NIBAN2 PE=1 SV=3	0.856382	1.35E-04

Q13045	FLII_HUMAN	Protein flightless-1 homolog OS=Homo sapiens OX=9606 GN=FLII PE=1 SV=2	0.822327	1.35E-04
P54687	BCAT1_HUMAN	Branched-chain-amino-acid aminotransferase cytosolic OS=Homo sapiens OX=9606 GN=BCAT1 PE=1 SV=3	0.838232	1.42E-04
Q15057	ACAP2_HUMAN	Arf-GAP with coiled-coil ANK repeat and PH domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ACAP2 PE=1 SV=3	0.904928	1.42E-04
Q13601	KRR1_HUMAN	KRR1 small subunit processome component homolog OS=Homo sapiens OX=9606 GN=KRR1 PE=1 SV=4	-0.90234	1.42E-04
Q8NCW5	NNRE_HUMAN	NAD(P)H-hydrate epimerase OS=Homo sapiens OX=9606 GN=NAXE PE=1 SV=2	0.844947	1.45E-04
Q03405	UPAR_HUMAN	Urokinase plasminogen activator surface receptor OS=Homo sapiens OX=9606 GN=PLAUR PE=1 SV=1	0.793436	1.48E-04
Q9BPW8	NIPS1_HUMAN	Protein NipSnap homolog 1 OS=Homo sapiens OX=9606 GN=NIPSNAP1 PE=1 SV=1	0.899543	1.48E-04
Q14671	PUM1_HUMAN	Pumilio homolog 1 OS=Homo sapiens OX=9606 GN=PUM1 PE=1 SV=3	0.898499	1.54E-04
Q07065	CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2	0.696241	1.56E-04
Q9BV57	MTND_HUMAN	1 2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens OX=9606 GN=ADI1 PE=1 SV=1	0.897902	1.57E-04
P30519	HMOX2_HUMAN	Heme oxygenase 2 OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=2	0.935335	1.61E-04
Q15024	EXOS7_HUMAN	Exosome complex component RRP42 OS=Homo sapiens OX=9606 GN=EXOSC7 PE=1 SV=3	0.895515	1.62E-04
O75886	STAM2_HUMAN	Signal transducing adapter molecule 2 OS=Homo sapiens OX=9606 GN=STAM2 PE=1 SV=1	0.893762	1.62E-04
Q8N5N7	RM50_HUMAN	39S ribosomal protein L50 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL50 PE=1 SV=2	0.895077	1.62E-04
O94888	UBXN7_HUMAN	UBX domain-containing protein 7 OS=Homo sapiens OX=9606 GN=UBXN7 PE=1 SV=2	0.893854	1.66E-04
Q8N684	CPSF7_HUMAN	Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens OX=9606 GN=CPSF7 PE=1 SV=1	0.714449	1.68E-04
Q7L5N7	PCAT2_HUMAN	Lysophosphatidylcholine acyltransferase 2 OS=Homo sapiens OX=9606 GN=LPCAT2 PE=1 SV=1	1.072358	1.68E-04
Q16763	UBE2S_HUMAN	Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens OX=9606 GN=UBE2S PE=1 SV=2	1.151008	1.75E-04
P43487	RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1	0.888827	1.77E-04
P50453	SPB9_HUMAN	Serpin B9 OS=Homo sapiens OX=9606 GN=SERPINB9 PE=1 SV=1	0.836024	1.77E-04
P24821	TENA_HUMAN	Tenascin OS=Homo sapiens OX=9606 GN=TNCP1 PE=1 SV=3	0.987264	1.81E-04
Q13510	ASAH1_HUMAN	Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=5	0.888969	1.86E-04
O60885	BRD4_HUMAN	Bromodomain-containing protein 4 OS=Homo sapiens OX=9606 GN=BRD4 PE=1 SV=2	1.258728	1.94E-04
P60709	ACTB_HUMAN	Actin cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1	0.883512	1.94E-04
P16435	NCPR_HUMAN	NADPH--cytochrome P450 reductase OS=Homo sapiens OX=9606 GN=POR PE=1 SV=2	0.869939	1.94E-04
P09884	DPOLA_HUMAN	DNA polymerase alpha catalytic subunit OS=Homo sapiens OX=9606 GN=POLA1 PE=1 SV=2	0.883166	1.99E-04
Q96CN7	ISOC1_HUMAN	Isochorismatase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ISOC1 PE=1 SV=3	0.877636	2.15E-04
O75381	PEX14_HUMAN	Peroxisomal membrane protein PEX14 OS=Homo sapiens OX=9606 GN=PEX14 PE=1 SV=1	0.873278	2.17E-04
Q9Y3B7	RM11_HUMAN	39S ribosomal protein L11 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL11 PE=1 SV=1	0.876073	2.19E-04
Q8TEQ6	GEM15_HUMAN	Gem-associated protein 5 OS=Homo sapiens OX=9606 GN=GEMIN5 PE=1 SV=3	0.721517	2.19E-04
P09543	CN37_HUMAN	2' 3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens OX=9606 GN=CNP PE=1 SV=2	0.795297	2.21E-04
P18615	NELFE_HUMAN	Negative elongation factor E OS=Homo sapiens OX=9606 GN=NELFE PE=1 SV=3	0.873226	2.21E-04
Q8TDN6	BRX1_HUMAN	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRX1 PE=1 SV=2	0.811436	2.32E-04
P49770	EI2BB_HUMAN	Translation initiation factor eIF-2B subunit beta OS=Homo sapiens OX=9606 GN=EIF2B2 PE=1 SV=3	0.872231	2.32E-04
Q7Z5L9	I2BP2_HUMAN	Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens OX=9606 GN=IRF2BP2 PE=1 SV=2	0.909668	2.32E-04
Q15436	SC23A_HUMAN	Protein transport protein Sec23A OS=Homo sapiens OX=9606 GN=SEC23A PE=1 SV=2	0.773338	2.41E-04
Q99653	CHP1_HUMAN	Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=3	0.868011	2.44E-04

Q96RS6	NUDC1_HUMAN	NudC domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NUDCD1 PE=1 SV=2	0.849975	2.48E-04
P46736	BRCC3_HUMAN	Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens OX=9606 GN=BRCC3 PE=1 SV=2	0.870515	2.52E-04
P09914	IFIT1_HUMAN	Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens OX=9606 GN=IFIT1 PE=1 SV=2	0.866733	2.53E-04
Q01085	TIAR_HUMAN	Nucleolysin TIAR OS=Homo sapiens OX=9606 GN=TIAL1 PE=1 SV=1	0.867397	2.57E-04
Q9NX14	NDUBB_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFB11 PE=1 SV=1	0.866852	2.58E-04
Q8IZ83	A16A1_HUMAN	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens OX=9606 GN=ALDH16A1 PE=1 SV=2	0.778943	2.58E-04
O95433	AHSA1_HUMAN	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens OX=9606 GN=AHSA1 PE=1 SV=1	0.894954	2.58E-04
P46934	NEDD4_HUMAN	E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens OX=9606 GN=NEDD4 PE=1 SV=4	0.730848	2.58E-04
Q7Z739	YTHD3_HUMAN	YTH domain-containing family protein 3 OS=Homo sapiens OX=9606 GN=YTHDF3 PE=1 SV=1	0.752867	2.60E-04
P34949	MPI_HUMAN	Mannose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=MPI PE=1 SV=2	0.86469	2.62E-04
P61758	PFD3_HUMAN	Prefoldin subunit 3 OS=Homo sapiens OX=9606 GN=VBP1 PE=1 SV=4	0.865956	2.62E-04
Q9BXY0	MAK16_HUMAN	Protein MAK16 homolog OS=Homo sapiens OX=9606 GN=MAK16 PE=1 SV=2	0.825212	2.70E-04
Q9P013	CWC15_HUMAN	Spliceosome-associated protein CWC15 homolog OS=Homo sapiens OX=9606 GN=CWC15 PE=1 SV=2	0.862426	2.72E-04
Q86Y82	STX12_HUMAN	Syntaxin-12 OS=Homo sapiens OX=9606 GN=STX12 PE=1 SV=1	0.86135	2.72E-04
Q9Y697	NFS1_HUMAN	Cysteine desulfurase mitochondrial OS=Homo sapiens OX=9606 GN=NFS1 PE=1 SV=3	0.858819	2.74E-04
Q9P270	SLAI2_HUMAN	SLAIN motif-containing protein 2 OS=Homo sapiens OX=9606 GN=SLAIN2 PE=1 SV=2	0.862364	2.78E-04
Q99700	ATX2_HUMAN	Ataxin-2 OS=Homo sapiens OX=9606 GN=ATXN2 PE=1 SV=2	0.875553	2.78E-04
P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens OX=9606 GN=PGAM1 PE=1 SV=2	0.845923	2.78E-04
Q5JPE7	NOMO2_HUMAN	Nodal modulator 2 OS=Homo sapiens OX=9606 GN=NOMO2 PE=1 SV=1	0.806594	2.78E-04
Q8WZA0	LZIC_HUMAN	Protein LZIC OS=Homo sapiens OX=9606 GN=LZIC PE=1 SV=1	1.075086	2.78E-04
Q9UHX1	PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1	0.7415	2.78E-04
O00625	PIR_HUMAN	Pirin OS=Homo sapiens OX=9606 GN=PIR PE=1 SV=1	0.985383	2.78E-04
P82909	RT36_HUMAN	28S ribosomal protein S36 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS36 PE=1 SV=2	0.934951	2.78E-04
O96005	CLPT1_HUMAN	Cleft lip and palate transmembrane protein 1 OS=Homo sapiens OX=9606 GN=CLPTM1 PE=1 SV=1	0.857574	2.80E-04
Q96EY8	MMAB_HUMAN	Corrinoid adenosyltransferase OS=Homo sapiens OX=9606 GN=MMAB PE=1 SV=1	0.860383	2.80E-04
Q07960	RHG01_HUMAN	Rho GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=ARHGAP1 PE=1 SV=1	0.861062	2.83E-04
P50995	ANX11_HUMAN	Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1 SV=1	0.789599	2.83E-04
P18583	SON_HUMAN	Protein SON OS=Homo sapiens OX=9606 GN=SON PE=1 SV=4	0.67885	2.95E-04
P30153	2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=4	0.723951	3.01E-04
Q14232	EI2BA_HUMAN	Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens OX=9606 GN=EIF2B1 PE=1 SV=1	0.855502	3.06E-04
Q32P44	EMAL3_HUMAN	Echinoderm microtubule-associated protein-like 3 OS=Homo sapiens OX=9606 GN=EML3 PE=1 SV=1	0.909717	3.13E-04
Q9BUF5	TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1	0.788334	3.19E-04
Q13618	CUL3_HUMAN	Cullin-3 OS=Homo sapiens OX=9606 GN=CUL3 PE=1 SV=2	0.752104	3.20E-04
Q9Y230	RUVB2_HUMAN	RuvB-like 2 OS=Homo sapiens OX=9606 GN=RUVBL2 PE=1 SV=3	0.763239	3.22E-04
Q6P1L8	RM14_HUMAN	39S ribosomal protein L14 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL14 PE=1 SV=1	0.850472	3.23E-04
Q12824	SNF5_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens OX=9606 GN=SMARCB1 PE=1 SV=2	0.850587	3.24E-04
Q13523	PRP4B_HUMAN	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3	0.847997	3.49E-04
Q13867	BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens OX=9606 GN=BLMH PE=1 SV=1	0.845462	3.57E-04

Q96GG9	DCNL1_HUMAN	DCN1-like protein 1 OS=Homo sapiens OX=9606 GN=DCUN1D1 PE=1 SV=1	0.842277	3.65E-04
P18827	SDC1_HUMAN	Syndecan-1 OS=Homo sapiens OX=9606 GN=SDC1 PE=1 SV=3	0.817623	3.65E-04
Q9Y3D7	TIM16_HUMAN	Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens OX=9606 GN=PAM16 PE=1 SV=2	0.846435	3.65E-04
Q8NFV4	ABHDB_HUMAN	Protein ABHD11 OS=Homo sapiens OX=9606 GN=ABHD11 PE=1 SV=1	0.844753	3.66E-04
P25788	PSA3_HUMAN	Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=2	0.844506	3.69E-04
P61289	PSME3_HUMAN	Proteasome activator complex subunit 3 OS=Homo sapiens OX=9606 GN=PSME3 PE=1 SV=1	1.158158	3.81E-04
P49354	FNTA_HUMAN	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens OX=9606 GN=FNTA PE=1 SV=1	0.841173	3.84E-04
Q6NZY4	ZCHC8_HUMAN	Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens OX=9606 GN=ZCHC8 PE=1 SV=2	0.748801	3.84E-04
O43847	NRDC_HUMAN	Nardilysin OS=Homo sapiens OX=9606 GN=NRDC PE=1 SV=3	0.967457	4.01E-04
Q9Y4E8	UBP15_HUMAN	Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens OX=9606 GN=USP15 PE=1 SV=3	0.878499	4.07E-04
P20700	LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2	0.748281	4.11E-04
Q9BY44	EIF2A_HUMAN	Eukaryotic translation initiation factor 2A OS=Homo sapiens OX=9606 GN=EIF2A PE=1 SV=3	0.699737	4.20E-04
Q13951	PEBB_HUMAN	Core-binding factor subunit beta OS=Homo sapiens OX=9606 GN=CBFB PE=1 SV=2	0.835733	4.23E-04
P78330	SERB_HUMAN	Phosphoserine phosphatase OS=Homo sapiens OX=9606 GN=PSPH PE=1 SV=2	0.83335	4.23E-04
Q8IV48	ERI1_HUMAN	3'-5' exoribonuclease 1 OS=Homo sapiens OX=9606 GN=ERI1 PE=1 SV=3	0.833924	4.28E-04
Q9BRX5	PSF3_HUMAN	DNA replication complex GINS protein PSF3 OS=Homo sapiens OX=9606 GN=GINS3 PE=1 SV=1	0.836005	4.28E-04
O43752	STX6_HUMAN	Syntaxin-6 OS=Homo sapiens OX=9606 GN=STX6 PE=1 SV=1	0.834639	4.28E-04
P62195	PRS8_HUMAN	26S proteasome regulatory subunit 8 OS=Homo sapiens OX=9606 GN=PSMC5 PE=1 SV=1	0.80771	4.28E-04
P25942	TNR5_HUMAN	Tumor necrosis factor receptor superfamily member 5 OS=Homo sapiens OX=9606 GN=CD40 PE=1 SV=1	0.833141	4.33E-04
Q9BTD8	RBM42_HUMAN	RNA-binding protein 42 OS=Homo sapiens OX=9606 GN=RBM42 PE=1 SV=1	0.829092	4.41E-04
Q9NWW8	BABA1_HUMAN	BRISC and BRCA1-A complex member 1 OS=Homo sapiens OX=9606 GN=BABAM1 PE=1 SV=1	0.831381	4.53E-04
P31948	STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1	0.768674	4.53E-04
Q9Y5X1	SNX9_HUMAN	Sorting nexin-9 OS=Homo sapiens OX=9606 GN=SNX9 PE=1 SV=1	0.833395	4.53E-04
Q9Y4P1	ATG4B_HUMAN	Cysteine protease ATG4B OS=Homo sapiens OX=9606 GN=ATG4B PE=1 SV=2	0.931064	4.59E-04
O15031	PLXB2_HUMAN	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	0.807355	4.59E-04
O14933	UBE2L6_HUMAN	Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens OX=9606 GN=UBE2L6 PE=1 SV=4	1.132507	4.66E-04
Q04760	LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapiens OX=9606 GN=GLO1 PE=1 SV=4	0.829994	4.73E-04
P63167	DYL1_HUMAN	Dynein light chain 1 cytoplasmic OS=Homo sapiens OX=9606 GN=DYNLL1 PE=1 SV=1	0.828615	4.81E-04
P18887	XRCC1_HUMAN	DNA repair protein XRCC1 OS=Homo sapiens OX=9606 GN=XRCC1 PE=1 SV=2	0.696405	4.81E-04
P82663	RT25_HUMAN	28S ribosomal protein S25 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS25 PE=1 SV=1	0.956279	4.81E-04
Q15018	ABRX2_HUMAN	BRISC complex subunit Abraxas 2 OS=Homo sapiens OX=9606 GN=ABRAXAS2 PE=1 SV=2	0.825691	4.81E-04
Q9BX55	AP1M1_HUMAN	AP-1 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP1M1 PE=1 SV=3	0.775456	4.81E-04
Q8NBF2	NHL2_HUMAN	NHL repeat-containing protein 2 OS=Homo sapiens OX=9606 GN=NHLRC2 PE=1 SV=1	0.827421	4.81E-04
Q6PD74	AAGAB_HUMAN	Alpha- and gamma-adaptin-binding protein p34 OS=Homo sapiens OX=9606 GN=AAGAB PE=1 SV=1	0.9262	4.92E-04
Q15165	PON2_HUMAN	Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=4	0.825769	4.92E-04
P51003	PAPOA_HUMAN	Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOLA PE=1 SV=4	0.952535	4.92E-04
Q12797	ASPH_HUMAN	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3	0.822002	4.92E-04
Q9UNQ2	DIM1_HUMAN	Probable dimethyladenosine transferase OS=Homo sapiens OX=9606 GN=DIMT1 PE=1 SV=1	0.82369	4.92E-04

O75152	ZC11A_HUMAN	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens OX=9606 GN=ZC3H11A PE=1 SV=3	0.822965	4.92E-04
Q71DI3	H32_HUMAN	Histone H3.2 OS=Homo sapiens OX=9606 GN=HIST2H3A PE=1 SV=3	0.823367	4.94E-04
P09758	TACD2_HUMAN	Tumor-associated calcium signal transducer 2 OS=Homo sapiens OX=9606 GN=TACSTD2 PE=1 SV=3	0.78958	5.00E-04
Q5TDH0	DDI2_HUMAN	Protein DDI1 homolog 2 OS=Homo sapiens OX=9606 GN=DDI2 PE=1 SV=1	0.820599	5.00E-04
Q9NUQ3	TXLNG_HUMAN	Gamma-taxilin OS=Homo sapiens OX=9606 GN=TXLNG PE=1 SV=2	0.821935	5.05E-04
Q96CS3	FAF2_HUMAN	FAS-associated factor 2 OS=Homo sapiens OX=9606 GN=FAF2 PE=1 SV=2	0.722846	5.11E-04
Q9UIQ6	LCAP_HUMAN	Leucyl-cystinyl aminopeptidase OS=Homo sapiens OX=9606 GN=LNPEP PE=1 SV=3	0.746325	5.11E-04
P28331	NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS1 PE=1 SV=3	0.60139	5.11E-04
P18074	ERCC2_HUMAN	General transcription and DNA repair factor IIH helicase subunit XPD OS=Homo sapiens OX=9606 GN=ERCC2 PE=1 SV=1	0.887466	5.11E-04
Q92922	SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens OX=9606 GN=SMARCC1 PE=1 SV=3	0.820665	5.11E-04
Q6P9B6	MEAK7_HUMAN	MTOR-associated protein MEAK7 OS=Homo sapiens OX=9606 GN=MEAK7 PE=1 SV=2	0.81921	5.20E-04
Q9NRL3	STRN4_HUMAN	Striatin-4 OS=Homo sapiens OX=9606 GN=STRN4 PE=1 SV=2	0.809036	5.22E-04
P20340	RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A PE=1 SV=3	0.817522	5.26E-04
P46063	RECQ1_HUMAN	ATP-dependent DNA helicase Q1 OS=Homo sapiens OX=9606 GN=RECQL PE=1 SV=3	0.728262	5.26E-04
P49407	ARRB1_HUMAN	Beta-arrestin-1 OS=Homo sapiens OX=9606 GN=ARRB1 PE=1 SV=2	0.814212	5.27E-04
O95865	DDAH2_HUMAN	N(G) N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=1	0.809333	5.30E-04
O60271	JIP4_HUMAN	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens OX=9606 GN=SPAG9 PE=1 SV=4	0.890052	5.33E-04
O95155	UBE4B_HUMAN	Ubiquitin conjugation factor E4 B OS=Homo sapiens OX=9606 GN=UBE4B PE=1 SV=1	0.857488	5.43E-04
Q13637	RAB32_HUMAN	Ras-related protein Rab-32 OS=Homo sapiens OX=9606 GN=RAB32 PE=1 SV=3	0.815743	5.46E-04
Q8N0X7	SPART_HUMAN	Spartin OS=Homo sapiens OX=9606 GN=SPART PE=1 SV=1	0.819975	5.60E-04
Q9H074	PAIP1_HUMAN	Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens OX=9606 GN=PAIP1 PE=1 SV=1	0.805678	5.73E-04
Q8N8S7	ENAH_HUMAN	Protein enabled homolog OS=Homo sapiens OX=9606 GN=ENAH PE=1 SV=2	0.812604	5.74E-04
Q99543	DNJC2_HUMAN	DnaJ homolog subfamily C member 2 OS=Homo sapiens OX=9606 GN=DNAJC2 PE=1 SV=4	0.811954	5.77E-04
P63220	RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens OX=9606 GN=RPS21 PE=1 SV=1	0.766486	5.80E-04
P13073	COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1 mitochondrial OS=Homo sapiens OX=9606 GN=COX41 PE=1 SV=1	0.811097	5.80E-04
Q13257	MD2L1_HUMAN	Mitotic spindle assembly checkpoint protein MAD2A OS=Homo sapiens OX=9606 GN=MAD2L1 PE=1 SV=1	0.812343	5.80E-04
P04818	TYSY_HUMAN	Thymidylate synthase OS=Homo sapiens OX=9606 GN=TYMS PE=1 SV=3	0.814389	5.80E-04
Q86VS8	HOOK3_HUMAN	Protein Hook homolog 3 OS=Homo sapiens OX=9606 GN=HOOK3 PE=1 SV=2	0.811607	5.82E-04
Q13641	TPBG_HUMAN	Trophoblast glycoprotein OS=Homo sapiens OX=9606 GN=TPBG PE=1 SV=1	0.811874	5.82E-04
Q9Y224	RTRAF_HUMAN	RNA transcription translation and transport factor protein OS=Homo sapiens OX=9606 GN=RTRAF PE=1 SV=1	0.703363	5.86E-04
O94855	SC24D_HUMAN	Protein transport protein Sec24D OS=Homo sapiens OX=9606 GN=SEC24D PE=1 SV=2	0.812098	5.86E-04
P84085	ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=2	0.809711	5.86E-04
Q14738	2A5D_HUMAN	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens OX=9606 GN=PPP2R5D PE=1 SV=1	0.753383	5.86E-04
Q00169	PIPNA_HUMAN	Phosphatidylinositol transfer protein alpha isoform OS=Homo sapiens OX=9606 GN=PIPNA PE=1 SV=2	0.808112	6.15E-04
Q9NYH9	UTP6_HUMAN	U3 small nucleolar RNA-associated protein 6 homolog OS=Homo sapiens OX=9606 GN=UTP6 PE=2 SV=2	0.807582	6.18E-04
Q9H488	OFUT1_HUMAN	GDP-fucose protein O-fucosyltransferase 1 OS=Homo sapiens OX=9606 GN=POFUT1 PE=1 SV=1	0.734584	6.22E-04
P23246	SFPQ_HUMAN	Splicing factor proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2	0.814519	6.26E-04

Q96ST2	IWS1_HUMAN	Protein IWS1 homolog OS=Homo sapiens OX=9606 GN=IWS1 PE=1 SV=2	0.805305	6.26E-04
Q92917	GPLOW_HUMAN	G-patch domain and KOW motifs-containing protein OS=Homo sapiens OX=9606 GN=GPLOW PE=1 SV=2	0.747546	6.34E-04
Q9UNW1	MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens OX=9606 GN=MINP1 PE=1 SV=1	0.804909	6.34E-04
O00204	ST2B1_HUMAN	Sulfotransferase 2B1 OS=Homo sapiens OX=9606 GN=SULT2B1 PE=1 SV=2	0.804696	6.34E-04
P27694	RFA1_HUMAN	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2	0.711948	6.34E-04
O43739	CYH3_HUMAN	Cytohesin-3 OS=Homo sapiens OX=9606 GN=CYTH3 PE=1 SV=2	0.805809	6.34E-04
Q99418	CYH2_HUMAN	Cytohesin-2 OS=Homo sapiens OX=9606 GN=CYTH2 PE=1 SV=2	0.805809	6.34E-04
Q7Z2W9	RM21_HUMAN	39S ribosomal protein L21 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL21 PE=1 SV=2	0.80514	6.37E-04
P32320	CDD_HUMAN	Cytidine deaminase OS=Homo sapiens OX=9606 GN=CDA PE=1 SV=2	0.802875	6.40E-04
Q7Z3K3	POGZ_HUMAN	Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=2	0.728615	6.56E-04
Q96A33	CCD47_HUMAN	Coiled-coil domain-containing protein 47 OS=Homo sapiens OX=9606 GN=CCDC47 PE=1 SV=1	0.779212	6.62E-04
Q08380	LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1	0.767841	6.62E-04
Q8N3F8	MILK1_HUMAN	MICAL-like protein 1 OS=Homo sapiens OX=9606 GN=MICALL1 PE=1 SV=2	0.801226	6.62E-04
Q7Z417	NUFP2_HUMAN	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens OX=9606 GN=NUFIP2 PE=1 SV=1	0.621368	6.64E-04
Q9H4A6	GOLP3_HUMAN	Golgi phosphoprotein 3 OS=Homo sapiens OX=9606 GN=GOLPH3 PE=1 SV=1	0.799027	6.64E-04
Q86W42	THOC6_HUMAN	THO complex subunit 6 homolog OS=Homo sapiens OX=9606 GN=THOC6 PE=1 SV=1	0.733164	6.66E-04
Q9NS86	LANC2_HUMAN	LanC-like protein 2 OS=Homo sapiens OX=9606 GN=LANCL2 PE=1 SV=1	0.801119	6.75E-04
Q9BUL8	PDC10_HUMAN	Programmed cell death protein 10 OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1	0.713318	6.88E-04
Q9UHR4	BI2L1_HUMAN	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Homo sapiens OX=9606 GN=BAIAP2L1 PE=1 SV=2	0.799667	7.04E-04
P48163	MAOX_HUMAN	NADP-dependent malic enzyme OS=Homo sapiens OX=9606 GN=ME1 PE=1 SV=1	0.799341	7.10E-04
Q5T6V5	QSPP_HUMAN	Queuosine salvage protein OS=Homo sapiens OX=9606 GN=C9orf64 PE=1 SV=1	0.859407	7.17E-04
P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=3	0.647157	7.17E-04
O00468	AGRIN_HUMAN	Agrin OS=Homo sapiens OX=9606 GN=AGRN PE=1 SV=6	0.774708	7.26E-04
P52292	IMA1_HUMAN	Importin subunit alpha-1 OS=Homo sapiens OX=9606 GN=KPNA2 PE=1 SV=1	0.643633	7.26E-04
Q9Y508	RN114_HUMAN	E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens OX=9606 GN=RNF114 PE=1 SV=1	0.79362	7.32E-04
Q92665	RT31_HUMAN	28S ribosomal protein S31 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS31 PE=1 SV=3	0.795022	7.35E-04
Q5BKZ1	ZN326_HUMAN	DBIRD complex subunit ZNF326 OS=Homo sapiens OX=9606 GN=ZNF326 PE=1 SV=2	0.773059	7.42E-04
Q8N766	EMC1_HUMAN	ER membrane protein complex subunit 1 OS=Homo sapiens OX=9606 GN=EMC1 PE=1 SV=1	0.678771	7.42E-04
Q9BY77	PDIP3_HUMAN	Polymerase delta-interacting protein 3 OS=Homo sapiens OX=9606 GN=POLDIP3 PE=1 SV=2	0.793676	7.62E-04
Q9BYD6	RM01_HUMAN	39S ribosomal protein L1 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL1 PE=1 SV=2	0.791601	7.76E-04
Q16186	ADRM1_HUMAN	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens OX=9606 GN=ADRM1 PE=1 SV=2	0.794522	7.76E-04
Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1 PE=1 SV=2	0.738642	7.76E-04
Q5W0V3	F16B1_HUMAN	Protein FAM160B1 OS=Homo sapiens OX=9606 GN=FAM160B1 PE=1 SV=1	0.794047	7.76E-04
P49642	PRI1_HUMAN	DNA primase small subunit OS=Homo sapiens OX=9606 GN=PRIM1 PE=1 SV=1	0.790015	7.82E-04
Q96T37	RBM15_HUMAN	RNA-binding protein 15 OS=Homo sapiens OX=9606 GN=RBM15 PE=1 SV=2	0.813392	7.87E-04
Q8N392	RHG18_HUMAN	Rho GTPase-activating protein 18 OS=Homo sapiens OX=9606 GN=ARHGAP18 PE=1 SV=3	0.789321	7.92E-04
P00491	PNPH_HUMAN	Purine nucleoside phosphorylase OS=Homo sapiens OX=9606 GN=PNP PE=1 SV=2	0.822523	7.96E-04
Q99567	NUP88_HUMAN	Nuclear pore complex protein Nup88 OS=Homo sapiens OX=9606 GN=NUP88 PE=1 SV=2	0.744219	7.96E-04

Q13561	DCTN2_HUMAN	Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=4	0.81031	7.96E-04
Q9Y5L0	TNPO3_HUMAN	Transportin-3 OS=Homo sapiens OX=9606 GN=TNPO3 PE=1 SV=3	0.76056	7.96E-04
Q9BTE7	DCN15_HUMAN	DCN1-like protein 5 OS=Homo sapiens OX=9606 GN=DCUN1D5 PE=1 SV=1	0.748636	7.96E-04
Q9NR45	SIAS_HUMAN	Sialic acid synthase OS=Homo sapiens OX=9606 GN=NANS PE=1 SV=2	0.735829	7.96E-04
Q9BYG3	MK67I_HUMAN	MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens OX=9606 GN=NIFK PE=1 SV=1	0.790847	7.96E-04
Q9UN86	G3BP2_HUMAN	Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens OX=9606 GN=G3BP2 PE=1 SV=2	0.788496	8.01E-04
Q9BT09	CNPY3_HUMAN	Protein canopy homolog 3 OS=Homo sapiens OX=9606 GN=CNPY3 PE=1 SV=1	0.791413	8.01E-04
P16278	BGAL_HUMAN	Beta-galactosidase OS=Homo sapiens OX=9606 GN=GLB1 PE=1 SV=2	0.787578	8.01E-04
P51570	GALK1_HUMAN	Galactokinase OS=Homo sapiens OX=9606 GN=GALK1 PE=1 SV=1	0.696666	8.01E-04
Q9Y4X5	ARI1_HUMAN	E3 ubiquitin-protein ligase ARIH1 OS=Homo sapiens OX=9606 GN=ARIH1 PE=1 SV=2	0.788661	8.01E-04
Q99614	TTC1_HUMAN	Tetratricopeptide repeat protein 1 OS=Homo sapiens OX=9606 GN=TTC1 PE=1 SV=1	0.707819	8.07E-04
P29353	SHC1_HUMAN	SHC-transforming protein 1 OS=Homo sapiens OX=9606 GN=SHC1 PE=1 SV=4	0.746218	8.07E-04
Q6UX04	CWC27_HUMAN	Spliceosome-associated protein CWC27 homolog OS=Homo sapiens OX=9606 GN=CWC27 PE=1 SV=1	0.788744	8.10E-04
Q96HY6	DDRKG_HUMAN	DDRKG domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DDRKG1 PE=1 SV=2	0.729392	8.18E-04
Q9GZM5	YIPF3_HUMAN	Protein YIPF3 OS=Homo sapiens OX=9606 GN=YIPF3 PE=1 SV=1	1.143386	8.20E-04
P51116	FXR2_HUMAN	Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens OX=9606 GN=FXR2 PE=1 SV=2	0.821222	8.20E-04
Q9NQR4	NIT2_HUMAN	Omega-amidase NIT2 OS=Homo sapiens OX=9606 GN=NIT2 PE=1 SV=1	0.623242	8.24E-04
Q8N6T3	ARFG1_HUMAN	ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=ARFGAP1 PE=1 SV=2	0.699069	8.27E-04
O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=IDH3B PE=1 SV=2	0.754959	8.46E-04
O00762	UBE2C_HUMAN	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens OX=9606 GN=UBE2C PE=1 SV=1	0.782575	8.57E-04
O75396	SEC22B_HUMAN	Vesicle-trafficking protein SEC22b OS=Homo sapiens OX=9606 GN=SEC22B PE=1 SV=4	0.758792	8.61E-04
P50402	EMD_HUMAN	Emerin OS=Homo sapiens OX=9606 GN=EMD PE=1 SV=1	0.753412	8.62E-04
Q9UNF1	MAGD2_HUMAN	Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGED2 PE=1 SV=2	0.78073	8.62E-04
P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens OX=9606 GN=NME2 PE=1 SV=1	0.832492	8.62E-04
O43681	ASNA_HUMAN	ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2	0.782591	8.67E-04
P20618	PSB1_HUMAN	Proteasome subunit beta type-1 OS=Homo sapiens OX=9606 GN=PSMB1 PE=1 SV=2	0.764351	8.79E-04
P42566	EPS15_HUMAN	Epidermal growth factor receptor substrate 15 OS=Homo sapiens OX=9606 GN=EPS15 PE=1 SV=2	0.703404	8.84E-04
Q16787	LAMA3_HUMAN	Laminin subunit alpha-3 OS=Homo sapiens OX=9606 GN=LAMA3 PE=1 SV=2	0.819187	8.92E-04
Q9H078	CLPB_HUMAN	Caseinolytic peptidase B protein homolog OS=Homo sapiens OX=9606 GN=CLPB PE=1 SV=1	0.716342	8.93E-04
Q92520	FAM3C_HUMAN	Protein FAM3C OS=Homo sapiens OX=9606 GN=FAM3C PE=1 SV=1	0.780417	8.93E-04
O75347	TBCA_HUMAN	Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=3	0.778888	9.02E-04
Q15750	TAB1_HUMAN	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens OX=9606 GN=TAB1 PE=1 SV=1	0.778234	9.02E-04
P60660	MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=2	0.759372	9.02E-04
Q9UPT5	EXOC7_HUMAN	Exocyst complex component 7 OS=Homo sapiens OX=9606 GN=EXOC7 PE=1 SV=3	0.782028	9.02E-04
Q9GZZ9	UBA5_HUMAN	Ubiquitin-like modifier-activating enzyme 5 OS=Homo sapiens OX=9606 GN=UBA5 PE=1 SV=1	0.78313	9.02E-04
P62330	ARF6_HUMAN	ADP-ribosylation factor 6 OS=Homo sapiens OX=9606 GN=ARF6 PE=1 SV=2	0.756915	9.08E-04
Q9UL15	BAG5_HUMAN	BAG family molecular chaperone regulator 5 OS=Homo sapiens OX=9606 GN=BAG5 PE=1 SV=1	0.922554	9.22E-04
Q9NYY8	FAKD2_HUMAN	FAST kinase domain-containing protein 2 mitochondrial OS=Homo sapiens OX=9606 GN=FASTKD2 PE=1 SV=1	0.776914	9.22E-04

Q9NYL9	TMOD3_HUMAN	Tropomodulin-3 OS=Homo sapiens OX=9606 GN=TMOD3 PE=1 SV=1	0.753584	9.25E-04
Q96KN1	LRAT2_HUMAN	Protein LRATD2 OS=Homo sapiens OX=9606 GN=LRATD2 PE=1 SV=1	0.775597	9.28E-04
O95232	LC7L3_HUMAN	Luc7-like protein 3 OS=Homo sapiens OX=9606 GN=LUC7L3 PE=1 SV=2	0.754034	9.28E-04
Q14137	BOP1_HUMAN	Ribosome biogenesis protein BOP1 OS=Homo sapiens OX=9606 GN=BOP1 PE=1 SV=2	0.768577	9.28E-04
P33176	KINH_HUMAN	Kinesin-1 heavy chain OS=Homo sapiens OX=9606 GN=KIF5B PE=1 SV=1	0.652401	9.30E-04
O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1	0.649873	9.39E-04
P06748	NPM_HUMAN	Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=2	0.664133	9.45E-04
O94874	UFL1_HUMAN	E3 UFM1-protein ligase 1 OS=Homo sapiens OX=9606 GN=UFL1 PE=1 SV=2	0.643689	9.50E-04
P05091	ALDH2_HUMAN	Aldehyde dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 PE=1 SV=2	0.774399	9.50E-04
P02649	APOE_HUMAN	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1	0.751028	9.50E-04
P60033	CD81_HUMAN	CD81 antigen OS=Homo sapiens OX=9606 GN=CD81 PE=1 SV=1	0.775068	9.50E-04
Q9Y3D6	FIS1_HUMAN	Mitochondrial fission 1 protein OS=Homo sapiens OX=9606 GN=FIS1 PE=1 SV=2	0.773708	9.50E-04
P34896	GLYC_HUMAN	Serine hydroxymethyltransferase cytosolic OS=Homo sapiens OX=9606 GN=SHMT1 PE=1 SV=1	0.674456	9.52E-04
O43251	RFOX2_HUMAN	RNA binding protein fox-1 homolog 2 OS=Homo sapiens OX=9606 GN=RBFox2 PE=1 SV=3	0.771146	9.76E-04
Q99447	PCYT2_HUMAN	Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens OX=9606 GN=PCYT2 PE=1 SV=1	0.770646	9.76E-04
P51784	UBP11_HUMAN	Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens OX=9606 GN=USP11 PE=1 SV=3	0.770177	9.85E-04
P07942	LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens OX=9606 GN=LAMB1 PE=1 SV=2	0.700215	9.87E-04
Q13190	STX5_HUMAN	Syntaxin-5 OS=Homo sapiens OX=9606 GN=STX5 PE=1 SV=2	0.769387	0.001009
Q16342	PDCD2_HUMAN	Programmed cell death protein 2 OS=Homo sapiens OX=9606 GN=PDCD2 PE=1 SV=2	0.907985	0.001028
O75175	CNOT3_HUMAN	CCR4-NOT transcription complex subunit 3 OS=Homo sapiens OX=9606 GN=CNOT3 PE=1 SV=1	0.768297	0.001028
P51151	RAB9A_HUMAN	Ras-related protein Rab-9A OS=Homo sapiens OX=9606 GN=RAB9A PE=1 SV=1	0.76753	0.001046
P48444	COPD_HUMAN	Coatamer subunit delta OS=Homo sapiens OX=9606 GN=ARCN1 PE=1 SV=1	0.871563	0.001046
Q6ZS17	RIPR1_HUMAN	Rho family-interacting cell polarization regulator 1 OS=Homo sapiens OX=9606 GN=RIPOR1 PE=1 SV=1	1.33044	0.001056
O94901	SUN1_HUMAN	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=3	0.764912	0.001065
Q9UBB4	ATX10_HUMAN	Ataxin-10 OS=Homo sapiens OX=9606 GN=ATXN10 PE=1 SV=1	0.842675	0.001065
Q9UK41	VPS28_HUMAN	Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens OX=9606 GN=VPS28 PE=1 SV=1	0.782128	0.001065
O15258	RER1_HUMAN	Protein RER1 OS=Homo sapiens OX=9606 GN=RER1 PE=1 SV=1	0.763024	0.00108
Q92890	UFD1_HUMAN	Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Homo sapiens OX=9606 GN=UFD1 PE=1 SV=3	0.754743	0.001084
P31937	3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=HIBADH PE=1 SV=2	0.759495	0.001089
Q10713	MPPA_HUMAN	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens OX=9606 GN=PMPCA PE=1 SV=2	0.762335	0.001089
Q9Y3B4	SF3B6_HUMAN	Splicing factor 3B subunit 6 OS=Homo sapiens OX=9606 GN=SF3B6 PE=1 SV=1	0.763419	0.001096
O00743	PPP6_HUMAN	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens OX=9606 GN=PPP6C PE=1 SV=1	0.703335	0.001099
O75431	MTX2_HUMAN	Metaxin-2 OS=Homo sapiens OX=9606 GN=MTX2 PE=1 SV=1	0.766778	0.001104
P80404	GABT_HUMAN	4-aminobutyrate aminotransferase mitochondrial OS=Homo sapiens OX=9606 GN=ABAT PE=1 SV=3	0.764309	0.001106
P20810	ICAL_HUMAN	Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=4	0.632332	0.001106
O14562	UBFD1_HUMAN	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens OX=9606 GN=UBFD1 PE=1 SV=2	0.761213	0.001111
O75223	GGCT_HUMAN	Gamma-glutamylcyclotransferase OS=Homo sapiens OX=9606 GN=GGCT PE=1 SV=1	0.762127	0.001134
P61964	WDR5_HUMAN	WD repeat-containing protein 5 OS=Homo sapiens OX=9606 GN=WDR5 PE=1 SV=1	0.764057	0.001136
Q15785	TOM34_HUMAN	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens OX=9606 GN=TOMM34 PE=1 SV=2	0.746271	0.001146

P61981	1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2	0.774624	0.001146
Q8NBJ7	SUMF2_HUMAN	Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=2	0.763782	0.001146
P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 PE=1 SV=1	0.658893	0.001146
Q08378	GOGA3_HUMAN	Golgin subfamily A member 3 OS=Homo sapiens OX=9606 GN=GOLGA3 PE=1 SV=2	0.76114	0.001146
Q99436	PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens OX=9606 GN=PSMB7 PE=1 SV=1	0.759791	0.001173
Q02790	FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens OX=9606 GN=FKBP4 PE=1 SV=3	0.805797	0.001173
Q9Y450	HBS1L_HUMAN	HBS1-like protein OS=Homo sapiens OX=9606 GN=HBS1L PE=1 SV=1	0.756534	0.001206
P07602	SAP_HUMAN	Prosaposin OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=2	0.758002	0.001206
Q15738	NSDHL_HUMAN	Sterol-4-alpha-carboxylate 3-dehydrogenase decarboxylating OS=Homo sapiens OX=9606 GN=NSDHL PE=1 SV=2	0.790182	0.001206
P22061	PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=4	0.73823	0.001206
Q86SF2	GALT7_HUMAN	N-acetylgalactosaminyltransferase 7 OS=Homo sapiens OX=9606 GN=GALNT7 PE=1 SV=1	0.784871	0.001219
O75915	PRAF3_HUMAN	PRA1 family protein 3 OS=Homo sapiens OX=9606 GN=ARL6IP5 PE=1 SV=1	0.756992	0.001219
Q13895	BYST_HUMAN	Bystin OS=Homo sapiens OX=9606 GN=BYSL PE=1 SV=3	0.758631	0.001222
O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens OX=9606 GN=CLIC1 PE=1 SV=4	0.672293	0.001225
O75663	TIPRL_HUMAN	TIP41-like protein OS=Homo sapiens OX=9606 GN=TIPRL PE=1 SV=2	0.755196	0.001265
P23434	GCSH_HUMAN	Glycine cleavage system H protein mitochondrial OS=Homo sapiens OX=9606 GN=GCSH PE=1 SV=2	0.753961	0.001268
O15212	PFD6_HUMAN	Prefoldin subunit 6 OS=Homo sapiens OX=9606 GN=PFDN6 PE=1 SV=1	0.682398	0.001271
Q13685	AAMP_HUMAN	Angio-associated migratory cell protein OS=Homo sapiens OX=9606 GN=AAMP PE=1 SV=2	0.755378	0.001271
P63241	IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=2	1.380749	0.001271
O43488	ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens OX=9606 GN=AKR7A2 PE=1 SV=3	0.882229	0.001271
O43719	HTSF1_HUMAN	HIV Tat-specific factor 1 OS=Homo sapiens OX=9606 GN=HTATSF1 PE=1 SV=1	0.834445	0.001286
Q05086	UBE3A_HUMAN	Ubiquitin-protein ligase E3A OS=Homo sapiens OX=9606 GN=UBE3A PE=1 SV=4	0.752809	0.001286
Q9GZL7	WDR12_HUMAN	Ribosome biogenesis protein WDR12 OS=Homo sapiens OX=9606 GN=WDR12 PE=1 SV=2	0.753939	0.001286
Q9UNE7	CHIP_HUMAN	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens OX=9606 GN=STUB1 PE=1 SV=2	0.751502	0.001286
Q9BXK5	B2L13_HUMAN	Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1	0.729216	0.001286
Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens OX=9606 GN=SH3BGL3 PE=1 SV=1	0.743241	0.001286
Q5TFE4	NT5D1_HUMAN	5'-nucleotidase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NT5DC1 PE=1 SV=1	0.669146	0.001286
Q32MZ4	LRRF1_HUMAN	Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens OX=9606 GN=LRRFIP1 PE=1 SV=2	0.813923	0.001301
Q09028	RBBP4_HUMAN	Histone-binding protein RBBP4 OS=Homo sapiens OX=9606 GN=RBBP4 PE=1 SV=3	0.742275	0.001304
Q8IYI6	EXOC8_HUMAN	Exocyst complex component 8 OS=Homo sapiens OX=9606 GN=EXOC8 PE=1 SV=2	0.751567	0.001313
Q14974	IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=2	0.608128	0.001313
P53041	PPP5_HUMAN	Serine/threonine-protein phosphatase 5 OS=Homo sapiens OX=9606 GN=PPP5C PE=1 SV=1	0.720398	0.001319
O95274	LYPD3_HUMAN	Ly6/PLAUR domain-containing protein 3 OS=Homo sapiens OX=9606 GN=LYPD3 PE=1 SV=2	0.752143	0.001319
Q9NX58	LYAR_HUMAN	Cell growth-regulating nucleolar protein OS=Homo sapiens OX=9606 GN=LYAR PE=1 SV=2	0.755554	0.001319
Q8TF05	PP4R1_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP4R1 PE=1 SV=1	0.915369	0.00132
P15374	UCHL3_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens OX=9606 GN=UCHL3 PE=1 SV=1	0.625835	0.001323
Q9BRJ2	RM45_HUMAN	39S ribosomal protein L45 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL45 PE=1 SV=2	0.750679	0.001323

Q8WZ82	OVCA2_HUMAN	Esterase OVCA2 OS=Homo sapiens OX=9606 GN=OVCA2 PE=1 SV=1	0.748534	0.00136
P20290	BTF3_HUMAN	Transcription factor BTF3 OS=Homo sapiens OX=9606 GN=BTF3 PE=1 SV=1	0.762108	0.001373
O15230	LAMA5_HUMAN	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	0.747465	0.001376
Q96AT9	RPE_HUMAN	Ribulose-phosphate 3-epimerase OS=Homo sapiens OX=9606 GN=RPE PE=1 SV=1	0.745487	0.001376
P25789	PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1	0.742464	0.001383
P55210	CASP7_HUMAN	Caspase-7 OS=Homo sapiens OX=9606 GN=CASP7 PE=1 SV=1	0.746714	0.001386
Q9Y3A5	SBDS_HUMAN	Ribosome maturation protein SBDS OS=Homo sapiens OX=9606 GN=SBDS PE=1 SV=4	0.745844	0.001386
Q8WUH6	TM263_HUMAN	Transmembrane protein 263 OS=Homo sapiens OX=9606 GN=TMEM263 PE=1 SV=1	1.319659	0.00139
Q14790	CASP8_HUMAN	Caspase-8 OS=Homo sapiens OX=9606 GN=CASP8 PE=1 SV=1	0.746646	0.001403
P53367	ARFP1_HUMAN	Arfaptin-1 OS=Homo sapiens OX=9606 GN=ARFIP1 PE=1 SV=2	0.67653	0.001409
Q9UKF6	CPSF3_HUMAN	Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens OX=9606 GN=CPSF3 PE=1 SV=1	0.743568	0.001433
O60256	KPRB_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens OX=9606 GN=PRPSAP2 PE=1 SV=1	0.745357	0.001433
Q8TCA0	LRC20_HUMAN	Leucine-rich repeat-containing protein 20 OS=Homo sapiens OX=9606 GN=LRRC20 PE=1 SV=1	0.979845	0.00144
Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a OS=Homo sapiens OX=9606 GN=SAR1A PE=1 SV=1	0.740376	0.001446
Q16222	UAP1_HUMAN	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens OX=9606 GN=UAP1 PE=1 SV=3	0.790849	0.001454
Q13217	DNJC3_HUMAN	DnaJ homolog subfamily C member 3 OS=Homo sapiens OX=9606 GN=DNAJC3 PE=1 SV=1	0.717381	0.001454
Q15075	EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens OX=9606 GN=EEA1 PE=1 SV=2	0.668241	0.001454
Q9H3R5	CENPH_HUMAN	Centromere protein H OS=Homo sapiens OX=9606 GN=CENPH PE=1 SV=1	0.743225	0.001454
P67870	CSK2B_HUMAN	Casein kinase II subunit beta OS=Homo sapiens OX=9606 GN=CSNK2B PE=1 SV=1	0.768245	0.001454
O14908	GIPC1_HUMAN	PDZ domain-containing protein GIPC1 OS=Homo sapiens OX=9606 GN=GIPC1 PE=1 SV=2	0.891209	0.001461
Q6NZ67	MZT2B_HUMAN	Mitotic-spindle organizing protein 2B OS=Homo sapiens OX=9606 GN=MZT2B PE=1 SV=1	0.742759	0.001463
O95453	PARN_HUMAN	Poly(A)-specific ribonuclease PARN OS=Homo sapiens OX=9606 GN=PARN PE=1 SV=1	0.741674	0.001463
Q15646	OASL_HUMAN	2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens OX=9606 GN=OASL PE=1 SV=2	0.743375	0.001463
P54136	SYRC_HUMAN	Arginine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=RARS1 PE=1 SV=2	0.662071	0.001463
Q9NQG5	RPR1B_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens OX=9606 GN=RPRD1B PE=1 SV=1	0.731922	0.001463
P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4	0.703799	0.001463
P19387	RPB3_HUMAN	DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens OX=9606 GN=POLR2C PE=1 SV=2	0.742568	0.001464
Q6YHK3	CD109_HUMAN	CD109 antigen OS=Homo sapiens OX=9606 GN=CD109 PE=1 SV=2	0.670432	0.001467
P35580	MYH10_HUMAN	Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3	0.606554	0.001478
O94804	STK10_HUMAN	Serine/threonine-protein kinase 10 OS=Homo sapiens OX=9606 GN=STK10 PE=1 SV=1	0.740149	0.001478
O95340	PAPS2_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens OX=9606 GN=PAPSS2 PE=1 SV=2	0.741062	0.001478
Q15050	RRS1_HUMAN	Ribosome biogenesis regulatory protein homolog OS=Homo sapiens OX=9606 GN=RRS1 PE=1 SV=2	0.758568	0.001486
Q8IWS0	PHF6_HUMAN	PHD finger protein 6 OS=Homo sapiens OX=9606 GN=PHF6 PE=1 SV=1	0.739764	0.001489
Q9BWU0	NADAP_HUMAN	Kanadaplin OS=Homo sapiens OX=9606 GN=SLC4A1AP PE=1 SV=1	0.67978	0.001494
Q8WWC4	MAIP1_HUMAN	m-AAA protease-interacting protein 1 mitochondrial OS=Homo sapiens OX=9606 GN=MAIP1 PE=1 SV=1	0.738255	0.001494
Q99961	SH3G1_HUMAN	Endophilin-A2 OS=Homo sapiens OX=9606 GN=SH3GL1 PE=1 SV=1	0.853689	0.001497
Q9NZL4	HPBP1_HUMAN	Hsp70-binding protein 1 OS=Homo sapiens OX=9606 GN=HSPBP1 PE=1 SV=2	0.715778	0.001505
Q7Z2K6	ERMP1_HUMAN	Endoplasmic reticulum metalloproteinase 1 OS=Homo sapiens OX=9606 GN=ERMP1 PE=1 SV=2	0.758596	0.001537

Q969G3	SMCE1_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=2	0.620152	0.001566
Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 PE=1 SV=2	0.726982	0.001567
P49589	SYCC_HUMAN	Cysteine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=CARS1 PE=1 SV=3	0.736153	0.001592
P24941	CDK2_HUMAN	Cyclin-dependent kinase 2 OS=Homo sapiens OX=9606 GN=CDK2 PE=1 SV=2	0.721449	0.0016
P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 PE=1 SV=2	0.734072	0.001601
P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4	0.723136	0.001601
P42167	LAP2B_HUMAN	Lamina-associated polypeptide 2 isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2	0.711408	0.00162
Q9UNH7	SNX6_HUMAN	Sorting nexin-6 OS=Homo sapiens OX=9606 GN=SNX6 PE=1 SV=1	0.782795	0.001651
P31146	COR1A_HUMAN	Coronin-1A OS=Homo sapiens OX=9606 GN=CORO1A PE=1 SV=4	0.733116	0.001671
P11234	RALB_HUMAN	Ras-related protein Ral-B OS=Homo sapiens OX=9606 GN=RALB PE=1 SV=1	0.733906	0.001671
Q724W1	DCXR_HUMAN	L-xylulose reductase OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=2	0.654865	0.001675
P31431	SDC4_HUMAN	Syndecan-4 OS=Homo sapiens OX=9606 GN=SDC4 PE=1 SV=2	0.778623	0.001684
P51648	AL3A2_HUMAN	Aldehyde dehydrogenase family 3 member A2 OS=Homo sapiens OX=9606 GN=ALDH3A2 PE=1 SV=1	0.735511	0.001692
Q07866	KLC1_HUMAN	Kinesin light chain 1 OS=Homo sapiens OX=9606 GN=KLC1 PE=1 SV=2	0.682173	0.001696
Q9NNW7	TRXR2_HUMAN	Thioredoxin reductase 2 mitochondrial OS=Homo sapiens OX=9606 GN=TXNRD2 PE=1 SV=3	0.934663	0.001697
Q92626	PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens OX=9606 GN=PXDN PE=1 SV=2	0.731102	0.001709
P68400	CSK21_HUMAN	Casein kinase II subunit alpha OS=Homo sapiens OX=9606 GN=CSNK2A1 PE=1 SV=1	0.834256	0.001722
O14964	HGS_HUMAN	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens OX=9606 GN=HGS PE=1 SV=1	0.728309	0.00173
O60248	SOX15_HUMAN	Protein SOX-15 OS=Homo sapiens OX=9606 GN=SOX15 PE=1 SV=1	0.832289	0.001743
Q96FV9	THOC1_HUMAN	THO complex subunit 1 OS=Homo sapiens OX=9606 GN=THOC1 PE=1 SV=1	0.730645	0.001756
P56945	BCAR1_HUMAN	Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens OX=9606 GN=BCAR1 PE=1 SV=2	0.75105	0.001756
P54105	ICLN_HUMAN	Methylosome subunit pICln OS=Homo sapiens OX=9606 GN=CLNS1A PE=1 SV=1	0.726239	0.001762
Q9BW27	NUP85_HUMAN	Nuclear pore complex protein Nup85 OS=Homo sapiens OX=9606 GN=NUP85 PE=1 SV=1	0.73163	0.001762
O43396	TXNL1_HUMAN	Thioredoxin-like protein 1 OS=Homo sapiens OX=9606 GN=TXNL1 PE=1 SV=3	0.877143	0.001762
P22087	FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens OX=9606 GN=FBL PE=1 SV=2	0.752997	0.001787
Q9UHD1	CHRD1_HUMAN	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CHORDC1 PE=1 SV=2	0.679355	0.001792
P08621	RU17_HUMAN	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 GN=SNRNP70 PE=1 SV=2	0.634178	0.001793
P09104	ENOG_HUMAN	Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=3	0.71751	0.001798
Q92878	RAD50_HUMAN	DNA repair protein RAD50 OS=Homo sapiens OX=9606 GN=RAD50 PE=1 SV=1	0.652853	0.001803
Q14318	FKBP8_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens OX=9606 GN=FKBP8 PE=1 SV=2	0.725998	0.001803
P11717	MPRI_HUMAN	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=IGF2R PE=1 SV=3	0.707549	0.001808
Q8TDD1	DDX54_HUMAN	ATP-dependent RNA helicase DDX54 OS=Homo sapiens OX=9606 GN=DDX54 PE=1 SV=2	0.727682	0.001813
Q9BRT2	UQCC2_HUMAN	Ubiquinol-cytochrome-c reductase complex assembly factor 2 OS=Homo sapiens OX=9606 GN=UQCC2 PE=1 SV=1	0.725551	0.001831
Q9NQ75	EXOS3_HUMAN	Exosome complex component RRP40 OS=Homo sapiens OX=9606 GN=EXOSC3 PE=1 SV=3	0.725965	0.001831
P56134	ATPK_HUMAN	ATP synthase subunit f mitochondrial OS=Homo sapiens OX=9606 GN=ATP5MF PE=1 SV=3	0.725354	0.00184
Q53GQ0	DHB12_HUMAN	Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens OX=9606 GN=HSD17B12 PE=1 SV=2	0.622066	0.00185
Q02809	PLOD1_HUMAN	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens OX=9606 GN=PLOD1 PE=1 SV=2	0.824377	0.00185
Q13596	SNX1_HUMAN	Sorting nexin-1 OS=Homo sapiens OX=9606 GN=SNX1 PE=1 SV=3	0.650591	0.001856

Q96J01	THOC3_HUMAN	THO complex subunit 3 OS=Homo sapiens OX=9606 GN=THOC3 PE=1 SV=1	0.725606	0.001873
Q15369	ELOC_HUMAN	Elongin-C OS=Homo sapiens OX=9606 GN=ELOC PE=1 SV=1	0.722972	0.001874
P18031	PTN1_HUMAN	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens OX=9606 GN=PTPN1 PE=1 SV=1	0.709826	0.001892
Q96S97	MYADM_HUMAN	Myeloid-associated differentiation marker OS=Homo sapiens OX=9606 GN=MYADM PE=1 SV=2	0.724004	0.001902
O60488	ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens OX=9606 GN=ACSL4 PE=1 SV=2	0.773091	0.00192
Q12805	FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens OX=9606 GN=EFEMP1 PE=1 SV=2	0.723735	0.001921
P23919	KTHY_HUMAN	Thymidylate kinase OS=Homo sapiens OX=9606 GN=DTYMK PE=1 SV=4	0.724271	0.001922
P12694	ODBA_HUMAN	2-oxoisovalerate dehydrogenase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=BCKDHA PE=1 SV=2	0.721829	0.001927
O15160	RPAC1_HUMAN	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens OX=9606 GN=POLR1C PE=1 SV=1	0.670611	0.001933
Q6P161	RM54_HUMAN	39S ribosomal protein L54 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL54 PE=1 SV=1	0.720924	0.001944
P50148	GNAQ_HUMAN	Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo sapiens OX=9606 GN=GNAQ PE=1 SV=4	1.040042	0.001944
P35241	RADI_HUMAN	Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1	0.751484	0.001946
Q9UNS2	CSN3_HUMAN	COP9 signalosome complex subunit 3 OS=Homo sapiens OX=9606 GN=COPS3 PE=1 SV=3	0.6594	0.001946
Q15836	VAMP3_HUMAN	Vesicle-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=VAMP3 PE=1 SV=3	1.035877	0.001983
Q9Y4R8	TELO2_HUMAN	Telomere length regulation protein TEL2 homolog OS=Homo sapiens OX=9606 GN=TELO2 PE=1 SV=2	0.719892	0.002016
Q9NZZ3	CHMP5_HUMAN	Charged multivesicular body protein 5 OS=Homo sapiens OX=9606 GN=CHMP5 PE=1 SV=1	0.719185	0.002037
O14618	CCS_HUMAN	Copper chaperone for superoxide dismutase OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1	0.718506	0.002037
Q92783	STAM1_HUMAN	Signal transducing adapter molecule 1 OS=Homo sapiens OX=9606 GN=STAM PE=1 SV=3	0.717688	0.002048
O60568	PLOD3_HUMAN	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	0.743225	0.002048
Q99816	TS101_HUMAN	Tumor susceptibility gene 101 protein OS=Homo sapiens OX=9606 GN=TS101 PE=1 SV=2	0.717614	0.002049
Q9P2I0	CPSF2_HUMAN	Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens OX=9606 GN=CPSF2 PE=1 SV=2	0.676212	0.002061
O95361	TRI16_HUMAN	Tripartite motif-containing protein 16 OS=Homo sapiens OX=9606 GN=TRIM16 PE=1 SV=3	0.731982	0.002061
P51812	KS6A3_HUMAN	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens OX=9606 GN=RPS6KA3 PE=1 SV=1	0.603459	0.002071
Q9NTZ6	RBM12_HUMAN	RNA-binding protein 12 OS=Homo sapiens OX=9606 GN=RBM12 PE=1 SV=1	0.730279	0.002073
Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=5	0.669921	0.002073
P61764	STXB1_HUMAN	Syntaxin-binding protein 1 OS=Homo sapiens OX=9606 GN=STXBP1 PE=1 SV=1	0.716581	0.002075
Q9Y2R9	RT07_HUMAN	28S ribosomal protein S7 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS7 PE=1 SV=2	0.716141	0.002078
P35611	ADDA_HUMAN	Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=2	0.719478	0.002078
O15427	MOT4_HUMAN	Monocarboxylate transporter 4 OS=Homo sapiens OX=9606 GN=SLC16A3 PE=1 SV=1	1.172481	0.002078
P14735	IDE_HUMAN	Insulin-degrading enzyme OS=Homo sapiens OX=9606 GN=IDE PE=1 SV=4	0.778676	0.002088
Q9UNL2	SSRG_HUMAN	Translocon-associated protein subunit gamma OS=Homo sapiens OX=9606 GN=SSR3 PE=1 SV=1	0.717979	0.002105
Q9Y376	CAB39_HUMAN	Calcium-binding protein 39 OS=Homo sapiens OX=9606 GN=CAB39 PE=1 SV=1	0.856636	0.002105
Q9H0B6	KLC2_HUMAN	Kinesin light chain 2 OS=Homo sapiens OX=9606 GN=KLC2 PE=1 SV=1	0.713339	0.002106
P39748	FEN1_HUMAN	Flap endonuclease 1 OS=Homo sapiens OX=9606 GN=FEN1 PE=1 SV=1	0.709019	0.002112
O75436	VP26A_HUMAN	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens OX=9606 GN=VPS26A PE=1 SV=2	0.758123	0.002118
Q5H9R7	PP6R3_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=2	0.727614	0.002119
Q9Y5Q9	TF3C3_HUMAN	General transcription factor 3C polypeptide 3 OS=Homo sapiens OX=9606 GN=GTF3C3 PE=1 SV=1	0.713696	0.002125

Q8NFZ8	CADM4_HUMAN	Cell adhesion molecule 4 OS=Homo sapiens OX=9606 GN=CADM4 PE=1 SV=1	0.713217	0.002151
P42785	PCP_HUMAN	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1	0.711254	0.002195
P14927	QCR7_HUMAN	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens OX=9606 GN=UQCRB PE=1 SV=2	0.71135	0.002195
Q15813	TBCE_HUMAN	Tubulin-specific chaperone E OS=Homo sapiens OX=9606 GN=TBCE PE=1 SV=1	0.68031	0.002195
Q9UKL0	RCOR1_HUMAN	REST corepressor 1 OS=Homo sapiens OX=9606 GN=RCOR1 PE=1 SV=2	0.711067	0.0022
P04920	B3A2_HUMAN	Anion exchange protein 2 OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=4	0.71522	0.0022
Q9NVD7	PARVA_HUMAN	Alpha-parvin OS=Homo sapiens OX=9606 GN=PARVA PE=1 SV=1	0.710778	0.0022
P22570	ADRO_HUMAN	NADPH:adrenodoxin oxidoreductase mitochondrial OS=Homo sapiens OX=9606 GN=FDXR PE=1 SV=3	0.648528	0.0022
Q6PKG0	LARP1_HUMAN	La-related protein 1 OS=Homo sapiens OX=9606 GN=LARP1 PE=1 SV=2	0.628351	0.002211
Q9BYD3	RM04_HUMAN	39S ribosomal protein L4 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL4 PE=1 SV=1	0.711805	0.002218
Q99598	TSNAX_HUMAN	Translin-associated protein X OS=Homo sapiens OX=9606 GN=TSNAX PE=1 SV=1	0.719202	0.002219
P36915	GNL1_HUMAN	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens OX=9606 GN=GNL1 PE=1 SV=2	0.799758	0.00222
Q13232	NDK3_HUMAN	Nucleoside diphosphate kinase 3 OS=Homo sapiens OX=9606 GN=NME3 PE=1 SV=2	0.710384	0.002221
Q8TEM1	PO210_HUMAN	Nuclear pore membrane glycoprotein 210 OS=Homo sapiens OX=9606 GN=NUP210 PE=1 SV=3	0.674809	0.002223
Q08209	PP2BA_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens OX=9606 GN=PPP3CA PE=1 SV=1	0.710561	0.002234
Q9Y6A5	TACC3_HUMAN	Transforming acidic coiled-coil-containing protein 3 OS=Homo sapiens OX=9606 GN=TACC3 PE=1 SV=1	0.672133	0.002241
P27797	CALR_HUMAN	Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1	0.723039	0.002273
Q9UGV2	NDRG3_HUMAN	Protein NDRG3 OS=Homo sapiens OX=9606 GN=NDRG3 PE=1 SV=2	0.77736	0.002275
P35754	GLRX1_HUMAN	Glutaredoxin-1 OS=Homo sapiens OX=9606 GN=GLRX PE=1 SV=2	0.707706	0.002276
Q2TAA2	IAH1_HUMAN	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens OX=9606 GN=IAH1 PE=1 SV=1	0.818205	0.002283
O75489	NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS3 PE=1 SV=1	0.673003	0.002285
Q9Y3Z3	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens OX=9606 GN=SAMHD1 PE=1 SV=2	0.658787	0.002285
Q5T1M5	FKB15_HUMAN	FK506-binding protein 15 OS=Homo sapiens OX=9606 GN=FKBP15 PE=1 SV=2	0.760304	0.002288
Q9P265	DIP2B_HUMAN	Disco-interacting protein 2 homolog B OS=Homo sapiens OX=9606 GN=DIP2B PE=1 SV=3	0.709338	0.002288
P24928	RPB1_HUMAN	DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens OX=9606 GN=POLR2A PE=1 SV=2	0.646965	0.002295
O60232	ZNRD2_HUMAN	Protein ZNRD2 OS=Homo sapiens OX=9606 GN=ZNRD2 PE=1 SV=1	0.708028	0.002302
P12955	PEPD_HUMAN	Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD PE=1 SV=3	0.790103	0.002324
Q96M27	PRRC1_HUMAN	Protein PRRC1 OS=Homo sapiens OX=9606 GN=PRRC1 PE=1 SV=1	0.708537	0.00234
Q9NUQ9	FA49B_HUMAN	Protein FAM49B OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1	0.703309	0.00234
P40926	MDHM_HUMAN	Malate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3	0.610113	0.00234
Q9NZT2	OGFR_HUMAN	Opioid growth factor receptor OS=Homo sapiens OX=9606 GN=OGFR PE=1 SV=3	0.876128	0.002352
Q13123	RED_HUMAN	Protein Red OS=Homo sapiens OX=9606 GN=IK PE=1 SV=3	0.700114	0.002359
Q9BY32	ITPA_HUMAN	Inosine triphosphate pyrophosphatase OS=Homo sapiens OX=9606 GN=ITPA PE=1 SV=2	0.704812	0.002382
P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSMC2 PE=1 SV=3	0.704817	0.002384
Q96T23	RSF1_HUMAN	Remodeling and spacing factor 1 OS=Homo sapiens OX=9606 GN=RSF1 PE=1 SV=2	0.704192	0.002385
Q96B97	SH3K1_HUMAN	SH3 domain-containing kinase-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3KBP1 PE=1 SV=2	0.67395	0.002387
Q99439	CNN2_HUMAN	Calponin-2 OS=Homo sapiens OX=9606 GN=CNN2 PE=1 SV=4	0.703495	0.002388
Q9GZN8	CT027_HUMAN	UPF0687 protein C20orf27 OS=Homo sapiens OX=9606 GN=C20orf27 PE=1 SV=3	0.705963	0.002393
O43583	DENR_HUMAN	Density-regulated protein OS=Homo sapiens OX=9606 GN=DENR PE=1 SV=2	0.703653	0.002393

Q96S66	CLCC1_HUMAN	Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 PE=1 SV=1	0.702817	0.002393
Q05639	EF1A2_HUMAN	Elongation factor 1-alpha 2 OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1	0.684353	0.002399
O14929	HAT1_HUMAN	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens OX=9606 GN=HAT1 PE=1 SV=1	0.726871	0.002399
O75477	ERLN1_HUMAN	Erlin-1 OS=Homo sapiens OX=9606 GN=ERLN1 PE=1 SV=2	0.70273	0.002399
Q9Y3B9	RRP15_HUMAN	RRP15-like protein OS=Homo sapiens OX=9606 GN=RRP15 PE=1 SV=2	0.703919	0.002399
Q13242	SRSF9_HUMAN	Serine/arginine-rich splicing factor 9 OS=Homo sapiens OX=9606 GN=SRSF9 PE=1 SV=1	0.76114	0.002429
O15382	BCAT2_HUMAN	Branched-chain-amino-acid aminotransferase mitochondrial OS=Homo sapiens OX=9606 GN=BCAT2 PE=1 SV=2	0.702672	0.002455
P0C0S5	H2AZ_HUMAN	Histone H2A.Z OS=Homo sapiens OX=9606 GN=H2AZ1 PE=1 SV=2	0.700479	0.002458
Q71UI9	H2AV_HUMAN	Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AVF PE=1 SV=3	0.700479	0.002458
P35269	T2FA_HUMAN	General transcription factor IIF subunit 1 OS=Homo sapiens OX=9606 GN=GTF2F1 PE=1 SV=2	0.703332	0.002471
Q13033	STRN3_HUMAN	Striatin-3 OS=Homo sapiens OX=9606 GN=STRN3 PE=1 SV=3	0.68966	0.002473
Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase AK3 mitochondrial OS=Homo sapiens OX=9606 GN=AK3 PE=1 SV=4	0.769148	0.002481
Q7L5D6	GET4_HUMAN	Golgi to ER traffic protein 4 homolog OS=Homo sapiens OX=9606 GN=GET4 PE=1 SV=1	0.70136	0.002481
P63208	SKP1_HUMAN	S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=2	0.713664	0.002481
P19388	RPAB1_HUMAN	DNA-directed RNA polymerases I II and III subunit RPABC1 OS=Homo sapiens OX=9606 GN=POLR2E PE=1 SV=4	0.699966	0.002481
Q96TC7	RMD3_HUMAN	Regulator of microtubule dynamics protein 3 OS=Homo sapiens OX=9606 GN=RMDN3 PE=1 SV=2	0.701178	0.002481
P51398	RT29_HUMAN	28S ribosomal protein S29 mitochondrial OS=Homo sapiens OX=9606 GN=DAP3 PE=1 SV=1	0.725561	0.002481
Q9Y3L3	3BP1_HUMAN	SH3 domain-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3BP1 PE=1 SV=3	0.700986	0.002481
Q53H82	LACB2_HUMAN	Endoribonuclease LACTB2 OS=Homo sapiens OX=9606 GN=LACTB2 PE=1 SV=2	0.707447	0.002481
Q8TD16	BICD2_HUMAN	Protein bicaudal D homolog 2 OS=Homo sapiens OX=9606 GN=BICD2 PE=1 SV=1	0.699621	0.002488
Q8NFH3	NUP43_HUMAN	Nucleoporin Nup43 OS=Homo sapiens OX=9606 GN=NUP43 PE=1 SV=1	0.77001	0.002496
Q96EE3	SEH1_HUMAN	Nucleoporin SEH1 OS=Homo sapiens OX=9606 GN=SEH1L PE=1 SV=3	0.701007	0.002503
Q9HD45	TM9S3_HUMAN	Transmembrane 9 superfamily member 3 OS=Homo sapiens OX=9606 GN=TM9SF3 PE=1 SV=2	0.583594	0.002513
Q7L0Y3	TM10C_HUMAN	tRNA methyltransferase 10 homolog C OS=Homo sapiens OX=9606 GN=TRMT10C PE=1 SV=2	0.690397	0.002513
P50895	BCAM_HUMAN	Basal cell adhesion molecule OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=2	0.974909	0.002522
Q00403	TF2B_HUMAN	Transcription initiation factor IIB OS=Homo sapiens OX=9606 GN=GTF2B PE=1 SV=1	0.699536	0.002522
Q9HD20	AT131_HUMAN	Manganese-transporting ATPase 13A1 OS=Homo sapiens OX=9606 GN=ATP13A1 PE=1 SV=2	0.699341	0.002522
P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1	0.68678	0.002522
P0DMV9	HS71B_HUMAN	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1	0.68678	0.002522
Q08945	SSRP1_HUMAN	FACT complex subunit SSRP1 OS=Homo sapiens OX=9606 GN=SSRP1 PE=1 SV=1	0.654391	0.002524
Q3ZCQ8	TIM50_HUMAN	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens OX=9606 GN=TIMM50 PE=1 SV=2	0.699203	0.002526
Q9UMX0	UBQL1_HUMAN	Ubiquilin-1 OS=Homo sapiens OX=9606 GN=UBQLN1 PE=1 SV=2	0.692843	0.002545
P06132	DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=Homo sapiens OX=9606 GN=UROD PE=1 SV=2	0.698998	0.002553
Q5T9A4	ATD3B_HUMAN	ATPase family AAA domain-containing protein 3B OS=Homo sapiens OX=9606 GN=ATAD3B PE=1 SV=1	0.698047	0.002561
Q01844	EWS_HUMAN	RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1	0.69584	0.002563
O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 OS=Homo sapiens OX=9606 GN=PGRMC2 PE=1 SV=1	0.733354	0.002564
Q9UK22	FBX2_HUMAN	F-box only protein 2 OS=Homo sapiens OX=9606 GN=FBXO2 PE=1 SV=2	0.801412	0.002578
P08559	ODPA_HUMAN	Pyruvate dehydrogenase E1 component subunit alpha somatic form mitochondrial OS=Homo sapiens OX=9606 GN=PDHA1 PE=1 SV=3	0.658963	0.002584

Q99538	LGMN_HUMAN	Legumain OS=Homo sapiens OX=9606 GN=LGMN PE=1 SV=1	0.697161	0.002584
P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Homo sapiens OX=9606 GN=PSMA2 PE=1 SV=2	0.730745	0.00261
O75718	CRTAP_HUMAN	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	0.695977	0.002618
P55209	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1	0.70242	0.002663
Q9NUU7	DD19A_HUMAN	ATP-dependent RNA helicase DDX19A OS=Homo sapiens OX=9606 GN=DDX19A PE=1 SV=1	0.693721	0.002667
Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=2	0.7037	0.002667
Q9Y3E5	PTH2_HUMAN	Peptidyl-tRNA hydrolase 2 mitochondrial OS=Homo sapiens OX=9606 GN=PTRH2 PE=1 SV=1	0.694849	0.002671
Q12849	GRSF1_HUMAN	G-rich sequence factor 1 OS=Homo sapiens OX=9606 GN=GRSF1 PE=1 SV=3	0.692896	0.002671
P49023	PAXI_HUMAN	Paxillin OS=Homo sapiens OX=9606 GN=PXN PE=1 SV=3	0.653039	0.002685
Q99615	DNJC7_HUMAN	DnaJ homolog subfamily C member 7 OS=Homo sapiens OX=9606 GN=DNAJC7 PE=1 SV=2	0.739319	0.002704
Q9UBL3	ASH2L_HUMAN	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens OX=9606 GN=ASH2L PE=1 SV=1	0.692463	0.002704
O94992	HEX1_HUMAN	Protein HEXIM1 OS=Homo sapiens OX=9606 GN=HEXIM1 PE=1 SV=1	0.769934	0.002704
Q9UJX2	CDC23_HUMAN	Cell division cycle protein 23 homolog OS=Homo sapiens OX=9606 GN=CDC23 PE=1 SV=3	0.69296	0.00271
P41743	KPCI_HUMAN	Protein kinase C iota type OS=Homo sapiens OX=9606 GN=PRKCI PE=1 SV=2	0.693631	0.00271
O43920	NDUS5_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens OX=9606 GN=NDUF55 PE=1 SV=3	0.810164	0.00271
P10515	ODP2_HUMAN	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex mitochondrial OS=Homo sapiens OX=9606 GN=DLAT PE=1 SV=3	0.767105	0.002713
P05120	PAI2_HUMAN	Plasminogen activator inhibitor 2 OS=Homo sapiens OX=9606 GN=SERPINB2 PE=1 SV=2	0.730302	0.002715
P62888	RL30_HUMAN	60S ribosomal protein L30 OS=Homo sapiens OX=9606 GN=RPL30 PE=1 SV=2	0.77249	0.002717
Q01658	NC2B_HUMAN	Protein Dr1 OS=Homo sapiens OX=9606 GN=DR1 PE=1 SV=1	0.69635	0.002721
Q96KB5	TOPK_HUMAN	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens OX=9606 GN=PBK PE=1 SV=3	0.691715	0.002721
Q9UI30	TR112_HUMAN	Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens OX=9606 GN=TRMT112 PE=1 SV=1	0.730295	0.002728
Q9HCY8	S10AE_HUMAN	Protein S100-A14 OS=Homo sapiens OX=9606 GN=S100A14 PE=1 SV=1	0.693267	0.002728
O00232	PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens OX=9606 GN=PSMD12 PE=1 SV=3	0.731368	0.002736
Q16698	DECR_HUMAN	2 4-dienoyl-CoA reductase mitochondrial OS=Homo sapiens OX=9606 GN=DECR1 PE=1 SV=1	0.691237	0.002747
Q9Y2W2	WBP11_HUMAN	WW domain-binding protein 11 OS=Homo sapiens OX=9606 GN=WBP11 PE=1 SV=1	0.652077	0.002747
P36957	ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex mitochondrial OS=Homo sapiens OX=9606 GN=DLST PE=1 SV=4	0.702785	0.00275
Q8IWE2	NXP20_HUMAN	Protein NOXP20 OS=Homo sapiens OX=9606 GN=FAM114A1 PE=1 SV=2	0.711217	0.002758
P29558	RBMS1_HUMAN	RNA-binding motif single-stranded-interacting protein 1 OS=Homo sapiens OX=9606 GN=RBMS1 PE=1 SV=3	0.692483	0.00276
Q9BV86	NTM1A_HUMAN	N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens OX=9606 GN=NTMT1 PE=1 SV=3	0.691324	0.002763
P12236	ADT3_HUMAN	ADP/ATP translocase 3 OS=Homo sapiens OX=9606 GN=SLC25A6 PE=1 SV=4	0.691878	0.002765
O75828	CBR3_HUMAN	Carbonyl reductase [NADPH] 3 OS=Homo sapiens OX=9606 GN=CBR3 PE=1 SV=3	0.687109	0.002776
P21589	5NTD_HUMAN	5'-nucleotidase OS=Homo sapiens OX=9606 GN=NT5E PE=1 SV=1	0.771461	0.002778
Q96IJ6	GMPPA_HUMAN	Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens OX=9606 GN=GMPPA PE=1 SV=1	0.689196	0.002787
O14979	HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens OX=9606 GN=HNRNPDL PE=1 SV=3	0.668064	0.002809
Q96EK5	KBP_HUMAN	KIF-binding protein OS=Homo sapiens OX=9606 GN=KIFBP PE=1 SV=1	0.683913	0.002822
O15355	PPM1G_HUMAN	Protein phosphatase 1G OS=Homo sapiens OX=9606 GN=PPM1G PE=1 SV=1	0.733	0.002838
P00533	EGFR_HUMAN	Epidermal growth factor receptor OS=Homo sapiens OX=9606 GN=EGFR PE=1 SV=2	0.696767	0.00284

Q16625	OCLN_HUMAN	Occludin OS=Homo sapiens OX=9606 GN=OCLN PE=1 SV=1	0.684557	0.002882
Q96I20	PAWR_HUMAN	PRKC apoptosis WT1 regulator protein OS=Homo sapiens OX=9606 GN=PAWR PE=1 SV=1	0.672628	0.002896
P54725	RD23A_HUMAN	UV excision repair protein RAD23 homolog A OS=Homo sapiens OX=9606 GN=RD23A PE=1 SV=1	0.686311	0.002896
P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 OS=Homo sapiens OX=9606 GN=DPP4 PE=1 SV=2	0.688262	0.002896
Q96LJ7	DHRS1_HUMAN	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens OX=9606 GN=DHRS1 PE=1 SV=1	0.686679	0.002939
P84095	RHOG_HUMAN	Rho-related GTP-binding protein RhoG OS=Homo sapiens OX=9606 GN=RHOG PE=1 SV=1	0.685167	0.002962
O15269	SPTC1_HUMAN	Serine palmitoyltransferase 1 OS=Homo sapiens OX=9606 GN=SPTLC1 PE=1 SV=1	0.682206	0.002978
Q98TY7	HGH1_HUMAN	Protein HGH1 homolog OS=Homo sapiens OX=9606 GN=HGH1 PE=1 SV=1	0.684198	0.002981
Q96JY6	PDLI2_HUMAN	PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1	0.658096	0.002983
P54920	SNAA_HUMAN	Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=3	0.624343	0.002986
P25685	DNJB1_HUMAN	DnaJ homolog subfamily B member 1 OS=Homo sapiens OX=9606 GN=DNAJB1 PE=1 SV=4	0.681748	0.002989
Q08257	QOR_HUMAN	Quinone oxidoreductase OS=Homo sapiens OX=9606 GN=CRYZ PE=1 SV=1	0.653892	0.003005
Q9H2U1	DHX36_HUMAN	ATP-dependent DNA/RNA helicase DHX36 OS=Homo sapiens OX=9606 GN=DHX36 PE=1 SV=2	0.684577	0.003028
O75153	CLU_HUMAN	Clustered mitochondria protein homolog OS=Homo sapiens OX=9606 GN=CLUH PE=1 SV=2	0.64261	0.003031
Q03519	TAP2_HUMAN	Antigen peptide transporter 2 OS=Homo sapiens OX=9606 GN=TAP2 PE=1 SV=1	0.682056	0.003041
Q9H7E9	CH033_HUMAN	UPF0488 protein C8orf33 OS=Homo sapiens OX=9606 GN=C8orf33 PE=1 SV=1	0.684159	0.003047
A8K023	WASH1_HUMAN	WASH complex subunit 1 OS=Homo sapiens OX=9606 GN=WASHC1 PE=1 SV=2	0.955434	0.003047
P0DP24	CALM2_HUMAN	Calmodulin-2 OS=Homo sapiens OX=9606 GN=CALM2 PE=1 SV=1	0.732912	0.003047
P0DP23	CALM1_HUMAN	Calmodulin-1 OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1	0.732912	0.003047
P0DP25	CALM3_HUMAN	Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1	0.732912	0.003047
P08648	ITA5_HUMAN	Integrin alpha-5 OS=Homo sapiens OX=9606 GN=ITGA5 PE=1 SV=2	0.677427	0.003064
P42574	CASP3_HUMAN	Caspase-3 OS=Homo sapiens OX=9606 GN=CASP3 PE=1 SV=2	0.682598	0.003065
Q9NT62	ATG3_HUMAN	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens OX=9606 GN=ATG3 PE=1 SV=1	0.680628	0.003065
Q9NWS0	PIHD1_HUMAN	PIH1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PIH1D1 PE=1 SV=1	0.683667	0.003065
Q9NPD8	UBE2T_HUMAN	Ubiquitin-conjugating enzyme E2 T OS=Homo sapiens OX=9606 GN=UBE2T PE=1 SV=1	0.681493	0.003102
Q7Z2T5	TRM1L_HUMAN	TRMT1-like protein OS=Homo sapiens OX=9606 GN=TRMT1L PE=1 SV=2	0.683956	0.003102
P36952	SPB5_HUMAN	Serin B5 OS=Homo sapiens OX=9606 GN=SERPINB5 PE=1 SV=2	0.639464	0.003102
O75821	EIF3G_HUMAN	Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens OX=9606 GN=EIF3G PE=1 SV=2	0.651236	0.003112
Q14966	ZN638_HUMAN	Zinc finger protein 638 OS=Homo sapiens OX=9606 GN=ZNF638 PE=1 SV=2	0.681246	0.003129
Q9Y6E2	BZW2_HUMAN	Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1	0.68065	0.003147
Q02252	MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 PE=1 SV=2	0.675038	0.003157
Q68EM7	RHG17_HUMAN	Rho GTPase-activating protein 17 OS=Homo sapiens OX=9606 GN=ARHGAP17 PE=1 SV=1	0.765535	0.003167
Q14690	RRP5_HUMAN	Protein RRP5 homolog OS=Homo sapiens OX=9606 GN=PDCD11 PE=1 SV=3	0.631458	0.00317
Q92542	NICA_HUMAN	Nicastrin OS=Homo sapiens OX=9606 GN=NCSTN PE=1 SV=2	0.78817	0.003198
Q6PGP7	TTC37_HUMAN	Tetratricopeptide repeat protein 37 OS=Homo sapiens OX=9606 GN=TTC37 PE=1 SV=1	0.677272	0.003198
O76003	GLRX3_HUMAN	Glutaredoxin-3 OS=Homo sapiens OX=9606 GN=GLRX3 PE=1 SV=2	0.663404	0.003218
P53582	MAP11_HUMAN	Methionine aminopeptidase 1 OS=Homo sapiens OX=9606 GN=METAP1 PE=1 SV=2	0.678072	0.003218
O43678	NDUA2_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens OX=9606 GN=NDUFA2 PE=1 SV=3	0.680823	0.00322
Q9Y281	COF2_HUMAN	Cofilin-2 OS=Homo sapiens OX=9606 GN=CFL2 PE=1 SV=1	0.613294	0.00322

Q08J23	NSUN2_HUMAN	RNA cytosine C(5)-methyltransferase NSUN2 OS=Homo sapiens OX=9606 GN=NSUN2 PE=1 SV=2	0.58431	0.00322
P23381	SYWC_HUMAN	Tryptophan--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=WARS1 PE=1 SV=2	0.84723	0.003235
O75340	PDCD6_HUMAN	Programmed cell death protein 6 OS=Homo sapiens OX=9606 GN=PDCD6 PE=1 SV=1	0.717353	0.003235
Q7Z4Q2	HEAT3_HUMAN	HEAT repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=HEATR3 PE=1 SV=2	0.67825	0.003235
Q9Y3I1	FBX7_HUMAN	F-box only protein 7 OS=Homo sapiens OX=9606 GN=FBXO7 PE=1 SV=1	0.678072	0.003235
Q9BR76	COR1B_HUMAN	Coronin-1B OS=Homo sapiens OX=9606 GN=CORO1B PE=1 SV=1	0.676039	0.003235
Q9Y3C6	PPIL1_HUMAN	Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens OX=9606 GN=PPIL1 PE=1 SV=1	0.677107	0.003245
O60749	SNX2_HUMAN	Sorting nexin-2 OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=2	0.624187	0.003286
Q9GZP4	PITH1_HUMAN	PITH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PITHD1 PE=1 SV=1	0.676018	0.003289
O14936	CSKP_HUMAN	Peripheral plasma membrane protein CASK OS=Homo sapiens OX=9606 GN=CASK PE=1 SV=3	0.677221	0.003307
P37108	SRP14_HUMAN	Signal recognition particle 14 kDa protein OS=Homo sapiens OX=9606 GN=SRP14 PE=1 SV=2	0.69822	0.003307
Q12933	TRAF2_HUMAN	TNF receptor-associated factor 2 OS=Homo sapiens OX=9606 GN=TRAF2 PE=1 SV=2	0.675832	0.003307
P36639	8ODP_HUMAN	7 8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens OX=9606 GN=NUDT1 PE=1 SV=3	0.703925	0.003307
P43897	EFTS_HUMAN	Elongation factor Ts mitochondrial OS=Homo sapiens OX=9606 GN=TSFM PE=1 SV=2	0.676651	0.003307
Q05519	SRS11_HUMAN	Serine/arginine-rich splicing factor 11 OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1	0.676812	0.003307
Q9BYD2	RM09_HUMAN	39S ribosomal protein L9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL9 PE=1 SV=2	0.675025	0.003307
P09972	ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=2	0.666874	0.003307
O43660	PLRG1_HUMAN	Pleiotropic regulator 1 OS=Homo sapiens OX=9606 GN=PLRG1 PE=1 SV=1	0.783791	0.003318
O15498	YKT6_HUMAN	Synaptobrevin homolog YKT6 OS=Homo sapiens OX=9606 GN=YKT6 PE=1 SV=1	0.67464	0.003327
O95881	TXD12_HUMAN	Thioredoxin domain-containing protein 12 OS=Homo sapiens OX=9606 GN=TXNDC12 PE=1 SV=1	0.739792	0.003327
A0AV96	RBM47_HUMAN	RNA-binding protein 47 OS=Homo sapiens OX=9606 GN=RBM47 PE=1 SV=2	0.660954	0.003327
Q96C36	P5CR2_HUMAN	Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens OX=9606 GN=PYCR2 PE=1 SV=1	0.678072	0.00333
P11766	ADHX_HUMAN	Alcohol dehydrogenase class-3 OS=Homo sapiens OX=9606 GN=ADH5 PE=1 SV=4	0.646922	0.003334
Q8TBX8	PI42C_HUMAN	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens OX=9606 GN=PIP4K2C PE=1 SV=3	0.871563	0.003345
Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=2	0.789687	0.003359
O43865	SAHH2_HUMAN	S-adenosylhomocysteine hydrolase-like protein 1 OS=Homo sapiens OX=9606 GN=AHCYL1 PE=1 SV=2	0.673907	0.003378
Q9H501	ESF1_HUMAN	ESF1 homolog OS=Homo sapiens OX=9606 GN=ESF1 PE=1 SV=1	0.727332	0.003381
Q6YP21	KAT3_HUMAN	Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens OX=9606 GN=KYAT3 PE=1 SV=1	0.63723	0.003398
Q9BYT8	NEUL_HUMAN	Neurolysin mitochondrial OS=Homo sapiens OX=9606 GN=NLN PE=1 SV=1	0.765702	0.003398
Q9NRW3	ABC3C_HUMAN	DNA dC->dU-editing enzyme APOBEC-3C OS=Homo sapiens OX=9606 GN=APOBEC3C PE=1 SV=2	0.673173	0.003398
Q6IBS0	TWF2_HUMAN	Twinfilin-2 OS=Homo sapiens OX=9606 GN=TWF2 PE=1 SV=2	0.641865	0.003398
Q9P035	HACD3_HUMAN	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=2	0.67319	0.003409
Q4G0N4	NAKD2_HUMAN	NAD kinase 2 mitochondrial OS=Homo sapiens OX=9606 GN=NADK2 PE=1 SV=2	0.669723	0.003412
O60664	PLIN3_HUMAN	Perilipin-3 OS=Homo sapiens OX=9606 GN=PLIN3 PE=1 SV=3	0.644052	0.003415
Q9P015	RM15_HUMAN	39S ribosomal protein L15 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL15 PE=1 SV=1	0.670559	0.003415
Q86WQ0	NR2CA_HUMAN	Nuclear receptor 2C2-associated protein OS=Homo sapiens OX=9606 GN=NR2C2AP PE=1 SV=1	0.671828	0.003415
Q15067	ACOX1_HUMAN	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens OX=9606 GN=ACOX1 PE=1 SV=3	0.62293	0.00345
Q92974	ARHG2_HUMAN	Rho guanine nucleotide exchange factor 2 OS=Homo sapiens OX=9606 GN=ARHGEF2 PE=1 SV=4	0.670026	0.003461

Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1	0.628504	0.00348
Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9 mitochondrial OS=Homo sapiens OX=9606 GN=ACOT9 PE=1 SV=2	0.712751	0.003494
Q9BQ67	GRWD1_HUMAN	Glutamate-rich WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=GRWD1 PE=1 SV=1	0.661945	0.003494
Q13751	LAMB3_HUMAN	Laminin subunit beta-3 OS=Homo sapiens OX=9606 GN=LAMB3 PE=1 SV=1	0.617577	0.003494
P54709	AT1B3_HUMAN	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens OX=9606 GN=ATP1B3 PE=1 SV=1	0.78787	0.003494
Q9Y5X3	SNX5_HUMAN	Sorting nexin-5 OS=Homo sapiens OX=9606 GN=SNX5 PE=1 SV=1	0.668744	0.003529
Q9H944	MED20_HUMAN	Mediator of RNA polymerase II transcription subunit 20 OS=Homo sapiens OX=9606 GN=MED20 PE=1 SV=1	0.66961	0.003529
O75841	UPK1B_HUMAN	Uroplakin-1b OS=Homo sapiens OX=9606 GN=UPK1B PE=1 SV=5	0.662938	0.003549
Q96QD9	UIF_HUMAN	UAP56-interacting factor OS=Homo sapiens OX=9606 GN=FYTTD1 PE=1 SV=3	0.869939	0.003569
Q9UBW8	CSN7A_HUMAN	COP9 signalosome complex subunit 7a OS=Homo sapiens OX=9606 GN=COP57A PE=1 SV=1	0.666032	0.003573
P04083	ANXA1_HUMAN	Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2	0.627064	0.003597
Q92615	LAR4B_HUMAN	La-related protein 4B OS=Homo sapiens OX=9606 GN=LARP4B PE=1 SV=3	0.667787	0.003597
Q5JWF2	GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens OX=9606 GN=GNAS PE=1 SV=2	0.684402	0.003612
Q01628	IFM3_HUMAN	Interferon-induced transmembrane protein 3 OS=Homo sapiens OX=9606 GN=IFITM3 PE=1 SV=2	0.668238	0.003612
Q9Y676	RT18B_HUMAN	28S ribosomal protein S18b mitochondrial OS=Homo sapiens OX=9606 GN=MRPS18B PE=1 SV=1	0.667844	0.003616
Q6YN16	HSDL2_HUMAN	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens OX=9606 GN=HSDL2 PE=1 SV=1	0.667831	0.003616
P20020	AT2B1_HUMAN	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens OX=9606 GN=ATP2B1 PE=1 SV=4	0.667017	0.003616
O15305	PMM2_HUMAN	Phosphomannomutase 2 OS=Homo sapiens OX=9606 GN=PMM2 PE=1 SV=1	0.937491	0.003616
P62266	RS23_HUMAN	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3	0.669123	0.003616
P63151	2ABA_HUMAN	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R2A PE=1 SV=1	0.623437	0.003616
P46937	YAP1_HUMAN	Transcriptional coactivator YAP1 OS=Homo sapiens OX=9606 GN=YAP1 PE=1 SV=2	0.651181	0.003616
Q9H9T3	ELP3_HUMAN	Elongator complex protein 3 OS=Homo sapiens OX=9606 GN=ELP3 PE=1 SV=2	0.775331	0.003616
Q13011	ECH1_HUMAN	Delta(3 5)-Delta(2 4)-dienoyl-CoA isomerase mitochondrial OS=Homo sapiens OX=9606 GN=ECH1 PE=1 SV=2	0.792578	0.003616
Q9UPN7	PP6R1_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP6R1 PE=1 SV=5	0.667716	0.003616
O43292	GPAA1_HUMAN	Glycosylphosphatidylinositol anchor attachment 1 protein OS=Homo sapiens OX=9606 GN=GPAA1 PE=1 SV=3	0.667023	0.00362
Q13243	SRSF5_HUMAN	Serine/arginine-rich splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 PE=1 SV=1	0.666044	0.003632
Q9Y6V7	DDX49_HUMAN	Probable ATP-dependent RNA helicase DDX49 OS=Homo sapiens OX=9606 GN=DDX49 PE=1 SV=1	0.667329	0.003632
P07311	ACYP1_HUMAN	Acylphosphatase-1 OS=Homo sapiens OX=9606 GN=ACYP1 PE=1 SV=2	0.665782	0.003635
Q96BW5	PTER_HUMAN	Phosphotriesterase-related protein OS=Homo sapiens OX=9606 GN=PTER PE=1 SV=1	0.666361	0.003656
Q9Y5K5	UCHL5_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens OX=9606 GN=UCHL5 PE=1 SV=3	0.660017	0.003668
Q13443	ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens OX=9606 GN=ADAM9 PE=1 SV=1	0.637643	0.003698
Q9NPQ8	RIC8A_HUMAN	Synembryn-A OS=Homo sapiens OX=9606 GN=RIC8A PE=1 SV=3	0.665052	0.003727
P05362	ICAM1_HUMAN	Intercellular adhesion molecule 1 OS=Homo sapiens OX=9606 GN=ICAM1 PE=1 SV=2	0.712147	0.003731
P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI2 PE=1 SV=3	0.580662	0.003744
P55809	SCOT1_HUMAN	Succinyl-CoA:3-ketoacid coenzyme A transferase 1 mitochondrial OS=Homo sapiens OX=9606 GN=OXCT1 PE=1 SV=1	0.664143	0.003809
P82673	RT35_HUMAN	28S ribosomal protein S35 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS35 PE=1 SV=1	0.663975	0.003821
P00374	DYR_HUMAN	Dihydrofolate reductase OS=Homo sapiens OX=9606 GN=DHFR PE=1 SV=2	0.659424	0.003834

P04792	HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2	0.638913	0.003834
P62495	ERF1_HUMAN	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens OX=9606 GN=ETF1 PE=1 SV=3	0.600644	0.003834
Q13347	EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens OX=9606 GN=EIF3I PE=1 SV=1	0.693299	0.003838
Q7Z478	DHX29_HUMAN	ATP-dependent RNA helicase DHX29 OS=Homo sapiens OX=9606 GN=DHX29 PE=1 SV=2	0.661759	0.003842
Q96B36	AKT1_HUMAN	Proline-rich AKT1 substrate 1 OS=Homo sapiens OX=9606 GN=AKT1S1 PE=1 SV=1	0.662147	0.003846
Q9Y6X4	F169A_HUMAN	Soluble lamin-associated protein of 75 kDa OS=Homo sapiens OX=9606 GN=FAM169A PE=1 SV=2	0.733144	0.003854
Q13153	PAK1_HUMAN	Serine/threonine-protein kinase PAK 1 OS=Homo sapiens OX=9606 GN=PAK1 PE=1 SV=2	0.663572	0.003854
P55735	SEC13_HUMAN	Protein SEC13 homolog OS=Homo sapiens OX=9606 GN=SEC13 PE=1 SV=3	0.581927	0.003871
P10586	PTPRF_HUMAN	Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens OX=9606 GN=PTPRF PE=1 SV=2	0.80458	0.00388
P62910	RL32_HUMAN	60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=2	0.618219	0.00388
Q14651	PLSI_HUMAN	Plastin-1 OS=Homo sapiens OX=9606 GN=PLS1 PE=1 SV=2	0.80551	0.003883
O95104	SCAF4_HUMAN	SR-related and CTD-associated factor 4 OS=Homo sapiens OX=9606 GN=SCAF4 PE=1 SV=3	0.662469	0.003883
Q6Y7W6	GGYF2_HUMAN	GRB10-interacting GYF protein 2 OS=Homo sapiens OX=9606 GN=GIGYF2 PE=1 SV=1	0.668549	0.003883
Q96PU5	NED4L_HUMAN	E3 ubiquitin-protein ligase NEDD4-like OS=Homo sapiens OX=9606 GN=NEDD4L PE=1 SV=2	0.661301	0.00391
Q15293	RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens OX=9606 GN=RCN1 PE=1 SV=1	0.674715	0.003914
P60983	GMFB_HUMAN	Glia maturation factor beta OS=Homo sapiens OX=9606 GN=GMFB PE=1 SV=2	0.662965	0.003918
Q9NPH2	INO1_HUMAN	Inositol-3-phosphate synthase 1 OS=Homo sapiens OX=9606 GN=ISYNA1 PE=1 SV=1	0.662344	0.003918
Q9UHY7	ENOPH_HUMAN	Enolase-phosphatase E1 OS=Homo sapiens OX=9606 GN=ENOPH1 PE=1 SV=1	0.659552	0.003918
O00267	SPT5H_HUMAN	Transcription elongation factor SPT5 OS=Homo sapiens OX=9606 GN=SUPT5H PE=1 SV=1	0.818586	0.003949
P23528	COF1_HUMAN	Cofilin-1 OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=3	0.654745	0.003954
Q53HL2	BOREA_HUMAN	Borealin OS=Homo sapiens OX=9606 GN=CDCA8 PE=1 SV=2	0.657894	0.003962
Q96S82	UBL7_HUMAN	Ubiquitin-like protein 7 OS=Homo sapiens OX=9606 GN=UBL7 PE=1 SV=2	0.660514	0.003962
P61225	RAP2B_HUMAN	Ras-related protein Rap-2b OS=Homo sapiens OX=9606 GN=RAP2B PE=1 SV=1	0.658443	0.003976
Q9Y265	RUVB1_HUMAN	RuvB-like 1 OS=Homo sapiens OX=9606 GN=RUVBL1 PE=1 SV=1	0.66956	0.003989
P10155	RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=RO60 PE=1 SV=2	0.68105	0.004035
Q5JRX3	PREP_HUMAN	Presequence protease mitochondrial OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=3	0.664195	0.004035
P30040	ERP29_HUMAN	Endoplasmic reticulum resident protein 29 OS=Homo sapiens OX=9606 GN=ERP29 PE=1 SV=4	0.703751	0.004068
Q92598	HS105_HUMAN	Heat shock protein 105 kDa OS=Homo sapiens OX=9606 GN=HSPH1 PE=1 SV=1	0.724247	0.004072
P60510	PP4C_HUMAN	Serine/threonine-protein phosphatase 4 catalytic subunit OS=Homo sapiens OX=9606 GN=PPP4C PE=1 SV=1	0.659494	0.004096
O60313	OPA1_HUMAN	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=3	0.754011	0.0041
Q13753	LAMC2_HUMAN	Laminin subunit gamma-2 OS=Homo sapiens OX=9606 GN=LAMC2 PE=1 SV=2	0.681448	0.004105
Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	0.604418	0.004118
P07948	LYN_HUMAN	Tyrosine-protein kinase Lyn OS=Homo sapiens OX=9606 GN=LYN PE=1 SV=3	0.649307	0.004118
P40121	CAPG_HUMAN	Macrophage-capping protein OS=Homo sapiens OX=9606 GN=CAPG PE=1 SV=2	0.65302	0.004118
Q15006	EMC2_HUMAN	ER membrane protein complex subunit 2 OS=Homo sapiens OX=9606 GN=EMC2 PE=1 SV=1	0.673216	0.004123
Q9ULR0	ISY1_HUMAN	Pre-mRNA-splicing factor ISY1 homolog OS=Homo sapiens OX=9606 GN=ISY1 PE=1 SV=3	0.656096	0.004147
Q8WUP2	FBLI1_HUMAN	Filamin-binding LIM protein 1 OS=Homo sapiens OX=9606 GN=FBLIM1 PE=1 SV=2	0.657382	0.004151
Q9NZ08	ERAP1_HUMAN	Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens OX=9606 GN=ERAP1 PE=1 SV=3	0.684089	0.004156

O00139	KIF2A_HUMAN	Kinesin-like protein KIF2A OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=3	0.742493	0.004161
O43264	ZW10_HUMAN	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens OX=9606 GN=ZW10 PE=1 SV=3	0.654591	0.004165
Q86SX6	GLRX5_HUMAN	Glutaredoxin-related protein 5 mitochondrial OS=Homo sapiens OX=9606 GN=GLRX5 PE=1 SV=2	0.656208	0.004175
P26006	ITA3_HUMAN	Integrin alpha-3 OS=Homo sapiens OX=9606 GN=ITGA3 PE=1 SV=5	0.653288	0.004179
Q15042	RB3GP_HUMAN	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens OX=9606 GN=RAB3GAP1 PE=1 SV=3	0.652557	0.004286
Q9UBQ5	EIF3K_HUMAN	Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens OX=9606 GN=EIF3K PE=1 SV=1	0.730915	0.004286
P61204	ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=2	0.664306	0.004286
P84077	ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapiens OX=9606 GN=ARF1 PE=1 SV=2	0.664306	0.004286
P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 PE=1 SV=2	0.676345	0.004286
O96019	ACL6A_HUMAN	Actin-like protein 6A OS=Homo sapiens OX=9606 GN=ACTL6A PE=1 SV=1	0.775568	0.004326
Q9H9J2	RM44_HUMAN	39S ribosomal protein L44 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL44 PE=1 SV=1	0.652608	0.004326
Q9UJU6	DBNL_HUMAN	Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1	0.690779	0.004331
Q03252	LMNB2_HUMAN	Lamin-B2 OS=Homo sapiens OX=9606 GN=LMNB2 PE=1 SV=4	0.714913	0.004336
Q9NYK5	RM39_HUMAN	39S ribosomal protein L39 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL39 PE=1 SV=3	0.656186	0.004346
P49903	SPS1_HUMAN	Selenide water dikinase 1 OS=Homo sapiens OX=9606 GN=SEPHS1 PE=1 SV=2	0.652404	0.004346
Q96PZ2	F111A_HUMAN	Protein FAM111A OS=Homo sapiens OX=9606 GN=FAM111A PE=1 SV=2	0.654119	0.004356
O60493	SNX3_HUMAN	Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 PE=1 SV=3	0.785735	0.004356
Q14126	DSG2_HUMAN	Desmoglein-2 OS=Homo sapiens OX=9606 GN=DSG2 PE=1 SV=2	0.667231	0.004356
P05556	ITB1_HUMAN	Integrin beta-1 OS=Homo sapiens OX=9606 GN=ITGB1 PE=1 SV=2	0.714004	0.004356
P07339	CATD_HUMAN	Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1	0.714458	0.004366
P38606	VATA_HUMAN	V-type proton ATPase catalytic subunit A OS=Homo sapiens OX=9606 GN=ATP6V1A PE=1 SV=2	0.641921	0.004366
P55145	MANF_HUMAN	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens OX=9606 GN=MANF PE=1 SV=3	0.607158	0.004401
Q6NXS1	IPP2B_HUMAN	Protein phosphatase inhibitor 2 family member B OS=Homo sapiens OX=9606 GN=PPP1R2B PE=1 SV=2	0.65101	0.004442
P41236	IPP2_HUMAN	Protein phosphatase inhibitor 2 OS=Homo sapiens OX=9606 GN=PPP1R2 PE=1 SV=2	0.65101	0.004442
O14907	TX1B3_HUMAN	Tax1-binding protein 3 OS=Homo sapiens OX=9606 GN=TAX1BP3 PE=1 SV=2	0.650015	0.004462
Q96EK6	GNA1_HUMAN	Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens OX=9606 GN=GNPNAT1 PE=1 SV=1	0.648646	0.004467
P11310	ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ACADM PE=1 SV=1	0.660275	0.004483
Q96JB5	CK5P3_HUMAN	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3 PE=1 SV=2	0.647956	0.004483
Q9Y673	ALG5_HUMAN	Dolichyl-phosphate beta-glucosyltransferase OS=Homo sapiens OX=9606 GN=ALG5 PE=1 SV=1	0.647686	0.004483
O43447	PPIH_HUMAN	Peptidyl-prolyl cis-trans isomerase H OS=Homo sapiens OX=9606 GN=PPIH PE=1 SV=1	0.698491	0.004488
P27816	MAP4_HUMAN	Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=3	0.683541	0.004499
Q00688	FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens OX=9606 GN=FKBP3 PE=1 SV=1	0.643713	0.004567
P41214	EIF2D_HUMAN	Eukaryotic translation initiation factor 2D OS=Homo sapiens OX=9606 GN=EIF2D PE=1 SV=3	0.647779	0.004583
P42892	ECE1_HUMAN	Endothelin-converting enzyme 1 OS=Homo sapiens OX=9606 GN=ECE1 PE=1 SV=2	0.64655	0.004609
Q6WKZ4	RFIP1_HUMAN	Rab11 family-interacting protein 1 OS=Homo sapiens OX=9606 GN=RAB11FIP1 PE=1 SV=3	0.648436	0.004625
Q6UN15	FIP1_HUMAN	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens OX=9606 GN=FIP1L1 PE=1 SV=1	0.61744	0.004625
P06733	ENOA_HUMAN	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2	0.64221	0.004631
Q7LGA3	HS2ST_HUMAN	Heparan sulfate 2-O-sulfotransferase 1 OS=Homo sapiens OX=9606 GN=HS2ST1 PE=1 SV=1	0.645439	0.004647
Q9Y2S7	PDIP2_HUMAN	Polymerase delta-interacting protein 2 OS=Homo sapiens OX=9606 GN=POLDIP2 PE=1 SV=1	0.645997	0.004658

O00560	SDCB1_HUMAN	Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1	0.679976	0.004658
O75934	SPF27_HUMAN	Pre-mRNA-splicing factor SPF27 OS=Homo sapiens OX=9606 GN=BCAS2 PE=1 SV=1	0.678072	0.004669
Q9Y285	SYFA_HUMAN	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=3	0.587814	0.004675
P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PEBP1 PE=1 SV=3	0.646174	0.00468
Q14574	DSC3_HUMAN	Desmocollin-3 OS=Homo sapiens OX=9606 GN=DSC3 PE=1 SV=3	0.644373	0.004746
O75150	BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens OX=9606 GN=RNF40 PE=1 SV=5	0.64302	0.004746
Q9H9Q2	CSN7B_HUMAN	COP9 signalosome complex subunit 7b OS=Homo sapiens OX=9606 GN=COPS7B PE=1 SV=1	0.588307	0.004746
Q93050	VPP1_HUMAN	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens OX=9606 GN=ATP6V0A1 PE=1 SV=3	0.644497	0.004747
Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2	0.687183	0.004747
Q9NRF8	PYRG2_HUMAN	CTP synthase 2 OS=Homo sapiens OX=9606 GN=CTPS2 PE=1 SV=1	0.640392	0.004747
P52758	RIDA_HUMAN	2-iminobutanoate/2-iminopropanoate deaminase OS=Homo sapiens OX=9606 GN=RIDA PE=1 SV=1	0.646921	0.004747
Q99661	KIF2C_HUMAN	Kinesin-like protein KIF2C OS=Homo sapiens OX=9606 GN=KIF2C PE=1 SV=2	0.682801	0.004774
O14579	COPE_HUMAN	Coatomer subunit epsilon OS=Homo sapiens OX=9606 GN=COPE PE=1 SV=3	0.618419	0.00478
P07954	FUMH_HUMAN	Fumarate hydratase mitochondrial OS=Homo sapiens OX=9606 GN=FH PE=1 SV=3	0.679042	0.004786
Q9UBS4	DJB11_HUMAN	DnaJ homolog subfamily B member 11 OS=Homo sapiens OX=9606 GN=DNAJB11 PE=1 SV=1	0.727839	0.004803
Q96I25	SPF45_HUMAN	Splicing factor 45 OS=Homo sapiens OX=9606 GN=RBM17 PE=1 SV=1	0.644114	0.004842
Q9BTX1	NDC1_HUMAN	Nucleoporin NDC1 OS=Homo sapiens OX=9606 GN=NDC1 PE=1 SV=2	0.644082	0.004853
P61966	AP1S1_HUMAN	AP-1 complex subunit sigma-1A OS=Homo sapiens OX=9606 GN=AP1S1 PE=1 SV=1	0.642843	0.004853
Q92797	SYMPK_HUMAN	Symplekin OS=Homo sapiens OX=9606 GN=SYMPK PE=1 SV=2	0.783887	0.004883
Q8WVC0	LEO1_HUMAN	RNA polymerase-associated protein LEO1 OS=Homo sapiens OX=9606 GN=LEO1 PE=1 SV=1	0.641515	0.004883
P16070	CD44_HUMAN	CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=3	0.647547	0.004883
P60953	CDC42_HUMAN	Cell division control protein 42 homolog OS=Homo sapiens OX=9606 GN=CDC42 PE=1 SV=2	0.641506	0.004889
Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 PE=1 SV=1	0.618701	0.004889
Q00577	PURA_HUMAN	Transcriptional activator protein Pur-alpha OS=Homo sapiens OX=9606 GN=PURA PE=1 SV=2	0.642106	0.004901
Q12888	TP53B_HUMAN	TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2	0.668967	0.004901
P14625	ENPL_HUMAN	Endoplasmic reticulum protein OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1	0.619728	0.00493
Q9NZI8	IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=1 SV=2	0.586656	0.004993
O00515	LAD1_HUMAN	Ladinin-1 OS=Homo sapiens OX=9606 GN=LAD1 PE=1 SV=2	0.591249	0.004999
P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens OX=9606 GN=GNB2 PE=1 SV=3	0.638801	0.005
Q9H3Z4	DNJC5_HUMAN	DnaJ homolog subfamily C member 5 OS=Homo sapiens OX=9606 GN=DNAJC5 PE=1 SV=1	1.467708	0.005
Q9UMS4	PRP19_HUMAN	Pre-mRNA-processing factor 19 OS=Homo sapiens OX=9606 GN=PRPF19 PE=1 SV=1	0.588172	0.005006
P07711	CATL1_HUMAN	Cathepsin L1 OS=Homo sapiens OX=9606 GN=CTSL PE=1 SV=2	0.637608	0.005024
P06396	GELS_HUMAN	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1	0.634867	0.00503
O15344	TRI18_HUMAN	E3 ubiquitin-protein ligase Midline-1 OS=Homo sapiens OX=9606 GN=MID1 PE=1 SV=1	0.639586	0.005059
Q9UJA5	TRM6_HUMAN	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens OX=9606 GN=TRMT6 PE=1 SV=1	0.637482	0.005077
Q2NL82	TSR1_HUMAN	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens OX=9606 GN=TSR1 PE=1 SV=1	0.827467	0.005078
Q9NVH1	DJC11_HUMAN	DnaJ homolog subfamily C member 11 OS=Homo sapiens OX=9606 GN=DNAJC11 PE=1 SV=2	0.639963	0.005078
P46782	RS5_HUMAN	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RP55 PE=1 SV=4	0.608313	0.005084
P33121	ACSL1_HUMAN	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens OX=9606 GN=ACSL1 PE=1 SV=1	0.633136	0.00509

Q969X6	UTP4_HUMAN	U3 small nucleolar RNA-associated protein 4 homolog OS=Homo sapiens OX=9606 GN=UTP4 PE=1 SV=1	0.720314	0.005097
O75348	VATG1_HUMAN	V-type proton ATPase subunit G 1 OS=Homo sapiens OX=9606 GN=ATP6V1G1 PE=1 SV=3	0.639178	0.005103
O00233	PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=3	0.639744	0.005129
Q8N1P7	CRBG2_HUMAN	Beta/gamma crystallin domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CRYBG2 PE=2 SV=2	0.635844	0.005129
P49406	RM19_HUMAN	39S ribosomal protein L19 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL19 PE=1 SV=2	0.639487	0.005129
P23497	SP100_HUMAN	Nuclear autoantigen Sp-100 OS=Homo sapiens OX=9606 GN=SP100 PE=1 SV=3	0.637849	0.005129
Q9UHV9	PFD2_HUMAN	Prefoldin subunit 2 OS=Homo sapiens OX=9606 GN=PFDN2 PE=1 SV=1	0.636965	0.005178
O43707	ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2	0.601334	0.005196
Q9NS69	TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens OX=9606 GN=TOMM22 PE=1 SV=3	0.652464	0.005202
Q9HAV4	XPO5_HUMAN	Exportin-5 OS=Homo sapiens OX=9606 GN=XPO5 PE=1 SV=1	0.592231	0.005209
Q13283	G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=1	0.68281	0.005227
P29317	EPHA2_HUMAN	Ephrin type-A receptor 2 OS=Homo sapiens OX=9606 GN=EPHA2 PE=1 SV=2	0.695533	0.005229
P22033	MUTA_HUMAN	Methylmalonyl-CoA mutase mitochondrial OS=Homo sapiens OX=9606 GN=MMUT PE=1 SV=4	0.635601	0.005242
P48147	PPCE_HUMAN	Prolyl endopeptidase OS=Homo sapiens OX=9606 GN=PREP PE=1 SV=2	0.691961	0.005242
P63279	UBC9_HUMAN	SUMO-conjugating enzyme UBC9 OS=Homo sapiens OX=9606 GN=UBE2I PE=1 SV=1	0.620356	0.005272
P04150	GCR_HUMAN	Glucocorticoid receptor OS=Homo sapiens OX=9606 GN=NR3C1 PE=1 SV=1	0.631156	0.005279
Q8TAQ2	SMRC2_HUMAN	SWI/SNF complex subunit SMARCC2 OS=Homo sapiens OX=9606 GN=SMARCC2 PE=1 SV=1	0.634055	0.005293
Q8NAV1	PR38A_HUMAN	Pre-mRNA-splicing factor 38A OS=Homo sapiens OX=9606 GN=PRPF38A PE=1 SV=1	0.719714	0.005293
P00441	SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD1 PE=1 SV=2	0.635767	0.005293
O43592	XPOT_HUMAN	Exportin-T OS=Homo sapiens OX=9606 GN=XPOT PE=1 SV=2	0.594283	0.005293
P31350	RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens OX=9606 GN=RRM2 PE=1 SV=1	0.616383	0.005344
O00217	NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS8 PE=1 SV=1	0.634015	0.005357
P22102	PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens OX=9606 GN=GART PE=1 SV=1	0.584157	0.005376
Q13505	MTX1_HUMAN	Metaxin-1 OS=Homo sapiens OX=9606 GN=MTX1 PE=1 SV=3	0.667572	0.005378
Q96D71	REPS1_HUMAN	RaBP1-associated Eps domain-containing protein 1 OS=Homo sapiens OX=9606 GN=REPS1 PE=1 SV=3	0.669904	0.005384
O75676	KS6A4_HUMAN	Ribosomal protein S6 kinase alpha-4 OS=Homo sapiens OX=9606 GN=RPS6KA4 PE=1 SV=1	0.631439	0.005391
Q9HAB8	PPCS_HUMAN	Phosphopantothenate--cysteine ligase OS=Homo sapiens OX=9606 GN=PPCS PE=1 SV=2	0.630853	0.005398
Q96FZ2	HMCES_HUMAN	Abasic site processing protein HMCES OS=Homo sapiens OX=9606 GN=HMCES PE=1 SV=1	0.89748	0.005442
Q9UMY4	SNX12_HUMAN	Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 PE=1 SV=4	0.631822	0.005449
Q96P70	IPO9_HUMAN	Importin-9 OS=Homo sapiens OX=9606 GN=IPO9 PE=1 SV=3	0.583333	0.005456
P05121	PAI1_HUMAN	Plasminogen activator inhibitor 1 OS=Homo sapiens OX=9606 GN=SERPINE1 PE=1 SV=1	0.780842	0.005463
Q96K17	BT3L4_HUMAN	Transcription factor BTF3 homolog 4 OS=Homo sapiens OX=9606 GN=BTF3L4 PE=1 SV=1	0.632761	0.005472
Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 PE=1 SV=1	0.644825	0.005472
Q9BWD1	THIC_HUMAN	Acetyl-CoA acetyltransferase cytosolic OS=Homo sapiens OX=9606 GN=ACAT2 PE=1 SV=2	0.666343	0.005472
Q9Y6W5	WASF2_HUMAN	Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens OX=9606 GN=WASF2 PE=1 SV=3	0.632746	0.005491
P08754	GNAI3_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha OS=Homo sapiens OX=9606 GN=GNAI3 PE=1 SV=3	0.621136	0.005498
Q15061	WDR43_HUMAN	WD repeat-containing protein 43 OS=Homo sapiens OX=9606 GN=WDR43 PE=1 SV=3	0.630934	0.005508
P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ACADVL PE=1 SV=1	0.651794	0.005508

P57735	RAB25_HUMAN	Ras-related protein Rab-25 OS=Homo sapiens OX=9606 GN=RAB25 PE=1 SV=2	0.629582	0.005508
Q12874	SF3A3_HUMAN	Splicing factor 3A subunit 3 OS=Homo sapiens OX=9606 GN=SF3A3 PE=1 SV=1	0.682594	0.005508
Q99805	TM9S2_HUMAN	Transmembrane 9 superfamily member 2 OS=Homo sapiens OX=9606 GN=TM9SF2 PE=1 SV=1	0.632883	0.00551
P53350	PLK1_HUMAN	Serine/threonine-protein kinase PLK1 OS=Homo sapiens OX=9606 GN=PLK1 PE=1 SV=1	0.632342	0.00551
P52434	RPAB3_HUMAN	DNA-directed RNA polymerases I II and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H PE=1 SV=4	0.630098	0.005524
Q9Y6G9	DC1L1_HUMAN	Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens OX=9606 GN=DYNC1LI1 PE=1 SV=3	0.750708	0.005524
P21283	VATC1_HUMAN	V-type proton ATPase subunit C 1 OS=Homo sapiens OX=9606 GN=ATP6V1C1 PE=1 SV=4	0.61838	0.005525
Q13188	STK3_HUMAN	Serine/threonine-protein kinase 3 OS=Homo sapiens OX=9606 GN=STK3 PE=1 SV=2	0.675597	0.005525
P57081	WDR4_HUMAN	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4 OS=Homo sapiens OX=9606 GN=WDR4 PE=1 SV=2	0.631077	0.005547
P35249	RFC4_HUMAN	Replication factor C subunit 4 OS=Homo sapiens OX=9606 GN=RFC4 PE=1 SV=2	0.649072	0.005554
Q9NP72	RAB18_HUMAN	Ras-related protein Rab-18 OS=Homo sapiens OX=9606 GN=RAB18 PE=1 SV=1	0.614109	0.005594
Q8NHH9	ATLA2_HUMAN	Atlastin-2 OS=Homo sapiens OX=9606 GN=ATL2 PE=1 SV=2	0.629456	0.005601
P17980	PRS6A_HUMAN	26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=3	0.635767	0.005609
Q8TAT6	NPL4_HUMAN	Nuclear protein localization protein 4 homolog OS=Homo sapiens OX=9606 GN=NPLOC4 PE=1 SV=3	0.626839	0.005616
P28072	PSB6_HUMAN	Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=4	0.640997	0.005623
Q9H0W9	CK054_HUMAN	Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1	0.709801	0.005627
Q9H8T0	AKTIP_HUMAN	AKT-interacting protein OS=Homo sapiens OX=9606 GN=AKTIP PE=1 SV=1	0.630095	0.005627
Q8NFQ8	TOIP2_HUMAN	Torsin-1A-interacting protein 2 OS=Homo sapiens OX=9606 GN=TOR1AIP2 PE=1 SV=1	0.631218	0.005627
P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=2	0.59071	0.005627
Q15435	PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1	0.710493	0.005654
Q12996	CSTF3_HUMAN	Cleavage stimulation factor subunit 3 OS=Homo sapiens OX=9606 GN=CSTF3 PE=1 SV=1	0.617594	0.005654
O00629	IMA3_HUMAN	Importin subunit alpha-3 OS=Homo sapiens OX=9606 GN=KPNA4 PE=1 SV=1	0.62192	0.005722
Q86VM9	ZCH18_HUMAN	Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18 PE=1 SV=2	0.626213	0.005729
Q9Y2Q5	LTOR2_HUMAN	Ragulator complex protein LAMTOR2 OS=Homo sapiens OX=9606 GN=LAMTOR2 PE=1 SV=1	0.624574	0.005737
Q66K74	MAP1S_HUMAN	Microtubule-associated protein 1S OS=Homo sapiens OX=9606 GN=MAP1S PE=1 SV=2	0.625983	0.005759
P09110	THIK_HUMAN	3-ketoacyl-CoA thiolase peroxisomal OS=Homo sapiens OX=9606 GN=ACAA1 PE=1 SV=2	0.627034	0.005759
Q9Y4L1	HYOU1_HUMAN	Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1	0.655251	0.005761
P11047	LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3	0.605721	0.005769
P47985	UCRI_HUMAN	Cytochrome b-c1 complex subunit Rieske mitochondrial OS=Homo sapiens OX=9606 GN=UQCRCF1 PE=1 SV=2	0.624032	0.005777
P49458	SRP09_HUMAN	Signal recognition particle 9 kDa protein OS=Homo sapiens OX=9606 GN=SRP9 PE=1 SV=2	0.765907	0.005799
P78344	IF4G2_HUMAN	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1	0.775335	0.005869
O14893	GEMI2_HUMAN	Gem-associated protein 2 OS=Homo sapiens OX=9606 GN=GEMIN2 PE=1 SV=1	1.055804	0.005876
Q13813	SPTN1_HUMAN	Spectrin alpha chain non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=3	0.61176	0.005886
Q9UKK9	NUDT5_HUMAN	ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1	0.625604	0.005886
Q15007	FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP OS=Homo sapiens OX=9606 GN=WTAP PE=1 SV=2	0.797436	0.005908
Q9BRP8	PYM1_HUMAN	Partner of Y14 and mago OS=Homo sapiens OX=9606 GN=PYM1 PE=1 SV=1	0.625663	0.005943
O95400	CD2B2_HUMAN	CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens OX=9606 GN=CD2BP2 PE=1 SV=1	0.622381	0.00598

Q86V81	THOC4_HUMAN	THO complex subunit 4 OS=Homo sapiens OX=9606 GN=ALYREF PE=1 SV=3	0.624911	0.00598
P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=4	0.66038	0.006004
Q8WWY3	PRP31_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens OX=9606 GN=PRPF31 PE=1 SV=2	0.621251	0.006004
Q13586	STIM1_HUMAN	Stromal interaction molecule 1 OS=Homo sapiens OX=9606 GN=STIM1 PE=1 SV=3	0.599754	0.006012
Q96AG4	LRC59_HUMAN	Leucine-rich repeat-containing protein 59 OS=Homo sapiens OX=9606 GN=LRRCS9 PE=1 SV=1	0.596422	0.006092
Q9H2P0	ADNP_HUMAN	Activity-dependent neuroprotector homeobox protein OS=Homo sapiens OX=9606 GN=ADNP PE=1 SV=1	0.625214	0.006092
O94906	PRP6_HUMAN	Pre-mRNA-processing factor 6 OS=Homo sapiens OX=9606 GN=PRPF6 PE=1 SV=1	0.589021	0.006115
P06756	ITAV_HUMAN	Integrin alpha-V OS=Homo sapiens OX=9606 GN=ITGAV PE=1 SV=2	0.68268	0.006131
O60762	DPM1_HUMAN	Dolichol-phosphate mannosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=DPM1 PE=1 SV=1	0.621426	0.006153
Q92597	NDRG1_HUMAN	Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1	0.619245	0.006162
O14737	PDCD5_HUMAN	Programmed cell death protein 5 OS=Homo sapiens OX=9606 GN=PDCD5 PE=1 SV=3	0.605721	0.006164
Q14435	GALT3_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 3 OS=Homo sapiens OX=9606 GN=GALNT3 PE=1 SV=2	0.617827	0.006164
P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 OS=Homo sapiens OX=9606 GN=PSMA1 PE=1 SV=1	0.620808	0.006201
Q16775	GLO2_HUMAN	Hydroxyacylglutathione hydrolase mitochondrial OS=Homo sapiens OX=9606 GN=HAGH PE=1 SV=2	0.620168	0.006231
P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha OS=Homo sapiens OX=9606 GN=GDI1 PE=1 SV=2	0.58679	0.006231
P51580	TPMT_HUMAN	Thiopurine S-methyltransferase OS=Homo sapiens OX=9606 GN=TPMT PE=1 SV=1	0.6192	0.006231
Q9Y5K8	VATD_HUMAN	V-type proton ATPase subunit D OS=Homo sapiens OX=9606 GN=ATP6V1D PE=1 SV=1	0.620494	0.006231
P04439	HLAA_HUMAN	HLA class I histocompatibility antigen A alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2	0.619996	0.006231
Q8NEF9	SRFB1_HUMAN	Serum response factor-binding protein 1 OS=Homo sapiens OX=9606 GN=SRFBP1 PE=1 SV=1	0.724133	0.006231
Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=3	0.618706	0.006233
Q8WTT2	NOC3L_HUMAN	Nucleolar complex protein 3 homolog OS=Homo sapiens OX=9606 GN=NOC3L PE=1 SV=1	1.205147	0.006233
O94925	GLSK_HUMAN	Glutaminase kidney isoform mitochondrial OS=Homo sapiens OX=9606 GN=GLS PE=1 SV=1	0.634867	0.006236
P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens OX=9606 GN=G6PD PE=1 SV=4	0.672749	0.006288
Q9P287	BCCIP_HUMAN	BRCA2 and CDKN1A-interacting protein OS=Homo sapiens OX=9606 GN=BCCIP PE=1 SV=1	0.73434	0.006296
Q13404	UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens OX=9606 GN=UBE2V1 PE=1 SV=2	0.619977	0.006299
Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens OX=9606 GN=MAPRE1 PE=1 SV=3	0.587273	0.006299
Q15382	RHEB_HUMAN	GTP-binding protein Rheb OS=Homo sapiens OX=9606 GN=RHEB PE=1 SV=1	0.61995	0.006345
Q99848	EBP2_HUMAN	Probable rRNA-processing protein EBP2 OS=Homo sapiens OX=9606 GN=EBNA1BP2 PE=1 SV=2	0.591061	0.006345
Q9NY12	GAR1_HUMAN	H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens OX=9606 GN=GAR1 PE=1 SV=1	0.622299	0.006368
Q71RC2	LARP4_HUMAN	La-related protein 4 OS=Homo sapiens OX=9606 GN=LARP4 PE=1 SV=3	0.620982	0.006377
P63104	1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1	0.618105	0.00638
Q8NFH5	NUP35_HUMAN	Nucleoporin NUP35 OS=Homo sapiens OX=9606 GN=NUP35 PE=1 SV=1	0.618499	0.00638
P10321	HLAC_HUMAN	HLA class I histocompatibility antigen C alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=3	0.612097	0.006442
Q53EL6	PDCD4_HUMAN	Programmed cell death protein 4 OS=Homo sapiens OX=9606 GN=PDCD4 PE=1 SV=2	0.61598	0.00645
Q15717	ELAV1_HUMAN	ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=2	0.589301	0.006489
Q9Y282	ERGI3_HUMAN	Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Homo sapiens OX=9606 GN=ERGIC3 PE=1 SV=1	0.615051	0.006573
P08779	K1C16_HUMAN	Keratin type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4	0.610053	0.006582

O14974	MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1	0.670432	0.006591
Q12979	ABR_HUMAN	Active breakpoint cluster region-related protein OS=Homo sapiens OX=9606 GN=ABR PE=1 SV=2	0.614203	0.0066
Q8WXF1	PSPC1_HUMAN	Paraspeckle component 1 OS=Homo sapiens OX=9606 GN=PSPC1 PE=1 SV=1	0.748461	0.00664
P48506	GSH1_HUMAN	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens OX=9606 GN=GCLC PE=1 SV=2	0.614086	0.00672
Q9BWM7	SFXN3_HUMAN	Sideroflexin-3 OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=3	0.612142	0.006744
P04080	CYTB_HUMAN	Cystatin-B OS=Homo sapiens OX=9606 GN=CSTB PE=1 SV=2	0.608391	0.006769
P36404	ARL2_HUMAN	ADP-ribosylation factor-like protein 2 OS=Homo sapiens OX=9606 GN=ARL2 PE=1 SV=4	0.613538	0.006779
Q2M389	WASC4_HUMAN	WASH complex subunit 4 OS=Homo sapiens OX=9606 GN=WASHC4 PE=1 SV=2	0.611269	0.006813
P42126	ECI1_HUMAN	Enoyl-CoA delta isomerase 1 mitochondrial OS=Homo sapiens OX=9606 GN=ECI1 PE=1 SV=1	0.614461	0.006813
Q14315	FLNC_HUMAN	Filamin-C OS=Homo sapiens OX=9606 GN=FLNC PE=1 SV=3	0.607158	0.006822
P30622	CLIP1_HUMAN	CAP-Gly domain-containing linker protein 1 OS=Homo sapiens OX=9606 GN=CLIP1 PE=1 SV=2	0.744974	0.006832
Q8IWX8	CHERP_HUMAN	Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens OX=9606 GN=CHERP PE=1 SV=3	0.612487	0.006841
P61960	UFM1_HUMAN	Ubiquitin-fold modifier 1 OS=Homo sapiens OX=9606 GN=UFM1 PE=1 SV=1	0.610908	0.006892
Q8IZL8	PELP1_HUMAN	Proline- glutamic acid- and leucine-rich protein 1 OS=Homo sapiens OX=9606 GN=PELP1 PE=1 SV=2	0.677228	0.006892
Q9Y2K7	KDM2A_HUMAN	Lysine-specific demethylase 2A OS=Homo sapiens OX=9606 GN=KDM2A PE=1 SV=3	0.610759	0.00692
Q13363	CTBP1_HUMAN	C-terminal-binding protein 1 OS=Homo sapiens OX=9606 GN=CTBP1 PE=1 SV=2	0.609306	0.00692
P61923	COPZ1_HUMAN	Coatamer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1	0.603448	0.00693
Q9Y547	IFT25_HUMAN	Intraflagellar transport protein 25 homolog OS=Homo sapiens OX=9606 GN=HSPB11 PE=1 SV=1	0.993411	0.007014
P43243	MATR3_HUMAN	Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=2	0.618129	0.007082
Q9H3P2	NELFA_HUMAN	Negative elongation factor A OS=Homo sapiens OX=9606 GN=NELFA PE=1 SV=3	0.601517	0.007092
Q86UE4	LYRIC_HUMAN	Protein LYRIC OS=Homo sapiens OX=9606 GN=MTDH PE=1 SV=2	0.619307	0.007134
Q14558	KPRA_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens OX=9606 GN=PRPSAP1 PE=1 SV=2	0.661198	0.007144
P99999	CYC_HUMAN	Cytochrome c OS=Homo sapiens OX=9606 GN=CYCS PE=1 SV=2	0.608429	0.007171
Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=2	0.626215	0.007181
Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H OS=Homo sapiens OX=9606 GN=EIF4H PE=1 SV=5	0.619998	0.007224
P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1	0.609969	0.007244
O00186	STXB3_HUMAN	Syntaxin-binding protein 3 OS=Homo sapiens OX=9606 GN=STXBP3 PE=1 SV=2	0.607482	0.007288
Q14157	UBP2L_HUMAN	Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L PE=1 SV=2	0.637245	0.007325
P26196	DDX6_HUMAN	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens OX=9606 GN=DDX6 PE=1 SV=2	0.583465	0.007369
O75832	PSD10_HUMAN	26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens OX=9606 GN=PSMD10 PE=1 SV=1	0.60747	0.007373
Q99733	NP1L4_HUMAN	Nucleosome assembly protein 1-like 4 OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1	0.605018	0.007425
Q4G0J3	LARP7_HUMAN	La-related protein 7 OS=Homo sapiens OX=9606 GN=LARP7 PE=1 SV=1	0.608202	0.007425
P62829	RL23_HUMAN	60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1	0.604263	0.007425
Q16740	CLPP_HUMAN	ATP-dependent Clp protease proteolytic subunit mitochondrial OS=Homo sapiens OX=9606 GN=CLPP PE=1 SV=1	0.642319	0.007425
Q9NRF9	DPOE3_HUMAN	DNA polymerase epsilon subunit 3 OS=Homo sapiens OX=9606 GN=POLE3 PE=1 SV=1	0.606336	0.007435
P54619	AAKG1_HUMAN	5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens OX=9606 GN=PRKAG1 PE=1 SV=1	0.604508	0.007447
Q9H8S9	MOB1A_HUMAN	MOB kinase activator 1A OS=Homo sapiens OX=9606 GN=MOB1A PE=1 SV=4	0.604242	0.007447
Q7L9L4	MOB1B_HUMAN	MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B PE=1 SV=3	0.604242	0.007447

P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1	0.603472	0.007447
Q9BV20	MTNA_HUMAN	Methylthioribose-1-phosphate isomerase OS=Homo sapiens OX=9606 GN=MR11 PE=1 SV=1	0.604271	0.007447
A0FGR8	ESYT2_HUMAN	Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1	0.705175	0.007468
P06493	CDK1_HUMAN	Cyclin-dependent kinase 1 OS=Homo sapiens OX=9606 GN=CDK1 PE=1 SV=3	0.694099	0.00753
P19623	SPEE_HUMAN	Spermidine synthase OS=Homo sapiens OX=9606 GN=SRM PE=1 SV=1	0.674243	0.007541
P22676	CALB2_HUMAN	Calretinin OS=Homo sapiens OX=9606 GN=CALB2 PE=2 SV=2	0.601082	0.007621
P22059	OSBP1_HUMAN	Oxysterol-binding protein 1 OS=Homo sapiens OX=9606 GN=OSBP PE=1 SV=1	0.600229	0.00766
Q9UJS0	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens OX=9606 GN=SLC25A13 PE=1 SV=2	0.62864	0.007671
O14818	PSA7_HUMAN	Proteasome subunit alpha type-7 OS=Homo sapiens OX=9606 GN=PSMA7 PE=1 SV=1	0.670041	0.0077
P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3	0.610433	0.007739
P30084	ECHM_HUMAN	Enoyl-CoA hydratase mitochondrial OS=Homo sapiens OX=9606 GN=ECHS1 PE=1 SV=4	0.633872	0.007744
P09132	SRP19_HUMAN	Signal recognition particle 19 kDa protein OS=Homo sapiens OX=9606 GN=SRP19 PE=1 SV=3	0.602469	0.007744
P16144	ITB4_HUMAN	Integrin beta-4 OS=Homo sapiens OX=9606 GN=ITGB4 PE=1 SV=5	0.605197	0.007766
Q9NR50	EI2BG_HUMAN	Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens OX=9606 GN=EIF2B3 PE=1 SV=1	0.602829	0.007766
Q9H0A0	NAT10_HUMAN	RNA cytidine acetyltransferase OS=Homo sapiens OX=9606 GN=NAT10 PE=1 SV=2	0.601219	0.007817
Q9BUR5	MIC26_HUMAN	MICOS complex subunit MIC26 OS=Homo sapiens OX=9606 GN=APOO PE=1 SV=1	1.449833	0.007846
P30154	2AAB_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=3	0.599955	0.007857
P11387	TOP1_HUMAN	DNA topoisomerase 1 OS=Homo sapiens OX=9606 GN=TOP1 PE=1 SV=2	0.612683	0.007887
P35270	SPRE_HUMAN	Sepiapterin reductase OS=Homo sapiens OX=9606 GN=SPR PE=1 SV=1	0.596772	0.007916
Q8N5K1	CISD2_HUMAN	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CISD2 PE=1 SV=1	0.600294	0.008001
O95219	SNX4_HUMAN	Sorting nexin-4 OS=Homo sapiens OX=9606 GN=SNX4 PE=1 SV=1	0.600616	0.008035
P62847	RS24_HUMAN	40S ribosomal protein S24 OS=Homo sapiens OX=9606 GN=RPS24 PE=1 SV=1	0.596458	0.00804
P52735	VAV2_HUMAN	Guanine nucleotide exchange factor VAV2 OS=Homo sapiens OX=9606 GN=VAV2 PE=1 SV=2	0.598597	0.00804
Q15434	RBMS2_HUMAN	RNA-binding motif single-stranded-interacting protein 2 OS=Homo sapiens OX=9606 GN=RBMS2 PE=1 SV=1	0.600745	0.008107
O94905	ERLN2_HUMAN	Erlin-2 OS=Homo sapiens OX=9606 GN=ERLIN2 PE=1 SV=1	0.712146	0.008161
Q8WYA6	CTBL1_HUMAN	Beta-catenin-like protein 1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1	0.594756	0.008205
P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=3	0.628169	0.008205
Q12792	TWF1_HUMAN	Twinfilin-1 OS=Homo sapiens OX=9606 GN=TWF1 PE=1 SV=3	0.644756	0.008205
P49593	PPM1F_HUMAN	Protein phosphatase 1F OS=Homo sapiens OX=9606 GN=PPM1F PE=1 SV=3	0.782993	0.008205
Q9H6F5	CCD86_HUMAN	Coiled-coil domain-containing protein 86 OS=Homo sapiens OX=9606 GN=CCDC86 PE=1 SV=1	0.596985	0.008205
Q9UNZ2	NSF1C_HUMAN	NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=2	0.611435	0.008205
Q15819	UB2V2_HUMAN	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens OX=9606 GN=UBE2V2 PE=1 SV=4	0.596876	0.008248
P62906	RL10A_HUMAN	60S ribosomal protein L10a OS=Homo sapiens OX=9606 GN=RPL10A PE=1 SV=2	0.582941	0.008248
Q16637	SMN_HUMAN	Survival motor neuron protein OS=Homo sapiens OX=9606 GN=SMN1 PE=1 SV=1	0.597108	0.00826
P52630	STAT2_HUMAN	Signal transducer and activator of transcription 2 OS=Homo sapiens OX=9606 GN=STAT2 PE=1 SV=1	0.600468	0.008272
Q9Y3B3	TMED7_HUMAN	Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens OX=9606 GN=TMED7 PE=1 SV=2	0.594398	0.008296
Q9H8Y8	GORS2_HUMAN	Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2 PE=1 SV=3	0.628357	0.008327
P62258	1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1	0.645424	0.008332

O00273	DFFA_HUMAN	DNA fragmentation factor subunit alpha OS=Homo sapiens OX=9606 GN=DFFA PE=1 SV=1	0.728838	0.008337
P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1 PE=1 SV=3	0.637124	0.008337
P32004	L1CAM_HUMAN	Neural cell adhesion molecule L1 OS=Homo sapiens OX=9606 GN=L1CAM PE=1 SV=2	0.593069	0.008368
Q9UQB8	BAIP2_HUMAN	Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens OX=9606 GN=BAIP2 PE=1 SV=1	0.664074	0.00838
P48507	GSHO_HUMAN	Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens OX=9606 GN=GCLM PE=1 SV=1	0.96384	0.008431
P46109	CRKL_HUMAN	Crk-like protein OS=Homo sapiens OX=9606 GN=CRKL PE=1 SV=1	0.712962	0.008488
Q727L1	SLN11_HUMAN	Schlafen family member 11 OS=Homo sapiens OX=9606 GN=SLFN11 PE=1 SV=2	0.617571	0.008493
Q9BW83	IFT27_HUMAN	Intraflagellar transport protein 27 homolog OS=Homo sapiens OX=9606 GN=IFT27 PE=1 SV=1	0.595434	0.008493
Q14353	GAMT_HUMAN	Guanidinoacetate N-methyltransferase OS=Homo sapiens OX=9606 GN=GAMT PE=1 SV=1	0.593747	0.008505
Q8NBJ4	GOLM1_HUMAN	Golgi membrane protein 1 OS=Homo sapiens OX=9606 GN=GOLM1 PE=1 SV=1	0.759621	0.008537
Q8NFW8	NEUA_HUMAN	N-acylneuraminate cytidyltransferase OS=Homo sapiens OX=9606 GN=CMAS PE=1 SV=2	0.590417	0.008569
Q92905	CSN5_HUMAN	COP9 signalosome complex subunit 5 OS=Homo sapiens OX=9606 GN=COP55 PE=1 SV=4	0.657922	0.008601
Q14241	ELOA1_HUMAN	Elongin-A OS=Homo sapiens OX=9606 GN=ELOA PE=1 SV=2	0.642072	0.008607
Q9NPD3	EXOS4_HUMAN	Exosome complex component RRP41 OS=Homo sapiens OX=9606 GN=EXOSC4 PE=1 SV=3	0.592549	0.008607
Q9UMS0	NFU1_HUMAN	NFU1 iron-sulfur cluster scaffold homolog mitochondrial OS=Homo sapiens OX=9606 GN=NFU1 PE=1 SV=2	0.590209	0.008619
O00487	PSDE_HUMAN	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens OX=9606 GN=PSMD14 PE=1 SV=1	0.580767	0.008645
P47813	IF1AX_HUMAN	Eukaryotic translation initiation factor 1A X-chromosomal OS=Homo sapiens OX=9606 GN=EIF1AX PE=1 SV=2	0.600481	0.00865
Q9Y2T2	AP3M1_HUMAN	AP-3 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP3M1 PE=1 SV=1	0.591924	0.008675
P62873	GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens OX=9606 GN=GNB1 PE=1 SV=3	0.592493	0.008675
P05026	AT1B1_HUMAN	Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens OX=9606 GN=ATP1B1 PE=1 SV=1	0.622466	0.008681
Q92575	UBXN4_HUMAN	UBX domain-containing protein 4 OS=Homo sapiens OX=9606 GN=UBXN4 PE=1 SV=2	0.659086	0.008681
P21333	FLNA_HUMAN	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4	0.604515	0.008686
Q9Y679	AUP1_HUMAN	Ancient ubiquitous protein 1 OS=Homo sapiens OX=9606 GN=AUP1 PE=1 SV=2	0.593959	0.008699
Q86X55	CARM1_HUMAN	Histone-arginine methyltransferase CARM1 OS=Homo sapiens OX=9606 GN=CARM1 PE=1 SV=3	0.592462	0.00873
O43324	MCA3_HUMAN	Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens OX=9606 GN=EEF1E1 PE=1 SV=1	0.593702	0.00873
P02786	TFR1_HUMAN	Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2	0.600996	0.008763
P35232	PHB_HUMAN	Prohibitin OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=1	0.648442	0.008789
O15400	STX7_HUMAN	Syntaxin-7 OS=Homo sapiens OX=9606 GN=STX7 PE=1 SV=4	0.590851	0.008806
P0DN76	U2AF5_HUMAN	Splicing factor U2AF 35 kDa subunit-like protein OS=Homo sapiens OX=9606 GN=U2AF1L5 PE=1 SV=1	0.662029	0.008806
Q01081	U2AF1_HUMAN	Splicing factor U2AF 35 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF1 PE=1 SV=3	0.662029	0.008806
P61019	RAB2A_HUMAN	Ras-related protein Rab-2A OS=Homo sapiens OX=9606 GN=RAB2A PE=1 SV=1	0.590862	0.008806
Q9Y223	GLCNE_HUMAN	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Homo sapiens OX=9606 GN=GNE PE=1 SV=1	0.73596	0.008806
Q9Y2Z0	SGT1_HUMAN	Protein SGT1 homolog OS=Homo sapiens OX=9606 GN=SUGT1 PE=1 SV=3	0.644244	0.008825
Q92896	GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sapiens OX=9606 GN=GLG1 PE=1 SV=2	0.704787	0.008879
Q16543	CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1	0.620527	0.008892
Q96B54	ZN428_HUMAN	Zinc finger protein 428 OS=Homo sapiens OX=9606 GN=ZNF428 PE=1 SV=2	0.58803	0.008946
Q92522	H1X_HUMAN	Histone H1x OS=Homo sapiens OX=9606 GN=H1FX PE=1 SV=1	0.589391	0.008959
Q9ULW0	TPX2_HUMAN	Targeting protein for Xklp2 OS=Homo sapiens OX=9606 GN=TPX2 PE=1 SV=2	0.589067	0.008965

Q01105	SET_HUMAN	Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=3	0.593951	0.008971
Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB PE=1 SV=4	0.629252	0.008971
P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1	0.638841	0.009026
P11802	CDK4_HUMAN	Cyclin-dependent kinase 4 OS=Homo sapiens OX=9606 GN=CDK4 PE=1 SV=2	0.587482	0.00906
O60828	PQBP1_HUMAN	Polyglutamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PQBP1 PE=1 SV=1	0.589281	0.009074
Q15758	AAAT_HUMAN	Neutral amino acid transporter B(0) OS=Homo sapiens OX=9606 GN=SLC1A5 PE=1 SV=2	0.668731	0.00908
Q7RTV0	PHF5A_HUMAN	PHD finger-like domain-containing protein 5A OS=Homo sapiens OX=9606 GN=PHF5A PE=1 SV=1	0.587402	0.00908
P07741	APT_HUMAN	Adenine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=2	0.637895	0.009086
P07858	CATB_HUMAN	Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3	0.602213	0.009086
Q9NUJ1	ABHDA_HUMAN	Mycophenolic acid acyl-glucuronide esterase mitochondrial OS=Homo sapiens OX=9606 GN=ABHD10 PE=1 SV=1	0.585521	0.00912
P62310	LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSM3 OS=Homo sapiens OX=9606 GN=LSM3 PE=1 SV=2	0.592194	0.009134
Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 OS=Homo sapiens OX=9606 GN=ERP44 PE=1 SV=1	0.588809	0.009188
Q86VR2	RETR3_HUMAN	Reticulophagy regulator 3 OS=Homo sapiens OX=9606 GN=RETREG3 PE=1 SV=1	0.588333	0.009188
Q9Y295	DRG1_HUMAN	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=DRG1 PE=1 SV=1	0.622362	0.009188
P33240	CSTF2_HUMAN	Cleavage stimulation factor subunit 2 OS=Homo sapiens OX=9606 GN=CSTF2 PE=1 SV=1	0.585983	0.009188
P27707	DCK_HUMAN	Deoxycytidine kinase OS=Homo sapiens OX=9606 GN=DCK PE=1 SV=1	0.586357	0.00923
O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1	0.59088	0.009244
Q16531	DDB1_HUMAN	DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DDB1 PE=1 SV=1	0.587888	0.009271
Q9GZT8	NIF3L_HUMAN	NIF3-like protein 1 OS=Homo sapiens OX=9606 GN=NIF3L1 PE=1 SV=2	0.615177	0.009271
Q9Y237	PIN4_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Homo sapiens OX=9606 GN=PIN4 PE=1 SV=1	0.703464	0.009328
Q9H3U1	UN45A_HUMAN	Protein unc-45 homolog A OS=Homo sapiens OX=9606 GN=UNC45A PE=1 SV=1	0.618625	0.009342
P23368	MAOM_HUMAN	NAD-dependent malic enzyme mitochondrial OS=Homo sapiens OX=9606 GN=ME2 PE=1 SV=1	0.582347	0.009443
O15260	SURF4_HUMAN	Surfeit locus protein 4 OS=Homo sapiens OX=9606 GN=SURF4 PE=1 SV=3	0.693617	0.009471
Q9Y512	SAM50_HUMAN	Sorting and assembly machinery component 50 homolog OS=Homo sapiens OX=9606 GN=SAMM50 PE=1 SV=3	0.58041	0.009529
O95394	AGM1_HUMAN	Phosphoacetylglucosamine mutase OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1	0.587098	0.00958
Q9C0C2	TB182_HUMAN	182 kDa tankyrase-1-binding protein OS=Homo sapiens OX=9606 GN=TNKS1BP1 PE=1 SV=4	0.6074	0.009594
Q9BVC4	LST8_HUMAN	Target of rapamycin complex subunit LST8 OS=Homo sapiens OX=9606 GN=MLST8 PE=1 SV=1	1.069096	0.009675
Q9Y263	PLAP_HUMAN	Phospholipase A-2-activating protein OS=Homo sapiens OX=9606 GN=PLAA PE=1 SV=2	0.700635	0.009704
Q96BP3	PPWD1_HUMAN	Peptidylprolyl isomerase domain and WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=PPWD1 PE=1 SV=1	0.58325	0.009719
Q5T6F2	UBAP2_HUMAN	Ubiquitin-associated protein 2 OS=Homo sapiens OX=9606 GN=UBAP2 PE=1 SV=1	0.602561	0.009748
P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein OS=Homo sapiens OX=9606 GN=VASP PE=1 SV=3	0.595961	0.00977

Appendix Table 3: 16HBE14o⁺ global proteome changes following DPCP exposure –

Proteins with a significant difference in abundance are presented according to descending log2 fold change.

A.2.5 Significant proteome changes in 16HE14o⁻ cells following exposure to PA

Accession	Uniprot ID	Description	Log2 Fold Change	P value (FDR)
Q15397	PUM3_HUMAN	Pumilio homolog 3 OS=Homo sapiens OX=9606 GN=PUM3 PE=1 SV=3	2.89802	7.26E-04
Q9Y2W6	TDRKH_HUMAN	Tudor and KH domain-containing protein OS=Homo sapiens OX=9606 GN=TDRKH PE=1 SV=2	2.555789	0.007918
P68431	H31_HUMAN	Histone H3.1 OS=Homo sapiens OX=9606 GN=H3C1 PE=1 SV=2	2.091326	1.14E-17
Q13126	MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP PE=1 SV=2	1.911749	1.14E-17
P62081	RS7_HUMAN	40S ribosomal protein S7 OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1	1.873438	1.14E-17
Q96T60	PNKP_HUMAN	Bifunctional polynucleotide phosphatase/kinase OS=Homo sapiens OX=9606 GN=PNKP PE=1 SV=1	1.803908	5.33E-05
Q8IYU8	MICU2_HUMAN	Calcium uptake protein 2 mitochondrial OS=Homo sapiens OX=9606 GN=MICU2 PE=1 SV=2	1.731113	1.83E-04
Q8NCF5	NF2IP_HUMAN	NFATC2-interacting protein OS=Homo sapiens OX=9606 GN=NFATC2IP PE=1 SV=1	1.703365	0.003547
Q9H1P3	OSBL2_HUMAN	Oxysterol-binding protein-related protein 2 OS=Homo sapiens OX=9606 GN=OSBPL2 PE=1 SV=1	1.632629	2.63E-08
P20591	MX1_HUMAN	Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens OX=9606 GN=MX1 PE=1 SV=4	1.609597	0.001564
Q9H7D7	WDR26_HUMAN	WD repeat-containing protein 26 OS=Homo sapiens OX=9606 GN=WDR26 PE=1 SV=3	1.601909	9.52E-13
O60885	BRD4_HUMAN	Bromodomain-containing protein 4 OS=Homo sapiens OX=9606 GN=BRD4 PE=1 SV=2	1.598684	3.70E-06
Q71DI3	H32_HUMAN	Histone H3.2 OS=Homo sapiens OX=9606 GN=HIST2H3A PE=1 SV=3	1.596039	4.09E-11
P42696	RBM34_HUMAN	RNA-binding protein 34 OS=Homo sapiens OX=9606 GN=RBM34 PE=1 SV=2	1.550855	2.39E-04
P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E OS=Homo sapiens OX=9606 GN=SNRPE PE=1 SV=1	1.491244	0.0016
O00505	IMA4_HUMAN	Importin subunit alpha-4 OS=Homo sapiens OX=9606 GN=KPNA3 PE=1 SV=2	1.459686	1.12E-10
Q8NFC6	BD1L1_HUMAN	Biorientation of chromosomes in cell division protein 1-like 1 OS=Homo sapiens OX=9606 GN=BOD1L1 PE=1 SV=2	1.459281	1.12E-10
P13995	MTDC_HUMAN	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD2 PE=1 SV=2	1.452032	1.36E-10
Q9Y2R4	DDX52_HUMAN	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens OX=9606 GN=DDX52 PE=1 SV=3	1.449091	0.003845
P62841	RS15_HUMAN	40S ribosomal protein S15 OS=Homo sapiens OX=9606 GN=RPS15 PE=1 SV=2	1.431279	3.57E-11
Q9Y3Y2	CHTOP_HUMAN	Chromatin target of PRMT1 protein OS=Homo sapiens OX=9606 GN=CHTOP PE=1 SV=2	1.429794	4.45E-06
Q8WTT2	NOC3L_HUMAN	Nucleolar complex protein 3 homolog OS=Homo sapiens OX=9606 GN=NOC3L PE=1 SV=1	1.421564	3.52E-04
Q9NXF1	TEX10_HUMAN	Testis-expressed protein 10 OS=Homo sapiens OX=9606 GN=TEX10 PE=1 SV=2	1.420038	3.34E-10
O43252	PAPS1_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens OX=9606 GN=PAPSS1 PE=1 SV=2	1.419225	3.34E-10
P82663	RT25_HUMAN	28S ribosomal protein S25 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS25 PE=1 SV=1	1.386838	6.51E-06
P32119	PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens OX=9606 GN=PRDX2 PE=1 SV=5	1.365914	0.005596
Q68E01	INT3_HUMAN	Integrator complex subunit 3 OS=Homo sapiens OX=9606 GN=INTS3 PE=1 SV=1	1.364725	0.004217
Q8N183	NDUF2_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 2 OS=Homo sapiens OX=9606 GN=NDUFAF2 PE=1 SV=1	1.35848	9.33E-04
Q9BYG5	PAR6B_HUMAN	Partitioning defective 6 homolog beta OS=Homo sapiens OX=9606 GN=PAR6B PE=1 SV=1	1.356694	1.13E-04
P25942	TNR5_HUMAN	Tumor necrosis factor receptor superfamily member 5 OS=Homo sapiens OX=9606 GN=CD40 PE=1 SV=1	1.343234	3.53E-09
Q9GZM5	YIPF3_HUMAN	Protein YIPF3 OS=Homo sapiens OX=9606 GN=YIPF3 PE=1 SV=1	1.338048	0.001163
Q96RE7	NACC1_HUMAN	Nucleus accumbens-associated protein 1 OS=Homo sapiens OX=9606 GN=NACC1 PE=1 SV=1	1.334285	3.29E-06
Q9NNW7	TRXR2_HUMAN	Thioredoxin reductase 2 mitochondrial OS=Homo sapiens OX=9606 GN=TXNRD2 PE=1 SV=3	1.303365	1.21E-08
P61204	ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=2	1.280108	2.63E-08

P84077	ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapiens OX=9606 GN=ARF1 PE=1 SV=2	1.280108	2.63E-08
P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNP2 PE=1 SV=1	1.279859	2.63E-08
Q6ZS17	RIPR1_HUMAN	Rho family-interacting cell polarization regulator 1 OS=Homo sapiens OX=9606 GN=RIPOR1 PE=1 SV=1	1.279345	2.29E-08
P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 OS=Homo sapiens OX=9606 GN=PTPN6 PE=1 SV=1	1.278163	2.43E-08
Q9NPI6	DCP1A_HUMAN	mRNA-decapping enzyme 1A OS=Homo sapiens OX=9606 GN=DCP1A PE=1 SV=3	1.259899	3.08E-06
Q9Y613	FHOD1_HUMAN	FH1/FH2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FHOD1 PE=1 SV=3	1.247686	5.43E-09
Q5ZPR3	CD276_HUMAN	CD276 antigen OS=Homo sapiens OX=9606 GN=CD276 PE=1 SV=1	1.247602	5.46E-08
O75923	DYSF_HUMAN	Dysferlin OS=Homo sapiens OX=9606 GN=DYSF PE=1 SV=1	1.241197	1.36E-10
Q9BRT3	MIEN1_HUMAN	Migration and invasion enhancer 1 OS=Homo sapiens OX=9606 GN=MIEN1 PE=1 SV=1	1.235256	2.97E-06
Q04446	GLGB_HUMAN	1 4-alpha-glucan-branching enzyme OS=Homo sapiens OX=9606 GN=GBE1 PE=1 SV=3	1.233888	7.79E-08
Q6IQ22	RAB12_HUMAN	Ras-related protein Rab-12 OS=Homo sapiens OX=9606 GN=RAB12 PE=1 SV=3	1.228035	8.57E-08
Q969V3	NCLN_HUMAN	Nicalin OS=Homo sapiens OX=9606 GN=NCLN PE=1 SV=2	1.227395	8.57E-08
P08237	PFKAM_HUMAN	ATP-dependent 6-phosphofructokinase muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=2	1.210666	3.18E-09
O14933	UB2L6_HUMAN	Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens OX=9606 GN=UBE2L6 PE=1 SV=4	1.210053	4.90E-06
Q9H0A8	COMD4_HUMAN	COMM domain-containing protein 4 OS=Homo sapiens OX=9606 GN=COMMD4 PE=1 SV=1	1.199482	0.003845
Q15418	KS6A1_HUMAN	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1 SV=2	1.195085	6.99E-11
Q8IWZ8	SUGP1_HUMAN	SURP and G-patch domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUGP1 PE=1 SV=2	1.187711	2.81E-07
O75152	ZC11A_HUMAN	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens OX=9606 GN=ZC3H11A PE=1 SV=3	1.182394	3.57E-07
Q9Y5Q9	TF3C3_HUMAN	General transcription factor 3C polypeptide 3 OS=Homo sapiens OX=9606 GN=GTF3C3 PE=1 SV=1	1.178233	3.42E-07
Q14671	PUM1_HUMAN	Pumilio homolog 1 OS=Homo sapiens OX=9606 GN=PUM1 PE=1 SV=3	1.175087	3.57E-07
Q16352	AINX_HUMAN	Alpha-internexin OS=Homo sapiens OX=9606 GN=INA PE=1 SV=2	1.174901	3.57E-07
Q8WVQ1	CANT1_HUMAN	Soluble calcium-activated nucleotidase 1 OS=Homo sapiens OX=9606 GN=CANT1 PE=1 SV=1	1.174371	3.57E-07
O00754	MA2B1_HUMAN	Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=3	1.172623	3.57E-07
Q16637	SMN_HUMAN	Survival motor neuron protein OS=Homo sapiens OX=9606 GN=SMN1 PE=1 SV=1	1.172375	7.12E-06
O75190	DNJB6_HUMAN	DnaJ homolog subfamily B member 6 OS=Homo sapiens OX=9606 GN=DNAJB6 PE=1 SV=2	1.168516	4.01E-07
Q53EL6	PDCD4_HUMAN	Programmed cell death protein 4 OS=Homo sapiens OX=9606 GN=PDCD4 PE=1 SV=2	1.160711	6.52E-07
P31949	S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens OX=9606 GN=S100A11 PE=1 SV=2	1.15794	4.76E-07
P45985	MP2K4_HUMAN	Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens OX=9606 GN=MAP2K4 PE=1 SV=1	1.157681	5.28E-07
O60825	F262_HUMAN	6-phosphofructo-2-kinase/fructose-2 6-bisphosphatase 2 OS=Homo sapiens OX=9606 GN=PFKFB2 PE=1 SV=2	1.157541	5.08E-07
Q9NY27	PP4R2_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PPP4R2 PE=1 SV=3	1.15555	9.16E-06
P10412	H14_HUMAN	Histone H1.4 OS=Homo sapiens OX=9606 GN=H1-4 PE=1 SV=2	1.153474	5.75E-07
O14972	VP26C_HUMAN	Vacuolar protein sorting-associated protein 26C OS=Homo sapiens OX=9606 GN=VPS26C PE=1 SV=1	1.152674	8.70E-04
Q9Y2D5	AKAP2_HUMAN	A-kinase anchor protein 2 OS=Homo sapiens OX=9606 GN=AKAP2 PE=1 SV=3	1.149364	6.09E-07
Q9H9E3	COG4_HUMAN	Conserved oligomeric Golgi complex subunit 4 OS=Homo sapiens OX=9606 GN=COG4 PE=1 SV=3	1.14711	6.09E-07
Q8NFZ8	CADM4_HUMAN	Cell adhesion molecule 4 OS=Homo sapiens OX=9606 GN=CADM4 PE=1 SV=1	1.145258	6.52E-07
Q13347	EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens OX=9606 GN=EIF3I PE=1 SV=1	1.134179	6.76E-05
Q8WUH6	TM263_HUMAN	Transmembrane protein 263 OS=Homo sapiens OX=9606 GN=TMEM263 PE=1 SV=1	1.123666	1.12E-06
P46977	STT3A_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens OX=9606 GN=STT3A PE=1 SV=2	1.123232	3.08E-06

Q15057	ACAP2_HUMAN	Arf-GAP with coiled-coil ANK repeat and PH domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ACAP2 PE=1 SV=3	1.119545	4.06E-05
P17676	CEBPB_HUMAN	CCAAT/enhancer-binding protein beta OS=Homo sapiens OX=9606 GN=CEBPB PE=1 SV=2	1.114333	1.33E-06
O75886	STAM2_HUMAN	Signal transducing adapter molecule 2 OS=Homo sapiens OX=9606 GN=STAM2 PE=1 SV=1	1.105586	1.79E-06
Q9NW64	RBM22_HUMAN	Pre-mRNA-splicing factor RBM22 OS=Homo sapiens OX=9606 GN=RBM22 PE=1 SV=1	1.102957	2.02E-06
P10586	PTPRF_HUMAN	Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens OX=9606 GN=PTPRF PE=1 SV=2	1.101506	2.07E-05
Q9UBV2	SEL1L_HUMAN	Protein sel-1 homolog 1 OS=Homo sapiens OX=9606 GN=SEL1L PE=1 SV=3	1.100209	2.06E-06
Q8WZA0	LZIC_HUMAN	Protein LZIC OS=Homo sapiens OX=9606 GN=LZIC PE=1 SV=1	1.099838	1.27E-04
P23368	MAOM_HUMAN	NAD-dependent malic enzyme mitochondrial OS=Homo sapiens OX=9606 GN=ME2 PE=1 SV=1	1.094879	2.57E-06
Q96TA1	NIBA2_HUMAN	Protein Niban 2 OS=Homo sapiens OX=9606 GN=NIBAN2 PE=1 SV=3	1.093831	4.94E-07
Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9 mitochondrial OS=Homo sapiens OX=9606 GN=ACOT9 PE=1 SV=2	1.09099	5.10E-08
Q9UL15	BAG5_HUMAN	BAG family molecular chaperone regulator 5 OS=Homo sapiens OX=9606 GN=BAG5 PE=1 SV=1	1.090792	2.43E-05
Q9UK76	JUP1_HUMAN	Jupiter microtubule associated homolog 1 OS=Homo sapiens OX=9606 GN=JPT1 PE=1 SV=3	1.086124	0.008301
P15144	AMPN_HUMAN	Aminopeptidase N OS=Homo sapiens OX=9606 GN=ANPEP PE=1 SV=4	1.084869	2.97E-06
Q03519	TAP2_HUMAN	Antigen peptide transporter 2 OS=Homo sapiens OX=9606 GN=TAP2 PE=1 SV=1	1.084755	2.98E-06
O95630	STABP_HUMAN	STAM-binding protein OS=Homo sapiens OX=9606 GN=STAMPB PE=1 SV=1	1.084475	0.009305
P20290	BTF3_HUMAN	Transcription factor BTF3 OS=Homo sapiens OX=9606 GN=BTF3 PE=1 SV=1	1.084036	2.81E-06
Q92785	REQU_HUMAN	Zinc finger protein ubi-d4 OS=Homo sapiens OX=9606 GN=DPF2 PE=1 SV=2	1.083348	3.00E-06
Q02252	MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 PE=1 SV=2	1.082967	2.98E-06
O95674	CDS2_HUMAN	Phosphatidate cytidylyltransferase 2 OS=Homo sapiens OX=9606 GN=CDS2 PE=1 SV=1	1.081603	2.89E-06
Q96EP5	DAZP1_HUMAN	DAZ-associated protein 1 OS=Homo sapiens OX=9606 GN=DAZAP1 PE=1 SV=1	1.081081	3.08E-06
O60256	KPRB_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens OX=9606 GN=PRPSAP2 PE=1 SV=1	1.08096	3.23E-06
Q7Z2T5	TRMT1L_HUMAN	TRMT1-like protein OS=Homo sapiens OX=9606 GN=TRMT1L PE=1 SV=2	1.080836	3.08E-06
Q8TEM1	PO210_HUMAN	Nuclear pore membrane glycoprotein 210 OS=Homo sapiens OX=9606 GN=NUP210 PE=1 SV=3	1.077055	3.42E-06
Q02487	DSC2_HUMAN	Desmocollin-2 OS=Homo sapiens OX=9606 GN=DSC2 PE=1 SV=1	1.076408	3.29E-06
Q96S97	MYADM_HUMAN	Myeloid-associated differentiation marker OS=Homo sapiens OX=9606 GN=MYADM PE=1 SV=2	1.074893	3.29E-06
Q13835	PKP1_HUMAN	Plakophilin-1 OS=Homo sapiens OX=9606 GN=PKP1 PE=1 SV=2	1.07269	0.004014
Q9BV38	WDR18_HUMAN	WD repeat-containing protein 18 OS=Homo sapiens OX=9606 GN=WDR18 PE=1 SV=2	1.072017	3.42E-06
O15498	YKT6_HUMAN	Synaptobrevin homolog YKT6 OS=Homo sapiens OX=9606 GN=YKT6 PE=1 SV=1	1.070522	3.77E-06
Q9UKS6	PACN3_HUMAN	Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens OX=9606 GN=PACSIN3 PE=1 SV=2	1.068697	3.70E-06
O95163	ELP1_HUMAN	Elongator complex protein 1 OS=Homo sapiens OX=9606 GN=ELP1 PE=1 SV=3	1.064973	2.11E-05
P51553	IDH3G_HUMAN	Isocitrate dehydrogenase [NAD] subunit gamma mitochondrial OS=Homo sapiens OX=9606 GN=IDH3G PE=1 SV=1	1.064718	4.56E-06
Q32P44	EMAL3_HUMAN	Echinoderm microtubule-associated protein-like 3 OS=Homo sapiens OX=9606 GN=EML3 PE=1 SV=1	1.062919	7.01E-06
Q5W0V3	F16B1_HUMAN	Protein FAM160B1 OS=Homo sapiens OX=9606 GN=FAM160B1 PE=1 SV=1	1.061296	4.17E-06
O60488	ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens OX=9606 GN=ACSL4 PE=1 SV=2	1.059484	1.11E-04
Q8WTW3	COG1_HUMAN	Conserved oligomeric Golgi complex subunit 1 OS=Homo sapiens OX=9606 GN=COG1 PE=1 SV=1	1.058965	4.17E-06
O43676	NDUB3_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 OS=Homo sapiens OX=9606 GN=NDUF3 PE=1 SV=3	1.058397	4.49E-06
P84243	H33_HUMAN	Histone H3.3 OS=Homo sapiens OX=9606 GN=H3-3A PE=1 SV=2	1.055755	4.57E-06

O14776	TCRG1_HUMAN	Transcription elongation regulator 1 OS=Homo sapiens OX=9606 GN=TCERG1 PE=1 SV=2	1.055688	0.003813
Q7KZ85	SPT6H_HUMAN	Transcription elongation factor SPT6 OS=Homo sapiens OX=9606 GN=SPT6H PE=1 SV=2	1.054156	7.72E-04
P41214	EIF2D_HUMAN	Eukaryotic translation initiation factor 2D OS=Homo sapiens OX=9606 GN=EIF2D PE=1 SV=3	1.051619	5.10E-06
Q6P1J9	CDC73_HUMAN	Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1	1.049864	1.66E-05
O15446	RPA34_HUMAN	DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens OX=9606 GN=CD3EAP PE=1 SV=1	1.048571	5.45E-06
Q6P587	FAHD1_HUMAN	Acylpyruvase FAHD1 mitochondrial OS=Homo sapiens OX=9606 GN=FAHD1 PE=1 SV=2	1.047656	5.97E-06
Q9Y6G9	DC1L1_HUMAN	Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens OX=9606 GN=DYNC1L1 PE=1 SV=3	1.044652	2.47E-05
Q96KG9	SCYL1_HUMAN	N-terminal kinase-like protein OS=Homo sapiens OX=9606 GN=SCYL1 PE=1 SV=1	1.044171	1.58E-08
Q96FV9	THOC1_HUMAN	THO complex subunit 1 OS=Homo sapiens OX=9606 GN=THOC1 PE=1 SV=1	1.038889	6.98E-06
Q0JRZ9	FCHO2_HUMAN	F-BAR domain only protein 2 OS=Homo sapiens OX=9606 GN=FCHO2 PE=1 SV=2	1.038309	7.01E-06
Q8TDD1	DDX54_HUMAN	ATP-dependent RNA helicase DDX54 OS=Homo sapiens OX=9606 GN=DDX54 PE=1 SV=2	1.037367	7.12E-06
Q6NYC1	JMJD6_HUMAN	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Homo sapiens OX=9606 GN=JMJD6 PE=1 SV=1	1.036069	7.01E-06
O75841	UPK1B_HUMAN	Uroplakin-1b OS=Homo sapiens OX=9606 GN=UPK1B PE=1 SV=5	1.034745	7.27E-06
P55809	SCOT1_HUMAN	Succinyl-CoA:3-ketoacid coenzyme A transferase 1 mitochondrial OS=Homo sapiens OX=9606 GN=OXCT1 PE=1 SV=1	1.033687	7.72E-06
Q15750	TAB1_HUMAN	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens OX=9606 GN=TAB1 PE=1 SV=1	1.031	7.72E-06
Q9H9J2	RM44_HUMAN	39S ribosomal protein L44 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL44 PE=1 SV=1	1.029692	7.76E-06
Q9BPX5	ARPSL_HUMAN	Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens OX=9606 GN=ARPC5L PE=1 SV=1	1.028634	7.97E-06
Q9NP81	SYSM_HUMAN	Serine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=SARS2 PE=1 SV=1	1.026282	8.33E-06
O43823	AKAP8_HUMAN	A-kinase anchor protein 8 OS=Homo sapiens OX=9606 GN=AKAP8 PE=1 SV=1	1.020381	1.00E-05
Q13555	KCC2G_HUMAN	Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Homo sapiens OX=9606 GN=CAMK2G PE=1 SV=4	1.019547	9.91E-06
Q8NFV4	ABHDB_HUMAN	Protein ABHD11 OS=Homo sapiens OX=9606 GN=ABHD11 PE=1 SV=1	1.019463	1.00E-05
Q6P9B6	MEAK7_HUMAN	MTOR-associated protein MEAK7 OS=Homo sapiens OX=9606 GN=MEAK7 PE=1 SV=2	1.017054	5.99E-05
P29353	SHC1_HUMAN	SHC-transforming protein 1 OS=Homo sapiens OX=9606 GN=SHC1 PE=1 SV=4	1.015825	5.34E-06
Q13136	LIPA1_HUMAN	Liprin-alpha-1 OS=Homo sapiens OX=9606 GN=PPFIA1 PE=1 SV=1	1.015653	0.002134
Q15477	SKIV2_HUMAN	Helicase SKI2W OS=Homo sapiens OX=9606 GN=SKIV2L PE=1 SV=3	1.014899	1.08E-05
P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3 PE=1 SV=2	1.014761	1.07E-05
Q8TAE8	G45IP_HUMAN	Growth arrest and DNA damage-inducible proteins-interacting protein 1 OS=Homo sapiens OX=9606 GN=GADD45GIP1 PE=1 SV=1	1.012932	0.003121
Q13190	STX5_HUMAN	Syntaxin-5 OS=Homo sapiens OX=9606 GN=STX5 PE=1 SV=2	1.01118	1.18E-05
Q4V328	GRAP1_HUMAN	GRIP1-associated protein 1 OS=Homo sapiens OX=9606 GN=GRIPAP1 PE=1 SV=2	1.010274	1.18E-05
Q96FZ2	HMCES_HUMAN	Abasic site processing protein HMCES OS=Homo sapiens OX=9606 GN=HMCES PE=1 SV=1	1.009507	0.006923
Q92783	STAM1_HUMAN	Signal transducing adapter molecule 1 OS=Homo sapiens OX=9606 GN=STAM PE=1 SV=3	1.009383	9.76E-08
P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=3	1.008064	3.97E-06
P48047	ATPO_HUMAN	ATP synthase subunit O mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PO PE=1 SV=1	1.005972	1.66E-05
O15031	PLXB2_HUMAN	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	1.004039	1.37E-04
P34949	MPI_HUMAN	Mannose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=MPI PE=1 SV=2	1.001291	1.47E-05
Q7Z3K3	POGZ_HUMAN	Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=2	1.000949	1.93E-05
P08047	SP1_HUMAN	Transcription factor Sp1 OS=Homo sapiens OX=9606 GN=SP1 PE=1 SV=3	0.9986	1.67E-05
Q9BUH6	PAXX_HUMAN	Protein PAXX OS=Homo sapiens OX=9606 GN=PAXX PE=1 SV=2	0.998327	1.62E-05

Q96JJ7	TMX3_HUMAN	Protein disulfide-isomerase TMX3 OS=Homo sapiens OX=9606 GN=TMX3 PE=1 SV=2	0.997725	5.40E-05
Q8IXB1	DJC10_HUMAN	DnaJ homolog subfamily C member 10 OS=Homo sapiens OX=9606 GN=DNAJC10 PE=1 SV=2	0.996682	0.001327
Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens OX=9606 GN=TGFBI PE=1 SV=1	0.996015	1.59E-05
Q13421	MSLN_HUMAN	Mesothelin OS=Homo sapiens OX=9606 GN=MSLN PE=1 SV=2	0.994963	1.60E-05
P40261	NNMT_HUMAN	Nicotinamide N-methyltransferase OS=Homo sapiens OX=9606 GN=NNMT PE=1 SV=1	0.991757	1.84E-05
P09543	CN37_HUMAN	2' 3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens OX=9606 GN=CNP PE=1 SV=2	0.991709	8.27E-07
Q9UIV1	CNOT7_HUMAN	CCR4-NOT transcription complex subunit 7 OS=Homo sapiens OX=9606 GN=CNOT7 PE=1 SV=3	0.989281	1.84E-05
Q15042	RB3GP_HUMAN	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens OX=9606 GN=RAB3GAP1 PE=1 SV=3	0.987695	3.68E-05
Q13155	AIMP2_HUMAN	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens OX=9606 GN=AIMP2 PE=1 SV=2	0.987526	1.97E-05
Q8NFU3	TSTD1_HUMAN	Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 PE=1 SV=3	0.986916	0.004014
Q96EY8	MMAB_HUMAN	Corrinoid adenosyltransferase OS=Homo sapiens OX=9606 GN=MMAB PE=1 SV=1	0.98656	2.03E-05
P46976	GLYG_HUMAN	Glycogenin-1 OS=Homo sapiens OX=9606 GN=GYG1 PE=1 SV=4	0.983938	2.09E-05
Q96E11	RRFM_HUMAN	Ribosome-recycling factor mitochondrial OS=Homo sapiens OX=9606 GN=MRRF PE=1 SV=1	0.983024	2.07E-05
P60033	CD81_HUMAN	CD81 antigen OS=Homo sapiens OX=9606 GN=CD81 PE=1 SV=1	0.981942	2.11E-05
Q16539	MK14_HUMAN	Mitogen-activated protein kinase 14 OS=Homo sapiens OX=9606 GN=MAPK14 PE=1 SV=3	0.981557	2.14E-05
Q96RT1	ERBIN_HUMAN	Erbin OS=Homo sapiens OX=9606 GN=ERBIN PE=1 SV=2	0.979748	1.60E-05
Q13523	PRP4B_HUMAN	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3	0.979587	2.20E-05
Q12933	TRAF2_HUMAN	TNF receptor-associated factor 2 OS=Homo sapiens OX=9606 GN=TRAF2 PE=1 SV=2	0.978044	2.20E-05
P50895	BCAM_HUMAN	Basal cell adhesion molecule OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=2	0.97674	4.61E-04
P28072	PSB6_HUMAN	Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=4	0.974329	2.40E-05
Q8WWA1	TMM40_HUMAN	Transmembrane protein 40 OS=Homo sapiens OX=9606 GN=TMEM40 PE=1 SV=2	0.972273	0.001584
Q8N5N7	RM50_HUMAN	39S ribosomal protein L50 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL50 PE=1 SV=2	0.971671	2.57E-05
Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 OS=Homo sapiens OX=9606 GN=ERP44 PE=1 SV=1	0.967864	3.94E-05
Q5TDH0	DDI2_HUMAN	Protein DDI1 homolog 2 OS=Homo sapiens OX=9606 GN=DDI2 PE=1 SV=1	0.96562	2.84E-05
Q7Z3T8	ZFY16_HUMAN	Zinc finger FYVE domain-containing protein 16 OS=Homo sapiens OX=9606 GN=ZFYVE16 PE=1 SV=3	0.963313	3.13E-05
Q9Y277	VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606 GN=VDAC3 PE=1 SV=1	0.963187	0.003436
Q9Y3A5	SBDS_HUMAN	Ribosome maturation protein SBDS OS=Homo sapiens OX=9606 GN=SBDS PE=1 SV=4	0.962726	1.49E-04
Q14353	GAMT_HUMAN	Guanidinoacetate N-methyltransferase OS=Homo sapiens OX=9606 GN=GAMT PE=1 SV=1	0.962111	3.15E-05
Q6NZ67	MZT2B_HUMAN	Mitotic-spindle organizing protein 2B OS=Homo sapiens OX=9606 GN=MZT2B PE=1 SV=1	0.961998	3.19E-05
Q10713	MPPA_HUMAN	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens OX=9606 GN=PMPA PE=1 SV=2	0.95907	3.46E-05
O94832	MYO1D_HUMAN	Unconventional myosin-IId OS=Homo sapiens OX=9606 GN=MYO1D PE=1 SV=2	0.957682	4.23E-04
Q13217	DNJC3_HUMAN	DnaJ homolog subfamily C member 3 OS=Homo sapiens OX=9606 GN=DNAJC3 PE=1 SV=1	0.957669	1.59E-05
O95858	TSN15_HUMAN	Tetraspanin-15 OS=Homo sapiens OX=9606 GN=TSPAN15 PE=1 SV=1	0.95626	4.80E-05
Q92538	GBF1_HUMAN	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=GBF1 PE=1 SV=2	0.956102	6.10E-05
Q99447	PCY2_HUMAN	Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens OX=9606 GN=PCYT2 PE=1 SV=1	0.955808	3.60E-05
Q96S82	UBL7_HUMAN	Ubiquitin-like protein 7 OS=Homo sapiens OX=9606 GN=UBL7 PE=1 SV=2	0.955501	3.60E-05
P62316	SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens OX=9606 GN=SNRPD2 PE=1 SV=1	0.955011	0.0071
Q92485	ASM3B_HUMAN	Acid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens OX=9606 GN=SMPDL3B PE=1 SV=2	0.95109	3.94E-05

Q06546	GABPA_HUMAN	GA-binding protein alpha chain OS=Homo sapiens OX=9606 GN=GABPA PE=1 SV=1	0.950359	3.97E-05
P20337	RAB3B_HUMAN	Ras-related protein Rab-3B OS=Homo sapiens OX=9606 GN=RAB3B PE=1 SV=2	0.949789	0.006568
Q14244	MAP7_HUMAN	Ensconsin OS=Homo sapiens OX=9606 GN=MAP7 PE=1 SV=1	0.94907	3.99E-05
Q9Y4W2	LAS1L_HUMAN	Ribosomal biogenesis protein LAS1L OS=Homo sapiens OX=9606 GN=LAS1L PE=1 SV=2	0.947717	4.31E-05
Q9BPW8	NIPS1_HUMAN	Protein NipSnap homolog 1 OS=Homo sapiens OX=9606 GN=NIPSNAP1 PE=1 SV=1	0.947505	3.93E-05
P82933	RT09_HUMAN	28S ribosomal protein S9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS9 PE=1 SV=2	0.945811	4.31E-05
Q9H0P0	5NT3A_HUMAN	Cytosolic 5'-nucleotidase 3A OS=Homo sapiens OX=9606 GN=NT5C3A PE=1 SV=3	0.945614	1.52E-04
Q96AC1	FERM2_HUMAN	Fermitin family homolog 2 OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1	0.942897	4.53E-05
Q9Y5L0	TNPO3_HUMAN	Transportin-3 OS=Homo sapiens OX=9606 GN=TNPO3 PE=1 SV=3	0.942714	4.51E-04
Q9H0A0	NAT10_HUMAN	RNA cytidine acetyltransferase OS=Homo sapiens OX=9606 GN=NAT10 PE=1 SV=2	0.941935	4.66E-05
Q9BU23	LMF2_HUMAN	Lipase maturation factor 2 OS=Homo sapiens OX=9606 GN=LMF2 PE=1 SV=2	0.940452	4.80E-05
Q9NQT5	EXOS3_HUMAN	Exosome complex component RRP40 OS=Homo sapiens OX=9606 GN=EXOSC3 PE=1 SV=3	0.94009	4.66E-05
O96005	CLPT1_HUMAN	Cleft lip and palate transmembrane protein 1 OS=Homo sapiens OX=9606 GN=CLPTM1 PE=1 SV=1	0.939458	5.43E-04
Q8WZ82	OVCA2_HUMAN	Esterase OVCA2 OS=Homo sapiens OX=9606 GN=OVCA2 PE=1 SV=1	0.939131	4.80E-05
Q9H2G2	SLK_HUMAN	STE20-like serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=SLK PE=1 SV=1	0.939032	4.80E-05
P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 OS=Homo sapiens OX=9606 GN=DPP4 PE=1 SV=2	0.93886	5.87E-04
Q9NWV8	BABA1_HUMAN	BRISC and BRCA1-A complex member 1 OS=Homo sapiens OX=9606 GN=BABAM1 PE=1 SV=1	0.938319	4.85E-05
Q6PD74	AAGAB_HUMAN	Alpha- and gamma-adaptin-binding protein p34 OS=Homo sapiens OX=9606 GN=AAGAB PE=1 SV=1	0.937982	4.88E-05
P32320	CDD_HUMAN	Cytidine deaminase OS=Homo sapiens OX=9606 GN=CDA PE=1 SV=2	0.937173	4.87E-05
P46934	NEDD4_HUMAN	E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens OX=9606 GN=NEDD4 PE=1 SV=4	0.937115	4.88E-05
Q13740	CD166_HUMAN	CD166 antigen OS=Homo sapiens OX=9606 GN=ALCAM PE=1 SV=2	0.936742	2.55E-05
Q12769	NU160_HUMAN	Nuclear pore complex protein Nup160 OS=Homo sapiens OX=9606 GN=NUP160 PE=1 SV=3	0.936521	4.88E-05
Q14181	DPOA2_HUMAN	DNA polymerase alpha subunit B OS=Homo sapiens OX=9606 GN=POLA2 PE=1 SV=2	0.936435	4.97E-05
Q8ND56	LS14A_HUMAN	Protein LSM14 homolog A OS=Homo sapiens OX=9606 GN=LSM14A PE=1 SV=3	0.932413	5.40E-05
P63172	DYLT1_HUMAN	Dynein light chain Tctex-type 1 OS=Homo sapiens OX=9606 GN=DYNLT1 PE=1 SV=1	0.929943	0.002382
Q15024	EXOS7_HUMAN	Exosome complex component RRP42 OS=Homo sapiens OX=9606 GN=EXOSC7 PE=1 SV=3	0.929117	5.68E-05
P16435	NCPR_HUMAN	NADPH--cytochrome P450 reductase OS=Homo sapiens OX=9606 GN=POR PE=1 SV=2	0.927982	1.01E-04
O60925	PFD1_HUMAN	Prefoldin subunit 1 OS=Homo sapiens OX=9606 GN=PFDN1 PE=1 SV=2	0.927576	5.76E-05
O94855	SC24D_HUMAN	Protein transport protein Sec24D OS=Homo sapiens OX=9606 GN=SEC24D PE=1 SV=2	0.923539	5.38E-05
P28062	PSB8_HUMAN	Proteasome subunit beta type-8 OS=Homo sapiens OX=9606 GN=PSMB8 PE=1 SV=3	0.921695	1.51E-04
Q9BSJ2	GCP2_HUMAN	Gamma-tubulin complex component 2 OS=Homo sapiens OX=9606 GN=TUBGCP2 PE=1 SV=2	0.920566	1.01E-05
Q16763	UBE2S_HUMAN	Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens OX=9606 GN=UBE2S PE=1 SV=2	0.92024	6.60E-05
P49914	MTHFS_HUMAN	5-formyltetrahydrofolate cyclo-ligase OS=Homo sapiens OX=9606 GN=MTHFS PE=1 SV=2	0.920212	6.23E-05
Q8N8S7	ENAH_HUMAN	Protein enabled homolog OS=Homo sapiens OX=9606 GN=ENAH PE=1 SV=2	0.918916	6.64E-05
P06865	HEXA_HUMAN	Beta-hexosaminidase subunit alpha OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=2	0.918612	6.76E-05
Q9BT09	CNPY3_HUMAN	Protein canopy homolog 3 OS=Homo sapiens OX=9606 GN=CNPY3 PE=1 SV=1	0.918598	6.75E-05
O00469	PLOD2_HUMAN	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens OX=9606 GN=PLOD2 PE=1 SV=2	0.917194	0.001739
Q9BST9	RTKN_HUMAN	Rhotekin OS=Homo sapiens OX=9606 GN=RTKN PE=1 SV=2	0.916627	6.94E-05

Q9Y3D7	TIM16_HUMAN	Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens OX=9606 GN=PAM16 PE=1 SV=2	0.916104	7.25E-05
Q16531	DDB1_HUMAN	DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DDB1 PE=1 SV=1	0.915484	4.64E-10
Q14192	FHL2_HUMAN	Four and a half LIM domains protein 2 OS=Homo sapiens OX=9606 GN=FHL2 PE=1 SV=3	0.913869	9.60E-07
Q13451	FKBP5_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens OX=9606 GN=FKBP5 PE=1 SV=2	0.913232	7.89E-05
Q9Y314	NOSIP_HUMAN	Nitric oxide synthase-interacting protein OS=Homo sapiens OX=9606 GN=NOSIP PE=1 SV=1	0.912828	1.29E-04
P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens OX=9606 GN=PGAM1 PE=1 SV=2	0.912537	4.16E-05
P61619	S61A1_HUMAN	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens OX=9606 GN=SEC61A1 PE=1 SV=2	0.912213	0.001646
P24752	THIL_HUMAN	Acetyl-CoA acetyltransferase mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 PE=1 SV=1	0.912138	5.39E-04
P51116	FXR2_HUMAN	Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens OX=9606 GN=FXR2 PE=1 SV=2	0.911644	7.60E-05
P12955	PEPD_HUMAN	Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD PE=1 SV=3	0.911514	4.76E-07
P16278	BGAL_HUMAN	Beta-galactosidase OS=Homo sapiens OX=9606 GN=GLB1 PE=1 SV=2	0.911145	7.44E-05
Q05086	UBE3A_HUMAN	Ubiquitin-protein ligase E3A OS=Homo sapiens OX=9606 GN=UBE3A PE=1 SV=4	0.910127	7.89E-05
P07948	LYN_HUMAN	Tyrosine-protein kinase Lyn OS=Homo sapiens OX=9606 GN=LYN PE=1 SV=3	0.910067	7.89E-05
Q5W111	SPRY7_HUMAN	SPRY domain-containing protein 7 OS=Homo sapiens OX=9606 GN=SPRYD7 PE=1 SV=2	0.910058	7.89E-05
Q8NFQ8	TOIP2_HUMAN	Torsin-1A-interacting protein 2 OS=Homo sapiens OX=9606 GN=TOR1AIP2 PE=1 SV=1	0.909377	8.55E-05
P52948	NUP98_HUMAN	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens OX=9606 GN=NUP98 PE=1 SV=4	0.909245	3.42E-06
Q3ZCW2	LEGL_HUMAN	Galectin-related protein OS=Homo sapiens OX=9606 GN=LGALS1 PE=1 SV=2	0.908284	6.76E-04
Q9Y224	RTRAF_HUMAN	RNA transcription translation and transport factor protein OS=Homo sapiens OX=9606 GN=RTRAF PE=1 SV=1	0.907866	3.29E-06
P43487	RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1	0.907661	0.003366
P31937	3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=HIBADH PE=1 SV=2	0.907422	8.44E-05
O00267	SPT5H_HUMAN	Transcription elongation factor SPT5 OS=Homo sapiens OX=9606 GN=SUPT5H PE=1 SV=1	0.907318	6.23E-05
Q9H4A6	GOLP3_HUMAN	Golgi phosphoprotein 3 OS=Homo sapiens OX=9606 GN=GOLPH3 PE=1 SV=1	0.907243	7.89E-05
Q9BZD4	NUF2_HUMAN	Kinetochore protein Nuf2 OS=Homo sapiens OX=9606 GN=NUF2 PE=1 SV=2	0.906747	0.001042
P49354	FNTA_HUMAN	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens OX=9606 GN=FNTA PE=1 SV=1	0.906468	8.47E-05
Q86VS8	HOOK3_HUMAN	Protein Hook homolog 3 OS=Homo sapiens OX=9606 GN=HOOK3 PE=1 SV=2	0.905717	8.47E-05
P78330	SERB_HUMAN	Phosphoserine phosphatase OS=Homo sapiens OX=9606 GN=PSPH PE=1 SV=2	0.905141	8.19E-05
P09110	THIK_HUMAN	3-ketoacyl-CoA thiolase peroxisomal OS=Homo sapiens OX=9606 GN=ACAA1 PE=1 SV=2	0.904745	8.70E-05
Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=OGDH PE=1 SV=3	0.903747	9.06E-09
O95218	ZRAB2_HUMAN	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ZRANB2 PE=1 SV=2	0.903744	8.93E-05
O75175	CNOT3_HUMAN	CCR4-NOT transcription complex subunit 3 OS=Homo sapiens OX=9606 GN=CNOT3 PE=1 SV=1	0.900718	9.26E-05
Q02809	PLOD1_HUMAN	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens OX=9606 GN=PLOD1 PE=1 SV=2	0.898296	2.11E-04
Q9Y696	CLIC4_HUMAN	Chloride intracellular channel protein 4 OS=Homo sapiens OX=9606 GN=CLIC4 PE=1 SV=4	0.89812	5.45E-05
P30084	ECHM_HUMAN	Enoyl-CoA hydratase mitochondrial OS=Homo sapiens OX=9606 GN=ECHS1 PE=1 SV=4	0.896907	4.80E-05
P35237	SPB6_HUMAN	Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=3	0.896649	0.002338
Q15165	PON2_HUMAN	Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=4	0.896492	1.01E-04
Q13492	PICAL_HUMAN	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens OX=9606 GN=PICALM PE=1 SV=2	0.896106	2.26E-04
O43488	ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens OX=9606 GN=AKR7A2 PE=1 SV=3	0.894887	5.61E-04

Q96CN7	ISOC1_HUMAN	Isochorismatase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ISOC1 PE=1 SV=3	0.894791	9.93E-05
Q8WUD1	RAB2B_HUMAN	Ras-related protein Rab-2B OS=Homo sapiens OX=9606 GN=RAB2B PE=1 SV=1	0.89439	1.05E-04
Q6L8Q7	PDE12_HUMAN	2' 5'-phosphodiesterase 12 OS=Homo sapiens OX=9606 GN=PDE12 PE=1 SV=2	0.894322	1.07E-04
Q86TU7	SETD3_HUMAN	Actin-histidine N-methyltransferase OS=Homo sapiens OX=9606 GN=SETD3 PE=1 SV=1	0.894	3.52E-04
Q9Y4P1	ATG4B_HUMAN	Cysteine protease ATG4B OS=Homo sapiens OX=9606 GN=ATG4B PE=1 SV=2	0.893942	5.49E-05
P22570	ADRO_HUMAN	NADPH:adrenodoxin oxidoreductase mitochondrial OS=Homo sapiens OX=9606 GN=FDXR PE=1 SV=3	0.893672	9.93E-05
P82909	RT36_HUMAN	28S ribosomal protein S36 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS36 PE=1 SV=2	0.892048	0.003117
Q8IYB5	SMAP1_HUMAN	Stromal membrane-associated protein 1 OS=Homo sapiens OX=9606 GN=SMAP1 PE=1 SV=2	0.891436	1.07E-04
P62873	GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens OX=9606 GN=GNB1 PE=1 SV=3	0.891114	1.09E-04
P78318	IGBP1_HUMAN	Immunoglobulin-binding protein 1 OS=Homo sapiens OX=9606 GN=IGBP1 PE=1 SV=1	0.890826	0.007311
Q96PZ2	F111A_HUMAN	Protein FAM111A OS=Homo sapiens OX=9606 GN=FAM111A PE=1 SV=2	0.890725	1.13E-04
Q12802	AKP13_HUMAN	A-kinase anchor protein 13 OS=Homo sapiens OX=9606 GN=AKAP13 PE=1 SV=2	0.889017	1.76E-04
Q96H20	SNF8_HUMAN	Vacuolar-sorting protein SNF8 OS=Homo sapiens OX=9606 GN=SNF8 PE=1 SV=1	0.888922	2.21E-04
P46736	BRCC3_HUMAN	Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens OX=9606 GN=BRCC3 PE=1 SV=2	0.888249	1.10E-04
Q14790	CASP8_HUMAN	Caspase-8 OS=Homo sapiens OX=9606 GN=CASP8 PE=1 SV=1	0.885767	1.20E-04
Q92922	SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens OX=9606 GN=SMARCC1 PE=1 SV=3	0.884923	1.34E-04
P47895	AL1A3_HUMAN	Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens OX=9606 GN=ALDH1A3 PE=1 SV=2	0.883837	5.26E-04
Q8TD16	BICD2_HUMAN	Protein bicaudal D homolog 2 OS=Homo sapiens OX=9606 GN=BICD2 PE=1 SV=1	0.883784	1.20E-04
O14530	TXND9_HUMAN	Thioredoxin domain-containing protein 9 OS=Homo sapiens OX=9606 GN=TXNDC9 PE=1 SV=2	0.883332	1.27E-04
Q12959	DLG1_HUMAN	Disks large homolog 1 OS=Homo sapiens OX=9606 GN=DLG1 PE=1 SV=2	0.881756	1.30E-04
Q99700	ATX2_HUMAN	Ataxin-2 OS=Homo sapiens OX=9606 GN=ATXN2 PE=1 SV=2	0.881544	2.96E-04
P62330	ARF6_HUMAN	ADP-ribosylation factor 6 OS=Homo sapiens OX=9606 GN=ARF6 PE=1 SV=2	0.881095	3.33E-05
Q14254	FLOT2_HUMAN	Flotillin-2 OS=Homo sapiens OX=9606 GN=FLOT2 PE=1 SV=2	0.880726	1.33E-04
Q6UX04	CWC27_HUMAN	Spliceosome-associated protein CWC27 homolog OS=Homo sapiens OX=9606 GN=CWC27 PE=1 SV=1	0.879808	5.60E-04
O00186	STXB3_HUMAN	Syntaxin-binding protein 3 OS=Homo sapiens OX=9606 GN=STXB3 PE=1 SV=2	0.878527	9.88E-04
P34896	GLYC_HUMAN	Serine hydroxymethyltransferase cytosolic OS=Homo sapiens OX=9606 GN=SHMT1 PE=1 SV=1	0.878321	1.58E-05
P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens OX=9606 GN=NME2 PE=1 SV=1	0.878093	6.39E-04
P55210	CASP7_HUMAN	Caspase-7 OS=Homo sapiens OX=9606 GN=CASP7 PE=1 SV=1	0.878077	1.40E-04
P39656	OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens OX=9606 GN=DDOST PE=1 SV=4	0.876672	1.14E-04
P84095	RHOG_HUMAN	Rho-related GTP-binding protein RhoG OS=Homo sapiens OX=9606 GN=RHOG PE=1 SV=1	0.876598	1.38E-04
P28370	SMCA1_HUMAN	Probable global transcription activator SNF2L1 OS=Homo sapiens OX=9606 GN=SMARCA1 PE=1 SV=2	0.87615	0.00665
O43818	U3IP2_HUMAN	U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens OX=9606 GN=RRP9 PE=1 SV=1	0.876076	0.006458
Q9Y4E8	UBP15_HUMAN	Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens OX=9606 GN=USP15 PE=1 SV=3	0.875814	1.32E-04
Q96HY6	DDRKG_HUMAN	DDRKG domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DDRKG1 PE=1 SV=2	0.875433	6.96E-05
Q9BZK7	TBL1R_HUMAN	F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens OX=9606 GN=TBL1XR1 PE=1 SV=1	0.874765	9.21E-05
P51151	RAB9A_HUMAN	Ras-related protein Rab-9A OS=Homo sapiens OX=9606 GN=RAB9A PE=1 SV=1	0.873243	1.48E-04
Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP] mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=4	0.872865	0.001886
Q6YHK3	CD109_HUMAN	CD109 antigen OS=Homo sapiens OX=9606 GN=CD109 PE=1 SV=2	0.872804	4.13E-05

P84085	ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=2	0.872367	1.47E-04
P36551	HEM6_HUMAN	Oxygen-dependent coproporphyrinogen-III oxidase mitochondrial OS=Homo sapiens OX=9606 GN=CPOX PE=1 SV=3	0.87192	7.63E-06
Q96EE3	SEH1_HUMAN	Nucleoporin SEH1 OS=Homo sapiens OX=9606 GN=SEH1L PE=1 SV=3	0.871847	1.55E-04
Q9BQ39	DDX50_HUMAN	ATP-dependent RNA helicase DDX50 OS=Homo sapiens OX=9606 GN=DDX50 PE=1 SV=1	0.871014	0.003086
Q5T9A4	ATD3B_HUMAN	ATPase family AAA domain-containing protein 3B OS=Homo sapiens OX=9606 GN=ATAD3B PE=1 SV=1	0.870999	1.52E-04
P07942	LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens OX=9606 GN=LAMB1 PE=1 SV=2	0.870821	2.62E-04
Q8N684	CPSF7_HUMAN	Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens OX=9606 GN=CPSF7 PE=1 SV=1	0.870143	9.76E-08
P53007	TXTP_HUMAN	Tricarboxylate transport protein mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A1 PE=1 SV=2	0.869987	1.55E-04
O75396	SC22B_HUMAN	Vesicle-trafficking protein SEC22b OS=Homo sapiens OX=9606 GN=SEC22B PE=1 SV=4	0.869477	2.36E-04
A1L0T0	ILVBL_HUMAN	Acetolactate synthase-like protein OS=Homo sapiens OX=9606 GN=ILVBL PE=1 SV=2	0.86935	3.13E-04
P52735	VAV2_HUMAN	Guanine nucleotide exchange factor VAV2 OS=Homo sapiens OX=9606 GN=VAV2 PE=1 SV=2	0.869223	1.57E-04
Q6DD88	ATLA3_HUMAN	Atlastin-3 OS=Homo sapiens OX=9606 GN=ATL3 PE=1 SV=1	0.868981	3.97E-06
Q9UPN7	PP6R1_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP6R1 PE=1 SV=5	0.867526	1.59E-04
Q93052	LPP_HUMAN	Lipoma-preferred partner OS=Homo sapiens OX=9606 GN=LPP PE=1 SV=1	0.867127	2.71E-04
P60709	ACTB_HUMAN	Actin cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1	0.866733	1.64E-04
Q15738	NSDHL_HUMAN	Sterol-4-alpha-carboxylate 3-dehydrogenase decarboxylating OS=Homo sapiens OX=9606 GN=NSDHL PE=1 SV=2	0.866126	2.45E-04
P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=2	0.866122	1.68E-04
Q9UJC3	HOOK1_HUMAN	Protein Hook homolog 1 OS=Homo sapiens OX=9606 GN=HOOK1 PE=1 SV=2	0.865176	4.86E-04
P16403	H12_HUMAN	Histone H1.2 OS=Homo sapiens OX=9606 GN=H1-2 PE=1 SV=2	0.865041	3.33E-05
Q9NRF8	PYRG2_HUMAN	CTP synthase 2 OS=Homo sapiens OX=9606 GN=CTPS2 PE=1 SV=1	0.86476	1.73E-04
Q9C0C9	UBE2O_HUMAN	(E3-independent) E2 ubiquitin-conjugating enzyme OS=Homo sapiens OX=9606 GN=UBE2O PE=1 SV=3	0.863914	1.74E-04
Q8NFH4	NUP37_HUMAN	Nucleoporin Nup37 OS=Homo sapiens OX=9606 GN=NUP37 PE=1 SV=1	0.862805	1.68E-04
P50453	SPB9_HUMAN	Serpin B9 OS=Homo sapiens OX=9606 GN=SERPINB9 PE=1 SV=1	0.862662	0.001053
Q9NZT2	OGFR_HUMAN	Opioid growth factor receptor OS=Homo sapiens OX=9606 GN=OGFR PE=1 SV=3	0.862018	6.68E-04
P29992	GNA11_HUMAN	Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens OX=9606 GN=GNA11 PE=1 SV=2	0.86012	1.84E-04
O95453	PARN_HUMAN	Poly(A)-specific ribonuclease PARN OS=Homo sapiens OX=9606 GN=PARN PE=1 SV=1	0.860063	1.82E-04
Q99567	NUP88_HUMAN	Nuclear pore complex protein Nup88 OS=Homo sapiens OX=9606 GN=NUP88 PE=1 SV=2	0.859368	0.001311
Q9ULC3	RAB23_HUMAN	Ras-related protein Rab-23 OS=Homo sapiens OX=9606 GN=RAB23 PE=1 SV=1	0.857583	1.86E-04
Q8N1G4	LRC47_HUMAN	Leucine-rich repeat-containing protein 47 OS=Homo sapiens OX=9606 GN=LRRC47 PE=1 SV=1	0.856619	2.07E-05
Q96A33	CCD47_HUMAN	Coiled-coil domain-containing protein 47 OS=Homo sapiens OX=9606 GN=CCDC47 PE=1 SV=1	0.856473	5.59E-05
P62195	PRS8_HUMAN	26S proteasome regulatory subunit 8 OS=Homo sapiens OX=9606 GN=PSMC5 PE=1 SV=1	0.856301	2.54E-04
Q7Z222	EFL1_HUMAN	Elongation factor-like GTPase 1 OS=Homo sapiens OX=9606 GN=EFL1 PE=1 SV=2	0.855874	2.07E-04
P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens OX=9606 GN=GNB2 PE=1 SV=3	0.855487	1.92E-04
O00217	NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS8 PE=1 SV=1	0.855262	1.88E-04
Q9Y5Y6	ST14_HUMAN	Suppressor of tumorigenicity 14 protein OS=Homo sapiens OX=9606 GN=ST14 PE=1 SV=2	0.855254	2.05E-04
Q15833	STXB2_HUMAN	Syntaxin-binding protein 2 OS=Homo sapiens OX=9606 GN=STXB2 PE=1 SV=2	0.855095	2.04E-04
O94776	MTA2_HUMAN	Metastasis-associated protein MTA2 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	0.854333	3.97E-05
O95865	DDAH2_HUMAN	N(G) N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=1	0.853812	1.32E-04

P61764	STXB1_HUMAN	Syntaxin-binding protein 1 OS=Homo sapiens OX=9606 GN=STXBP1 PE=1 SV=1	0.853019	2.09E-04
Q93008	USP9X_HUMAN	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens OX=9606 GN=USP9X PE=1 SV=3	0.852119	0.001579
Q9BUL8	PDC10_HUMAN	Programmed cell death protein 10 OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1	0.850936	2.08E-04
Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosomes protein 3 OS=Homo sapiens OX=9606 GN=SMC3 PE=1 SV=2	0.850892	1.08E-04
Q12797	ASPH_HUMAN	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3	0.850544	2.16E-04
O00193	SMAP_HUMAN	Small acidic protein OS=Homo sapiens OX=9606 GN=SMAP PE=1 SV=1	0.850307	7.37E-04
O60216	RAD21_HUMAN	Double-strand-break repair protein rad21 homolog OS=Homo sapiens OX=9606 GN=RAD21 PE=1 SV=2	0.849598	0.008301
Q9NV96	CC50A_HUMAN	Cell cycle control protein 50A OS=Homo sapiens OX=9606 GN=TMEM30A PE=1 SV=1	0.849583	2.16E-04
Q96A65	EXOC4_HUMAN	Exocyst complex component 4 OS=Homo sapiens OX=9606 GN=EXOC4 PE=1 SV=1	0.849521	0.003431
Q9H936	GHC1_HUMAN	Mitochondrial glutamate carrier 1 OS=Homo sapiens OX=9606 GN=SLC25A22 PE=1 SV=1	0.849294	2.08E-04
P35580	MYH10_HUMAN	Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3	0.849203	9.12E-05
Q14651	PLS1_HUMAN	Plastin-1 OS=Homo sapiens OX=9606 GN=PLS1 PE=1 SV=2	0.848418	1.36E-04
P35611	ADDA_HUMAN	Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=2	0.847669	5.93E-04
Q5JWF2	GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens OX=9606 GN=GNAS PE=1 SV=2	0.847517	6.76E-04
P50443	S26A2_HUMAN	Sulfate transporter OS=Homo sapiens OX=9606 GN=SLC26A2 PE=1 SV=2	0.846983	2.31E-04
Q8N6T3	ARFG1_HUMAN	ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=ARFGAP1 PE=1 SV=2	0.846677	2.98E-05
Q92626	PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens OX=9606 GN=PXDN PE=1 SV=2	0.846354	4.25E-05
Q8NBU5	ATAD1_HUMAN	ATPase family AAA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ATAD1 PE=1 SV=1	0.846349	2.37E-04
Q9UFC0	LRWD1_HUMAN	Leucine-rich repeat and WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=LRWD1 PE=1 SV=2	0.843689	2.39E-04
Q12824	SNF5_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens OX=9606 GN=SMARCB1 PE=1 SV=2	0.842773	2.43E-04
O95155	UBE4B_HUMAN	Ubiquitin conjugation factor E4 B OS=Homo sapiens OX=9606 GN=UBE4B PE=1 SV=1	0.840749	3.42E-04
Q15018	ABRX2_HUMAN	BRISC complex subunit Abraxas 2 OS=Homo sapiens OX=9606 GN=ABRAXAS2 PE=1 SV=2	0.840542	2.60E-04
P10155	RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=RO60 PE=1 SV=2	0.84047	5.82E-04
Q96L92	SNX27_HUMAN	Sorting nexin-27 OS=Homo sapiens OX=9606 GN=SNX27 PE=1 SV=2	0.840104	0.002664
O95372	LYPA2_HUMAN	Acyl-protein thioesterase 2 OS=Homo sapiens OX=9606 GN=LYPLA2 PE=1 SV=1	0.838974	2.78E-04
Q00688	FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens OX=9606 GN=FKBP3 PE=1 SV=1	0.838957	5.26E-04
Q14690	RRP5_HUMAN	Protein RRP5 homolog OS=Homo sapiens OX=9606 GN=PDCD11 PE=1 SV=3	0.838796	1.72E-04
O14828	SCAM3_HUMAN	Secretory carrier-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=SCAMP3 PE=1 SV=3	0.838551	4.86E-04
Q8N392	RHG18_HUMAN	Rho GTPase-activating protein 18 OS=Homo sapiens OX=9606 GN=ARHGAP18 PE=1 SV=3	0.838124	2.66E-04
Q9UPT5	EXOC7_HUMAN	Exocyst complex component 7 OS=Homo sapiens OX=9606 GN=EXOC7 PE=1 SV=3	0.837972	0.005504
P78344	IF4G2_HUMAN	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1	0.837284	0.001056
Q96B26	EXOS8_HUMAN	Exosome complex component RRP43 OS=Homo sapiens OX=9606 GN=EXOSC8 PE=1 SV=1	0.836647	2.79E-04
P49770	EI2BB_HUMAN	Translation initiation factor eIF-2B subunit beta OS=Homo sapiens OX=9606 GN=EIF2B2 PE=1 SV=3	0.836212	2.84E-04
O15160	RPAC1_HUMAN	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens OX=9606 GN=POLR1C PE=1 SV=1	0.834586	8.87E-05
Q86SF2	GALT7_HUMAN	N-acetylgalactosaminyltransferase 7 OS=Homo sapiens OX=9606 GN=GALNT7 PE=1 SV=1	0.834188	5.26E-04
Q9H074	PAIP1_HUMAN	Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens OX=9606 GN=PAIP1 PE=1 SV=1	0.833589	7.92E-04
Q00169	PIPNA_HUMAN	Phosphatidylinositol transfer protein alpha isoform OS=Homo sapiens OX=9606 GN=PIPNA PE=1 SV=2	0.833318	2.89E-04

P05187	PPB1_HUMAN	Alkaline phosphatase placental type OS=Homo sapiens OX=9606 GN=ALPP PE=1 SV=2	0.83289	2.37E-04
Q9NRW3	ABC3C_HUMAN	DNA dC->dU-editing enzyme APOBEC-3C OS=Homo sapiens OX=9606 GN=APOBEC3C PE=1 SV=2	0.83274	2.91E-04
O15230	LAMA5_HUMAN	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	0.832681	0.003997
O75431	MTX2_HUMAN	Metaxin-2 OS=Homo sapiens OX=9606 GN=MTX2 PE=1 SV=1	0.832319	3.02E-04
Q9H0B6	KLC2_HUMAN	Kinesin light chain 2 OS=Homo sapiens OX=9606 GN=KLC2 PE=1 SV=1	0.832247	2.94E-04
Q9UNF1	MAGD2_HUMAN	Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGED2 PE=1 SV=2	0.832242	9.14E-04
P49591	SYSC_HUMAN	Serine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=SARS1 PE=1 SV=3	0.831909	0.002319
P23743	DGKA_HUMAN	Diacylglycerol kinase alpha OS=Homo sapiens OX=9606 GN=DGKA PE=1 SV=3	0.831436	8.94E-05
Q96EY1	DNJA3_HUMAN	DnaJ homolog subfamily A member 3 mitochondrial OS=Homo sapiens OX=9606 GN=DNAJA3 PE=1 SV=2	0.831263	2.84E-04
Q9H2M9	RBGPR_HUMAN	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens OX=9606 GN=RAB3GAP2 PE=1 SV=1	0.831246	3.01E-04
Q9UNL2	SSRG_HUMAN	Translocon-associated protein subunit gamma OS=Homo sapiens OX=9606 GN=SSR3 PE=1 SV=1	0.83119	3.10E-04
P60983	GMFB_HUMAN	Glia maturation factor beta OS=Homo sapiens OX=9606 GN=GMFB PE=1 SV=2	0.830075	3.22E-04
P11234	RALB_HUMAN	Ras-related protein Ral-B OS=Homo sapiens OX=9606 GN=RALB PE=1 SV=1	0.829454	3.19E-04
Q9Y678	COPG1_HUMAN	Coatomer subunit gamma-1 OS=Homo sapiens OX=9606 GN=COPG1 PE=1 SV=1	0.827914	0.002485
P42566	EPS15_HUMAN	Epidermal growth factor receptor substrate 15 OS=Homo sapiens OX=9606 GN=EPS15 PE=1 SV=2	0.825971	1.97E-04
P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR2A PE=1 SV=2	0.82556	5.56E-04
O95817	BAG3_HUMAN	BAG family molecular chaperone regulator 3 OS=Homo sapiens OX=9606 GN=BAG3 PE=1 SV=3	0.8254	3.29E-04
Q9H7E9	CH033_HUMAN	UPF0488 protein C8orf33 OS=Homo sapiens OX=9606 GN=C8orf33 PE=1 SV=1	0.825054	0.003106
Q96AT9	RPE_HUMAN	Ribulose-phosphate 3-epimerase OS=Homo sapiens OX=9606 GN=RPE PE=1 SV=1	0.824831	3.19E-04
Q99614	TTC1_HUMAN	Tetratricopeptide repeat protein 1 OS=Homo sapiens OX=9606 GN=TTC1 PE=1 SV=1	0.824571	6.23E-05
Q9Y6A5	TACC3_HUMAN	Transforming acidic coiled-coil-containing protein 3 OS=Homo sapiens OX=9606 GN=TACC3 PE=1 SV=1	0.823098	7.76E-06
Q9BTE7	DCNL5_HUMAN	DCN1-like protein 5 OS=Homo sapiens OX=9606 GN=DCUN1D5 PE=1 SV=1	0.822527	6.92E-04
Q16718	NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=3	0.822491	5.78E-04
Q86X55	CARM1_HUMAN	Histone-arginine methyltransferase CARM1 OS=Homo sapiens OX=9606 GN=CARM1 PE=1 SV=3	0.822383	3.59E-04
Q96RS6	NUDC1_HUMAN	NudC domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NUDCD1 PE=1 SV=2	0.822075	9.83E-04
Q13011	ECH1_HUMAN	Delta(3 5)-Delta(2 4)-dienoyl-CoA isomerase mitochondrial OS=Homo sapiens OX=9606 GN=ECH1 PE=1 SV=2	0.821743	0.00247
Q96T37	RBM15_HUMAN	RNA-binding protein 15 OS=Homo sapiens OX=9606 GN=RBM15 PE=1 SV=2	0.821547	9.42E-05
Q9Y3C4	TPRKB_HUMAN	EKC/KEOPS complex subunit TPRKB OS=Homo sapiens OX=9606 GN=TPRKB PE=1 SV=1	0.821126	0.009076
P13010	XRCC5_HUMAN	X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1 SV=3	0.820851	2.81E-04
P18615	NELFE_HUMAN	Negative elongation factor E OS=Homo sapiens OX=9606 GN=NELFE PE=1 SV=3	0.820256	0.001126
P49585	PCYT1A_HUMAN	Choline-phosphate cytidyltransferase A OS=Homo sapiens OX=9606 GN=PCYT1A PE=1 SV=2	0.820064	3.65E-04
Q14241	ELOA1_HUMAN	Elongin-A OS=Homo sapiens OX=9606 GN=ELOA PE=1 SV=2	0.819279	3.46E-04
Q9Y5X1	SNX9_HUMAN	Sorting nexin-9 OS=Homo sapiens OX=9606 GN=SNX9 PE=1 SV=1	0.818393	7.02E-04
O75477	ERLN1_HUMAN	Erlin-1 OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=2	0.817889	3.74E-04
Q9BYD2	RM09_HUMAN	39S ribosomal protein L9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL9 PE=1 SV=2	0.817219	0.001775
Q9NX47	MARH5_HUMAN	E3 ubiquitin-protein ligase MARCHF5 OS=Homo sapiens OX=9606 GN=MARCHF5 PE=1 SV=1	0.817093	3.71E-04
Q8N766	EMC1_HUMAN	ER membrane protein complex subunit 1 OS=Homo sapiens OX=9606 GN=EMC1 PE=1 SV=1	0.816995	3.54E-05
Q13753	LAMC2_HUMAN	Laminin subunit gamma-2 OS=Homo sapiens OX=9606 GN=LAMC2 PE=1 SV=2	0.816665	5.57E-04

Q5JRX3	PREP_HUMAN	Presequence protease mitochondrial OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=3	0.81649	3.57E-05
P20700	LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2	0.816464	5.47E-05
Q5T6V5	QSPH_HUMAN	Queuosine salvage protein OS=Homo sapiens OX=9606 GN=C9orf64 PE=1 SV=1	0.816149	3.95E-04
Q8IWS0	PHF6_HUMAN	PHD finger protein 6 OS=Homo sapiens OX=9606 GN=PHF6 PE=1 SV=1	0.814794	3.95E-04
Q15075	EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens OX=9606 GN=EEA1 PE=1 SV=2	0.814611	7.02E-05
P08133	ANXA6_HUMAN	Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3	0.814586	7.89E-05
P49247	RPIA_HUMAN	Ribose-5-phosphate isomerase OS=Homo sapiens OX=9606 GN=RPIA PE=1 SV=3	0.813519	4.07E-04
P46199	IF2M_HUMAN	Translation initiation factor IF-2 mitochondrial OS=Homo sapiens OX=9606 GN=MTIF2 PE=1 SV=2	0.813492	4.12E-04
Q86TI2	DPP9_HUMAN	Dipeptidyl peptidase 9 OS=Homo sapiens OX=9606 GN=DPP9 PE=1 SV=3	0.813155	4.05E-04
P55265	DSRAD_HUMAN	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=4	0.812731	6.49E-04
Q5RKV6	EXOS6_HUMAN	Exosome complex component MTR3 OS=Homo sapiens OX=9606 GN=EXOSC6 PE=1 SV=1	0.811584	4.21E-04
P54725	RD23A_HUMAN	UV excision repair protein RAD23 homolog A OS=Homo sapiens OX=9606 GN=RD23A PE=1 SV=1	0.811507	4.21E-04
P54652	HSP72_HUMAN	Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1	0.810708	1.64E-04
Q9BY77	PDIP3_HUMAN	Polymerase delta-interacting protein 3 OS=Homo sapiens OX=9606 GN=POLDIP3 PE=1 SV=2	0.810468	0.001813
Q13546	RIPK1_HUMAN	Receptor-interacting serine/threonine-protein kinase 1 OS=Homo sapiens OX=9606 GN=RIPK1 PE=1 SV=3	0.810006	4.09E-04
Q8TDN6	BRX1_HUMAN	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRX1 PE=1 SV=2	0.809759	0.007034
Q9UHY1	NRBP_HUMAN	Nuclear receptor-binding protein OS=Homo sapiens OX=9606 GN=NRBP1 PE=1 SV=1	0.808848	3.74E-04
Q7Z2W9	RM21_HUMAN	39S ribosomal protein L21 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL21 PE=1 SV=2	0.808297	4.50E-04
Q6P1N0	C2D1A_HUMAN	Coiled-coil and C2 domain-containing protein 1A OS=Homo sapiens OX=9606 GN=CC2D1A PE=1 SV=1	0.808114	0.001003
Q8WUP2	FBLI1_HUMAN	Filamin-binding LIM protein 1 OS=Homo sapiens OX=9606 GN=FBLIM1 PE=1 SV=2	0.807227	4.60E-04
Q70J99	UN13D_HUMAN	Protein unc-13 homolog D OS=Homo sapiens OX=9606 GN=UNC13D PE=1 SV=1	0.807101	0.001956
P00813	ADA_HUMAN	Adenosine deaminase OS=Homo sapiens OX=9606 GN=ADA PE=1 SV=3	0.80689	0.001896
Q9NS86	LANC2_HUMAN	LanC-like protein 2 OS=Homo sapiens OX=9606 GN=LANCL2 PE=1 SV=1	0.80672	4.60E-04
P04632	CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1	0.806305	1.68E-04
P36639	8ODP_HUMAN	7 8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens OX=9606 GN=NUDT1 PE=1 SV=3	0.806058	0.00667
Q13561	DCTN2_HUMAN	Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=4	0.805918	8.85E-04
Q9BV20	MTNA_HUMAN	Methylthioribose-1-phosphate isomerase OS=Homo sapiens OX=9606 GN=MRI1 PE=1 SV=1	0.805725	4.59E-04
P62266	RS23_HUMAN	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3	0.805301	4.91E-04
Q14839	CHD4_HUMAN	Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens OX=9606 GN=CHD4 PE=1 SV=2	0.805233	0.002071
Q14166	TTL12_HUMAN	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens OX=9606 GN=TTL12 PE=1 SV=2	0.805222	5.56E-05
Q9NY33	DPP3_HUMAN	Dipeptidyl peptidase 3 OS=Homo sapiens OX=9606 GN=DPP3 PE=1 SV=2	0.804347	8.57E-08
P28070	PSB4_HUMAN	Proteasome subunit beta type-4 OS=Homo sapiens OX=9606 GN=PSMB4 PE=1 SV=4	0.803956	2.04E-04
Q9UBL3	ASH2L_HUMAN	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens OX=9606 GN=ASH2L PE=1 SV=1	0.803823	4.80E-04
Q9NR50	EI2BG_HUMAN	Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens OX=9606 GN=EIF2B3 PE=1 SV=1	0.803747	5.26E-04
Q9UNH7	SNX6_HUMAN	Sorting nexin-6 OS=Homo sapiens OX=9606 GN=SNX6 PE=1 SV=1	0.803104	5.78E-04
Q9UBD5	ORC3_HUMAN	Origin recognition complex subunit 3 OS=Homo sapiens OX=9606 GN=ORC3 PE=1 SV=1	0.802963	4.86E-04
O15067	PUR4_HUMAN	Phosphoribosylformylglycinamide synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1 SV=4	0.802918	4.78E-04
Q9BW27	NUP85_HUMAN	Nuclear pore complex protein Nup85 OS=Homo sapiens OX=9606 GN=NUP85 PE=1 SV=1	0.802592	4.87E-04

P08779	K1C16_HUMAN	Keratin type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4	0.80247	4.60E-04
Q8NCW5	NNRE_HUMAN	NAD(P)H-hydrate epimerase OS=Homo sapiens OX=9606 GN=NAXE PE=1 SV=2	0.802214	4.00E-04
O94915	FRYL_HUMAN	Protein furry homolog-like OS=Homo sapiens OX=9606 GN=FRYL PE=1 SV=2	0.801738	0.002489
P68400	CSK21_HUMAN	Casein kinase II subunit alpha OS=Homo sapiens OX=9606 GN=CSNK2A1 PE=1 SV=1	0.80158	0.002863
Q14746	COG2_HUMAN	Conserved oligomeric Golgi complex subunit 2 OS=Homo sapiens OX=9606 GN=COG2 PE=1 SV=1	0.801096	0.00843
Q14289	FAK2_HUMAN	Protein-tyrosine kinase 2-beta OS=Homo sapiens OX=9606 GN=PTK2B PE=1 SV=2	0.801081	4.86E-04
Q13618	CUL3_HUMAN	Cullin-3 OS=Homo sapiens OX=9606 GN=CUL3 PE=1 SV=2	0.800248	7.34E-04
O15258	RER1_HUMAN	Protein RER1 OS=Homo sapiens OX=9606 GN=RER1 PE=1 SV=1	0.80023	4.68E-04
Q6WKZ4	RFIP1_HUMAN	Rab11 family-interacting protein 1 OS=Homo sapiens OX=9606 GN=RAB11FIP1 PE=1 SV=3	0.800098	5.10E-04
P78316	NOP14_HUMAN	Nucleolar protein 14 OS=Homo sapiens OX=9606 GN=NOP14 PE=1 SV=3	0.799131	5.26E-04
Q16787	LAMA3_HUMAN	Laminin subunit alpha-3 OS=Homo sapiens OX=9606 GN=LAMA3 PE=1 SV=2	0.799024	6.82E-04
O15269	SPTC1_HUMAN	Serine palmitoyltransferase 1 OS=Homo sapiens OX=9606 GN=SPTLC1 PE=1 SV=1	0.798918	4.86E-04
O43719	HTSF1_HUMAN	HIV Tat-specific factor 1 OS=Homo sapiens OX=9606 GN=HTATSF1 PE=1 SV=1	0.798779	7.92E-04
Q12874	SF3A3_HUMAN	Splicing factor 3A subunit 3 OS=Homo sapiens OX=9606 GN=SF3A3 PE=1 SV=1	0.798551	6.35E-04
Q99543	DNJC2_HUMAN	DnaJ homolog subfamily C member 2 OS=Homo sapiens OX=9606 GN=DNAJC2 PE=1 SV=4	0.798478	5.96E-04
Q9UJZ1	STML2_HUMAN	Stomatin-like protein 2 mitochondrial OS=Homo sapiens OX=9606 GN=STOML2 PE=1 SV=1	0.798457	7.97E-04
Q8WX92	NELFB_HUMAN	Negative elongation factor B OS=Homo sapiens OX=9606 GN=NELFB PE=1 SV=1	0.798366	5.26E-04
O75347	TBCA_HUMAN	Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=3	0.798174	5.12E-04
Q96C36	P5CR2_HUMAN	Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens OX=9606 GN=PYCR2 PE=1 SV=1	0.79787	5.26E-04
O60248	SOX15_HUMAN	Protein SOX-15 OS=Homo sapiens OX=9606 GN=SOX15 PE=1 SV=1	0.797541	0.005118
Q2M389	WASC4_HUMAN	WASH complex subunit 4 OS=Homo sapiens OX=9606 GN=WASHC4 PE=1 SV=2	0.796782	9.83E-04
P43897	EFTS_HUMAN	Elongation factor Ts mitochondrial OS=Homo sapiens OX=9606 GN=TSFM PE=1 SV=2	0.796726	5.30E-04
P05091	ALDH2_HUMAN	Aldehyde dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 PE=1 SV=2	0.795452	5.39E-04
P57735	RAB25_HUMAN	Ras-related protein Rab-25 OS=Homo sapiens OX=9606 GN=RAB25 PE=1 SV=2	0.795421	5.30E-04
P08754	GNAI3_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha OS=Homo sapiens OX=9606 GN=GNAI3 PE=1 SV=3	0.795228	6.44E-04
Q96S66	CLCC1_HUMAN	Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 PE=1 SV=1	0.794755	5.26E-04
Q9Y3D6	FIS1_HUMAN	Mitochondrial fission 1 protein OS=Homo sapiens OX=9606 GN=FIS1 PE=1 SV=2	0.794431	5.39E-04
P19387	RPB3_HUMAN	DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens OX=9606 GN=POLR2C PE=1 SV=2	0.79351	5.82E-04
P41236	IPP2_HUMAN	Protein phosphatase inhibitor 2 OS=Homo sapiens OX=9606 GN=PPP1R2 PE=1 SV=2	0.793162	5.62E-04
Q6NXS1	IPP2B_HUMAN	Protein phosphatase inhibitor 2 family member B OS=Homo sapiens OX=9606 GN=PPP1R2B PE=1 SV=2	0.793162	5.62E-04
O60232	ZNRD2_HUMAN	Protein ZNRD2 OS=Homo sapiens OX=9606 GN=ZNRD2 PE=1 SV=1	0.793156	5.48E-04
Q969X6	UTP4_HUMAN	U3 small nucleolar RNA-associated protein 4 homolog OS=Homo sapiens OX=9606 GN=UTP4 PE=1 SV=1	0.793153	5.36E-04
P37235	HPCL1_HUMAN	Hippocalcin-like protein 1 OS=Homo sapiens OX=9606 GN=HPCAL1 PE=1 SV=3	0.792749	0.002189
P51648	AL3A2_HUMAN	Aldehyde dehydrogenase family 3 member A2 OS=Homo sapiens OX=9606 GN=ALDH3A2 PE=1 SV=1	0.792033	5.60E-04
Q9Y697	NFS1_HUMAN	Cysteine desulfurase mitochondrial OS=Homo sapiens OX=9606 GN=NFS1 PE=1 SV=3	0.791875	5.64E-04
O76094	SRP72_HUMAN	Signal recognition particle subunit SRP72 OS=Homo sapiens OX=9606 GN=SRP72 PE=1 SV=3	0.791797	0.00459
P24821	TENA_HUMAN	Tenascin OS=Homo sapiens OX=9606 GN=TNC PE=1 SV=3	0.791775	7.51E-05
O94888	UBXN7_HUMAN	UBX domain-containing protein 7 OS=Homo sapiens OX=9606 GN=UBXN7 PE=1 SV=2	0.791437	5.57E-04

O00625	PIR_HUMAN	Pirin OS=Homo sapiens OX=9606 GN=PIR PE=1 SV=1	0.791135	0.002565
O14936	CSKP_HUMAN	Peripheral plasma membrane protein CASK OS=Homo sapiens OX=9606 GN=CASK PE=1 SV=3	0.791039	5.64E-04
P21589	5NTD_HUMAN	5'-nucleotidase OS=Homo sapiens OX=9606 GN=NT5E PE=1 SV=1	0.790725	5.26E-04
P18827	SDC1_HUMAN	Syndecan-1 OS=Homo sapiens OX=9606 GN=SDC1 PE=1 SV=3	0.790077	4.20E-04
P36543	VATE1_HUMAN	V-type proton ATPase subunit E 1 OS=Homo sapiens OX=9606 GN=ATP6V1E1 PE=1 SV=1	0.790059	5.64E-04
Q14978	NOLC1_HUMAN	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens OX=9606 GN=NOLC1 PE=1 SV=2	0.789433	5.82E-04
O94992	HEX11_HUMAN	Protein HEXIM1 OS=Homo sapiens OX=9606 GN=HEXIM1 PE=1 SV=1	0.789042	5.82E-04
Q8TBX8	PI42C_HUMAN	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens OX=9606 GN=PIP4K2C PE=1 SV=3	0.788852	0.009487
P60660	MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=2	0.788716	5.82E-04
Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=SUCLG2 PE=1 SV=2	0.787498	6.65E-04
Q92896	GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sapiens OX=9606 GN=GLG1 PE=1 SV=2	0.787095	0.002338
P20674	COX5A_HUMAN	Cytochrome c oxidase subunit 5A mitochondrial OS=Homo sapiens OX=9606 GN=COX5A PE=1 SV=2	0.786128	0.007293
O00743	PPP6_HUMAN	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens OX=9606 GN=PPP6C PE=1 SV=1	0.785398	3.74E-04
Q8N806	UBR7_HUMAN	Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens OX=9606 GN=UBR7 PE=1 SV=2	0.785366	5.98E-04
A6NHR9	SMHD1_HUMAN	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SMCHD1 PE=1 SV=2	0.784987	1.59E-04
Q9BRX5	PSF3_HUMAN	DNA replication complex GINS protein PSF3 OS=Homo sapiens OX=9606 GN=GINS3 PE=1 SV=1	0.784138	6.18E-04
Q13951	PEBB_HUMAN	Core-binding factor subunit beta OS=Homo sapiens OX=9606 GN=CBFB PE=1 SV=2	0.783909	6.02E-04
P33176	KINH_HUMAN	Kinesin-1 heavy chain OS=Homo sapiens OX=9606 GN=KIF5B PE=1 SV=1	0.783508	0.001159
Q9P287	BCCIP_HUMAN	BRCA2 and CDKN1A-interacting protein OS=Homo sapiens OX=9606 GN=BCCIP PE=1 SV=1	0.782154	0.001255
Q9Y3B7	RM11_HUMAN	39S ribosomal protein L11 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL11 PE=1 SV=1	0.781828	6.17E-04
P63167	DYL1_HUMAN	Dynein light chain 1 cytoplasmic OS=Homo sapiens OX=9606 GN=DYNLL1 PE=1 SV=1	0.781794	6.25E-04
Q9BY32	ITPA_HUMAN	Inosine triphosphate pyrophosphatase OS=Homo sapiens OX=9606 GN=ITPA PE=1 SV=2	0.781336	4.68E-04
P23921	RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens OX=9606 GN=RRM1 PE=1 SV=1	0.781153	9.53E-04
Q8WU90	ZC3HF_HUMAN	Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens OX=9606 GN=ZC3H15 PE=1 SV=1	0.780925	6.12E-04
O75390	CISY_HUMAN	Citrate synthase mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=2	0.78087	2.67E-04
Q14980	NUMA1_HUMAN	Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=2	0.780722	0.003991
O60313	OPA1_HUMAN	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=3	0.780455	0.001807
Q9BTT0	AN32E_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens OX=9606 GN=ANP32E PE=1 SV=1	0.78017	0.002877
Q96TC7	RMD3_HUMAN	Regulator of microtubule dynamics protein 3 OS=Homo sapiens OX=9606 GN=RMDN3 PE=1 SV=2	0.780076	9.48E-04
Q2NKK8	ERC6L_HUMAN	DNA excision repair protein ERCC-6-like OS=Homo sapiens OX=9606 GN=ERCC6L PE=1 SV=1	0.77981	6.42E-04
P09914	IFIT1_HUMAN	Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens OX=9606 GN=IFIT1 PE=1 SV=2	0.779428	6.28E-04
O43920	NDUS5_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens OX=9606 GN=NDUF55 PE=1 SV=3	0.779364	0.001148
Q9Y3I1	FBX7_HUMAN	F-box only protein 7 OS=Homo sapiens OX=9606 GN=FBXO7 PE=1 SV=1	0.779324	6.46E-04
P14927	QCR7_HUMAN	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens OX=9606 GN=UQCRB PE=1 SV=2	0.779102	6.49E-04
P41743	KPCI_HUMAN	Protein kinase C iota type OS=Homo sapiens OX=9606 GN=PRKCI PE=1 SV=2	0.7779	6.51E-04
Q92797	SYMPK_HUMAN	Symplekin OS=Homo sapiens OX=9606 GN=SYMPK PE=1 SV=2	0.776945	0.001737
Q99961	SH3G1_HUMAN	Endophilin-A2 OS=Homo sapiens OX=9606 GN=SH3GL1 PE=1 SV=1	0.776932	0.002745
Q8IVF2	AHNAK2_HUMAN	Protein AHNAK2 OS=Homo sapiens OX=9606 GN=AHNAK2 PE=1 SV=2	0.776783	7.54E-04

Q7Z7L1	SLN11_HUMAN	Schlafen family member 11 OS=Homo sapiens OX=9606 GN=SLFN11 PE=1 SV=2	0.776593	6.76E-04
Q15398	DLGP5_HUMAN	Disks large-associated protein 5 OS=Homo sapiens OX=9606 GN=DLGAP5 PE=1 SV=2	0.776464	6.76E-04
Q9Y450	HBS1L_HUMAN	HBS1-like protein OS=Homo sapiens OX=9606 GN=HBS1L PE=1 SV=1	0.776387	6.84E-04
P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 PE=1 SV=2	0.776328	9.39E-05
Q9ULZ3	ASC_HUMAN	Apoptosis-associated speck-like protein containing a CARD OS=Homo sapiens OX=9606 GN=PYCARD PE=1 SV=2	0.776138	2.97E-04
Q96MU7	YTDC1_HUMAN	YTH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=YTHDC1 PE=1 SV=3	0.775696	6.87E-04
P0DP24	CALM2_HUMAN	Calmodulin-2 OS=Homo sapiens OX=9606 GN=CALM2 PE=1 SV=1	0.775612	0.001148
P0DP23	CALM1_HUMAN	Calmodulin-1 OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1	0.775612	0.001148
P0DP25	CALM3_HUMAN	Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1	0.775612	0.001148
Q8NBF2	NHLC2_HUMAN	NHL repeat-containing protein 2 OS=Homo sapiens OX=9606 GN=NLRC2 PE=1 SV=1	0.775484	0.001619
P49589	SYCC_HUMAN	Cysteine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=CARS1 PE=1 SV=3	0.775461	6.86E-04
Q9BQE3	TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1	0.775376	6.82E-04
O75955	FLOT1_HUMAN	Flotillin-1 OS=Homo sapiens OX=9606 GN=FLOT1 PE=1 SV=3	0.774933	1.75E-04
Q9H0W9	CK054_HUMAN	Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1	0.774841	7.35E-04
P30153	2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=4	0.774468	1.48E-04
Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A OS=Homo sapiens OX=9606 GN=SMC1A PE=1 SV=2	0.774293	0.005912
P19784	CSK22_HUMAN	Casein kinase II subunit alpha' OS=Homo sapiens OX=9606 GN=CSNK2A2 PE=1 SV=1	0.774103	0.001775
Q9ULW0	TPX2_HUMAN	Targeting protein for Xklp2 OS=Homo sapiens OX=9606 GN=TPX2 PE=1 SV=2	0.774007	7.07E-04
P00390	GSHR_HUMAN	Glutathione reductase mitochondrial OS=Homo sapiens OX=9606 GN=GSR PE=1 SV=2	0.773601	8.96E-05
O95361	TRI16_HUMAN	Tripartite motif-containing protein 16 OS=Homo sapiens OX=9606 GN=TRIM16 PE=1 SV=3	0.773356	1.33E-04
Q86V81	THOC4_HUMAN	THO complex subunit 4 OS=Homo sapiens OX=9606 GN=ALYREF PE=1 SV=3	0.773115	7.61E-04
Q8WWC4	MAIP1_HUMAN	m-AAA protease-interacting protein 1 mitochondrial OS=Homo sapiens OX=9606 GN=MAIP1 PE=1 SV=1	0.773017	7.37E-04
O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=IDH3B PE=1 SV=2	0.772785	0.002471
Q99459	CDC5L_HUMAN	Cell division cycle 5-like protein OS=Homo sapiens OX=9606 GN=CDC5L PE=1 SV=2	0.772516	0.001153
Q01085	TIAR_HUMAN	Nucleolysin TIAR OS=Homo sapiens OX=9606 GN=TIAL1 PE=1 SV=1	0.772065	7.18E-04
P29590	PML_HUMAN	Protein PML OS=Homo sapiens OX=9606 GN=PML PE=1 SV=3	0.771765	3.71E-04
Q9UGV2	NDRG3_HUMAN	Protein NDRG3 OS=Homo sapiens OX=9606 GN=NDRG3 PE=1 SV=2	0.771731	8.94E-04
Q9BV86	NTM1A_HUMAN	N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens OX=9606 GN=NTMT1 PE=1 SV=3	0.771629	7.34E-04
Q8IZP0	ABI1_HUMAN	Abl interactor 1 OS=Homo sapiens OX=9606 GN=ABI1 PE=1 SV=4	0.771254	7.58E-04
Q13123	RED_HUMAN	Protein Red OS=Homo sapiens OX=9606 GN=IK PE=1 SV=3	0.771247	4.40E-04
Q9Y2K7	KDM2A_HUMAN	Lysine-specific demethylase 2A OS=Homo sapiens OX=9606 GN=KDM2A PE=1 SV=3	0.770945	7.54E-04
P27707	DCK_HUMAN	Deoxycytidine kinase OS=Homo sapiens OX=9606 GN=DCK PE=1 SV=1	0.770518	7.54E-04
Q9ULR0	ISY1_HUMAN	Pre-mRNA-splicing factor ISY1 homolog OS=Homo sapiens OX=9606 GN=ISY1 PE=1 SV=3	0.770421	7.41E-04
O75663	TIPRL_HUMAN	TIP41-like protein OS=Homo sapiens OX=9606 GN=TIPRL PE=1 SV=2	0.769943	7.35E-04
Q9Y5X3	SNX5_HUMAN	Sorting nexin-5 OS=Homo sapiens OX=9606 GN=SNX5 PE=1 SV=1	0.769146	7.63E-04
P68036	UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens OX=9606 GN=UBE2L3 PE=1 SV=1	0.768674	7.74E-04
Q08209	PP2BA_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens OX=9606 GN=PPP3CA PE=1 SV=1	0.768588	7.54E-04
Q96J01	THOC3_HUMAN	THO complex subunit 3 OS=Homo sapiens OX=9606 GN=THOC3 PE=1 SV=1	0.767879	2.71E-04
P04439	HLAA_HUMAN	HLA class I histocompatibility antigen A alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2	0.767518	7.60E-04

O75381	PEX14_HUMAN	Peroxisomal membrane protein PEX14 OS=Homo sapiens OX=9606 GN=PEX14 PE=1 SV=1	0.766841	6.84E-04
P17655	CAN2_HUMAN	Calpain-2 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN2 PE=1 SV=6	0.766749	7.43E-04
O94973	AP2A2_HUMAN	AP-2 complex subunit alpha-2 OS=Homo sapiens OX=9606 GN=AP2A2 PE=1 SV=2	0.766619	0.001653
P49915	GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=GMPS PE=1 SV=1	0.765954	7.89E-04
Q8WYA6	CTBL1_HUMAN	Beta-catenin-like protein 1 OS=Homo sapiens OX=9606 GN=CTNBL1 PE=1 SV=1	0.765729	0.002877
O75832	PSD10_HUMAN	26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens OX=9606 GN=PSMD10 PE=1 SV=1	0.765535	7.61E-04
P52292	IMA1_HUMAN	Importin subunit alpha-1 OS=Homo sapiens OX=9606 GN=KPNA2 PE=1 SV=1	0.765502	2.21E-04
Q9H773	DCTP1_HUMAN	dCTP pyrophosphatase 1 OS=Homo sapiens OX=9606 GN=DCTPP1 PE=1 SV=1	0.764845	3.22E-04
Q9BRX8	PXL2A_HUMAN	Peroxisome-like 2A OS=Homo sapiens OX=9606 GN=PRXL2A PE=1 SV=3	0.764638	8.10E-04
O00161	SNP23_HUMAN	Synaptosomal-associated protein 23 OS=Homo sapiens OX=9606 GN=SNAP23 PE=1 SV=1	0.764536	0.001463
Q49A26	GLYR1_HUMAN	Putative oxidoreductase GLYR1 OS=Homo sapiens OX=9606 GN=GLYR1 PE=1 SV=4	0.764335	8.09E-04
Q9H3R5	CENPH_HUMAN	Centromere protein H OS=Homo sapiens OX=9606 GN=CENPH PE=1 SV=1	0.762721	8.14E-04
Q9NP61	ARFG3_HUMAN	ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens OX=9606 GN=ARFGAP3 PE=1 SV=1	0.762627	8.41E-04
Q6XQN6	PNCB_HUMAN	Nicotinate phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=NAPRT PE=1 SV=2	0.762549	0.001239
Q7Z2K6	ERMP1_HUMAN	Endoplasmic reticulum metalloproteinase 1 OS=Homo sapiens OX=9606 GN=ERMP1 PE=1 SV=2	0.762418	9.54E-04
Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1 PE=1 SV=2	0.761782	0.001227
P57088	TMM33_HUMAN	Transmembrane protein 33 OS=Homo sapiens OX=9606 GN=TMEM33 PE=1 SV=2	0.761672	0.005137
P61201	CSN2_HUMAN	COP9 signalosome complex subunit 2 OS=Homo sapiens OX=9606 GN=COPS2 PE=1 SV=1	0.761467	3.74E-04
O94804	STK10_HUMAN	Serine/threonine-protein kinase 10 OS=Homo sapiens OX=9606 GN=STK10 PE=1 SV=1	0.761087	8.12E-04
O15382	BCAT2_HUMAN	Branched-chain-amino-acid aminotransferase mitochondrial OS=Homo sapiens OX=9606 GN=BCAT2 PE=1 SV=2	0.760971	8.41E-04
P49903	SPS1_HUMAN	Selenide water dikinase 1 OS=Homo sapiens OX=9606 GN=SEPHS1 PE=1 SV=2	0.760316	8.44E-04
Q5H9R7	PP6R3_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=2	0.759977	0.008635
P57764	GSDMD_HUMAN	Gasdermin-D OS=Homo sapiens OX=9606 GN=GSDMD PE=1 SV=1	0.75977	0.002271
P26358	DNMT1_HUMAN	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens OX=9606 GN=DNMT1 PE=1 SV=2	0.759754	0.004963
Q96IJ6	GMPPA_HUMAN	Mannose-1-phosphate guanylttransferase alpha OS=Homo sapiens OX=9606 GN=GMPPA PE=1 SV=1	0.759414	8.41E-04
Q14C86	GAPD1_HUMAN	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=GAPVD1 PE=1 SV=2	0.75884	6.10E-04
Q9GZZ9	UBA5_HUMAN	Ubiquitin-like modifier-activating enzyme 5 OS=Homo sapiens OX=9606 GN=UBA5 PE=1 SV=1	0.75876	8.85E-04
Q96QR8	PURB_HUMAN	Transcriptional activator protein Pur-beta OS=Homo sapiens OX=9606 GN=PURB PE=1 SV=3	0.758757	8.85E-04
O94905	ERLN2_HUMAN	Erlin-2 OS=Homo sapiens OX=9606 GN=ERLIN2 PE=1 SV=1	0.758631	6.35E-04
P50148	GNAQ_HUMAN	Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo sapiens OX=9606 GN=GNAQ PE=1 SV=4	0.758499	0.001322
Q9UNW1	MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens OX=9606 GN=MINPP1 PE=1 SV=1	0.75763	8.99E-04
Q96GG9	DCN1_HUMAN	DCN1-like protein 1 OS=Homo sapiens OX=9606 GN=DCUN1D1 PE=1 SV=1	0.757488	8.76E-04
Q9NTZ6	RBM12_HUMAN	RNA-binding protein 12 OS=Homo sapiens OX=9606 GN=RBM12 PE=1 SV=1	0.757363	9.02E-04
P54578	UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens OX=9606 GN=USP14 PE=1 SV=3	0.757321	8.79E-04
O75150	BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens OX=9606 GN=RNFB40 PE=1 SV=5	0.756123	0.001239
Q9Y333	LSM2_HUMAN	U6 snRNA-associated Sm-like protein LSM2 OS=Homo sapiens OX=9606 GN=LSM2 PE=1 SV=1	0.755763	9.09E-04
Q12846	STX4_HUMAN	Syntaxin-4 OS=Homo sapiens OX=9606 GN=STX4 PE=1 SV=2	0.755547	9.02E-04
A0AVT1	UBA6_HUMAN	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens OX=9606 GN=UBA6 PE=1 SV=1	0.755457	0.004164

Q15020	SART3_HUMAN	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens OX=9606 GN=SART3 PE=1 SV=1	0.754039	0.009889
Q6PI48	SYDM_HUMAN	Aspartate--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1	0.754018	0.009889
Q9BYD3	RM04_HUMAN	39S ribosomal protein L4 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL4 PE=1 SV=1	0.753872	9.47E-04
Q86XL3	ANKL2_HUMAN	Ankyrin repeat and LEM domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ANKL2 PE=1 SV=4	0.753827	9.40E-04
Q8NEU8	DP13B_HUMAN	DCC-interacting protein 13-beta OS=Homo sapiens OX=9606 GN=APPL2 PE=1 SV=3	0.753786	9.48E-04
P29083	T2EA_HUMAN	General transcription factor IIE subunit 1 OS=Homo sapiens OX=9606 GN=GTF2E1 PE=1 SV=2	0.753478	0.001396
P61020	RAB5B_HUMAN	Ras-related protein Rab-5B OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1	0.753427	9.71E-04
O43148	MCES_HUMAN	mRNA cap guanine-N7 methyltransferase OS=Homo sapiens OX=9606 GN=RNMT PE=1 SV=1	0.753146	9.09E-04
Q8TE77	SSH3_HUMAN	Protein phosphatase Slingshot homolog 3 OS=Homo sapiens OX=9606 GN=SSH3 PE=1 SV=2	0.753085	9.26E-04
P05120	PAI2_HUMAN	Plasminogen activator inhibitor 2 OS=Homo sapiens OX=9606 GN=SERPINB2 PE=1 SV=2	0.752213	4.91E-04
Q9Y4R8	TELO2_HUMAN	Telomere length regulation protein TEL2 homolog OS=Homo sapiens OX=9606 GN=TELO2 PE=1 SV=2	0.752202	9.83E-04
P02649	APOE_HUMAN	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1	0.752048	4.20E-04
P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta OS=Homo sapiens OX=9606 GN=HEXB PE=1 SV=3	0.751951	0.002745
Q9BXW7	HDHD5_HUMAN	Haloacid dehalogenase-like hydrolase domain-containing 5 OS=Homo sapiens OX=9606 GN=HDHD5 PE=1 SV=1	0.751827	0.006522
Q5T1M5	FKB15_HUMAN	FK506-binding protein 15 OS=Homo sapiens OX=9606 GN=FKBP15 PE=1 SV=2	0.751775	0.001678
Q99575	POP1_HUMAN	Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens OX=9606 GN=POP1 PE=1 SV=2	0.751578	9.61E-04
O43172	PRP4_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens OX=9606 GN=PRPF4 PE=1 SV=2	0.751393	0.004652
P61923	COPZ1_HUMAN	Coatmer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1	0.750886	9.47E-04
Q14789	GOLGB1_HUMAN	Golgin subfamily B member 1 OS=Homo sapiens OX=9606 GN=GOLGB1 PE=1 SV=2	0.750817	0.00678
Q9Y3T9	NOC2L_HUMAN	Nucleolar complex protein 2 homolog OS=Homo sapiens OX=9606 GN=NOC2L PE=1 SV=4	0.74941	0.001004
O75116	ROCK2_HUMAN	Rho-associated protein kinase 2 OS=Homo sapiens OX=9606 GN=ROCK2 PE=1 SV=4	0.749244	0.00101
O76021	RL1D1_HUMAN	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RSL1D1 PE=1 SV=3	0.748889	2.12E-04
P27694	RFA1_HUMAN	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2	0.748796	5.82E-04
P11047	LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3	0.748527	8.00E-05
P04183	KITH_HUMAN	Thymidine kinase cytosolic OS=Homo sapiens OX=9606 GN=TK1 PE=1 SV=2	0.748302	6.10E-04
Q16204	CCDC6_HUMAN	Coiled-coil domain-containing protein 6 OS=Homo sapiens OX=9606 GN=CCDC6 PE=1 SV=2	0.748006	1.88E-04
Q96CW5	GCP3_HUMAN	Gamma-tubulin complex component 3 OS=Homo sapiens OX=9606 GN=TUBGCP3 PE=1 SV=2	0.747907	0.001755
Q9NVX2	NLE1_HUMAN	Notchless protein homolog 1 OS=Homo sapiens OX=9606 GN=NLE1 PE=1 SV=4	0.747373	0.003094
P63220	RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens OX=9606 GN=RPS21 PE=1 SV=1	0.747332	0.001485
Q04760	LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapiens OX=9606 GN=GLO1 PE=1 SV=4	0.747317	0.001017
L0R6Q1	S35U4_HUMAN	SLC35A4 upstream open reading frame protein OS=Homo sapiens OX=9606 GN=SLC35A4 PE=3 SV=1	0.747091	0.007652
O15260	SURF4_HUMAN	Surfeit locus protein 4 OS=Homo sapiens OX=9606 GN=SURF4 PE=1 SV=3	0.747056	9.83E-04
P43304	GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=GPD2 PE=1 SV=3	0.746989	7.40E-06
P30260	CDC27_HUMAN	Cell division cycle protein 27 homolog OS=Homo sapiens OX=9606 GN=CDC27 PE=1 SV=2	0.746501	0.00252
Q6NZY4	ZCHC8_HUMAN	Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens OX=9606 GN=ZCHC8 PE=1 SV=2	0.746402	2.58E-04
P48449	ERG7_HUMAN	Lanosterol synthase OS=Homo sapiens OX=9606 GN=LSS PE=1 SV=1	0.745848	0.001205
O95881	TXD12_HUMAN	Thioredoxin domain-containing protein 12 OS=Homo sapiens OX=9606 GN=TXNDC12 PE=1 SV=1	0.745427	0.001063

Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 PE=1 SV=2	0.745358	8.59E-04
Q9Y446	PKP3_HUMAN	Plakophilin-3 OS=Homo sapiens OX=9606 GN=PKP3 PE=1 SV=1	0.745295	0.002129
Q8IV48	ERI1_HUMAN	3'-5' exoribonuclease 1 OS=Homo sapiens OX=9606 GN=ERI1 PE=1 SV=3	0.745284	0.001047
P06576	ATPB_HUMAN	ATP synthase subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=3	0.745093	3.73E-06
O95486	SC24A_HUMAN	Protein transport protein Sec24A OS=Homo sapiens OX=9606 GN=SEC24A PE=1 SV=2	0.745064	0.001092
Q86XP3	DDX42_HUMAN	ATP-dependent RNA helicase DDX42 OS=Homo sapiens OX=9606 GN=DDX42 PE=1 SV=1	0.744263	4.64E-04
P00374	DYR_HUMAN	Dihydrofolate reductase OS=Homo sapiens OX=9606 GN=DHFR PE=1 SV=2	0.743276	0.001009
P42285	MTREX_HUMAN	Exosome RNA helicase MTR4 OS=Homo sapiens OX=9606 GN=MTREX PE=1 SV=3	0.743267	2.20E-05
Q9C0C2	TB182_HUMAN	182 kDa tankyrase-1-binding protein OS=Homo sapiens OX=9606 GN=TNKS1BP1 PE=1 SV=4	0.742723	0.003678
Q14997	PSME4_HUMAN	Proteasome activator complex subunit 4 OS=Homo sapiens OX=9606 GN=PSME4 PE=1 SV=2	0.742717	0.001063
O75410	TACC1_HUMAN	Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=2	0.742327	0.003107
Q92614	MY18A_HUMAN	Unconventional myosin-XVIIIa OS=Homo sapiens OX=9606 GN=MYO18A PE=1 SV=3	0.741877	0.001106
Q5TFE4	NT5D1_HUMAN	5'-nucleotidase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NT5DC1 PE=1 SV=1	0.741318	5.57E-04
Q00610	CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=5	0.741088	8.41E-04
Q96EK5	KBP_HUMAN	KIF-binding protein OS=Homo sapiens OX=9606 GN=KIFBP PE=1 SV=1	0.741057	0.001148
Q14258	TRI25_HUMAN	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens OX=9606 GN=TRIM25 PE=1 SV=2	0.74101	7.86E-07
Q8NBN3	TM87A_HUMAN	Transmembrane protein 87A OS=Homo sapiens OX=9606 GN=TMEM87A PE=1 SV=3	0.740753	0.001117
Q00796	DHSO_HUMAN	Sorbitol dehydrogenase OS=Homo sapiens OX=9606 GN=SORD PE=1 SV=4	0.740568	0.003159
Q969G3	SMCE1_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=2	0.740523	7.51E-05
Q15436	SC23A_HUMAN	Protein transport protein Sec23A OS=Homo sapiens OX=9606 GN=SEC23A PE=1 SV=2	0.739215	1.64E-04
P52888	THOP1_HUMAN	Thimet oligopeptidase OS=Homo sapiens OX=9606 GN=THOP1 PE=1 SV=2	0.739169	0.001148
P08243	ASNS_HUMAN	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=ASNS PE=1 SV=4	0.738843	0.001161
O43237	DC1L2_HUMAN	Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1L2 PE=1 SV=1	0.738838	1.13E-04
O95104	SCAF4_HUMAN	SR-related and CTD-associated factor 4 OS=Homo sapiens OX=9606 GN=SCAF4 PE=1 SV=3	0.738341	0.001269
P27797	CALR_HUMAN	Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1	0.738231	0.001585
Q9P015	RM15_HUMAN	39S ribosomal protein L15 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL15 PE=1 SV=1	0.73818	0.001163
Q12888	TP53B_HUMAN	TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2	0.738139	0.001004
Q15785	TOM34_HUMAN	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens OX=9606 GN=TOMM34 PE=1 SV=2	0.737814	9.06E-04
Q9BRR6	ADPGK_HUMAN	ADP-dependent glucokinase OS=Homo sapiens OX=9606 GN=ADPGK PE=1 SV=1	0.737715	0.001255
P23497	SP100_HUMAN	Nuclear autoantigen Sp-100 OS=Homo sapiens OX=9606 GN=SP100 PE=1 SV=3	0.737635	0.001194
P54619	AAKG1_HUMAN	5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens OX=9606 GN=PRKAG1 PE=1 SV=1	0.737289	0.00116
P49321	NASP_HUMAN	Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=2	0.736966	3.10E-04
O75439	MPPB_HUMAN	Mitochondrial-processing peptidase subunit beta OS=Homo sapiens OX=9606 GN=PMPCB PE=1 SV=2	0.736532	0.001322
Q5T6F2	UBAP2_HUMAN	Ubiquitin-associated protein 2 OS=Homo sapiens OX=9606 GN=UBAP2 PE=1 SV=1	0.736028	0.004229
Q2TAY7	SMU1_HUMAN	WD40 repeat-containing protein SMU1 OS=Homo sapiens OX=9606 GN=SMU1 PE=1 SV=2	0.73596	1.72E-04
Q9Y263	PLAP_HUMAN	Phospholipase A-2-activating protein OS=Homo sapiens OX=9606 GN=PLAA PE=1 SV=2	0.735321	0.001175
Q99653	CHP1_HUMAN	Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=3	0.735297	0.001619

P30085	KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens OX=9606 GN=CMKP1 PE=1 SV=3	0.735183	0.001205
Q8WVJ2	NUDC2_HUMAN	NudC domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NUDC2 PE=1 SV=1	0.735028	0.003878
Q8N3D4	EH1L1_HUMAN	EH domain-binding protein 1-like protein 1 OS=Homo sapiens OX=9606 GN=EHP1L1 PE=1 SV=2	0.73489	6.92E-04
Q9NYY8	FAKD2_HUMAN	FAST kinase domain-containing protein 2 mitochondrial OS=Homo sapiens OX=9606 GN=FASTKD2 PE=1 SV=1	0.734189	0.001256
P61011	SRP54_HUMAN	Signal recognition particle 54 kDa protein OS=Homo sapiens OX=9606 GN=SRP54 PE=1 SV=1	0.733653	0.006696
Q86V48	LUZP1_HUMAN	Leucine zipper protein 1 OS=Homo sapiens OX=9606 GN=LUZP1 PE=1 SV=2	0.733524	0.009357
P18031	PTN1_HUMAN	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens OX=9606 GN=PTN1 PE=1 SV=1	0.733467	3.91E-04
P16144	ITB4_HUMAN	Integrin beta-4 OS=Homo sapiens OX=9606 GN=ITGB4 PE=1 SV=5	0.733309	5.82E-04
Q92520	FAM3C_HUMAN	Protein FAM3C OS=Homo sapiens OX=9606 GN=FAM3C PE=1 SV=1	0.733175	0.001268
P31431	SDC4_HUMAN	Syndecan-4 OS=Homo sapiens OX=9606 GN=SDC4 PE=1 SV=2	0.732896	0.001711
Q13637	RAB32_HUMAN	Ras-related protein Rab-32 OS=Homo sapiens OX=9606 GN=RAB32 PE=1 SV=3	0.732534	0.001254
P22061	PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=4	0.732184	0.001795
P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase mitochondrial OS=Homo sapiens OX=9606 GN=PRDX3 PE=1 SV=3	0.731994	0.00128
P42785	PCP_HUMAN	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1	0.731691	0.001255
Q13243	SRSF5_HUMAN	Serine/arginine-rich splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 PE=1 SV=1	0.731632	0.001298
Q01105	SET_HUMAN	Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=3	0.731612	9.06E-04
Q9Y6D5	BIG2_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens OX=9606 GN=ARFGEF2 PE=1 SV=3	0.731332	8.67E-04
Q86Y56	DAAF5_HUMAN	Dynein assembly factor 5 axonemal OS=Homo sapiens OX=9606 GN=DAAF5 PE=1 SV=4	0.731292	0.004119
P49790	NU153_HUMAN	Nuclear pore complex protein Nup153 OS=Homo sapiens OX=9606 GN=NUP153 PE=1 SV=2	0.731065	6.83E-05
Q3LXA3	TKFC_HUMAN	Triokinase/FMN cyclase OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=2	0.730525	7.27E-04
P57081	WDR4_HUMAN	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4 OS=Homo sapiens OX=9606 GN=WDR4 PE=1 SV=2	0.730004	0.00127
Q92888	ARHG1_HUMAN	Rho guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=ARHGEF1 PE=1 SV=2	0.729706	0.002495
Q13131	AAPK1_HUMAN	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens OX=9606 GN=PRKAA1 PE=1 SV=4	0.729611	0.008467
Q15642	CIP4_HUMAN	Cdc42-interacting protein 4 OS=Homo sapiens OX=9606 GN=TRIP10 PE=1 SV=3	0.729302	0.001299
Q96AB3	ISOC2_HUMAN	Isochorismatase domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ISOC2 PE=1 SV=1	0.729241	0.001322
Q9Y262	EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1	0.728928	6.04E-04
Q00577	PURA_HUMAN	Transcriptional activator protein Pur-alpha OS=Homo sapiens OX=9606 GN=PURA PE=1 SV=2	0.728521	0.001255
O43678	NDUA2_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens OX=9606 GN=NDUFA2 PE=1 SV=3	0.728128	0.001393
Q9UHV9	PFD2_HUMAN	Prefoldin subunit 2 OS=Homo sapiens OX=9606 GN=PFDN2 PE=1 SV=1	0.727822	0.001343
Q9P0V9	SEP10_HUMAN	Septin-10 OS=Homo sapiens OX=9606 GN=SEPTIN10 PE=1 SV=2	0.72772	0.001148
Q92878	RAD50_HUMAN	DNA repair protein RAD50 OS=Homo sapiens OX=9606 GN=RAD50 PE=1 SV=1	0.727653	0.001389
Q14558	KPRA_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens OX=9606 GN=PRPSAP1 PE=1 SV=2	0.727541	0.007293
P46734	MP2K3_HUMAN	Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens OX=9606 GN=MAP2K3 PE=1 SV=2	0.727517	2.68E-04
Q96D71	REPS1_HUMAN	RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens OX=9606 GN=REPS1 PE=1 SV=3	0.72702	3.95E-04
O95400	CD2B2_HUMAN	CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens OX=9606 GN=CD2BP2 PE=1 SV=1	0.726808	0.001378
Q9NZB2	F120A_HUMAN	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A PE=1 SV=2	0.726239	0.003353
P39687	AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32A PE=1 SV=1	0.726114	0.001564
P18074	ERCC2_HUMAN	General transcription and DNA repair factor IIH helicase subunit XPD OS=Homo sapiens OX=9606 GN=ERCC2 PE=1 SV=1	0.725876	0.001358

Q96S44	PRPK_HUMAN	EKC/KEOPS complex subunit TP53RK OS=Homo sapiens OX=9606 GN=TP53RK PE=1 SV=2	0.725306	0.001358
Q9NX14	NDUBB_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11 mitochondrial OS=Homo sapiens OX=9606 GN=NDUBB11 PE=1 SV=1	0.724638	0.001716
Q16795	NDUA9_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9 mitochondrial OS=Homo sapiens OX=9606 GN=NDUA9 PE=1 SV=2	0.724481	0.005818
Q9BVL2	NUP58_HUMAN	Nucleoporin p58/p45 OS=Homo sapiens OX=9606 GN=NUP58 PE=1 SV=1	0.724476	0.001396
P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit mitochondrial OS=Homo sapiens OX=9606 GN=SDHA PE=1 SV=2	0.724452	0.001017
Q96KR1	ZFR_HUMAN	Zinc finger RNA-binding protein OS=Homo sapiens OX=9606 GN=ZFR PE=1 SV=2	0.724441	0.001363
Q8TDX7	NEK7_HUMAN	Serine/threonine-protein kinase Nek7 OS=Homo sapiens OX=9606 GN=NEK7 PE=1 SV=1	0.724277	0.001441
P25789	PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1	0.723806	0.001441
Q15102	PA1B3_HUMAN	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens OX=9606 GN=PAFAH1B3 PE=1 SV=1	0.72338	0.001441
Q13033	STRN3_HUMAN	Striatin-3 OS=Homo sapiens OX=9606 GN=STRN3 PE=1 SV=3	0.72278	0.006428
Q9Y2A7	NCKP1_HUMAN	Nck-associated protein 1 OS=Homo sapiens OX=9606 GN=NCKAP1 PE=1 SV=1	0.722606	5.35E-04
Q13257	MD2L1_HUMAN	Mitotic spindle assembly checkpoint protein MAD2A OS=Homo sapiens OX=9606 GN=MAD2L1 PE=1 SV=1	0.722466	0.001441
P48444	COPD_HUMAN	Coatomer subunit delta OS=Homo sapiens OX=9606 GN=ARCN1 PE=1 SV=1	0.722436	9.19E-04
Q9NQR4	NIT2_HUMAN	Omega-amidase NIT2 OS=Homo sapiens OX=9606 GN=NIT2 PE=1 SV=1	0.722271	6.10E-04
Q9Y230	RUVB2_HUMAN	RuvB-like 2 OS=Homo sapiens OX=9606 GN=RUVBL2 PE=1 SV=3	0.722112	0.002008
P53350	PLK1_HUMAN	Serine/threonine-protein kinase PLK1 OS=Homo sapiens OX=9606 GN=PLK1 PE=1 SV=1	0.722101	0.001441
Q969U7	PSMG2_HUMAN	Proteasome assembly chaperone 2 OS=Homo sapiens OX=9606 GN=PSMG2 PE=1 SV=1	0.721979	0.001481
Q01813	PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase platelet type OS=Homo sapiens OX=9606 GN=PFKP PE=1 SV=2	0.721517	0.008923
Q6P3X3	TTC27_HUMAN	Tetratricopeptide repeat protein 27 OS=Homo sapiens OX=9606 GN=TTC27 PE=1 SV=1	0.720962	0.001452
Q9UNN5	FAF1_HUMAN	FAS-associated factor 1 OS=Homo sapiens OX=9606 GN=FAF1 PE=1 SV=2	0.72083	0.001478
Q96BW5	PTER_HUMAN	Phosphotriesterase-related protein OS=Homo sapiens OX=9606 GN=PTER PE=1 SV=1	0.720484	0.001239
P04150	GCR_HUMAN	Glucocorticoid receptor OS=Homo sapiens OX=9606 GN=NR3C1 PE=1 SV=1	0.720322	0.008476
Q15008	PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens OX=9606 GN=PSMD6 PE=1 SV=1	0.720268	5.59E-04
Q86UE4	LYRIC_HUMAN	Protein LYRIC OS=Homo sapiens OX=9606 GN=MTDH PE=1 SV=2	0.720127	0.002227
Q01780	EXOSX_HUMAN	Exosome component 10 OS=Homo sapiens OX=9606 GN=EXOSC10 PE=1 SV=2	0.719999	0.007034
Q9UBS4	DJB11_HUMAN	DnaJ homolog subfamily B member 11 OS=Homo sapiens OX=9606 GN=DNAJB11 PE=1 SV=1	0.719996	3.74E-04
Q9P265	DIP2B_HUMAN	Disco-interacting protein 2 homolog B OS=Homo sapiens OX=9606 GN=DIP2B PE=1 SV=3	0.719892	0.001484
P36915	GNL1_HUMAN	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens OX=9606 GN=GNL1 PE=1 SV=2	0.719762	0.003003
O75131	CPNE3_HUMAN	Copine-3 OS=Homo sapiens OX=9606 GN=CPNE3 PE=1 SV=1	0.719203	0.004856
Q8NC56	LEMD2_HUMAN	LEM domain-containing protein 2 OS=Homo sapiens OX=9606 GN=LEMD2 PE=1 SV=1	0.719142	0.001622
O43292	GPAA1_HUMAN	Glycosylphosphatidylinositol anchor attachment 1 protein OS=Homo sapiens OX=9606 GN=GPAA1 PE=1 SV=3	0.718973	0.00151
Q96KN1	LRAT2_HUMAN	Protein LRATD2 OS=Homo sapiens OX=9606 GN=LRATD2 PE=1 SV=1	0.718721	0.0015
Q8TAQ2	SMRC2_HUMAN	SWI/SNF complex subunit SMARCC2 OS=Homo sapiens OX=9606 GN=SMARCC2 PE=1 SV=1	0.718541	0.002352
Q9Y295	DRG1_HUMAN	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=DRG1 PE=1 SV=1	0.718347	0.001266
Q16537	2A5E_HUMAN	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform OS=Homo sapiens OX=9606 GN=PPP2R5E PE=1 SV=1	0.718296	0.001561
P07954	FUMH_HUMAN	Fumarate hydratase mitochondrial OS=Homo sapiens OX=9606 GN=FMH PE=1 SV=3	0.718107	0.004336

P30419	NMT1_HUMAN	Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens OX=9606 GN=NMT1 PE=1 SV=2	0.718038	0.004888
Q99615	DNJC7_HUMAN	DnaJ homolog subfamily C member 7 OS=Homo sapiens OX=9606 GN=DNAJC7 PE=1 SV=2	0.717998	0.00247
Q16740	CLPP_HUMAN	ATP-dependent Clp protease proteolytic subunit mitochondrial OS=Homo sapiens OX=9606 GN=CLPP PE=1 SV=1	0.717778	0.001544
Q92542	NICA_HUMAN	Nicastrin OS=Homo sapiens OX=9606 GN=NCSTN PE=1 SV=2	0.717397	0.005111
Q9UJA5	TRM6_HUMAN	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens OX=9606 GN=TRMT6 PE=1 SV=1	0.71721	0.00198
O43752	STX6_HUMAN	Syntaxin-6 OS=Homo sapiens OX=9606 GN=STX6 PE=1 SV=1	0.717118	0.001561
Q9NPD8	UBE2T_HUMAN	Ubiquitin-conjugating enzyme E2 T OS=Homo sapiens OX=9606 GN=UBE2T PE=1 SV=1	0.716987	0.001543
Q53H82	LACB2_HUMAN	Endoribonuclease LACTB2 OS=Homo sapiens OX=9606 GN=LACTB2 PE=1 SV=2	0.7169	0.001561
Q9Y3D9	RT23_HUMAN	28S ribosomal protein S23 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS23 PE=1 SV=2	0.716863	0.001543
P11717	MPRI_HUMAN	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=IGF2R PE=1 SV=3	0.716663	0.001657
Q0VDF9	HSP7E_HUMAN	Heat shock 70 kDa protein 14 OS=Homo sapiens OX=9606 GN=HSPA14 PE=1 SV=1	0.716338	0.001501
P18858	DNL1_HUMAN	DNA ligase 1 OS=Homo sapiens OX=9606 GN=LIG1 PE=1 SV=1	0.716308	0.003437
P15586	GNS_HUMAN	N-acetylglucosamine-6-sulfatase OS=Homo sapiens OX=9606 GN=GNS PE=1 SV=3	0.716008	0.001584
P49642	PRI1_HUMAN	DNA primase small subunit OS=Homo sapiens OX=9606 GN=PRIM1 PE=1 SV=1	0.715355	0.001567
P30622	CLIP1_HUMAN	CAP-Gly domain-containing linker protein 1 OS=Homo sapiens OX=9606 GN=CLIP1 PE=1 SV=2	0.715161	8.85E-04
Q99829	CPNE1_HUMAN	Copine-1 OS=Homo sapiens OX=9606 GN=CPNE1 PE=1 SV=1	0.714931	0.001465
P49406	RM19_HUMAN	39S ribosomal protein L19 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL19 PE=1 SV=2	0.714797	0.001587
Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB PE=1 SV=4	0.714737	0.001423
Q8TEQ6	GEM15_HUMAN	Gem-associated protein 5 OS=Homo sapiens OX=9606 GN=GEMIN5 PE=1 SV=3	0.714711	7.35E-04
Q96552	PIGS_HUMAN	GPI transamidase component PIG-S OS=Homo sapiens OX=9606 GN=PIGS PE=1 SV=3	0.71466	5.82E-04
Q6P1L8	RM14_HUMAN	39S ribosomal protein L14 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL14 PE=1 SV=1	0.714159	0.001584
P06493	CDK1_HUMAN	Cyclin-dependent kinase 1 OS=Homo sapiens OX=9606 GN=CDK1 PE=1 SV=3	0.714143	0.001105
Q99538	LGMN_HUMAN	Legumain OS=Homo sapiens OX=9606 GN=LGMN PE=1 SV=1	0.714114	0.001561
Q9NYL9	TMOD3_HUMAN	Tropomodulin-3 OS=Homo sapiens OX=9606 GN=TMOD3 PE=1 SV=1	0.714079	6.35E-04
O60869	EDF1_HUMAN	Endothelial differentiation-related factor 1 OS=Homo sapiens OX=9606 GN=EDF1 PE=1 SV=1	0.714004	4.82E-04
Q14574	DSC3_HUMAN	Desmocollin-3 OS=Homo sapiens OX=9606 GN=DSC3 PE=1 SV=3	0.713914	0.001587
P49590	SYHM_HUMAN	Histidine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=HARS2 PE=1 SV=1	0.713851	0.001619
Q9UBB4	ATX10_HUMAN	Ataxin-10 OS=Homo sapiens OX=9606 GN=ATXN10 PE=1 SV=1	0.713825	0.002966
P18887	XRCC1_HUMAN	DNA repair protein XRCC1 OS=Homo sapiens OX=9606 GN=XRCC1 PE=1 SV=2	0.713627	0.001652
Q92598	HS105_HUMAN	Heat shock protein 105 kDa OS=Homo sapiens OX=9606 GN=HSPH1 PE=1 SV=1	0.713411	0.007386
Q9Y3L3	3BP1_HUMAN	SH3 domain-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3BP1 PE=1 SV=3	0.713364	0.001622
Q9BQA1	MEP50_HUMAN	Methylosome protein 50 OS=Homo sapiens OX=9606 GN=WDR77 PE=1 SV=1	0.713178	0.008591
Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=4	0.71297	0.001084
P61981	1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2	0.71292	0.002271
O75915	PRAF3_HUMAN	PRA1 family protein 3 OS=Homo sapiens OX=9606 GN=ARL6IP5 PE=1 SV=1	0.712808	0.001587
Q9UJH6	SHPK_HUMAN	Sedoheptulokinase OS=Homo sapiens OX=9606 GN=SHPK PE=1 SV=3	0.712613	7.11E-04
Q9NVI7	ATD3A_HUMAN	ATPase family AAA domain-containing protein 3A OS=Homo sapiens OX=9606 GN=ATAD3A PE=1 SV=2	0.712095	0.001595
Q9Y5Q8	TF3C5_HUMAN	General transcription factor 3C polypeptide 5 OS=Homo sapiens OX=9606 GN=GTF3C5 PE=1 SV=2	0.711431	0.001631
O00560	SDCB1_HUMAN	Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1	0.711308	0.004808

Q86SX6	GLRX5_HUMAN	Glutaredoxin-related protein 5 mitochondrial OS=Homo sapiens OX=9606 GN=GLRX5 PE=1 SV=2	0.711289	0.001646
Q68EM7	RHG17_HUMAN	Rho GTPase-activating protein 17 OS=Homo sapiens OX=9606 GN=ARHGAP17 PE=1 SV=1	0.71118	0.004966
Q9P2J5	SYLC_HUMAN	Leucine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=LARS1 PE=1 SV=2	0.711126	0.001777
Q9Y6W5	WASF2_HUMAN	Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens OX=9606 GN=WASF2 PE=1 SV=3	0.711013	0.001602
Q8IXI1	MIRO2_HUMAN	Mitochondrial Rho GTPase 2 OS=Homo sapiens OX=9606 GN=RHOT2 PE=1 SV=2	0.710813	0.002725
Q53H12	AGK_HUMAN	Acylglycerol kinase mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=2	0.710682	0.001664
Q99661	KIF2C_HUMAN	Kinesin-like protein KIF2C OS=Homo sapiens OX=9606 GN=KIF2C PE=1 SV=2	0.710406	0.0043
O75746	CMC1_HUMAN	Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens OX=9606 GN=SLC25A12 PE=1 SV=2	0.710295	0.002994
P42892	ECE1_HUMAN	Endothelin-converting enzyme 1 OS=Homo sapiens OX=9606 GN=ECE1 PE=1 SV=2	0.709658	0.0037
P11310	ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ACADM PE=1 SV=1	0.709461	0.005504
Q8WXI9	P66B_HUMAN	Transcriptional repressor p66-beta OS=Homo sapiens OX=9606 GN=GATAD2B PE=1 SV=1	0.709168	0.001673
Q9Y2R9	RT07_HUMAN	28S ribosomal protein S7 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS7 PE=1 SV=2	0.708984	0.001711
Q9Y6M1	IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2 PE=1 SV=2	0.708951	5.01E-04
Q9NZI8	IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=1 SV=2	0.708727	0.001477
O95084	PRS23_HUMAN	Serine protease 23 OS=Homo sapiens OX=9606 GN=PRSS23 PE=1 SV=1	0.708637	0.001716
Q8IX12	CCAR1_HUMAN	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens OX=9606 GN=CCAR1 PE=1 SV=2	0.708447	0.009281
Q15029	U5S1_HUMAN	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=EFTUD2 PE=1 SV=1	0.708183	0.009446
O95274	LYPD3_HUMAN	Ly6/PLAUR domain-containing protein 3 OS=Homo sapiens OX=9606 GN=LYPD3 PE=1 SV=2	0.707854	0.001665
Q9BWM7	SFXN3_HUMAN	Sideroflexin-3 OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=3	0.707789	0.001678
Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2 OS=Homo sapiens OX=9606 GN=SPCS2 PE=1 SV=3	0.707659	0.001349
P04818	TYSY_HUMAN	Thymidylate synthase OS=Homo sapiens OX=9606 GN=TYMS PE=1 SV=3	0.707469	0.001321
Q14974	IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=2	0.70731	0.007416
Q00403	TF2B_HUMAN	Transcription initiation factor IIB OS=Homo sapiens OX=9606 GN=GTF2B PE=1 SV=1	0.707254	0.001716
Q9BT78	CSN4_HUMAN	COP9 signalosome complex subunit 4 OS=Homo sapiens OX=9606 GN=COPS4 PE=1 SV=1	0.706669	0.001673
Q9Y679	AUP1_HUMAN	Ancient ubiquitous protein 1 OS=Homo sapiens OX=9606 GN=AUP1 PE=1 SV=2	0.706217	0.001827
Q92890	UFD1_HUMAN	Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Homo sapiens OX=9606 GN=UFD1 PE=1 SV=3	0.705896	0.007034
P62857	RS28_HUMAN	40S ribosomal protein S28 OS=Homo sapiens OX=9606 GN=RPS28 PE=1 SV=1	0.705114	0.008469
Q13867	BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens OX=9606 GN=BLMH PE=1 SV=1	0.704692	0.001821
P0C0S5	H2AZ_HUMAN	Histone H2A.Z OS=Homo sapiens OX=9606 GN=H2AZ1 PE=1 SV=2	0.703598	0.001821
Q71UI9	H2AV_HUMAN	Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AFV PE=1 SV=3	0.703598	0.001821
Q8NBJ7	SUMF2_HUMAN	Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=2	0.703557	0.001789
Q9UHY7	ENOPH_HUMAN	Enolase-phosphatase E1 OS=Homo sapiens OX=9606 GN=ENOPH1 PE=1 SV=1	0.703519	0.001533
P78346	RPP30_HUMAN	Ribonuclease P protein subunit p30 OS=Homo sapiens OX=9606 GN=RPP30 PE=1 SV=1	0.703247	0.001827
Q8TCG1	CIP2A_HUMAN	Protein CIP2A OS=Homo sapiens OX=9606 GN=CIP2A PE=1 SV=2	0.702892	0.001807
Q9NVH1	DJC11_HUMAN	DnaJ homolog subfamily C member 11 OS=Homo sapiens OX=9606 GN=DNAJC11 PE=1 SV=2	0.702724	0.001875
Q8TE68	ES8L1_HUMAN	Epidermal growth factor receptor kinase substrate 8-like protein 1 OS=Homo sapiens OX=9606 GN=EPS8L1 PE=1 SV=3	0.702646	0.008967
P26368	U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=1 SV=4	0.702614	0.004044
P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4	0.702559	9.43E-04

Q12792	TWF1_HUMAN	Twinfilin-1 OS=Homo sapiens OX=9606 GN=TWF1 PE=1 SV=3	0.702456	0.001881
Q96KB5	TOPK_HUMAN	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens OX=9606 GN=PBK PE=1 SV=3	0.702284	0.001846
Q9NYL4	FKB11_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP11 OS=Homo sapiens OX=9606 GN=FKBP11 PE=1 SV=1	0.702249	0.00186
P21399	ACOC_HUMAN	Cytoplasmic aconitate hydratase OS=Homo sapiens OX=9606 GN=ACO1 PE=1 SV=3	0.701368	0.004549
Q6UN15	FIP1_HUMAN	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens OX=9606 GN=FIP1L1 PE=1 SV=1	0.701308	0.001471
P40222	TXLNA_HUMAN	Alpha-taxilin OS=Homo sapiens OX=9606 GN=TXLNA PE=1 SV=3	0.701178	0.001595
O60271	JIP4_HUMAN	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens OX=9606 GN=SPAG9 PE=1 SV=4	0.700578	0.001149
Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1 PE=1 SV=2	0.70044	0.003876
O75694	NU155_HUMAN	Nuclear pore complex protein Nup155 OS=Homo sapiens OX=9606 GN=NUP155 PE=1 SV=1	0.70044	0.005801
P35241	RADI_HUMAN	Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1	0.700259	0.002523
Q07065	CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2	0.700104	3.46E-05
P31948	STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1	0.700075	8.09E-04
A0AV96	RBM47_HUMAN	RNA-binding protein 47 OS=Homo sapiens OX=9606 GN=RBM47 PE=1 SV=2	0.700027	7.54E-04
Q9H2P0	ADNP_HUMAN	Activity-dependent neuroprotector homeobox protein OS=Homo sapiens OX=9606 GN=ADNP PE=1 SV=1	0.700003	0.001958
Q14435	GALT3_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 3 OS=Homo sapiens OX=9606 GN=GALNT3 PE=1 SV=2	0.699928	0.001821
Q9UNE7	CHIP_HUMAN	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens OX=9606 GN=STUB1 PE=1 SV=2	0.699683	0.001883
Q96I20	PAWR_HUMAN	PRKC apoptosis WT1 regulator protein OS=Homo sapiens OX=9606 GN=PAWR PE=1 SV=1	0.699643	0.001175
P61964	WDR5_HUMAN	WD repeat-containing protein 5 OS=Homo sapiens OX=9606 GN=WDR5 PE=1 SV=1	0.699231	0.001511
P53041	PPP5_HUMAN	Serine/threonine-protein phosphatase 5 OS=Homo sapiens OX=9606 GN=PPP5C PE=1 SV=1	0.698998	0.001441
Q5K651	SAMD9_HUMAN	Sterile alpha motif domain-containing protein 9 OS=Homo sapiens OX=9606 GN=SAMD9 PE=1 SV=1	0.698923	0.001963
O94826	TOM70_HUMAN	Mitochondrial import receptor subunit TOM70 OS=Homo sapiens OX=9606 GN=TOMM70 PE=1 SV=1	0.698583	0.001297
Q9H2U1	DHX36_HUMAN	ATP-dependent DNA/RNA helicase DHX36 OS=Homo sapiens OX=9606 GN=DHX36 PE=1 SV=2	0.697948	0.001971
O94760	DDAH1_HUMAN	N(G) N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens OX=9606 GN=DDAH1 PE=1 SV=3	0.697741	0.005604
Q8IZ83	A16A1_HUMAN	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens OX=9606 GN=ALDH16A1 PE=1 SV=2	0.697044	0.002029
Q9Y282	ERGI3_HUMAN	Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Homo sapiens OX=9606 GN=ERGIC3 PE=1 SV=1	0.696581	0.001996
Q99590	SCAFB_HUMAN	Protein SCAF11 OS=Homo sapiens OX=9606 GN=SCAF11 PE=1 SV=2	0.696543	0.001978
Q9BRQ8	FSP1_HUMAN	Ferroptosis suppressor protein 1 OS=Homo sapiens OX=9606 GN=AIFM2 PE=1 SV=1	0.696334	0.002008
Q9UNX4	WDR3_HUMAN	WD repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=WDR3 PE=1 SV=1	0.696278	0.009987
Q9NS69	TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens OX=9606 GN=TOMM22 PE=1 SV=3	0.69625	0.001969
P52732	KIF11_HUMAN	Kinesin-like protein KIF11 OS=Homo sapiens OX=9606 GN=KIF11 PE=1 SV=2	0.696072	5.45E-05
Q05639	EF1A2_HUMAN	Elongation factor 1-alpha 2 OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1	0.696052	0.001846
P37108	SRP14_HUMAN	Signal recognition particle 14 kDa protein OS=Homo sapiens OX=9606 GN=SRP14 PE=1 SV=2	0.695266	0.002015
P06396	GELS_HUMAN	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1	0.695145	0.001494
Q9BYD1	RM13_HUMAN	39S ribosomal protein L13 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL13 PE=1 SV=1	0.695079	0.002105
P30876	RPB2_HUMAN	DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=1	0.694751	0.003168
Q96MW1	CCD43_HUMAN	Coiled-coil domain-containing protein 43 OS=Homo sapiens OX=9606 GN=CCDC43 PE=1 SV=2	0.694655	0.002024
Q15054	DPOD3_HUMAN	DNA polymerase delta subunit 3 OS=Homo sapiens OX=9606 GN=POLD3 PE=1 SV=2	0.694494	0.00204
Q13596	SNX1_HUMAN	Sorting nexin-1 OS=Homo sapiens OX=9606 GN=SNX1 PE=1 SV=3	0.694192	6.63E-04

O00159	MYO1C_HUMAN	Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4	0.693679	0.002683
P07339	CATD_HUMAN	Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1	0.693629	0.00339
Q01658	NC2B_HUMAN	Protein Dr1 OS=Homo sapiens OX=9606 GN=DR1 PE=1 SV=1	0.693473	0.002131
O43592	XPOT_HUMAN	Exportin-T OS=Homo sapiens OX=9606 GN=XPOT PE=1 SV=2	0.693111	0.002003
P62834	RAP1A_HUMAN	Ras-related protein Rap-1A OS=Homo sapiens OX=9606 GN=RAP1A PE=1 SV=1	0.692693	0.002024
Q01970	PLCB3_HUMAN	1-phosphatidylinositol 4 5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens OX=9606 GN=PLCB3 PE=1 SV=2	0.692633	8.46E-04
Q7Z4Q2	HEAT3_HUMAN	HEAT repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=HEATR3 PE=1 SV=2	0.69242	0.002102
P67870	CSK2B_HUMAN	Casein kinase II subunit beta OS=Homo sapiens OX=9606 GN=CSNK2B PE=1 SV=1	0.692236	0.003781
Q9H3U1	UN45A_HUMAN	Protein unc-45 homolog A OS=Homo sapiens OX=9606 GN=UNC45A PE=1 SV=1	0.692087	0.002129
P80404	GABT_HUMAN	4-aminobutyrate aminotransferase mitochondrial OS=Homo sapiens OX=9606 GN=ABAT PE=1 SV=3	0.692002	0.002151
Q02790	FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens OX=9606 GN=FKBP4 PE=1 SV=3	0.691878	0.001017
Q96JY6	PDLI2_HUMAN	PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1	0.691294	0.004104
O14562	UBFD1_HUMAN	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens OX=9606 GN=UBFD1 PE=1 SV=2	0.690746	0.004755
P38606	VATA_HUMAN	V-type proton ATPase catalytic subunit A OS=Homo sapiens OX=9606 GN=ATP6V1A PE=1 SV=2	0.690464	0.001038
Q9HCS7	SYF1_HUMAN	Pre-mRNA-splicing factor SYF1 OS=Homo sapiens OX=9606 GN=XAB2 PE=1 SV=2	0.690413	0.001204
O95340	PAPS2_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens OX=9606 GN=PAPSS2 PE=1 SV=2	0.690412	0.002173
Q8NI27	THOC2_HUMAN	THO complex subunit 2 OS=Homo sapiens OX=9606 GN=THOC2 PE=1 SV=2	0.690333	0.002219
P07355	ANXA2_HUMAN	Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2	0.690055	0.009121
Q96SU4	OSBL9_HUMAN	Oxysterol-binding protein-related protein 9 OS=Homo sapiens OX=9606 GN=OSBPL9 PE=1 SV=2	0.69005	0.002319
O15344	TRI18_HUMAN	E3 ubiquitin-protein ligase Midline-1 OS=Homo sapiens OX=9606 GN=MID1 PE=1 SV=1	0.690015	0.002211
Q8IZL8	PELP1_HUMAN	Proline- glutamic acid- and leucine-rich protein 1 OS=Homo sapiens OX=9606 GN=PELP1 PE=1 SV=2	0.68984	0.004084
Q13177	PAK2_HUMAN	Serine/threonine-protein kinase PAK 2 OS=Homo sapiens OX=9606 GN=PAK2 PE=1 SV=3	0.689782	5.82E-04
O00410	IPO5_HUMAN	Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4	0.68966	9.83E-05
Q96ME1	FXL18_HUMAN	F-box/LRR-repeat protein 18 OS=Homo sapiens OX=9606 GN=FBXL18 PE=1 SV=2	0.689161	0.002191
P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=2	0.689043	7.40E-06
P50897	PPT1_HUMAN	Palmitoyl-protein thioesterase 1 OS=Homo sapiens OX=9606 GN=PPT1 PE=1 SV=1	0.688921	0.002633
Q9Y394	DHRS7_HUMAN	Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 PE=1 SV=1	0.688578	0.002235
P05787	K2C8_HUMAN	Keratin type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7	0.687553	0.002623
Q9UNZ2	NSF1C_HUMAN	NSF1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSF1C PE=1 SV=2	0.687489	0.009208
O14579	COPE_HUMAN	Coatomer subunit epsilon OS=Homo sapiens OX=9606 GN=COPE PE=1 SV=3	0.687467	0.002229
P55010	IF5_HUMAN	Eukaryotic translation initiation factor 5 OS=Homo sapiens OX=9606 GN=EIF5 PE=1 SV=2	0.687146	0.005545
P28340	DPOD1_HUMAN	DNA polymerase delta catalytic subunit OS=Homo sapiens OX=9606 GN=POLD1 PE=1 SV=2	0.687086	7.41E-05
P49588	SYAC_HUMAN	Alanine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=AARS1 PE=1 SV=2	0.687077	0.00752
Q14807	KIF22_HUMAN	Kinesin-like protein KIF22 OS=Homo sapiens OX=9606 GN=KIF22 PE=1 SV=5	0.687077	0.002319
Q7Z406	MYH14_HUMAN	Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=2	0.68704	5.52E-04
P16402	H13_HUMAN	Histone H1.3 OS=Homo sapiens OX=9606 GN=H1-3 PE=1 SV=2	0.686957	0.00252
Q9GZZ1	NAA50_HUMAN	N-alpha-acetyltransferase 50 OS=Homo sapiens OX=9606 GN=NAA50 PE=1 SV=1	0.686808	0.002319
O75489	NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS3 PE=1 SV=1	0.686786	0.00129
Q00535	CDK5_HUMAN	Cyclin-dependent-like kinase 5 OS=Homo sapiens OX=9606 GN=CDK5 PE=1 SV=3	0.686768	0.003845

Q06124	PTN11_HUMAN	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 PE=1 SV=3	0.686662	0.004365
P36776	LONM_HUMAN	Lon protease homolog mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 PE=1 SV=2	0.68613	0.009382
O60568	PLOD3_HUMAN	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	0.68596	0.004573
P48147	PPCE_HUMAN	Prolyl endopeptidase OS=Homo sapiens OX=9606 GN=PREP PE=1 SV=2	0.685588	4.08E-04
Q9BUF5	TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1	0.684898	0.004211
P42167	LAP2B_HUMAN	Lamina-associated polypeptide 2 isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2	0.68476	0.002338
O00139	KIF2A_HUMAN	Kinesin-like protein KIF2A OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=3	0.684736	0.002385
P54136	SYRC_HUMAN	Arginine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=RARS1 PE=1 SV=2	0.68438	0.001174
Q15293	RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens OX=9606 GN=RCN1 PE=1 SV=1	0.684285	0.005319
O60306	AQR_HUMAN	RNA helicase aquarius OS=Homo sapiens OX=9606 GN=AQR PE=1 SV=4	0.684126	0.002341
Q9P035	HACD3_HUMAN	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=2	0.683825	0.003082
P51784	UBP11_HUMAN	Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens OX=9606 GN=USP11 PE=1 SV=3	0.68362	0.002349
Q12805	FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens OX=9606 GN=EFEMP1 PE=1 SV=2	0.6833	0.002464
Q12788	TBL3_HUMAN	Transducin beta-like protein 3 OS=Homo sapiens OX=9606 GN=TBL3 PE=1 SV=2	0.683143	1.97E-04
Q07866	KLC1_HUMAN	Kinesin light chain 1 OS=Homo sapiens OX=9606 GN=KLC1 PE=1 SV=2	0.683092	0.001221
P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PEBP1 PE=1 SV=3	0.68226	0.002501
Q9H9A6	LRC40_HUMAN	Leucine-rich repeat-containing protein 40 OS=Homo sapiens OX=9606 GN=LRR40 PE=1 SV=1	0.681999	0.009106
Q16850	CP51A_HUMAN	Lanosterol 14-alpha demethylase OS=Homo sapiens OX=9606 GN=CYP51A1 PE=1 SV=3	0.681212	0.001807
P36952	SPB5_HUMAN	Serpin B5 OS=Homo sapiens OX=9606 GN=SERPINB5 PE=1 SV=2	0.681192	0.005545
Q7LOY3	TM10C_HUMAN	tRNA methyltransferase 10 homolog C OS=Homo sapiens OX=9606 GN=TRMT10C PE=1 SV=2	0.680868	9.06E-04
P12931	SRC_HUMAN	Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens OX=9606 GN=SRC PE=1 SV=3	0.680613	0.002471
Q9HC07	TM165_HUMAN	Transmembrane protein 165 OS=Homo sapiens OX=9606 GN=TMEM165 PE=1 SV=1	0.68054	0.002295
O75676	KS6A4_HUMAN	Ribosomal protein S6 kinase alpha-4 OS=Homo sapiens OX=9606 GN=RPS6KA4 PE=1 SV=1	0.680531	0.00251
Q9UI12	VATH_HUMAN	V-type proton ATPase subunit H OS=Homo sapiens OX=9606 GN=ATP6V1H PE=1 SV=1	0.680449	0.002471
Q9H8S9	MOB1A_HUMAN	MOB kinase activator 1A OS=Homo sapiens OX=9606 GN=MOB1A PE=1 SV=4	0.680045	0.002438
Q7L9L4	MOB1B_HUMAN	MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B PE=1 SV=3	0.680045	0.002438
P25788	PSA3_HUMAN	Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=2	0.679804	0.002532
P06756	ITAV_HUMAN	Integrin alpha-V OS=Homo sapiens OX=9606 GN=ITGAV PE=1 SV=2	0.67979	4.58E-05
P32929	CGL_HUMAN	Cystathionine gamma-lyase OS=Homo sapiens OX=9606 GN=CTH PE=1 SV=3	0.679741	0.005118
Q14669	TRIPC_HUMAN	E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens OX=9606 GN=TRIP12 PE=1 SV=1	0.679604	0.001716
Q12849	GRSF1_HUMAN	G-rich sequence factor 1 OS=Homo sapiens OX=9606 GN=GRSF1 PE=1 SV=3	0.679599	0.002432
Q99816	TS101_HUMAN	Tumor susceptibility gene 101 protein OS=Homo sapiens OX=9606 GN=TS101 PE=1 SV=2	0.679589	0.002495
P33993	MCM7_HUMAN	DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=1 SV=4	0.679427	0.002085
Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta OS=Homo sapiens OX=9606 GN=CCT7 PE=1 SV=2	0.678973	2.07E-05
Q8IYB1	M21D2_HUMAN	Protein MB21D2 OS=Homo sapiens OX=9606 GN=MB21D2 PE=1 SV=3	0.678799	0.002495
Q13526	PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens OX=9606 GN=PIN1 PE=1 SV=1	0.678738	0.002555
Q14318	FKBP8_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens OX=9606 GN=FKBP8 PE=1 SV=2	0.678693	5.66E-04

Q9Y3Z3	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens OX=9606 GN=SAMHD1 PE=1 SV=2	0.678256	6.28E-04
Q9Y5K8	VATD_HUMAN	V-type proton ATPase subunit D OS=Homo sapiens OX=9606 GN=ATP6V1D PE=1 SV=1	0.677835	0.002568
Q9BTD8	RBM42_HUMAN	RNA-binding protein 42 OS=Homo sapiens OX=9606 GN=RBM42 PE=1 SV=1	0.67758	0.0015
P06132	DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=Homo sapiens OX=9606 GN=UROD PE=1 SV=2	0.677579	0.006078
Q01650	LAT1_HUMAN	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens OX=9606 GN=SLC7A5 PE=1 SV=2	0.677524	0.002589
Q2TAA2	IAH1_HUMAN	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens OX=9606 GN=IAH1 PE=1 SV=1	0.677321	0.002592
Q8TC07	TBC15_HUMAN	TBC1 domain family member 15 OS=Homo sapiens OX=9606 GN=TBC1D15 PE=1 SV=2	0.677087	0.003052
Q9UID3	VPS51_HUMAN	Vacuolar protein sorting-associated protein 51 homolog OS=Homo sapiens OX=9606 GN=VPS51 PE=1 SV=2	0.676838	0.003929
P09104	ENOG_HUMAN	Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=3	0.676405	0.001664
P51398	RT29_HUMAN	28S ribosomal protein S29 mitochondrial OS=Homo sapiens OX=9606 GN=DAP3 PE=1 SV=1	0.676231	0.00258
Q32MZ4	LRRF1_HUMAN	Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens OX=9606 GN=LRRFIP1 PE=1 SV=2	0.67611	0.00251
Q9Y281	COF2_HUMAN	Cofilin-2 OS=Homo sapiens OX=9606 GN=CFL2 PE=1 SV=1	0.675594	0.001175
Q96ST2	IWS1_HUMAN	Protein IWS1 homolog OS=Homo sapiens OX=9606 GN=IWS1 PE=1 SV=2	0.675454	0.002633
Q96T51	RUFY1_HUMAN	RUN and FYVE domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RUFY1 PE=1 SV=2	0.67516	0.002608
P35270	SPRE_HUMAN	Sepiapterin reductase OS=Homo sapiens OX=9606 GN=SPR PE=1 SV=1	0.674858	0.002642
P46459	NSF_HUMAN	Vesicle-fusing ATPase OS=Homo sapiens OX=9606 GN=NSF PE=1 SV=3	0.67423	0.003478
Q9H3P2	NELFA_HUMAN	Negative elongation factor A OS=Homo sapiens OX=9606 GN=NELFA PE=1 SV=3	0.674195	0.003719
P20810	ICAL_HUMAN	Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=4	0.673896	0.003007
P43243	MATR3_HUMAN	Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=2	0.673482	0.002513
O75436	VP26A_HUMAN	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens OX=9606 GN=VPS26A PE=1 SV=2	0.673102	0.004164
Q7Z739	YTHD3_HUMAN	YTH domain-containing family protein 3 OS=Homo sapiens OX=9606 GN=YTHDF3 PE=1 SV=1	0.673066	0.006696
P22223	CADH3_HUMAN	Cadherin-3 OS=Homo sapiens OX=9606 GN=CDH3 PE=1 SV=2	0.672885	0.004014
P00533	EGFR_HUMAN	Epidermal growth factor receptor OS=Homo sapiens OX=9606 GN=EGFR PE=1 SV=2	0.672835	7.49E-04
Q9UKK9	NUDT5_HUMAN	ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1	0.672817	0.002801
Q4KMP7	TB10B_HUMAN	TBC1 domain family member 10B OS=Homo sapiens OX=9606 GN=TBC1D10B PE=1 SV=3	0.672787	0.002661
Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=5	0.672644	0.001023
Q15067	ACOX1_HUMAN	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens OX=9606 GN=ACOX1 PE=1 SV=3	0.672498	0.00258
O15020	SPTN2_HUMAN	Spectrin beta chain non-erythrocytic 2 OS=Homo sapiens OX=9606 GN=SPTBN2 PE=1 SV=3	0.672352	0.002029
O95433	AHSA1_HUMAN	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens OX=9606 GN=AHSA1 PE=1 SV=1	0.672114	0.008261
P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1	0.671926	0.002738
P07814	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens OX=9606 GN=EPRS1 PE=1 SV=5	0.671921	8.53E-07
P19388	RPAB1_HUMAN	DNA-directed RNA polymerases I II and III subunit RPABC1 OS=Homo sapiens OX=9606 GN=POLR2E PE=1 SV=4	0.671902	0.002758
P50402	EMD_HUMAN	Emerin OS=Homo sapiens OX=9606 GN=EMD PE=1 SV=1	0.671864	0.002818
P28290	ITPI2_HUMAN	Protein ITPRID2 OS=Homo sapiens OX=9606 GN=ITPRID2 PE=1 SV=3	0.671734	0.001311
Q9NQG5	RPR1B_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens OX=9606 GN=RPRED1B PE=1 SV=1	0.671717	0.004036
P09972	ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=2	0.671652	0.001862
Q92973	TNPO1_HUMAN	Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 PE=1 SV=2	0.671652	0.004428
Q9Y3X0	CCDC9_HUMAN	Coiled-coil domain-containing protein 9 OS=Homo sapiens OX=9606 GN=CCDC9 PE=1 SV=1	0.671454	0.002791
O00622	CCN1_HUMAN	CCN family member 1 OS=Homo sapiens OX=9606 GN=CCN1 PE=1 SV=1	0.671442	0.007949

O60749	SNX2_HUMAN	Sorting nexin-2 OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=2	0.671377	0.002424
Q9Y508	RN114_HUMAN	E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens OX=9606 GN=RNF114 PE=1 SV=1	0.671237	0.002758
Q9Y223	GLCNE_HUMAN	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Homo sapiens OX=9606 GN=GNE PE=1 SV=1	0.671143	0.008113
Q9NZJ7	MTCH1_HUMAN	Mitochondrial carrier homolog 1 OS=Homo sapiens OX=9606 GN=MTCH1 PE=1 SV=1	0.671127	0.002721
O14964	HGS_HUMAN	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens OX=9606 GN=HGS PE=1 SV=1	0.671084	0.002787
Q16186	ADRM1_HUMAN	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens OX=9606 GN=ADRM1 PE=1 SV=2	0.670671	0.003492
Q6P2E9	EDC4_HUMAN	Enhancer of mRNA-decapping protein 4 OS=Homo sapiens OX=9606 GN=EDC4 PE=1 SV=1	0.670668	2.48E-04
Q9NV06	DCA13_HUMAN	DDB1- and CUL4-associated factor 13 OS=Homo sapiens OX=9606 GN=DCAF13 PE=1 SV=2	0.670505	0.002829
P39748	FEN1_HUMAN	Flap endonuclease 1 OS=Homo sapiens OX=9606 GN=FEN1 PE=1 SV=1	0.670463	0.003923
Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 PE=1 SV=1	0.670416	0.001267
P21283	VATC1_HUMAN	V-type proton ATPase subunit C 1 OS=Homo sapiens OX=9606 GN=ATP6V1C1 PE=1 SV=4	0.670362	0.006078
Q9UNQ2	DIM1_HUMAN	Probable dimethyladenosine transferase OS=Homo sapiens OX=9606 GN=DIMT1 PE=1 SV=1	0.67021	0.002859
O15042	SR140_HUMAN	U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens OX=9606 GN=U2SURP PE=1 SV=2	0.670083	0.00298
Q9Y624	JAM1_HUMAN	Junctional adhesion molecule A OS=Homo sapiens OX=9606 GN=F11R PE=1 SV=1	0.669948	0.009571
Q9NZ08	ERAP1_HUMAN	Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens OX=9606 GN=ERAP1 PE=1 SV=3	0.669793	0.004596
Q9NUQ7	UFSP2_HUMAN	Ufm1-specific protease 2 OS=Homo sapiens OX=9606 GN=UFSP2 PE=1 SV=3	0.669672	0.002855
Q15434	RBMS2_HUMAN	RNA-binding motif single-stranded-interacting protein 2 OS=Homo sapiens OX=9606 GN=RBMS2 PE=1 SV=1	0.669622	0.002877
Q9UJU6	DBNL_HUMAN	Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1	0.669555	0.001349
Q9Y265	RUVB1_HUMAN	RuvB-like 1 OS=Homo sapiens OX=9606 GN=RUVBL1 PE=1 SV=1	0.669478	0.00444
Q16643	DREB_HUMAN	Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4	0.669149	0.002471
Q9BW83	IFT27_HUMAN	Intraflagellar transport protein 27 homolog OS=Homo sapiens OX=9606 GN=IFT27 PE=1 SV=1	0.669075	0.002966
O95833	CLIC3_HUMAN	Chloride intracellular channel protein 3 OS=Homo sapiens OX=9606 GN=CLIC3 PE=1 SV=2	0.669054	9.64E-04
Q9Y2T3	GUAD_HUMAN	Guanine deaminase OS=Homo sapiens OX=9606 GN=GDA PE=1 SV=1	0.668856	0.003105
P00491	PNPH_HUMAN	Purine nucleoside phosphorylase OS=Homo sapiens OX=9606 GN=PNP PE=1 SV=2	0.668851	0.00247
O60762	DPM1_HUMAN	Dolichol-phosphate mannosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=DPM1 PE=1 SV=1	0.668392	0.002894
Q8N5K1	CISD2_HUMAN	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CISD2 PE=1 SV=1	0.668355	0.002626
Q9Y365	STA10_HUMAN	START domain-containing protein 10 OS=Homo sapiens OX=9606 GN=STARD10 PE=1 SV=2	0.668241	0.005319
Q9UHD8	SEPT9_HUMAN	Septin-9 OS=Homo sapiens OX=9606 GN=SEPTIN9 PE=1 SV=2	0.668225	0.008923
P20618	PSB1_HUMAN	Proteasome subunit beta type-1 OS=Homo sapiens OX=9606 GN=PSMB1 PE=1 SV=2	0.668067	0.006923
Q9H8H0	NOL11_HUMAN	Nucleolar protein 11 OS=Homo sapiens OX=9606 GN=NOL11 PE=1 SV=1	0.667819	0.001678
Q9UKN8	TF3C4_HUMAN	General transcription factor 3C polypeptide 4 OS=Homo sapiens OX=9606 GN=GTF3C4 PE=1 SV=2	0.66778	0.002945
Q5BKZ1	ZN326_HUMAN	DBIRD complex subunit ZNF326 OS=Homo sapiens OX=9606 GN=ZNF326 PE=1 SV=2	0.667618	0.001707
O43290	SNUT1_HUMAN	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens OX=9606 GN=SART1 PE=1 SV=1	0.667566	0.002489
P19623	SPEE_HUMAN	Spermidine synthase OS=Homo sapiens OX=9606 GN=SRM PE=1 SV=1	0.667545	0.005903
O14929	HAT1_HUMAN	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens OX=9606 GN=HAT1 PE=1 SV=1	0.667425	0.001255
Q96JB5	CK5P3_HUMAN	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3 PE=1 SV=2	0.667097	0.002977
O75792	RNH2A_HUMAN	Ribonuclease H2 subunit A OS=Homo sapiens OX=9606 GN=RNASEH2A PE=1 SV=2	0.667088	0.002946

O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1	0.666926	1.12E-04
O75940	SPF30_HUMAN	Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens OX=9606 GN=SMNDC1 PE=1 SV=1	0.666706	0.003781
P40121	CAPG_HUMAN	Macrophage-capping protein OS=Homo sapiens OX=9606 GN=CAPG PE=1 SV=2	0.66663	0.005152
Q86Y39	NDUAB_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens OX=9606 GN=NDUFA11 PE=1 SV=3	0.666263	0.002998
Q9UKF6	CPSF3_HUMAN	Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens OX=9606 GN=CPSF3 PE=1 SV=1	0.666115	0.003111
O43156	TTI1_HUMAN	TELO2-interacting protein 1 homolog OS=Homo sapiens OX=9606 GN=TTI1 PE=1 SV=3	0.66577	0.002966
Q15717	ELAV1_HUMAN	ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=2	0.665707	0.00247
Q16543	CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1	0.665696	0.008408
Q14331	FRG1_HUMAN	Protein FRG1 OS=Homo sapiens OX=9606 GN=FRG1 PE=1 SV=1	0.665619	0.002966
P51452	DUS3_HUMAN	Dual specificity protein phosphatase 3 OS=Homo sapiens OX=9606 GN=DUSP3 PE=1 SV=1	0.665581	0.008293
Q53EP0	FND3B_HUMAN	Fibronectin type III domain-containing protein 3B OS=Homo sapiens OX=9606 GN=FND3B PE=1 SV=2	0.665544	0.002966
P07602	SAP_HUMAN	Prosaposin OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=2	0.66495	0.003002
P48634	PRC2A_HUMAN	Protein PRRC2A OS=Homo sapiens OX=9606 GN=PRRC2A PE=1 SV=3	0.664931	5.21E-04
O95394	AGM1_HUMAN	Phosphoacetylglucosamine mutase OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1	0.66458	0.006827
O60437	PEPL_HUMAN	Periplakin OS=Homo sapiens OX=9606 GN=PPL PE=1 SV=4	0.664473	0.001476
P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSMC2 PE=1 SV=3	0.664233	0.006064
Q9NXR7	BABA2_HUMAN	BRISC and BRCA1-A complex member 2 OS=Homo sapiens OX=9606 GN=BABAM2 PE=1 SV=2	0.664014	0.003074
Q9NWU5	RM22_HUMAN	39S ribosomal protein L22 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL22 PE=1 SV=1	0.664005	0.003069
Q13443	ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens OX=9606 GN=ADAM9 PE=1 SV=1	0.664005	0.006634
Q9Y570	PPME1_HUMAN	Protein phosphatase methylesterase 1 OS=Homo sapiens OX=9606 GN=PPME1 PE=1 SV=3	0.663896	0.004076
P51153	RAB13_HUMAN	Ras-related protein Rab-13 OS=Homo sapiens OX=9606 GN=RAB13 PE=1 SV=1	0.66355	0.002994
P17858	PFKAL_HUMAN	ATP-dependent 6-phosphofructokinase liver type OS=Homo sapiens OX=9606 GN=PFKL PE=1 SV=6	0.663534	0.005885
Q9Y3E5	PTH2_HUMAN	Peptidyl-tRNA hydrolase 2 mitochondrial OS=Homo sapiens OX=9606 GN=PTRH2 PE=1 SV=1	0.663428	0.003003
Q9GZR7	DDX24_HUMAN	ATP-dependent RNA helicase DDX24 OS=Homo sapiens OX=9606 GN=DDX24 PE=1 SV=1	0.66325	0.00306
Q9Y5K5	UCHL5_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens OX=9606 GN=UCHL5 PE=1 SV=3	0.663093	0.001858
Q9NTJ3	SMC4_HUMAN	Structural maintenance of chromosomes protein 4 OS=Homo sapiens OX=9606 GN=SMC4 PE=1 SV=2	0.662922	0.001869
Q14141	SEPT6_HUMAN	Septin-6 OS=Homo sapiens OX=9606 GN=SEPTIN6 PE=1 SV=4	0.662826	5.86E-04
Q9NRL3	STRN4_HUMAN	Striatin-4 OS=Homo sapiens OX=9606 GN=STRN4 PE=1 SV=2	0.66225	0.002319
P40855	PEX19_HUMAN	Peroxisomal biogenesis factor 19 OS=Homo sapiens OX=9606 GN=PEX19 PE=1 SV=1	0.66217	0.003151
P11766	ADHX_HUMAN	Alcohol dehydrogenase class-3 OS=Homo sapiens OX=9606 GN=ADH5 PE=1 SV=4	0.662157	0.003705
P22676	CALB2_HUMAN	Calretinin OS=Homo sapiens OX=9606 GN=CALB2 PE=2 SV=2	0.662112	0.00295
Q8WWY3	PRP31_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens OX=9606 GN=PRPF31 PE=1 SV=2	0.662084	0.001185
Q9Y2Q3	GSTK1_HUMAN	Glutathione S-transferase kappa 1 OS=Homo sapiens OX=9606 GN=GSTK1 PE=1 SV=3	0.661666	0.003211
P52434	RPAB3_HUMAN	DNA-directed RNA polymerases I II and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H PE=1 SV=4	0.661633	0.003163
P54920	SNAA_HUMAN	Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=3	0.660998	0.001827
P56134	ATPK_HUMAN	ATP synthase subunit f mitochondrial OS=Homo sapiens OX=9606 GN=ATP5MF PE=1 SV=3	0.660985	0.003069
Q9UBQ5	EIF3K_HUMAN	Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens OX=9606 GN=EIF3K PE=1 SV=1	0.660789	0.004131
O43660	PLRG1_HUMAN	Pleiotropic regulator 1 OS=Homo sapiens OX=9606 GN=PLRG1 PE=1 SV=1	0.660463	0.004076

Q10471	GALT2_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens OX=9606 GN=GALNT2 PE=1 SV=1	0.659376	0.004966
Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3	0.65936	8.61E-04
P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=3	0.659295	0.004596
Q13085	ACACA_HUMAN	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACACA PE=1 SV=2	0.659284	0.002492
P56945	BCAR1_HUMAN	Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens OX=9606 GN=BCAR1 PE=1 SV=2	0.659115	0.007241
O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens OX=9606 GN=CLIC1 PE=1 SV=4	0.659089	9.47E-04
Q9NP72	RAB18_HUMAN	Ras-related protein Rab-18 OS=Homo sapiens OX=9606 GN=RAB18 PE=1 SV=1	0.658963	0.002498
Q9H9Q2	CSN7B_HUMAN	COP9 signalosome complex subunit 7b OS=Homo sapiens OX=9606 GN=COPS7B PE=1 SV=1	0.658524	0.001469
P61106	RAB14_HUMAN	Ras-related protein Rab-14 OS=Homo sapiens OX=9606 GN=RAB14 PE=1 SV=4	0.658508	0.005545
Q9BYG3	MK67I_HUMAN	MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens OX=9606 GN=NIFK PE=1 SV=1	0.658008	3.76E-04
Q13895	BYST_HUMAN	Bystin OS=Homo sapiens OX=9606 GN=BYSL PE=1 SV=3	0.657838	0.003308
P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDI PE=1 SV=3	0.657719	0.00309
P38432	COIL_HUMAN	Coilin OS=Homo sapiens OX=9606 GN=COIL PE=1 SV=1	0.657719	0.003312
Q96P70	IPO9_HUMAN	Importin-9 OS=Homo sapiens OX=9606 GN=IPO9 PE=1 SV=3	0.657499	0.008953
P37198	NUP62_HUMAN	Nuclear pore glycoprotein p62 OS=Homo sapiens OX=9606 GN=NUP62 PE=1 SV=3	0.657339	0.002471
P63151	2ABA_HUMAN	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R2A PE=1 SV=1	0.657196	0.009987
P25205	MCM3_HUMAN	DNA replication licensing factor MCM3 OS=Homo sapiens OX=9606 GN=MCM3 PE=1 SV=3	0.656997	0.008618
P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=4	0.656516	0.001205
Q96CM8	ACSF2_HUMAN	Medium-chain acyl-CoA ligase ACSF2 mitochondrial OS=Homo sapiens OX=9606 GN=ACSF2 PE=1 SV=2	0.656377	0.005247
P10321	HLAC_HUMAN	HLA class I histocompatibility antigen C alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=3	0.656306	0.002829
Q13813	SPTN1_HUMAN	Spectrin alpha chain non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=3	0.655074	0.004343
Q14126	DSG2_HUMAN	Desmoglein-2 OS=Homo sapiens OX=9606 GN=DSG2 PE=1 SV=2	0.655007	0.001566
P20340	RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A PE=1 SV=3	0.654822	0.002994
O43583	DENR_HUMAN	Density-regulated protein OS=Homo sapiens OX=9606 GN=DENR PE=1 SV=2	0.654688	0.003438
P08648	ITA5_HUMAN	Integrin alpha-5 OS=Homo sapiens OX=9606 GN=ITGA5 PE=1 SV=2	0.654655	0.004963
Q9UHD2	TBK1_HUMAN	Serine/threonine-protein kinase TBK1 OS=Homo sapiens OX=9606 GN=TBK1 PE=1 SV=1	0.654519	0.003386
P50748	KNTC1_HUMAN	Kinetochore-associated protein 1 OS=Homo sapiens OX=9606 GN=KNTC1 PE=1 SV=1	0.654417	0.003464
P50579	MAP2_HUMAN	Methionine aminopeptidase 2 OS=Homo sapiens OX=9606 GN=METAP2 PE=1 SV=1	0.653719	0.00409
Q06265	EXOS9_HUMAN	Exosome complex component RRP45 OS=Homo sapiens OX=9606 GN=EXOSC9 PE=1 SV=3	0.653317	0.003479
Q16401	PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens OX=9606 GN=PSMD5 PE=1 SV=3	0.653148	0.001234
Q96J02	ITCH_HUMAN	E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens OX=9606 GN=ITCH PE=1 SV=2	0.653101	0.006978
O95373	IPO7_HUMAN	Importin-7 OS=Homo sapiens OX=9606 GN=IPO7 PE=1 SV=1	0.653041	0.007212
Q9BYJ9	YTHD1_HUMAN	YTH domain-containing family protein 1 OS=Homo sapiens OX=9606 GN=YTHDF1 PE=1 SV=1	0.65283	0.003588
Q7Z478	DHX29_HUMAN	ATP-dependent RNA helicase DHX29 OS=Homo sapiens OX=9606 GN=DHX29 PE=1 SV=2	0.65277	0.003479
P35579	MYH9_HUMAN	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4	0.652505	1.53E-04
Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=2	0.651802	0.002438
Q9Y512	SAM50_HUMAN	Sorting and assembly machinery component 50 homolog OS=Homo sapiens OX=9606 GN=SAMM50 PE=1 SV=3	0.651458	0.004294
Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase AK3 mitochondrial OS=Homo sapiens OX=9606 GN=AK3 PE=1 SV=4	0.651285	0.004381

Q13751	LAMB3_HUMAN	Laminin subunit beta-3 OS=Homo sapiens OX=9606 GN=LAMB3 PE=1 SV=1	0.651247	0.00364
Q9Y3B2	EXOS1_HUMAN	Exosome complex component CSL4 OS=Homo sapiens OX=9606 GN=EXOSC1 PE=1 SV=1	0.651005	0.003655
Q96B97	SH3K1_HUMAN	SH3 domain-containing kinase-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3KBP1 PE=1 SV=2	0.650741	0.002808
P31146	COR1A_HUMAN	Coronin-1A OS=Homo sapiens OX=9606 GN=CORO1A PE=1 SV=4	0.650534	0.00366
P62310	LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSM3 OS=Homo sapiens OX=9606 GN=LSM3 PE=1 SV=2	0.650519	0.00357
P35606	COPB2_HUMAN	Coatamer subunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2	0.650293	4.91E-04
Q86SQ0	PHLB2_HUMAN	Pleckstrin homology-like domain family B member 2 OS=Homo sapiens OX=9606 GN=PHLDB2 PE=1 SV=2	0.650289	0.003655
Q8TC12	RDH11_HUMAN	Retinol dehydrogenase 11 OS=Homo sapiens OX=9606 GN=RDH11 PE=1 SV=2	0.649901	0.003557
Q9Y4W6	AFG32_HUMAN	AFG3-like protein 2 OS=Homo sapiens OX=9606 GN=AFG3L2 PE=1 SV=2	0.64929	0.008663
Q8NFH5	NUP35_HUMAN	Nucleoporin NUP35 OS=Homo sapiens OX=9606 GN=NUP35 PE=1 SV=1	0.648861	0.003766
P33991	MCM4_HUMAN	DNA replication licensing factor MCM4 OS=Homo sapiens OX=9606 GN=MCM4 PE=1 SV=5	0.648436	0.003878
Q9NPH2	INO1_HUMAN	Inositol-3-phosphate synthase 1 OS=Homo sapiens OX=9606 GN=ISYNA1 PE=1 SV=1	0.648424	0.007287
P13489	RINI_HUMAN	Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=2	0.648372	0.001358
P62820	RAB1A_HUMAN	Ras-related protein Rab-1A OS=Homo sapiens OX=9606 GN=RAB1A PE=1 SV=3	0.64827	1.52E-04
P35613	BASI_HUMAN	Basigin OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=2	0.648107	0.003797
Q9H0D6	XRN2_HUMAN	5'-3' exoribonuclease 2 OS=Homo sapiens OX=9606 GN=XRN2 PE=1 SV=1	0.647862	0.002668
Q9NVI1	FANCI_HUMAN	Fanconi anemia group I protein OS=Homo sapiens OX=9606 GN=FANCI PE=1 SV=4	0.64784	0.003673
Q6ZRV2	FA83H_HUMAN	Protein FAM83H OS=Homo sapiens OX=9606 GN=FAM83H PE=1 SV=3	0.647798	0.001533
P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI2 PE=1 SV=3	0.647763	0.006961
Q9NQW7	XPP1_HUMAN	Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1 PE=1 SV=3	0.647596	0.002804
O43681	ASNA_HUMAN	ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2	0.647463	0.003473
O14734	ACOT8_HUMAN	Acyl-coenzyme A thioesterase 8 OS=Homo sapiens OX=9606 GN=ACOT8 PE=1 SV=1	0.64741	0.00378
P46778	RL21_HUMAN	60S ribosomal protein L21 OS=Homo sapiens OX=9606 GN=RPL21 PE=1 SV=2	0.647365	0.003557
O00425	IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP3 PE=1 SV=2	0.64663	0.008484
Q8NFJ5	RAI3_HUMAN	Retinoic acid-induced protein 3 OS=Homo sapiens OX=9606 GN=GPRC5A PE=1 SV=2	0.646555	0.008303
Q8N3F8	MILK1_HUMAN	MICAL-like protein 1 OS=Homo sapiens OX=9606 GN=MICALL1 PE=1 SV=2	0.64652	0.003824
Q9Y6M5	ZNT1_HUMAN	Zinc transporter 1 OS=Homo sapiens OX=9606 GN=SLC30A1 PE=1 SV=3	0.646485	0.003741
Q9UBU9	NXF1_HUMAN	Nuclear RNA export factor 1 OS=Homo sapiens OX=9606 GN=NXF1 PE=1 SV=1	0.64615	0.003803
P11802	CDK4_HUMAN	Cyclin-dependent kinase 4 OS=Homo sapiens OX=9606 GN=CDK4 PE=1 SV=2	0.645973	0.003824
Q6DKI1	RL7L_HUMAN	60S ribosomal protein L7-like 1 OS=Homo sapiens OX=9606 GN=RPL7L1 PE=1 SV=2	0.645898	0.003889
Q9UKL0	RCOR1_HUMAN	REST corepressor 1 OS=Homo sapiens OX=9606 GN=RCOR1 PE=1 SV=2	0.645406	0.003861
Q14257	RCN2_HUMAN	Reticulocalbin-2 OS=Homo sapiens OX=9606 GN=RCN2 PE=1 SV=1	0.644867	0.009091
Q13505	MTX1_HUMAN	Metaxin-1 OS=Homo sapiens OX=9606 GN=MTX1 PE=1 SV=3	0.644812	0.004164
Q9Y6E2	BZW2_HUMAN	Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1	0.644785	0.003808
P53396	ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens OX=9606 GN=ACLY PE=1 SV=3	0.644464	5.95E-04
O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1	0.644456	0.002829
P58107	EPIPL_HUMAN	Epiplakin OS=Homo sapiens OX=9606 GN=EPPK1 PE=1 SV=3	0.644278	0.004381
Q96FX7	TRM61_HUMAN	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens OX=9606 GN=TRMT61A PE=1 SV=1	0.644102	0.003985

Q9UGP8	SEC63_HUMAN	Translocation protein SEC63 homolog OS=Homo sapiens OX=9606 GN=SEC63 PE=1 SV=2	0.643763	0.003403
Q9P2I0	CPSF2_HUMAN	Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens OX=9606 GN=CPSF2 PE=1 SV=2	0.643658	0.003845
P16989	YBOX3_HUMAN	Y-box-binding protein 3 OS=Homo sapiens OX=9606 GN=YBX3 PE=1 SV=4	0.643465	0.003117
P10768	ESTD_HUMAN	S-formylglutathione hydrolase OS=Homo sapiens OX=9606 GN=ESD PE=1 SV=2	0.643454	0.008869
Q15269	PWP2_HUMAN	Periodic tryptophan protein 2 homolog OS=Homo sapiens OX=9606 GN=PWP2 PE=2 SV=2	0.643395	0.004002
Q9H6S3	ES8L2_HUMAN	Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens OX=9606 GN=EPS8L2 PE=1 SV=2	0.64286	0.001579
P51531	SMCA2_HUMAN	Probable global transcription activator SNF2L2 OS=Homo sapiens OX=9606 GN=SMARCA2 PE=1 SV=2	0.642788	0.004024
Q92620	PRP16_HUMAN	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 OS=Homo sapiens OX=9606 GN=DHX38 PE=1 SV=2	0.642767	0.003985
Q8TF05	PP4R1_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP4R1 PE=1 SV=1	0.64246	0.004013
P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3	0.642329	0.008422
Q9NR12	PDLI7_HUMAN	PDZ and LIM domain protein 7 OS=Homo sapiens OX=9606 GN=PDLIM7 PE=1 SV=1	0.641865	0.002966
Q9Y2T2	AP3M1_HUMAN	AP-3 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP3M1 PE=1 SV=1	0.641669	0.004038
Q9BRJ6	CG050_HUMAN	Uncharacterized protein C7orf50 OS=Homo sapiens OX=9606 GN=C7orf50 PE=1 SV=1	0.641632	0.004164
Q8NCH0	CHSTE_HUMAN	Carbohydrate sulfotransferase 14 OS=Homo sapiens OX=9606 GN=CHST14 PE=1 SV=2	0.641546	0.004014
Q9BTY7	HGH1_HUMAN	Protein HGH1 homolog OS=Homo sapiens OX=9606 GN=HGH1 PE=1 SV=1	0.641546	0.004036
P09132	SRP19_HUMAN	Signal recognition particle 19 kDa protein OS=Homo sapiens OX=9606 GN=SRP19 PE=1 SV=3	0.640971	0.004137
Q9NWS0	PIHD1_HUMAN	PIH1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PIH1D1 PE=1 SV=1	0.640727	0.004014
P42126	ECI1_HUMAN	Enoyl-CoA delta isomerase 1 mitochondrial OS=Homo sapiens OX=9606 GN=ECI1 PE=1 SV=1	0.640658	0.004024
Q13057	COASY_HUMAN	Bifunctional coenzyme A synthase OS=Homo sapiens OX=9606 GN=COASY PE=1 SV=4	0.640604	0.00326
Q13619	CUL4A_HUMAN	Cullin-4A OS=Homo sapiens OX=9606 GN=CUL4A PE=1 SV=3	0.640458	0.009581
P18583	SON_HUMAN	Protein SON OS=Homo sapiens OX=9606 GN=SON PE=1 SV=4	0.640423	9.21E-04
Q8TAT6	NPL4_HUMAN	Nuclear protein localization protein 4 homolog OS=Homo sapiens OX=9606 GN=NPLOC4 PE=1 SV=3	0.639997	0.003183
Q86VM9	ZCH18_HUMAN	Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18 PE=1 SV=2	0.639907	0.005766
Q9UIQ6	LCAP_HUMAN	Leucyl-cystinyl aminopeptidase OS=Homo sapiens OX=9606 GN=LNPEP PE=1 SV=3	0.639389	3.04E-04
Q8IYI6	EXOC8_HUMAN	Exocyst complex component 8 OS=Homo sapiens OX=9606 GN=EXOC8 PE=1 SV=2	0.639297	0.004096
Q9H6T3	RPAP3_HUMAN	RNA polymerase II-associated protein 3 OS=Homo sapiens OX=9606 GN=RPAP3 PE=1 SV=2	0.638962	0.003468
Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=2	0.638569	0.003795
P61225	RAP2B_HUMAN	Ras-related protein Rap-2b OS=Homo sapiens OX=9606 GN=RAP2B PE=1 SV=1	0.638544	0.004131
O95861	BPNT1_HUMAN	3'-(2') 5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1	0.638359	0.006543
Q99598	TSNAX_HUMAN	Translin-associated protein X OS=Homo sapiens OX=9606 GN=TSNAX PE=1 SV=1	0.638051	0.009477
O75223	GGCT_HUMAN	Gamma-glutamylcyclotransferase OS=Homo sapiens OX=9606 GN=GGCT PE=1 SV=1	0.638029	0.007212
P54687	BCAT1_HUMAN	Branched-chain-amino-acid aminotransferase cytosolic OS=Homo sapiens OX=9606 GN=BCAT1 PE=1 SV=3	0.637944	0.003761
P22234	PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo sapiens OX=9606 GN=PAICS PE=1 SV=3	0.637632	0.00715
Q14694	UBP10_HUMAN	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens OX=9606 GN=USP10 PE=1 SV=2	0.637529	0.00306
Q96CS3	FAF2_HUMAN	FAS-associated factor 2 OS=Homo sapiens OX=9606 GN=FAF2 PE=1 SV=2	0.636713	0.003151
P22059	OSBP1_HUMAN	Oxysterol-binding protein 1 OS=Homo sapiens OX=9606 GN=OSBP PE=1 SV=1	0.636125	0.003078
Q5UIP0	RIF1_HUMAN	Telomere-associated protein RIF1 OS=Homo sapiens OX=9606 GN=RIF1 PE=1 SV=2	0.636112	0.007671

O95232	LC7L3_HUMAN	Luc7-like protein 3 OS=Homo sapiens OX=9606 GN=LUC7L3 PE=1 SV=2	0.636037	0.003188
P35269	T2FA_HUMAN	General transcription factor IIF subunit 1 OS=Homo sapiens OX=9606 GN=GTF2F1 PE=1 SV=2	0.635566	0.007357
Q15393	SF3B3_HUMAN	Splicing factor 3B subunit 3 OS=Homo sapiens OX=9606 GN=SF3B3 PE=1 SV=4	0.635277	0.002946
Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1	0.63441	0.004708
Q9NUU7	DD19A_HUMAN	ATP-dependent RNA helicase DDX19A OS=Homo sapiens OX=9606 GN=DDX19A PE=1 SV=1	0.634141	0.004372
P23229	ITA6_HUMAN	Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 PE=1 SV=5	0.633952	0.009342
P53582	MAP11_HUMAN	Methionine aminopeptidase 1 OS=Homo sapiens OX=9606 GN=METAP1 PE=1 SV=2	0.633758	0.002504
Q99805	TM9S2_HUMAN	Transmembrane 9 superfamily member 2 OS=Homo sapiens OX=9606 GN=TM9SF2 PE=1 SV=1	0.63356	0.004434
Q03426	KIME_HUMAN	Mevalonate kinase OS=Homo sapiens OX=9606 GN=MVK PE=1 SV=1	0.633525	0.007598
P46782	RS5_HUMAN	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RP55 PE=1 SV=4	0.633519	0.003859
P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=4	0.633483	8.97E-05
O94979	SC31A_HUMAN	Protein transport protein Sec31A OS=Homo sapiens OX=9606 GN=SEC31A PE=1 SV=3	0.633218	0.001716
O14907	TX1B3_HUMAN	Tax1-binding protein 3 OS=Homo sapiens OX=9606 GN=TAX1BP3 PE=1 SV=2	0.632932	0.004549
P39023	RL3_HUMAN	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2	0.632383	0.004024
Q724V5	HDGR2_HUMAN	Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens OX=9606 GN=HDGFL2 PE=1 SV=1	0.632025	0.004447
P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ACADVL PE=1 SV=1	0.631461	0.009136
O60884	DNJA2_HUMAN	DnaJ homolog subfamily A member 2 OS=Homo sapiens OX=9606 GN=DNAJA2 PE=1 SV=1	0.630983	0.006864
P30040	ERP29_HUMAN	Endoplasmic reticulum resident protein 29 OS=Homo sapiens OX=9606 GN=ERP29 PE=1 SV=4	0.630846	0.003106
P30154	2AAB_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=3	0.630837	0.005545
O75717	WDHD1_HUMAN	WD repeat and HMG-box DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=WDHD1 PE=1 SV=1	0.630412	0.003797
Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=2	0.630398	0.008439
P99999	CYC_HUMAN	Cytochrome c OS=Homo sapiens OX=9606 GN=CYCS PE=1 SV=2	0.629912	0.004826
Q7L1Q6	BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=BZW1 PE=1 SV=1	0.629776	0.004102
O95219	SNX4_HUMAN	Sorting nexin-4 OS=Homo sapiens OX=9606 GN=SNX4 PE=1 SV=1	0.629475	0.009296
Q9H944	MED20_HUMAN	Mediator of RNA polymerase II transcription subunit 20 OS=Homo sapiens OX=9606 GN=MED20 PE=1 SV=1	0.629271	0.004694
Q9Y673	ALG5_HUMAN	Dolichyl-phosphate beta-glucosyltransferase OS=Homo sapiens OX=9606 GN=ALG5 PE=1 SV=1	0.629022	0.004659
Q9BPX3	CND3_HUMAN	Condensin complex subunit 3 OS=Homo sapiens OX=9606 GN=NCAPG PE=1 SV=1	0.629018	0.001918
Q96I24	FUBP3_HUMAN	Far upstream element-binding protein 3 OS=Homo sapiens OX=9606 GN=FUBP3 PE=1 SV=2	0.628993	0.003314
Q9BQ52	RNZ2_HUMAN	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens OX=9606 GN=ELAC2 PE=1 SV=2	0.628906	0.004677
P11586	C1TC_HUMAN	C-1-tetrahydrofolate synthase cytoplasmic OS=Homo sapiens OX=9606 GN=MTHFD1 PE=1 SV=3	0.628874	0.001753
O15264	MK13_HUMAN	Mitogen-activated protein kinase 13 OS=Homo sapiens OX=9606 GN=MAPK13 PE=1 SV=1	0.628827	0.004757
Q6PIU2	NCEH1_HUMAN	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens OX=9606 GN=NCEH1 PE=1 SV=3	0.628762	0.009041
Q8TCS8	PNPT1_HUMAN	Polyribonucleotide nucleotidyltransferase 1 mitochondrial OS=Homo sapiens OX=9606 GN=PNPT1 PE=1 SV=2	0.62823	0.009717
O60610	DIAP1_HUMAN	Protein diaphanous homolog 1 OS=Homo sapiens OX=9606 GN=DIAPH1 PE=1 SV=2	0.628206	7.16E-04
Q9GZN8	CT027_HUMAN	UPF0687 protein C20orf27 OS=Homo sapiens OX=9606 GN=C20orf27 PE=1 SV=3	0.627908	0.004918
O14618	CCS_HUMAN	Copper chaperone for superoxide dismutase OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1	0.627824	0.004757
Q9Y3I0	RTCB_HUMAN	RNA-splicing ligase RtcB homolog OS=Homo sapiens OX=9606 GN=RTCB PE=1 SV=1	0.627582	0.003308

Q8IXM2	BAP18_HUMAN	Chromatin complexes subunit BAP18 OS=Homo sapiens OX=9606 GN=BAP18 PE=1 SV=1	0.627582	0.004603
Q9Y2W2	WBP11_HUMAN	WW domain-binding protein 11 OS=Homo sapiens OX=9606 GN=WBP11 PE=1 SV=1	0.627467	0.001059
P46937	YAP1_HUMAN	Transcriptional coactivator YAP1 OS=Homo sapiens OX=9606 GN=YAP1 PE=1 SV=2	0.627313	0.004049
P35249	RFC4_HUMAN	Replication factor C subunit 4 OS=Homo sapiens OX=9606 GN=RFC4 PE=1 SV=2	0.6267	0.005854
Q9UBC2	EP15R_HUMAN	Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens OX=9606 GN=EPS15L1 PE=1 SV=1	0.626509	0.009733
Q9NVD7	PARVA_HUMAN	Alpha-parvin OS=Homo sapiens OX=9606 GN=PARVA PE=1 SV=1	0.625921	0.004937
Q9BQG0	MBB1A_HUMAN	Myb-binding protein 1A OS=Homo sapiens OX=9606 GN=MYBBP1A PE=1 SV=2	0.625328	0.006573
Q8N1P7	CRBG2_HUMAN	Beta/gamma crystallin domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CRYBG2 PE=2 SV=2	0.62521	0.005015
P07858	CATB_HUMAN	Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3	0.624738	0.009663
P60510	PP4C_HUMAN	Serine/threonine-protein phosphatase 4 catalytic subunit OS=Homo sapiens OX=9606 GN=PPP4C PE=1 SV=1	0.624265	0.003653
Q9Y5K6	CD2AP_HUMAN	CD2-associated protein OS=Homo sapiens OX=9606 GN=CD2AP PE=1 SV=1	0.624227	0.003505
O75475	PSIP1_HUMAN	PC4 and SFRS1-interacting protein OS=Homo sapiens OX=9606 GN=PSIP1 PE=1 SV=1	0.62404	0.004515
Q8TED0	UTP15_HUMAN	U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens OX=9606 GN=UTP15 PE=1 SV=3	0.624032	0.006041
Q92621	NU205_HUMAN	Nuclear pore complex protein Nup205 OS=Homo sapiens OX=9606 GN=NUP205 PE=1 SV=3	0.623778	1.64E-04
Q92522	H1X_HUMAN	Histone H1x OS=Homo sapiens OX=9606 GN=H1FX PE=1 SV=1	0.623604	0.005152
Q9H2U2	IPYR2_HUMAN	Inorganic pyrophosphatase 2 mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 PE=1 SV=2	0.623188	0.003291
O15212	PFD6_HUMAN	Prefoldin subunit 6 OS=Homo sapiens OX=9606 GN=PFDN6 PE=1 SV=1	0.623101	0.001322
P09758	TACD2_HUMAN	Tumor-associated calcium signal transducer 2 OS=Homo sapiens OX=9606 GN=TACSTD2 PE=1 SV=3	0.62293	0.003921
Q9H6Z4	RANB3_HUMAN	Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=1	0.622806	0.002839
Q13188	STK3_HUMAN	Serine/threonine-protein kinase 3 OS=Homo sapiens OX=9606 GN=STK3 PE=1 SV=2	0.622789	0.008401
P26196	DDX6_HUMAN	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens OX=9606 GN=DDX6 PE=1 SV=2	0.622639	0.00417
P04637	P53_HUMAN	Cellular tumor antigen p53 OS=Homo sapiens OX=9606 GN=TP53 PE=1 SV=4	0.622369	0.00508
P78347	GTF2I_HUMAN	General transcription factor II-I OS=Homo sapiens OX=9606 GN=GTF2I PE=1 SV=2	0.621961	5.82E-04
P25325	THTM_HUMAN	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens OX=9606 GN=MPST PE=1 SV=3	0.62182	0.005319
O00116	ADAS_HUMAN	Alkylidihydroxyacetonephosphate synthase peroxisomal OS=Homo sapiens OX=9606 GN=AGPS PE=1 SV=1	0.621693	0.003183
P00505	AATM_HUMAN	Aspartate aminotransferase mitochondrial OS=Homo sapiens OX=9606 GN=GOT2 PE=1 SV=3	0.621138	0.006978
Q14376	GALE_HUMAN	UDP-glucose 4-epimerase OS=Homo sapiens OX=9606 GN=GALE PE=1 SV=2	0.621093	0.001148
Q9Y676	RT18B_HUMAN	28S ribosomal protein S18b mitochondrial OS=Homo sapiens OX=9606 GN=MRPS18B PE=1 SV=1	0.621024	0.005239
P51812	KS6A3_HUMAN	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens OX=9606 GN=RPS6KA3 PE=1 SV=1	0.620998	6.10E-04
Q15435	PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1	0.620942	0.0071
Q99436	PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens OX=9606 GN=PSMB7 PE=1 SV=1	0.620548	0.005219
O43707	ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2	0.620019	0.00196
Q14CX7	NAA25_HUMAN	N-alpha-acetyltransferase 25 NatB auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA25 PE=1 SV=1	0.619992	0.003755
Q9NT62	ATG3_HUMAN	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens OX=9606 GN=ATG3 PE=1 SV=1	0.619909	0.005533
Q16222	UAP1_HUMAN	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens OX=9606 GN=UAP1 PE=1 SV=3	0.619894	0.002488
P62993	GRB2_HUMAN	Growth factor receptor-bound protein 2 OS=Homo sapiens OX=9606 GN=GRB2 PE=1 SV=1	0.619354	0.00508
O94874	UFL1_HUMAN	E3 UFM1-protein ligase 1 OS=Homo sapiens OX=9606 GN=UFL1 PE=1 SV=2	0.619189	0.001519
Q86X76	NIT1_HUMAN	Deaminated glutathione amidase OS=Homo sapiens OX=9606 GN=NIT1 PE=1 SV=2	0.61914	0.005287

Q9BXY0	MAK16_HUMAN	Protein MAK16 homolog OS=Homo sapiens OX=9606 GN=MAK16 PE=1 SV=2	0.618942	0.002209
O60828	PQBP1_HUMAN	Polyglutamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PQBP1 PE=1 SV=1	0.618729	0.005388
Q14498	RBM39_HUMAN	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2	0.618571	0.003583
Q86Y82	STX12_HUMAN	Syntaxin-12 OS=Homo sapiens OX=9606 GN=STX12 PE=1 SV=1	0.618571	0.009415
Q9UBW8	CSN7A_HUMAN	COP9 signalosome complex subunit 7a OS=Homo sapiens OX=9606 GN=COPS7A PE=1 SV=1	0.618519	0.00508
Q99426	TBCB_HUMAN	Tubulin-folding cofactor B OS=Homo sapiens OX=9606 GN=TBCB PE=1 SV=2	0.618208	0.003155
Q96F27	CHMP6_HUMAN	Charged multivesicular body protein 6 OS=Homo sapiens OX=9606 GN=CHMP6 PE=1 SV=3	0.618164	0.005504
Q9UHB9	SRP68_HUMAN	Signal recognition particle subunit SRP68 OS=Homo sapiens OX=9606 GN=SRP68 PE=1 SV=2	0.618067	0.001619
P43246	MSH2_HUMAN	DNA mismatch repair protein Msh2 OS=Homo sapiens OX=9606 GN=MSH2 PE=1 SV=1	0.617913	0.003117
Q13137	CACO2_HUMAN	Calcium-binding and coiled-coil domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CALCOCO2 PE=1 SV=1	0.61782	0.005717
Q9BY44	EIF2A_HUMAN	Eukaryotic translation initiation factor 2A OS=Homo sapiens OX=9606 GN=EIF2A PE=1 SV=3	0.617324	0.005148
O43264	ZW10_HUMAN	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens OX=9606 GN=ZW10 PE=1 SV=3	0.617024	0.005533
Q9Y320	TMX2_HUMAN	Thioredoxin-related transmembrane protein 2 OS=Homo sapiens OX=9606 GN=TMX2 PE=1 SV=1	0.616887	0.005549
Q52LJ0	FA98B_HUMAN	Protein FAM98B OS=Homo sapiens OX=9606 GN=FAM98B PE=1 SV=2	0.61642	0.005545
Q9NR45	SIAS_HUMAN	Sialic acid synthase OS=Homo sapiens OX=9606 GN=NANS PE=1 SV=2	0.616259	0.002994
Q15369	ELOC_HUMAN	Elongin-C OS=Homo sapiens OX=9606 GN=ELOC PE=1 SV=1	0.616187	0.005525
Q9Y490	TLN1_HUMAN	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3	0.616151	0.008055
Q9UI09	NDUAC_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Homo sapiens OX=9606 GN=NDUFA12 PE=1 SV=1	0.61609	0.005533
Q92615	LAR4B_HUMAN	La-related protein 4B OS=Homo sapiens OX=9606 GN=LARP4B PE=1 SV=3	0.616033	0.005533
Q5SRE5	NU188_HUMAN	Nucleoporin NUP188 homolog OS=Homo sapiens OX=9606 GN=NUP188 PE=1 SV=1	0.616025	0.005545
O14908	GIPC1_HUMAN	PDZ domain-containing protein GIPC1 OS=Homo sapiens OX=9606 GN=GIPC1 PE=1 SV=2	0.61582	0.00137
P14625	ENPL_HUMAN	Endoplasmic reticulum protein OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1	0.615448	8.96E-04
O76071	CIAO1_HUMAN	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens OX=9606 GN=CIAO1 PE=1 SV=1	0.615374	0.005504
Q92817	EVPL_HUMAN	Envoplakin OS=Homo sapiens OX=9606 GN=EVPL PE=1 SV=3	0.615245	8.41E-04
Q01804	OTUD4_HUMAN	OTU domain-containing protein 4 OS=Homo sapiens OX=9606 GN=OTUD4 PE=1 SV=4	0.615109	0.005796
O14896	IRF6_HUMAN	Interferon regulatory factor 6 OS=Homo sapiens OX=9606 GN=IRF6 PE=1 SV=1	0.61471	0.008246
O15213	WDR46_HUMAN	WD repeat-containing protein 46 OS=Homo sapiens OX=9606 GN=WDR46 PE=1 SV=3	0.614626	0.007597
O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 OS=Homo sapiens OX=9606 GN=PGRC2 PE=1 SV=1	0.614317	0.006453
P36404	ARL2_HUMAN	ADP-ribosylation factor-like protein 2 OS=Homo sapiens OX=9606 GN=ARL2 PE=1 SV=4	0.614174	0.005801
P05026	AT1B1_HUMAN	Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens OX=9606 GN=ATP1B1 PE=1 SV=1	0.614154	0.007659
P02786	TFR1_HUMAN	Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2	0.613911	0.008469
O75348	VATG1_HUMAN	V-type proton ATPase subunit G 1 OS=Homo sapiens OX=9606 GN=ATP6V1G1 PE=1 SV=3	0.613556	0.00581
Q03252	LMNB2_HUMAN	Lamin-B2 OS=Homo sapiens OX=9606 GN=LMNB2 PE=1 SV=4	0.613408	0.003068
O95777	LSM8_HUMAN	U6 snRNA-associated Sm-like protein LSM8 OS=Homo sapiens OX=9606 GN=LSM8 PE=1 SV=3	0.613264	0.005788
Q9NUJ1	ABHDA_HUMAN	Mycophenolic acid acyl-glucuronide esterase mitochondrial OS=Homo sapiens OX=9606 GN=ABHD10 PE=1 SV=1	0.61317	0.008953
Q96I25	SPF45_HUMAN	Splicing factor 45 OS=Homo sapiens OX=9606 GN=RBM17 PE=1 SV=1	0.612261	0.006031
Q8NHV4	NEDD1_HUMAN	Protein NEDD1 OS=Homo sapiens OX=9606 GN=NEDD1 PE=1 SV=1	0.611888	0.00585
P51570	GALK1_HUMAN	Galactokinase OS=Homo sapiens OX=9606 GN=GALK1 PE=1 SV=1	0.611804	0.005504
P19404	NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFV2 PE=1 SV=2	0.611246	0.005827

Q5T0Z8	CF132_HUMAN	Uncharacterized protein C6orf132 OS=Homo sapiens OX=9606 GN=C6orf132 PE=1 SV=4	0.610748	0.005903
P63010	AP2B1_HUMAN	AP-2 complex subunit beta OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1	0.610514	0.006073
P61966	AP1S1_HUMAN	AP-1 complex subunit sigma-1A OS=Homo sapiens OX=9606 GN=AP1S1 PE=1 SV=1	0.610053	0.006022
Q9UQ80	PA2G4_HUMAN	Proliferation-associated protein 2G4 OS=Homo sapiens OX=9606 GN=PA2G4 PE=1 SV=3	0.609737	0.008869
P29966	MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens OX=9606 GN=MARCS PE=1 SV=4	0.609292	0.008671
P54709	AT1B3_HUMAN	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens OX=9606 GN=ATP1B3 PE=1 SV=1	0.608885	0.001569
Q9GZL7	WDR12_HUMAN	Ribosome biogenesis protein WDR12 OS=Homo sapiens OX=9606 GN=WDR12 PE=1 SV=2	0.608494	0.006195
Q96N66	MBOA7_HUMAN	Lysophospholipid acyltransferase 7 OS=Homo sapiens OX=9606 GN=MBOA7 PE=1 SV=2	0.608345	0.006195
O00232	PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens OX=9606 GN=PSMD12 PE=1 SV=3	0.607813	0.00695
Q9NZZ3	CHMP5_HUMAN	Charged multivesicular body protein 5 OS=Homo sapiens OX=9606 GN=CHMP5 PE=1 SV=1	0.607683	0.006267
O95571	ETHE1_HUMAN	Persulfide dioxygenase ETHE1 mitochondrial OS=Homo sapiens OX=9606 GN=ETHE1 PE=1 SV=2	0.607325	0.009366
P33121	ACSL1_HUMAN	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens OX=9606 GN=ACSL1 PE=1 SV=1	0.6071	0.004038
P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 OS=Homo sapiens OX=9606 GN=CAPZA1 PE=1 SV=3	0.607076	0.007962
Q9BW19	KIFC1_HUMAN	Kinesin-like protein KIFC1 OS=Homo sapiens OX=9606 GN=KIFC1 PE=1 SV=2	0.606847	0.006315
Q04323	UBXN1_HUMAN	UBX domain-containing protein 1 OS=Homo sapiens OX=9606 GN=UBXN1 PE=1 SV=2	0.606788	0.006219
P13073	COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1 mitochondrial OS=Homo sapiens OX=9606 GN=COX41 PE=1 SV=1	0.606756	0.006291
Q12965	MYO1E_HUMAN	Unconventional myosin-Ie OS=Homo sapiens OX=9606 GN=MYO1E PE=1 SV=2	0.606658	0.007211
Q9H9B4	SFXN1_HUMAN	Sideroflexin-1 OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=4	0.606253	0.004881
Q5T0W9	FA83B_HUMAN	Protein FAM83B OS=Homo sapiens OX=9606 GN=FAM83B PE=1 SV=1	0.605821	0.006458
Q92696	PGTA_HUMAN	Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens OX=9606 GN=RABGGTA PE=1 SV=2	0.605602	0.007264
P55735	SEC13_HUMAN	Protein SEC13 homolog OS=Homo sapiens OX=9606 GN=SEC13 PE=1 SV=3	0.605435	0.005145
P0DN76	U2AF5_HUMAN	Splicing factor U2AF 35 kDa subunit-like protein OS=Homo sapiens OX=9606 GN=U2AF1L5 PE=1 SV=1	0.605369	0.008872
Q01081	U2AF1_HUMAN	Splicing factor U2AF 35 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF1 PE=1 SV=3	0.605369	0.008872
Q9HCU5	PREB_HUMAN	Prolactin regulatory element-binding protein OS=Homo sapiens OX=9606 GN=PREB PE=1 SV=2	0.60514	0.006598
Q86VR2	RETR3_HUMAN	Reticulophagy regulator 3 OS=Homo sapiens OX=9606 GN=RETREG3 PE=1 SV=1	0.60507	0.006598
Q9UHD1	CHRD1_HUMAN	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CHORDC1 PE=1 SV=2	0.604954	0.00148
O00629	IMA3_HUMAN	Importin subunit alpha-3 OS=Homo sapiens OX=9606 GN=KPNA4 PE=1 SV=1	0.604895	0.006598
Q13616	CUL1_HUMAN	Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=2	0.604636	0.001484
Q6Y7W6	GGYF2_HUMAN	GRB10-interacting GYF protein 2 OS=Homo sapiens OX=9606 GN=GIGYF2 PE=1 SV=1	0.604263	0.002994
Q9NR46	SHLB2_HUMAN	Endophilin-B2 OS=Homo sapiens OX=9606 GN=SH3GLB2 PE=1 SV=1	0.604243	0.00984
O75964	ATP5L_HUMAN	ATP synthase subunit g mitochondrial OS=Homo sapiens OX=9606 GN=ATP5MG PE=1 SV=3	0.603973	0.006634
P48506	GSH1_HUMAN	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens OX=9606 GN=GCLC PE=1 SV=2	0.603699	0.006598
Q13310	PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1	0.603655	0.004596
P04083	ANXA1_HUMAN	Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2	0.60355	0.001621
P60953	CDC42_HUMAN	Cell division control protein 42 homolog OS=Homo sapiens OX=9606 GN=CDC42 PE=1 SV=2	0.603294	0.00665
P53367	ARFP1_HUMAN	Arfaptin-1 OS=Homo sapiens OX=9606 GN=ARFIP1 PE=1 SV=2	0.602665	0.004008
Q9UBQ7	GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens OX=9606 GN=GRHPR PE=1 SV=1	0.602535	0.007659
Q9NX62	IMPA3_HUMAN	Golgi-resident adenosine 3' 5'-bisphosphate 3'-phosphatase OS=Homo sapiens OX=9606 GN=IMPAD1 PE=1 SV=1	0.602285	0.006681

P14923	PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3	0.601836	1.73E-04
Q96EK6	GNA1_HUMAN	Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens OX=9606 GN=GNPNAT1 PE=1 SV=1	0.601538	0.006403
P15880	RS2_HUMAN	40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2	0.601332	0.007016
Q9NZL4	HPBP1_HUMAN	Hsp70-binding protein 1 OS=Homo sapiens OX=9606 GN=HSPBP1 PE=1 SV=2	0.601301	0.004757
Q9Y2H6	FND3A_HUMAN	Fibronectin type-III domain-containing protein 3A OS=Homo sapiens OX=9606 GN=FND3A PE=1 SV=4	0.601076	0.002658
O75340	PDCD6_HUMAN	Programmed cell death protein 6 OS=Homo sapiens OX=9606 GN=PDCD6 PE=1 SV=1	0.601029	0.006769
P62253	UB2G1_HUMAN	Ubiquitin-conjugating enzyme E2 G1 OS=Homo sapiens OX=9606 GN=UBE2G1 PE=1 SV=3	0.600985	0.006923
P35914	HMGCL_HUMAN	Hydroxymethylglutaryl-CoA lyase mitochondrial OS=Homo sapiens OX=9606 GN=HMGCL PE=1 SV=2	0.600783	0.006759
Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	0.599678	0.003199
Q00653	NFKB2_HUMAN	Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens OX=9606 GN=NFKB2 PE=1 SV=4	0.599588	5.90E-04
P49005	DPOD2_HUMAN	DNA polymerase delta subunit 2 OS=Homo sapiens OX=9606 GN=POLD2 PE=1 SV=1	0.599486	0.006923
Q3ZCQ8	TIM50_HUMAN	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens OX=9606 GN=TIMM50 PE=1 SV=2	0.599257	0.00402
P25685	DNJB1_HUMAN	DnaJ homolog subfamily B member 1 OS=Homo sapiens OX=9606 GN=DNAJB1 PE=1 SV=4	0.599198	0.001217
Q13868	EXOS2_HUMAN	Exosome complex component RRP4 OS=Homo sapiens OX=9606 GN=EXOSC2 PE=1 SV=2	0.599151	0.009415
Q8WVM8	SCFD1_HUMAN	Sec1 family domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SCFD1 PE=1 SV=4	0.598919	0.00508
Q9HD45	TM9S3_HUMAN	Transmembrane 9 superfamily member 3 OS=Homo sapiens OX=9606 GN=TM9SF3 PE=1 SV=2	0.598763	0.006738
O43739	CYH3_HUMAN	Cytohesin-3 OS=Homo sapiens OX=9606 GN=CYTH3 PE=1 SV=2	0.598597	0.0071
Q99418	CYH2_HUMAN	Cytohesin-2 OS=Homo sapiens OX=9606 GN=CYTH2 PE=1 SV=2	0.598597	0.0071
Q9BRT2	UQCC2_HUMAN	Ubiquinol-cytochrome-c reductase complex assembly factor 2 OS=Homo sapiens OX=9606 GN=UQCC2 PE=1 SV=1	0.598131	0.006978
P12694	ODBA_HUMAN	2-oxoisovalerate dehydrogenase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=BCKDHA PE=1 SV=2	0.597745	0.007034
O43809	CPSF5_HUMAN	Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens OX=9606 GN=NUDT21 PE=1 SV=1	0.59761	0.004055
Q9BTE1	DCTN5_HUMAN	Dynactin subunit 5 OS=Homo sapiens OX=9606 GN=DCTN5 PE=1 SV=1	0.597086	0.007034
Q9Y2U8	MAN1_HUMAN	Inner nuclear membrane protein Man1 OS=Homo sapiens OX=9606 GN=LEMD3 PE=1 SV=2	0.597077	0.006978
O43747	AP1G1_HUMAN	AP-1 complex subunit gamma-1 OS=Homo sapiens OX=9606 GN=AP1G1 PE=1 SV=5	0.596915	0.002877
P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1	0.596701	0.001595
Q6UB35	C1TM_HUMAN	Monofunctional C1-tetrahydrofolate synthase mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD1L PE=1 SV=1	0.59561	0.0081
P56211	ARP19_HUMAN	cAMP-regulated phosphoprotein 19 OS=Homo sapiens OX=9606 GN=ARPP19 PE=1 SV=2	0.595569	0.007252
Q5JTH9	RRP12_HUMAN	RRP12-like protein OS=Homo sapiens OX=9606 GN=RRP12 PE=1 SV=2	0.595569	0.007241
Q01082	SPTB2_HUMAN	Spectrin beta chain non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTBN1 PE=1 SV=2	0.595407	0.009987
P49959	MRE11_HUMAN	Double-strand break repair protein MRE11 OS=Homo sapiens OX=9606 GN=MRE11 PE=1 SV=3	0.5954	0.003451
Q15437	SC23B_HUMAN	Protein transport protein Sec23B OS=Homo sapiens OX=9606 GN=SEC23B PE=1 SV=2	0.595073	0.004556
Q86V21	AACS_HUMAN	Acetoacetyl-CoA synthetase OS=Homo sapiens OX=9606 GN=AACS PE=1 SV=1	0.594881	0.007139
P55209	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1	0.594581	0.006978
P21333	FLNA_HUMAN	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4	0.594566	0.008632
Q9NR30	DDX21_HUMAN	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5	0.594501	0.004078
Q96C86	DCPS_HUMAN	m7GpppX diphosphatase OS=Homo sapiens OX=9606 GN=DCPS PE=1 SV=2	0.594373	0.007299
P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2 mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=3	0.594286	0.009366
Q9Y2X7	GIT1_HUMAN	ARF GTPase-activating protein GIT1 OS=Homo sapiens OX=9606 GN=GIT1 PE=1 SV=2	0.59426	0.007275

Q15382	RHEB_HUMAN	GTP-binding protein Rheb OS=Homo sapiens OX=9606 GN=RHEB PE=1 SV=1	0.594252	0.007598
Q6NZI2	CAVN1_HUMAN	Caveolae-associated protein 1 OS=Homo sapiens OX=9606 GN=CAVIN1 PE=1 SV=1	0.593751	0.001664
P35573	GDE_HUMAN	Glycogen debranching enzyme OS=Homo sapiens OX=9606 GN=AGL PE=1 SV=3	0.59368	0.002994
P42704	LPPRC_HUMAN	Leucine-rich PPR motif-containing protein mitochondrial OS=Homo sapiens OX=9606 GN=LPPRC PE=1 SV=3	0.593601	0.007508
O60888	CUTA_HUMAN	Protein CutA OS=Homo sapiens OX=9606 GN=CUTA PE=1 SV=2	0.593566	0.007445
P49327	FAS_HUMAN	Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3	0.59323	0.001185
Q14573	ITPR3_HUMAN	Inositol 1 4 5-trisphosphate receptor type 3 OS=Homo sapiens OX=9606 GN=ITPR3 PE=1 SV=2	0.592951	0.002718
Q96K37	S35E1_HUMAN	Solute carrier family 35 member E1 OS=Homo sapiens OX=9606 GN=SLC35E1 PE=1 SV=2	0.592576	0.007416
P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 PE=1 SV=2	0.592172	0.00764
P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4	0.592032	0.001807
P40938	RFC3_HUMAN	Replication factor C subunit 3 OS=Homo sapiens OX=9606 GN=RFC3 PE=1 SV=2	0.59172	0.00497
P05386	RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Homo sapiens OX=9606 GN=RPLP1 PE=1 SV=1	0.591571	0.007838
Q6ZUT6	CCD9B_HUMAN	Coiled-coil domain-containing protein 9B OS=Homo sapiens OX=9606 GN=CCDC9B PE=1 SV=1	0.591513	0.007299
Q15645	PCH2_HUMAN	Pachytene checkpoint protein 2 homolog OS=Homo sapiens OX=9606 GN=TRIP13 PE=1 SV=2	0.590728	0.002994
Q92900	RENT1_HUMAN	Regulator of nonsense transcripts 1 OS=Homo sapiens OX=9606 GN=UPF1 PE=1 SV=2	0.590016	1.87E-04
O00203	AP3B1_HUMAN	AP-3 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP3B1 PE=1 SV=3	0.589555	0.004757
Q14315	FLNC_HUMAN	Filamin-C OS=Homo sapiens OX=9606 GN=FLNC PE=1 SV=3	0.589258	0.007034
P62805	H4_HUMAN	Histone H4 OS=Homo sapiens OX=9606 GN=H4C1 PE=1 SV=2	0.589221	0.007322
Q9HCY8	S10AE_HUMAN	Protein S100-A14 OS=Homo sapiens OX=9606 GN=S100A14 PE=1 SV=1	0.589212	0.008011
O15355	PPM1G_HUMAN	Protein phosphatase 1G OS=Homo sapiens OX=9606 GN=PPM1G PE=1 SV=1	0.588883	0.008996
P62753	RS6_HUMAN	40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1	0.588805	0.008635
Q08J23	NSUN2_HUMAN	RNA cytosine C(5)-methyltransferase NSUN2 OS=Homo sapiens OX=9606 GN=NSUN2 PE=1 SV=2	0.588764	4.95E-04
Q08378	GOGA3_HUMAN	Golgin subfamily A member 3 OS=Homo sapiens OX=9606 GN=GOLGA3 PE=1 SV=2	0.588558	1.52E-04
Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 OS=Homo sapiens OX=9606 GN=GCN1 PE=1 SV=6	0.588262	0.004153
P24941	CDK2_HUMAN	Cyclin-dependent kinase 2 OS=Homo sapiens OX=9606 GN=CDK2 PE=1 SV=2	0.588068	0.003287
O76003	GLRX3_HUMAN	Glutaredoxin-3 OS=Homo sapiens OX=9606 GN=GLRX3 PE=1 SV=2	0.587692	0.001662
Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A OS=Homo sapiens OX=9606 GN=DHX9 PE=1 SV=4	0.587437	0.002471
Q13098	CSN1_HUMAN	COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=4	0.587382	0.006854
Q9HAV7	GRPE1_HUMAN	GrpE protein homolog 1 mitochondrial OS=Homo sapiens OX=9606 GN=GRPEL1 PE=1 SV=2	0.587254	0.006243
P62910	RL32_HUMAN	60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=2	0.58716	0.005549
Q04637	IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=4	0.58632	0.001903
P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1	0.586204	0.006759
Q9Y220	SGT1_HUMAN	Protein SGT1 homolog OS=Homo sapiens OX=9606 GN=SUGT1 PE=1 SV=3	0.586186	0.005015
Q13620	CUL4B_HUMAN	Cullin-4B OS=Homo sapiens OX=9606 GN=CUL4B PE=1 SV=4	0.58597	0.008144
Q9H8Y8	GORS2_HUMAN	Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2 PE=1 SV=3	0.585886	0.007351
Q7L576	CYFP1_HUMAN	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1	0.58579	0.003438
P21281	VATB2_HUMAN	V-type proton ATPase subunit B brain isoform OS=Homo sapiens OX=9606 GN=ATP6V1B2 PE=1 SV=3	0.585364	0.003861
Q9H078	CLPB_HUMAN	Caseinolytic peptidase B protein homolog OS=Homo sapiens OX=9606 GN=CLPB PE=1 SV=1	0.584963	0.001017

O00273	DFFA_HUMAN	DNA fragmentation factor subunit alpha OS=Homo sapiens OX=9606 GN=DFFA PE=1 SV=1	0.584963	0.005307
Q16851	UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens OX=9606 GN=UGP2 PE=1 SV=5	0.584963	0.005463
O00204	ST2B1_HUMAN	Sulfotransferase 2B1 OS=Homo sapiens OX=9606 GN=SULT2B1 PE=1 SV=2	0.584963	0.008261
Q9BV57	MTND_HUMAN	1 2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens OX=9606 GN=ADI1 PE=1 SV=1	0.584963	0.008303
Q12979	ABR_HUMAN	Active breakpoint cluster region-related protein OS=Homo sapiens OX=9606 GN=ABR PE=1 SV=2	0.584357	0.008254
P52630	STAT2_HUMAN	Signal transducer and activator of transcription 2 OS=Homo sapiens OX=9606 GN=STAT2 PE=1 SV=1	0.584017	0.008303
P11908	PRPS2_HUMAN	Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens OX=9606 GN=PRPS2 PE=1 SV=2	0.583792	0.008335
P62495	ERF1_HUMAN	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens OX=9606 GN=ETF1 PE=1 SV=3	0.583584	0.002019
Q96S84	SRPK1_HUMAN	SRSF protein kinase 1 OS=Homo sapiens OX=9606 GN=SRPK1 PE=1 SV=2	0.583415	0.008408
Q15050	RRS1_HUMAN	Ribosome biogenesis regulatory protein homolog OS=Homo sapiens OX=9606 GN=RRS1 PE=1 SV=2	0.583342	0.008484
P52294	IMA5_HUMAN	Importin subunit alpha-5 OS=Homo sapiens OX=9606 GN=KPNA1 PE=1 SV=3	0.583312	0.008453
Q96920	FAKD4_HUMAN	FAST kinase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=TBRG4 PE=1 SV=1	0.582861	0.008469
O00178	GTPB1_HUMAN	GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP1 PE=1 SV=3	0.58272	0.008635
P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens OX=9606 GN=PPP1CB PE=1 SV=3	0.582584	0.008349
Q9P0I2	EMC3_HUMAN	ER membrane protein complex subunit 3 OS=Homo sapiens OX=9606 GN=EMC3 PE=1 SV=3	0.582563	0.008432
P28331	NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS1 PE=1 SV=3	0.582332	4.71E-04
Q13423	NNTM_HUMAN	NAD(P) transhydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=3	0.581991	0.008476
P32004	L1CAM_HUMAN	Neural cell adhesion molecule L1 OS=Homo sapiens OX=9606 GN=L1CAM PE=1 SV=2	0.581832	0.00843
Q9BXK5	B2L13_HUMAN	Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1	0.581528	0.005267
P41252	SYIC_HUMAN	Isoleucine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=IARS1 PE=1 SV=2	0.581126	0.002399
P06733	ENOA_HUMAN	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2	0.58111	0.004708
Q9NPQ8	RIC8A_HUMAN	Synembryn-A OS=Homo sapiens OX=9606 GN=RIC8A PE=1 SV=3	0.580145	0.008663
Q16777	H2A2C_HUMAN	Histone H2A type 2-C OS=Homo sapiens OX=9606 GN=HIST2H2AC PE=1 SV=4	-1.14103	0.001239
Q6FI13	H2A2A_HUMAN	Histone H2A type 2-A OS=Homo sapiens OX=9606 GN=HIST2H2AA3 PE=1 SV=3	-1.14103	0.001239
P02768	ALBU_HUMAN	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2	-1.24735	4.23E-10
Q5RI15	COX20_HUMAN	Cytochrome c oxidase assembly protein COX20 mitochondrial OS=Homo sapiens OX=9606 GN=COX20 PE=1 SV=2	-1.84912	5.93E-07

Appendix Table 4: 16HBE14o⁻ global proteome changes following phthalic anhydride exposure – Proteins with a significant difference in abundance are presented according to descending log2 fold change.

A.2.6 Significant proteome changes in 16HE140⁻ cells following exposure to TDI

Accession	Uniprot ID	Description	Log2 Fold Change	P value (FDR)
P13645	K1C10_HUMAN	Keratin type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6	3.493507	5.02E-18
P04264	K2C1_HUMAN	Keratin type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6	3.15613	5.02E-18
O15530	PDPK1_HUMAN	3-phosphoinositide-dependent protein kinase 1 OS=Homo sapiens OX=9606 GN=PDPK1 PE=1 SV=1	3.076993	0.005045
Q6NXE6	ARMC6_HUMAN	Armadillo repeat-containing protein 6 OS=Homo sapiens OX=9606 GN=ARMC6 PE=1 SV=2	3.061445	4.14E-09
Q9BW92	SYTM_HUMAN	Threonine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=TARS2 PE=1 SV=1	2.381116	5.64E-09
P22681	CBL_HUMAN	E3 ubiquitin-protein ligase CBL OS=Homo sapiens OX=9606 GN=CBL PE=1 SV=2	2.155984	2.06E-04
P01583	IL1A_HUMAN	Interleukin-1 alpha OS=Homo sapiens OX=9606 GN=IL1A PE=1 SV=1	2.002742	3.30E-06
Q9HD20	AT131_HUMAN	Manganese-transporting ATPase 13A1 OS=Homo sapiens OX=9606 GN=ATP13A1 PE=1 SV=2	1.826807	8.98E-04
Q9BX40	LS14B_HUMAN	Protein LSM14 homolog B OS=Homo sapiens OX=9606 GN=LSM14B PE=1 SV=1	1.761974	5.02E-18
Q6ZS17	RIPR1_HUMAN	Rho family-interacting cell polarization regulator 1 OS=Homo sapiens OX=9606 GN=RIPOR1 PE=1 SV=1	1.756281	5.02E-18
Q15024	EXOS7_HUMAN	Exosome complex component RRP42 OS=Homo sapiens OX=9606 GN=EXOSC7 PE=1 SV=3	1.707416	5.02E-18
O75923	DYSF_HUMAN	Dysferlin OS=Homo sapiens OX=9606 GN=DYSF PE=1 SV=1	1.696089	1.20E-05
Q5ZPR3	CD276_HUMAN	CD276 antigen OS=Homo sapiens OX=9606 GN=CD276 PE=1 SV=1	1.68608	5.02E-18
Q99575	POP1_HUMAN	Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens OX=9606 GN=POP1 PE=1 SV=2	1.676021	5.02E-18
Q71DI3	H32_HUMAN	Histone H3.2 OS=Homo sapiens OX=9606 GN=HIST2H3A PE=1 SV=3	1.640847	2.60E-13
Q9NXF1	TEX10_HUMAN	Testis-expressed protein 10 OS=Homo sapiens OX=9606 GN=TEX10 PE=1 SV=2	1.63743	9.75E-14
P42696	RBM34_HUMAN	RNA-binding protein 34 OS=Homo sapiens OX=9606 GN=RBM34 PE=1 SV=2	1.61168	6.27E-04
O75054	IGSF3_HUMAN	Immunoglobulin superfamily member 3 OS=Homo sapiens OX=9606 GN=IGSF3 PE=2 SV=3	1.595756	8.87E-04
P62841	RS15_HUMAN	40S ribosomal protein S15 OS=Homo sapiens OX=9606 GN=RPS15 PE=1 SV=2	1.555738	3.13E-13
Q9BUR5	MIC26_HUMAN	MICOS complex subunit MIC26 OS=Homo sapiens OX=9606 GN=APOO PE=1 SV=1	1.54675	0.001442
Q15057	ACAP2_HUMAN	Arf-GAP with coiled-coil ANK repeat and PH domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ACAP2 PE=1 SV=3	1.524653	6.00E-12
Q9Y2D5	AKAP2_HUMAN	A-kinase anchor protein 2 OS=Homo sapiens OX=9606 GN=AKAP2 PE=1 SV=3	1.524163	5.79E-11
Q9Y6X4	F169A_HUMAN	Soluble lamin-associated protein of 75 kDa OS=Homo sapiens OX=9606 GN=FAM169A PE=1 SV=2	1.477134	5.25E-11
Q6P6C2	ALKB5_HUMAN	RNA demethylase ALKBH5 OS=Homo sapiens OX=9606 GN=ALKBH5 PE=1 SV=2	1.471707	0.004084
Q969U7	PSMG2_HUMAN	Proteasome assembly chaperone 2 OS=Homo sapiens OX=9606 GN=PSMG2 PE=1 SV=1	1.444037	1.04E-10
Q14155	ARHG7_HUMAN	Rho guanine nucleotide exchange factor 7 OS=Homo sapiens OX=9606 GN=ARHGEF7 PE=1 SV=2	1.434801	1.37E-10
Q9UPT5	EXOC7_HUMAN	Exocyst complex component 7 OS=Homo sapiens OX=9606 GN=EXOC7 PE=1 SV=3	1.432363	4.56E-08
Q9GZM5	YIPF3_HUMAN	Protein YIPF3 OS=Homo sapiens OX=9606 GN=YIPF3 PE=1 SV=1	1.429954	6.38E-04
Q5T9A4	ATD3B_HUMAN	ATPase family AAA domain-containing protein 3B OS=Homo sapiens OX=9606 GN=ATAD3B PE=1 SV=1	1.408966	3.50E-10
Q96FJ2	DYL2_HUMAN	Dynein light chain 2 cytoplasmic OS=Homo sapiens OX=9606 GN=DYNLL2 PE=1 SV=1	1.394191	3.12E-07
Q9NW64	RBM22_HUMAN	Pre-mRNA-splicing factor RBM22 OS=Homo sapiens OX=9606 GN=RBM22 PE=1 SV=1	1.391812	1.99E-11
Q96AC1	FERM2_HUMAN	Fermitin family homolog 2 OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1	1.388987	6.11E-10
Q9H3Z4	DNJC5_HUMAN	DnaJ homolog subfamily C member 5 OS=Homo sapiens OX=9606 GN=DNAJC5 PE=1 SV=1	1.38495	0.001676
Q92626	PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens OX=9606 GN=PXDN PE=1 SV=2	1.379733	1.31E-07

Q9BZJ0	CRNL1_HUMAN	Crooked neck-like protein 1 OS=Homo sapiens OX=9606 GN=CRNL1 PE=1 SV=4	1.370399	1.17E-09
Q14512	FGFP1_HUMAN	Fibroblast growth factor-binding protein 1 OS=Homo sapiens OX=9606 GN=FGFBP1 PE=1 SV=1	1.369173	1.78E-04
O15446	RPA34_HUMAN	DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens OX=9606 GN=CD3EAP PE=1 SV=1	1.363547	1.32E-09
P14635	CCNB1_HUMAN	G2/mitotic-specific cyclin-B1 OS=Homo sapiens OX=9606 GN=CCNB1 PE=1 SV=1	1.35714	6.08E-05
Q8N392	RHG18_HUMAN	Rho GTPase-activating protein 18 OS=Homo sapiens OX=9606 GN=ARHGAP18 PE=1 SV=3	1.349378	1.97E-09
Q92974	ARHG2_HUMAN	Rho guanine nucleotide exchange factor 2 OS=Homo sapiens OX=9606 GN=ARHGEF2 PE=1 SV=4	1.342269	1.56E-12
P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNP2 PE=1 SV=1	1.341664	2.53E-09
Q6IQ22	RAB12_HUMAN	Ras-related protein Rab-12 OS=Homo sapiens OX=9606 GN=RAB12 PE=1 SV=3	1.339332	2.88E-09
Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=2	1.333424	2.17E-05
P68431	H31_HUMAN	Histone H3.1 OS=Homo sapiens OX=9606 GN=H3C1 PE=1 SV=2	1.331404	6.00E-12
Q12846	STX4_HUMAN	Syntaxin-4 OS=Homo sapiens OX=9606 GN=STX4 PE=1 SV=2	1.32855	3.66E-09
Q9UBV2	SE1L1_HUMAN	Protein sel-1 homolog 1 OS=Homo sapiens OX=9606 GN=SEL1L PE=1 SV=3	1.316282	4.97E-04
Q9Y613	FHOD1_HUMAN	FH1/FH2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FHOD1 PE=1 SV=3	1.308122	1.17E-09
Q92783	STAM1_HUMAN	Signal transducing adapter molecule 1 OS=Homo sapiens OX=9606 GN=STAM PE=1 SV=3	1.305432	7.15E-09
O95352	ATG7_HUMAN	Ubiquitin-like modifier-activating enzyme ATG7 OS=Homo sapiens OX=9606 GN=ATG7 PE=1 SV=1	1.302927	3.29E-04
O75431	MTX2_HUMAN	Metaxin-2 OS=Homo sapiens OX=9606 GN=MTX2 PE=1 SV=1	1.295194	8.69E-09
Q9BVC4	LST8_HUMAN	Target of rapamycin complex subunit LST8 OS=Homo sapiens OX=9606 GN=MLST8 PE=1 SV=1	1.291356	0.001895
Q92769	HDAC2_HUMAN	Histone deacetylase 2 OS=Homo sapiens OX=9606 GN=HDAC2 PE=1 SV=2	1.289878	1.07E-08
Q14192	FHL2_HUMAN	Four and a half LIM domains protein 2 OS=Homo sapiens OX=9606 GN=FHL2 PE=1 SV=3	1.288469	5.64E-11
E9PAV3	NACAM_HUMAN	Nascent polypeptide-associated complex subunit alpha muscle-specific form OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=1	1.287458	1.28E-08
P07947	YES_HUMAN	Tyrosine-protein kinase Yes OS=Homo sapiens OX=9606 GN=YES1 PE=1 SV=3	1.281882	1.31E-08
O14933	UB2L6_HUMAN	Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Homo sapiens OX=9606 GN=UBE2L6 PE=1 SV=4	1.27745	1.42E-08
P40306	PSB10_HUMAN	Proteasome subunit beta type-10 OS=Homo sapiens OX=9606 GN=PSMB10 PE=1 SV=1	1.271989	1.89E-08
Q9UHR4	BI2L1_HUMAN	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Homo sapiens OX=9606 GN=BAIAP2L1 PE=1 SV=2	1.262487	7.45E-04
Q99700	ATX2_HUMAN	Ataxin-2 OS=Homo sapiens OX=9606 GN=ATXN2 PE=1 SV=2	1.248522	4.19E-05
Q6P587	FAHD1_HUMAN	Acylpyruvase FAHD1 mitochondrial OS=Homo sapiens OX=9606 GN=FAHD1 PE=1 SV=2	1.247356	3.69E-08
Q13835	PKP1_HUMAN	Plakophilin-1 OS=Homo sapiens OX=9606 GN=PKP1 PE=1 SV=2	1.244361	4.09E-08
Q8WWA1	TMM40_HUMAN	Transmembrane protein 40 OS=Homo sapiens OX=9606 GN=TMEM40 PE=1 SV=2	1.23618	4.63E-08
P46977	STT3A_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens OX=9606 GN=STT3A PE=1 SV=2	1.233405	4.83E-08
Q9Y3D6	FIS1_HUMAN	Mitochondrial fission 1 protein OS=Homo sapiens OX=9606 GN=FIS1 PE=1 SV=2	1.232818	5.32E-08
P61764	STXB1_HUMAN	Syntaxin-binding protein 1 OS=Homo sapiens OX=9606 GN=STXBP1 PE=1 SV=1	1.227226	5.46E-08
P61619	S61A1_HUMAN	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens OX=9606 GN=SEC61A1 PE=1 SV=2	1.224118	6.37E-08
Q05086	UBE3A_HUMAN	Ubiquitin-protein ligase E3A OS=Homo sapiens OX=9606 GN=UBE3A PE=1 SV=4	1.221862	6.51E-08
Q9Y2Q5	LTOR2_HUMAN	Ragulator complex protein LAMTOR2 OS=Homo sapiens OX=9606 GN=LAMTOR2 PE=1 SV=1	1.21487	8.00E-08
Q0JR29	FCHO2_HUMAN	F-BAR domain only protein 2 OS=Homo sapiens OX=9606 GN=FCHO2 PE=1 SV=2	1.214859	7.88E-08
Q53EU6	GPAT3_HUMAN	Glycerol-3-phosphate acyltransferase 3 OS=Homo sapiens OX=9606 GN=GPAT3 PE=1 SV=2	1.212167	3.38E-05
Q96RT1	ERBIN_HUMAN	Erbin OS=Homo sapiens OX=9606 GN=ERBIN PE=1 SV=2	1.208403	4.24E-05
Q9NY27	PP4R2_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PPP4R2 PE=1 SV=3	1.207423	7.58E-08

P15144	AMPN_HUMAN	Aminopeptidase N OS=Homo sapiens OX=9606 GN=ANPEP PE=1 SV=4	1.203891	1.10E-07
Q13469	NFAC2_HUMAN	Nuclear factor of activated T-cells cytoplasmic 2 OS=Homo sapiens OX=9606 GN=NFATC2 PE=1 SV=2	1.198381	1.28E-07
Q9NYB9	ABI2_HUMAN	Abl interactor 2 OS=Homo sapiens OX=9606 GN=ABI2 PE=1 SV=1	1.19546	0.001918
O95858	TSN15_HUMAN	Tetraspanin-15 OS=Homo sapiens OX=9606 GN=TSPAN15 PE=1 SV=1	1.192645	1.43E-07
Q7Z2W9	RM21_HUMAN	39S ribosomal protein L21 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL21 PE=1 SV=2	1.191544	1.54E-07
Q14244	MAP7_HUMAN	Enscosin OS=Homo sapiens OX=9606 GN=MAP7 PE=1 SV=1	1.189314	1.49E-07
Q14241	ELOA1_HUMAN	Elongin-A OS=Homo sapiens OX=9606 GN=ELOA PE=1 SV=2	1.183533	6.76E-04
Q6L8Q7	PDE12_HUMAN	2' 5'-phosphodiesterase 12 OS=Homo sapiens OX=9606 GN=PDE12 PE=1 SV=2	1.179674	4.60E-04
Q9BUH6	PAXX_HUMAN	Protein PAXX OS=Homo sapiens OX=9606 GN=PAXX PE=1 SV=2	1.179063	0.005881
Q12769	NU160_HUMAN	Nuclear pore complex protein Nup160 OS=Homo sapiens OX=9606 GN=NUP160 PE=1 SV=3	1.17877	2.11E-07
O95163	ELP1_HUMAN	Elongator complex protein 1 OS=Homo sapiens OX=9606 GN=ELP1 PE=1 SV=3	1.177684	1.77E-09
O14972	VP26C_HUMAN	Vacuolar protein sorting-associated protein 26C OS=Homo sapiens OX=9606 GN=VPS26C PE=1 SV=1	1.17067	8.39E-05
Q96EP5	DAZP1_HUMAN	DAZ-associated protein 1 OS=Homo sapiens OX=9606 GN=DAZAP1 PE=1 SV=1	1.167754	2.90E-07
P05091	ALDH2_HUMAN	Aldehyde dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 PE=1 SV=2	1.161751	4.14E-09
O43920	NDUS5_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens OX=9606 GN=NDUFS5 PE=1 SV=3	1.158317	6.69E-05
O75841	UPK1B_HUMAN	Uroplakin-1b OS=Homo sapiens OX=9606 GN=UPK1B PE=1 SV=5	1.157541	3.64E-07
Q9H7Z7	PGES2_HUMAN	Prostaglandin E synthase 2 OS=Homo sapiens OX=9606 GN=PTGES2 PE=1 SV=1	1.1493	4.65E-07
Q9HAU0	PKHA5_HUMAN	Pleckstrin homology domain-containing family A member 5 OS=Homo sapiens OX=9606 GN=PLEKHA5 PE=1 SV=1	1.143159	3.50E-07
Q03519	TAP2_HUMAN	Antigen peptide transporter 2 OS=Homo sapiens OX=9606 GN=TAP2 PE=1 SV=1	1.140317	6.21E-07
Q9H2G2	SLK_HUMAN	STE20-like serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=SLK PE=1 SV=1	1.136166	3.21E-06
Q16637	SMN_HUMAN	Survival motor neuron protein OS=Homo sapiens OX=9606 GN=SMN1 PE=1 SV=1	1.134546	7.03E-07
Q8N8S7	ENAH_HUMAN	Protein enabled homolog OS=Homo sapiens OX=9606 GN=ENAH PE=1 SV=2	1.133721	7.03E-07
Q06546	GABPA_HUMAN	GA-binding protein alpha chain OS=Homo sapiens OX=9606 GN=GABPA PE=1 SV=1	1.128711	7.93E-07
O75152	ZC11A_HUMAN	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens OX=9606 GN=ZC3H11A PE=1 SV=3	1.127994	7.77E-07
Q9NV96	CC50A_HUMAN	Cell cycle control protein 50A OS=Homo sapiens OX=9606 GN=TMEM30A PE=1 SV=1	1.127825	7.77E-07
Q96FZ2	HMCES_HUMAN	Abasic site processing protein HMCES OS=Homo sapiens OX=9606 GN=HMCES PE=1 SV=1	1.127715	7.77E-07
Q96RE7	NACC1_HUMAN	Nucleus accumbens-associated protein 1 OS=Homo sapiens OX=9606 GN=NACC1 PE=1 SV=1	1.126177	0.001111
Q02487	DSC2_HUMAN	Desmocollin-2 OS=Homo sapiens OX=9606 GN=DSC2 PE=1 SV=1	1.125187	8.49E-07
Q9BW60	ELOV1_HUMAN	Elongation of very long chain fatty acids protein 1 OS=Homo sapiens OX=9606 GN=ELOVL1 PE=1 SV=1	1.123515	7.93E-07
Q9BRP8	PYM1_HUMAN	Partner of Y14 and mago OS=Homo sapiens OX=9606 GN=PYM1 PE=1 SV=1	1.123434	0.006666
Q9NX14	NDUBB_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFB11 PE=1 SV=1	1.123249	2.11E-07
P45985	MP2K4_HUMAN	Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens OX=9606 GN=MAP2K4 PE=1 SV=1	1.119847	9.60E-07
Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens OX=9606 GN=TGFBI PE=1 SV=1	1.117348	1.03E-06
Q9C0C9	UBE2O_HUMAN	(E3-independent) E2 ubiquitin-conjugating enzyme OS=Homo sapiens OX=9606 GN=UBE2O PE=1 SV=3	1.11173	1.77E-05
Q6PK04	CC137_HUMAN	Coiled-coil domain-containing protein 137 OS=Homo sapiens OX=9606 GN=CCDC137 PE=1 SV=1	1.111161	0.009269
O60885	BRD4_HUMAN	Bromodomain-containing protein 4 OS=Homo sapiens OX=9606 GN=BRD4 PE=1 SV=2	1.110445	0.001605
Q9NVZ3	NECP2_HUMAN	Adaptin ear-binding coat-associated protein 2 OS=Homo sapiens OX=9606 GN=NECAP2 PE=1 SV=1	1.106389	1.25E-06
Q5XKP0	MIC13_HUMAN	MICOS complex subunit MIC13 OS=Homo sapiens OX=9606 GN=MICOS13 PE=1 SV=1	1.105652	1.18E-06

O15260	SURF4_HUMAN	Surfeit locus protein 4 OS=Homo sapiens OX=9606 GN=SURF4 PE=1 SV=3	1.105248	1.18E-06
Q9NYH9	UTP6_HUMAN	U3 small nucleolar RNA-associated protein 6 homolog OS=Homo sapiens OX=9606 GN=UTP6 PE=2 SV=2	1.104869	1.25E-06
P52948	NUP98_HUMAN	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens OX=9606 GN=NUP98 PE=1 SV=4	1.10473	2.15E-08
P26885	FKBP2_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Homo sapiens OX=9606 GN=FKBP2 PE=1 SV=2	1.104093	1.38E-06
O15230	LAMA5_HUMAN	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	1.102051	6.93E-05
Q9NQT4	EXOS5_HUMAN	Exosome complex component RRP46 OS=Homo sapiens OX=9606 GN=EXOSC5 PE=1 SV=1	1.098794	6.87E-07
Q8NFH4	NUP37_HUMAN	Nucleoporin Nup37 OS=Homo sapiens OX=9606 GN=NUP37 PE=1 SV=1	1.09727	2.11E-05
Q8NFV4	ABHDB_HUMAN	Protein ABHD11 OS=Homo sapiens OX=9606 GN=ABHD11 PE=1 SV=1	1.094789	1.65E-06
P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 OS=Homo sapiens OX=9606 GN=PTPN6 PE=1 SV=1	1.093687	4.21E-06
Q9BV38	WDR18_HUMAN	WD repeat-containing protein 18 OS=Homo sapiens OX=9606 GN=WDR18 PE=1 SV=2	1.093517	3.24E-04
P60709	ACTB_HUMAN	Actin cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1	1.092993	1.72E-06
P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens OX=9606 GN=NME2 PE=1 SV=1	1.091148	8.82E-06
Q8TAE8	G45IP_HUMAN	Growth arrest and DNA damage-inducible proteins-interacting protein 1 OS=Homo sapiens OX=9606 GN=GADD45GIP1 PE=1 SV=1	1.089619	1.81E-06
Q2NL82	TSR1_HUMAN	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens OX=9606 GN=TSR1 PE=1 SV=1	1.089361	8.03E-05
Q9NRW3	ABC3C_HUMAN	DNA dC->dU-editing enzyme APOBEC-3C OS=Homo sapiens OX=9606 GN=APOBEC3C PE=1 SV=2	1.08913	1.79E-06
O75150	BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens OX=9606 GN=RN40 PE=1 SV=5	1.088901	1.56E-06
Q8WZ82	OVCA2_HUMAN	Esterase OVCA2 OS=Homo sapiens OX=9606 GN=OVCA2 PE=1 SV=1	1.087463	1.88E-06
P55809	SCOT1_HUMAN	Succinyl-CoA:3-ketoacid coenzyme A transferase 1 mitochondrial OS=Homo sapiens OX=9606 GN=OXCT1 PE=1 SV=1	1.083987	2.11E-06
Q9P270	SLAI2_HUMAN	SLAIN motif-containing protein 2 OS=Homo sapiens OX=9606 GN=SLAIN2 PE=1 SV=2	1.082462	0.007871
Q12805	FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens OX=9606 GN=EFEMP1 PE=1 SV=2	1.082407	2.14E-06
O00754	MA2B1_HUMAN	Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=3	1.082192	9.89E-04
Q03405	UPAR_HUMAN	Urokinase plasminogen activator surface receptor OS=Homo sapiens OX=9606 GN=PLAUR PE=1 SV=1	1.081981	2.03E-06
P51003	PAPOA_HUMAN	Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOLA PE=1 SV=4	1.081959	7.13E-04
O95674	CDS2_HUMAN	Phosphatidate cytidyltransferase 2 OS=Homo sapiens OX=9606 GN=CDS2 PE=1 SV=1	1.081603	2.04E-06
Q8TDB4	HUMMR_HUMAN	Protein MGARP OS=Homo sapiens OX=9606 GN=MGARP PE=1 SV=1	1.081476	0.00882
O95453	PARN_HUMAN	Poly(A)-specific ribonuclease PARN OS=Homo sapiens OX=9606 GN=PARN PE=1 SV=1	1.080947	2.14E-06
Q9BPX5	ARPSL_HUMAN	Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens OX=9606 GN=ARPC5L PE=1 SV=1	1.079755	2.29E-06
Q8NC56	LEMD2_HUMAN	LEM domain-containing protein 2 OS=Homo sapiens OX=9606 GN=LEMD2 PE=1 SV=1	1.076701	7.41E-06
Q12959	DLG1_HUMAN	Disks large homolog 1 OS=Homo sapiens OX=9606 GN=DLG1 PE=1 SV=2	1.07639	2.40E-06
Q6ZRP7	QSOX2_HUMAN	Sulfhydryl oxidase 2 OS=Homo sapiens OX=9606 GN=QSOX2 PE=1 SV=3	1.073116	4.50E-04
Q96JJ7	TMX3_HUMAN	Protein disulfide-isomerase TMX3 OS=Homo sapiens OX=9606 GN=TMX3 PE=1 SV=2	1.072579	4.38E-05
Q658Y4	F91A1_HUMAN	Protein FAM91A1 OS=Homo sapiens OX=9606 GN=FAM91A1 PE=1 SV=3	1.072196	2.75E-06
Q15477	SKIV2_HUMAN	Helicase SKI2W OS=Homo sapiens OX=9606 GN=SKIV2L PE=1 SV=3	1.072052	2.63E-06
O14936	CSKP_HUMAN	Peripheral plasma membrane protein CASK OS=Homo sapiens OX=9606 GN=CASK PE=1 SV=3	1.070289	2.75E-06
Q02252	MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial OS=Homo sapiens OX=9606 GN=ALDH6A1 PE=1 SV=2	1.068078	2.63E-06
Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2 OS=Homo sapiens OX=9606 GN=SPCS2 PE=1 SV=3	1.067939	7.77E-07

Q9Y2J4	AMOL2_HUMAN	Angiotensin-like protein 2 OS=Homo sapiens OX=9606 GN=AMOTL2 PE=1 SV=3	1.067497	2.94E-06
P47895	AL1A3_HUMAN	Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens OX=9606 GN=ALDH1A3 PE=1 SV=2	1.065802	6.66E-05
P25942	TNR5_HUMAN	Tumor necrosis factor receptor superfamily member 5 OS=Homo sapiens OX=9606 GN=CD40 PE=1 SV=1	1.063062	2.98E-06
P50570	DYN2_HUMAN	Dynamin-2 OS=Homo sapiens OX=9606 GN=DNM2 PE=1 SV=2	1.061532	4.32E-06
P84085	ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens OX=9606 GN=ARF5 PE=1 SV=2	1.061401	3.01E-06
O60488	ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens OX=9606 GN=ACSL4 PE=1 SV=2	1.060542	4.99E-06
Q15269	PWP2_HUMAN	Periodic tryptophan protein 2 homolog OS=Homo sapiens OX=9606 GN=PWP2 PE=2 SV=2	1.059028	1.31E-05
O75147	OBSL1_HUMAN	Obscurin-like protein 1 OS=Homo sapiens OX=9606 GN=OBSL1 PE=1 SV=4	1.058679	3.30E-06
Q96ST2	IWS1_HUMAN	Protein IWS1 homolog OS=Homo sapiens OX=9606 GN=IWS1 PE=1 SV=2	1.058402	3.30E-06
Q7Z2T5	TRM1L_HUMAN	TRMT1-like protein OS=Homo sapiens OX=9606 GN=TRMT1L PE=1 SV=2	1.058093	3.30E-06
P49247	RPIA_HUMAN	Ribose-5-phosphate isomerase OS=Homo sapiens OX=9606 GN=RPIA PE=1 SV=3	1.057374	3.45E-06
Q53EP0	FND3B_HUMAN	Fibronectin type III domain-containing protein 3B OS=Homo sapiens OX=9606 GN=FND3B PE=1 SV=2	1.056489	5.85E-06
Q8IZ83	A16A1_HUMAN	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens OX=9606 GN=ALDH16A1 PE=1 SV=2	1.054742	0.001521
P35237	SPB6_HUMAN	Serpin B6 OS=Homo sapiens OX=9606 GN=SERPINB6 PE=1 SV=3	1.054004	1.48E-04
Q96EY8	MMAB_HUMAN	Corrinoid adenosyltransferase OS=Homo sapiens OX=9606 GN=MMAB PE=1 SV=1	1.052543	3.78E-06
Q9UKS6	PACN3_HUMAN	Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens OX=9606 GN=PACSIN3 PE=1 SV=2	1.052321	3.85E-06
Q9Y3I1	FBX7_HUMAN	F-box only protein 7 OS=Homo sapiens OX=9606 GN=FBXO7 PE=1 SV=1	1.052073	3.78E-06
Q9Y2R4	DDX52_HUMAN	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens OX=9606 GN=DDX52 PE=1 SV=3	1.051864	3.85E-06
A6NDB9	PALM3_HUMAN	Paralemmin-3 OS=Homo sapiens OX=9606 GN=PALM3 PE=1 SV=2	1.051605	3.85E-06
P43246	MSH2_HUMAN	DNA mismatch repair protein Msh2 OS=Homo sapiens OX=9606 GN=MSH2 PE=1 SV=1	1.050814	9.70E-06
O00267	SPT5H_HUMAN	Transcription elongation factor SPT5 OS=Homo sapiens OX=9606 GN=SPT5H PE=1 SV=1	1.048856	3.95E-04
Q9H061	T126A_HUMAN	Transmembrane protein 126A OS=Homo sapiens OX=9606 GN=TMEM126A PE=1 SV=1	1.045851	5.13E-04
P26358	DNMT1_HUMAN	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens OX=9606 GN=DNMT1 PE=1 SV=2	1.044978	1.83E-05
Q7KZ85	SPT6H_HUMAN	Transcription elongation factor SPT6 OS=Homo sapiens OX=9606 GN=SPT6H PE=1 SV=2	1.044633	9.70E-06
P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens OX=9606 GN=SNRPD1 PE=1 SV=1	1.043431	4.45E-06
Q9BTT6	LRRC1_HUMAN	Leucine-rich repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=LRRC1 PE=1 SV=1	1.041584	1.09E-04
P12931	SRC_HUMAN	Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens OX=9606 GN=SRC PE=1 SV=3	1.041442	4.58E-06
P04150	GCR_HUMAN	Glucocorticoid receptor OS=Homo sapiens OX=9606 GN=NR3C1 PE=1 SV=1	1.041257	8.31E-06
Q9UHG3	PCYOX_HUMAN	Prenylcysteine oxidase 1 OS=Homo sapiens OX=9606 GN=PCYOX1 PE=1 SV=3	1.04105	3.29E-05
O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 SV=1	1.041044	0.009786
Q9NWW8	BABA1_HUMAN	BRIS and BRCA1-A complex member 1 OS=Homo sapiens OX=9606 GN=BABAM1 PE=1 SV=1	1.040658	4.80E-06
O94776	MTA2_HUMAN	Metastasis-associated protein MTA2 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	1.040379	1.42E-06
Q6P161	RM54_HUMAN	39S ribosomal protein L54 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL54 PE=1 SV=1	1.039903	4.80E-06
P33527	MRP1_HUMAN	Multidrug resistance-associated protein 1 OS=Homo sapiens OX=9606 GN=ABCC1 PE=1 SV=3	1.038729	4.99E-06
Q07960	RHG01_HUMAN	Rho GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=ARHGAP1 PE=1 SV=1	1.038638	4.60E-06
Q13347	EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens OX=9606 GN=EIF3I PE=1 SV=1	1.037849	1.17E-09
P02751	FINC_HUMAN	Fibronectin OS=Homo sapiens OX=9606 GN=FN1 PE=1 SV=5	1.037608	7.78E-06
Q9P013	CWC15_HUMAN	Spliceosome-associated protein CWC15 homolog OS=Homo sapiens OX=9606 GN=CWC15 PE=1 SV=2	1.037111	4.99E-06

Q53LP3	SWAHC_HUMAN	Ankyrin repeat domain-containing protein SOWAHC OS=Homo sapiens OX=9606 GN=SOWAHC PE=1 SV=1	1.036712	5.01E-06
P46736	BRCC3_HUMAN	Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens OX=9606 GN=BRCC3 PE=1 SV=2	1.036007	5.14E-06
P51116	FXR2_HUMAN	Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens OX=9606 GN=FXR2 PE=1 SV=2	1.035275	5.14E-06
P34949	MPI_HUMAN	Mannose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=MPI PE=1 SV=2	1.035088	5.14E-06
Q9H845	ACAD9_HUMAN	Complex I assembly factor ACAD9 mitochondrial OS=Homo sapiens OX=9606 GN=ACAD9 PE=1 SV=1	1.034167	3.17E-06
Q92614	MY18A_HUMAN	Unconventional myosin-XVIIIa OS=Homo sapiens OX=9606 GN=MYO18A PE=1 SV=3	1.033726	4.03E-05
Q6NYC1	JMJD6_HUMAN	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Homo sapiens OX=9606 GN=JMJD6 PE=1 SV=1	1.033616	1.02E-04
O95232	LC7L3_HUMAN	Luc7-like protein 3 OS=Homo sapiens OX=9606 GN=LUC7L3 PE=1 SV=2	1.033601	9.06E-06
P01111	RASN_HUMAN	GTPase NRas OS=Homo sapiens OX=9606 GN=NRAS PE=1 SV=1	1.03264	5.52E-06
Q8N3F8	MILK1_HUMAN	MICAL-like protein 1 OS=Homo sapiens OX=9606 GN=MICALL1 PE=1 SV=2	1.032488	5.36E-06
O60825	F262_HUMAN	6-phosphofructo-2-kinase/fructose-2-6-bisphosphatase 2 OS=Homo sapiens OX=9606 GN=PFKFB2 PE=1 SV=2	1.032421	5.45E-06
Q9NZJ7	MTCH1_HUMAN	Mitochondrial carrier homolog 1 OS=Homo sapiens OX=9606 GN=MTCH1 PE=1 SV=1	1.030081	6.03E-06
Q9Y6G9	DC1L1_HUMAN	Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens OX=9606 GN=DYNC1LI1 PE=1 SV=3	1.029606	2.66E-05
P49770	EI2BB_HUMAN	Translation initiation factor eIF-2B subunit beta OS=Homo sapiens OX=9606 GN=EIF2B2 PE=1 SV=3	1.029363	5.64E-06
P49591	SYSC_HUMAN	Serine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=SARS1 PE=1 SV=3	1.027307	3.71E-05
O15121	DEGS1_HUMAN	Sphingolipid delta(4)-desaturase DES1 OS=Homo sapiens OX=9606 GN=DEGS1 PE=1 SV=1	1.026851	0.008894
Q8N5N7	RM50_HUMAN	39S ribosomal protein L50 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL50 PE=1 SV=2	1.026293	0.001603
Q9NXR7	BABA2_HUMAN	BRISC and BRCA1-A complex member 2 OS=Homo sapiens OX=9606 GN=BABAM2 PE=1 SV=2	1.02357	6.74E-06
P07948	LYN_HUMAN	Tyrosine-protein kinase Lyn OS=Homo sapiens OX=9606 GN=LYN PE=1 SV=3	1.023476	1.20E-04
P09132	SRP19_HUMAN	Signal recognition particle 19 kDa protein OS=Homo sapiens OX=9606 GN=SRP19 PE=1 SV=3	1.023327	6.53E-06
Q96T23	RSF1_HUMAN	Remodeling and spacing factor 1 OS=Homo sapiens OX=9606 GN=RSF1 PE=1 SV=2	1.023105	5.47E-06
Q9BZK7	TBL1R_HUMAN	F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens OX=9606 GN=TBL1XR1 PE=1 SV=1	1.022765	2.49E-05
Q8WUP2	FBLI1_HUMAN	Filamin-binding LIM protein 1 OS=Homo sapiens OX=9606 GN=FBLIM1 PE=1 SV=2	1.022216	6.84E-06
Q13011	ECH1_HUMAN	Delta(3 5)-Delta(2 4)-dienoyl-CoA isomerase mitochondrial OS=Homo sapiens OX=9606 GN=ECH1 PE=1 SV=2	1.019916	3.28E-05
P46976	GLYG_HUMAN	Glycogenin-1 OS=Homo sapiens OX=9606 GN=GYG1 PE=1 SV=4	1.018568	7.46E-06
Q14790	CASP8_HUMAN	Caspase-8 OS=Homo sapiens OX=9606 GN=CASP8 PE=1 SV=1	1.01782	7.46E-06
P07996	TSP1_HUMAN	Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1 PE=1 SV=2	1.017339	3.60E-05
Q9BZF9	UACA_HUMAN	Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens OX=9606 GN=UACA PE=1 SV=2	1.017045	2.71E-06
P50443	S26A2_HUMAN	Sulfate transporter OS=Homo sapiens OX=9606 GN=SLC26A2 PE=1 SV=2	1.016626	0.002077
Q96TA1	NIBA2_HUMAN	Protein Niban 2 OS=Homo sapiens OX=9606 GN=NIBAN2 PE=1 SV=3	1.014477	0.002813
Q92922	SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens OX=9606 GN=SMARCC1 PE=1 SV=3	1.014355	2.94E-06
Q93052	LPP_HUMAN	Lipoma-preferred partner OS=Homo sapiens OX=9606 GN=LPP PE=1 SV=1	1.013768	1.03E-06
Q13042	CDC16_HUMAN	Cell division cycle protein 16 homolog OS=Homo sapiens OX=9606 GN=CDC16 PE=1 SV=2	1.013697	3.67E-04
Q9BPW8	NIPS1_HUMAN	Protein NipSnap homolog 1 OS=Homo sapiens OX=9606 GN=NIPSNAP1 PE=1 SV=1	1.012831	0.005064
O95274	LYPD3_HUMAN	Ly6/PLAUR domain-containing protein 3 OS=Homo sapiens OX=9606 GN=LYPD3 PE=1 SV=2	1.012379	8.71E-06
Q8NI27	THOC2_HUMAN	THO complex subunit 2 OS=Homo sapiens OX=9606 GN=THOC2 PE=1 SV=2	1.012323	8.48E-06
Q9NYY8	FAKD2_HUMAN	FAST kinase domain-containing protein 2 mitochondrial OS=Homo sapiens OX=9606 GN=FASTKD2 PE=1 SV=1	1.011055	8.56E-06
Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1 PE=1 SV=2	1.010769	6.47E-06

Q14671	PUM1_HUMAN	Pumilio homolog 1 OS=Homo sapiens OX=9606 GN=PUM1 PE=1 SV=3	1.01061	8.55E-06
Q9H6T3	RPAP3_HUMAN	RNA polymerase II-associated protein 3 OS=Homo sapiens OX=9606 GN=RPAP3 PE=1 SV=2	1.01055	1.36E-06
Q2NKX8	ERC6L_HUMAN	DNA excision repair protein ERCC-6-like OS=Homo sapiens OX=9606 GN=ERCC6L PE=1 SV=1	1.009632	8.82E-06
O95490	AGRL2_HUMAN	Adhesion G protein-coupled receptor L2 OS=Homo sapiens OX=9606 GN=AGRL2 PE=1 SV=2	1.009563	8.74E-06
Q9BY44	EIF2A_HUMAN	Eukaryotic translation initiation factor 2A OS=Homo sapiens OX=9606 GN=EIF2A PE=1 SV=3	1.009124	6.51E-08
O95361	TRI16_HUMAN	Tripartite motif-containing protein 16 OS=Homo sapiens OX=9606 GN=TRIM16 PE=1 SV=3	1.008592	3.45E-05
O75843	AP1G2_HUMAN	AP-1 complex subunit gamma-like 2 OS=Homo sapiens OX=9606 GN=AP1G2 PE=1 SV=1	1.004717	9.60E-06
Q9Y4P3	TBL2_HUMAN	Transducin beta-like protein 2 OS=Homo sapiens OX=9606 GN=TBL2 PE=1 SV=1	1.002618	3.16E-06
P32322	P5CR1_HUMAN	Pyrroline-5-carboxylate reductase 1 mitochondrial OS=Homo sapiens OX=9606 GN=P5CR1 PE=1 SV=2	1.001051	3.56E-05
Q15311	RBP1_HUMAN	RalA-binding protein 1 OS=Homo sapiens OX=9606 GN=RALBP1 PE=1 SV=3	1.000854	0.001577
Q5T0W9	FA83B_HUMAN	Protein FAM83B OS=Homo sapiens OX=9606 GN=FAM83B PE=1 SV=1	1.000564	1.01E-05
P16403	H12_HUMAN	Histone H1.2 OS=Homo sapiens OX=9606 GN=H1-2 PE=1 SV=2	1	6.50E-05
O43752	STX6_HUMAN	Syntaxin-6 OS=Homo sapiens OX=9606 GN=STX6 PE=1 SV=1	1	0.00311
P63151	2ABA_HUMAN	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R2A PE=1 SV=1	0.999327	3.15E-06
Q6YHK3	CD109_HUMAN	CD109 antigen OS=Homo sapiens OX=9606 GN=CD109 PE=1 SV=2	0.999163	1.77E-08
Q9UBU9	NXF1_HUMAN	Nuclear RNA export factor 1 OS=Homo sapiens OX=9606 GN=NXF1 PE=1 SV=1	0.998493	1.02E-05
Q9Y6C9	MTCH2_HUMAN	Mitochondrial carrier homolog 2 OS=Homo sapiens OX=9606 GN=MTCH2 PE=1 SV=1	0.997951	1.08E-05
Q15042	RB3GP_HUMAN	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens OX=9606 GN=RAB3GAP1 PE=1 SV=3	0.997574	1.98E-05
Q8N3D4	EH1L1_HUMAN	EH domain-binding protein 1-like protein 1 OS=Homo sapiens OX=9606 GN=EHBP1L1 PE=1 SV=2	0.993764	2.69E-04
Q9BTC0	DIDO1_HUMAN	Death-inducer obliterator 1 OS=Homo sapiens OX=9606 GN=DIDO1 PE=1 SV=5	0.993231	6.39E-05
Q9GZR7	DDX24_HUMAN	ATP-dependent RNA helicase DDX24 OS=Homo sapiens OX=9606 GN=DDX24 PE=1 SV=1	0.99189	4.56E-05
Q5QJE6	TDIF2_HUMAN	Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens OX=9606 GN=DNTP2 PE=1 SV=2	0.990662	4.11E-04
Q9Y5Y2	NUBP2_HUMAN	Cytosolic Fe-S cluster assembly factor NUBP2 OS=Homo sapiens OX=9606 GN=NUBP2 PE=1 SV=1	0.989388	1.31E-05
Q9H1E3	NUCKS_HUMAN	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens OX=9606 GN=NUCKS1 PE=1 SV=1	0.989029	1.31E-05
Q7KZI7	MARK2_HUMAN	Serine/threonine-protein kinase MARK2 OS=Homo sapiens OX=9606 GN=MARK2 PE=1 SV=2	0.988548	9.08E-04
Q6ZRV2	FA83H_HUMAN	Protein FAM83H OS=Homo sapiens OX=9606 GN=FAM83H PE=1 SV=3	0.988538	1.09E-04
Q9H0B6	KLC2_HUMAN	Kinesin light chain 2 OS=Homo sapiens OX=9606 GN=KLC2 PE=1 SV=1	0.98805	1.31E-05
Q9Y4W2	LAS1L_HUMAN	Ribosomal biogenesis protein LAS1L OS=Homo sapiens OX=9606 GN=LAS1L PE=1 SV=2	0.987745	2.94E-06
O00139	KIF2A_HUMAN	Kinesin-like protein KIF2A OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=3	0.98705	1.31E-05
Q9Y3A5	SBDS_HUMAN	Ribosome maturation protein SBDS OS=Homo sapiens OX=9606 GN=SBDS PE=1 SV=4	0.986125	3.79E-04
Q15833	STXB2_HUMAN	Syntaxin-binding protein 2 OS=Homo sapiens OX=9606 GN=STXB2 PE=1 SV=2	0.985239	1.41E-05
Q14669	TRIP12_HUMAN	E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens OX=9606 GN=TRIP12 PE=1 SV=1	0.984947	3.46E-05
O95786	DDX58_HUMAN	Antiviral innate immune response receptor RIG-I OS=Homo sapiens OX=9606 GN=DDX58 PE=1 SV=2	0.98371	1.41E-05
P28290	ITPI2_HUMAN	Protein ITPRID2 OS=Homo sapiens OX=9606 GN=ITPRID2 PE=1 SV=3	0.983626	7.75E-05
P80404	GABT_HUMAN	4-aminobutyrate aminotransferase mitochondrial OS=Homo sapiens OX=9606 GN=ABAT PE=1 SV=3	0.983559	1.49E-05
Q7Z3K3	POGZ_HUMAN	Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=2	0.983283	2.03E-05
Q9BX55	AP1M1_HUMAN	AP-1 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP1M1 PE=1 SV=3	0.983004	3.57E-04

Q9BT09	CNPY3_HUMAN	Protein canopy homolog 3 OS=Homo sapiens OX=9606 GN=CNPY3 PE=1 SV=1	0.982945	1.48E-05
P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=2	0.982545	1.46E-05
Q9Y4E8	UBP15_HUMAN	Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens OX=9606 GN=USP15 PE=1 SV=3	0.981155	8.34E-04
Q13740	CD166_HUMAN	CD166 antigen OS=Homo sapiens OX=9606 GN=ALCAM PE=1 SV=2	0.980664	1.16E-05
O94804	STK10_HUMAN	Serine/threonine-protein kinase 10 OS=Homo sapiens OX=9606 GN=STK10 PE=1 SV=1	0.978877	1.53E-05
Q9UL15	BAG5_HUMAN	BAG family molecular chaperone regulator 5 OS=Homo sapiens OX=9606 GN=BAG5 PE=1 SV=1	0.978041	2.22E-04
Q99567	NUP88_HUMAN	Nuclear pore complex protein Nup88 OS=Homo sapiens OX=9606 GN=NUP88 PE=1 SV=2	0.977151	7.39E-05
Q15061	WDR43_HUMAN	WD repeat-containing protein 43 OS=Homo sapiens OX=9606 GN=WDR43 PE=1 SV=3	0.976111	1.71E-05
P41240	CSK_HUMAN	Tyrosine-protein kinase CSK OS=Homo sapiens OX=9606 GN=CSK PE=1 SV=1	0.975107	1.70E-05
Q6IBS0	TWF2_HUMAN	Twinfilin-2 OS=Homo sapiens OX=9606 GN=TWF2 PE=1 SV=2	0.974909	3.30E-06
Q5T1M5	FKB15_HUMAN	FK506-binding protein 15 OS=Homo sapiens OX=9606 GN=FKBP15 PE=1 SV=2	0.974838	1.71E-06
A0FGR8	ESYT2_HUMAN	Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1	0.973964	1.14E-05
P61981	1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2	0.973933	2.19E-05
Q49A26	GLYR1_HUMAN	Putative oxidoreductase GLYR1 OS=Homo sapiens OX=9606 GN=GLYR1 PE=1 SV=4	0.972344	1.79E-05
P08047	SP1_HUMAN	Transcription factor Sp1 OS=Homo sapiens OX=9606 GN=SP1 PE=1 SV=3	0.971739	1.75E-05
P07602	SAP_HUMAN	Prosaposin OS=Homo sapiens OX=9606 GN=PSAP PE=1 SV=2	0.97164	1.98E-05
Q96AB3	ISOC2_HUMAN	Isochorismatase domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ISOC2 PE=1 SV=1	0.970423	6.60E-04
Q99436	PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens OX=9606 GN=PSMB7 PE=1 SV=1	0.969926	1.83E-05
Q6NZ67	MZT2B_HUMAN	Mitotic-spindle organizing protein 2B OS=Homo sapiens OX=9606 GN=MZT2B PE=1 SV=1	0.969808	1.95E-05
Q10713	MPPA_HUMAN	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens OX=9606 GN=PMPA PE=1 SV=2	0.969412	1.93E-05
Q9UK76	JUPI1_HUMAN	Jupiter microtubule associated homolog 1 OS=Homo sapiens OX=9606 GN=JPT1 PE=1 SV=3	0.96935	1.83E-05
P98194	AT2C1_HUMAN	Calcium-transporting ATPase type 2C member 1 OS=Homo sapiens OX=9606 GN=ATP2C1 PE=1 SV=3	0.969313	7.39E-05
P06132	DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=Homo sapiens OX=9606 GN=UROD PE=1 SV=2	0.968291	3.42E-05
P43686	PRS6B_HUMAN	26S proteasome regulatory subunit 6B OS=Homo sapiens OX=9606 GN=PSMC4 PE=1 SV=2	0.967326	0.001835
P28062	PSB8_HUMAN	Proteasome subunit beta type-8 OS=Homo sapiens OX=9606 GN=PSMB8 PE=1 SV=3	0.96721	5.14E-06
P12694	ODBA_HUMAN	2-oxoisovalerate dehydrogenase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=BCKDHA PE=1 SV=2	0.966344	2.00E-05
Q92797	SYMPK_HUMAN	Symplekin OS=Homo sapiens OX=9606 GN=SYMPK PE=1 SV=2	0.965816	6.32E-05
P08237	PFKAM_HUMAN	ATP-dependent 6-phosphofructokinase muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=2	0.965804	4.60E-05
P49589	SYCC_HUMAN	Cysteine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=CARS1 PE=1 SV=3	0.96573	2.00E-05
Q15418	KS6A1_HUMAN	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1 SV=2	0.965146	8.45E-05
Q04446	GLGB_HUMAN	1 4-alpha-glucan-branching enzyme OS=Homo sapiens OX=9606 GN=GBE1 PE=1 SV=3	0.964973	2.03E-05
P42167	LAP2B_HUMAN	Lamina-associated polypeptide 2 isoforms beta/gamma OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2	0.964916	2.01E-05
O75746	CMC1_HUMAN	Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens OX=9606 GN=SLC25A12 PE=1 SV=2	0.963598	9.13E-05
O00468	AGRIN_HUMAN	Agrin OS=Homo sapiens OX=9606 GN=AGRN PE=1 SV=6	0.963183	1.15E-04
O43598	DNPH1_HUMAN	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 OS=Homo sapiens OX=9606 GN=DNPH1 PE=1 SV=1	0.963177	2.08E-05
Q2M389	WASC4_HUMAN	WASH complex subunit 4 OS=Homo sapiens OX=9606 GN=WASHC4 PE=1 SV=2	0.963124	2.03E-05
Q9BTY7	HGH1_HUMAN	Protein HGH1 homolog OS=Homo sapiens OX=9606 GN=HGH1 PE=1 SV=1	0.962687	2.01E-05
P17676	CEBPB_HUMAN	CCAAT/enhancer-binding protein beta OS=Homo sapiens OX=9606 GN=CEBPB PE=1 SV=2	0.962489	2.14E-05

Q9ULC3	RAB23_HUMAN	Ras-related protein Rab-23 OS=Homo sapiens OX=9606 GN=RAB23 PE=1 SV=1	0.961994	2.04E-05
P53384	NUBP1_HUMAN	Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens OX=9606 GN=NUBP1 PE=1 SV=2	0.961723	2.13E-05
P05121	PAI1_HUMAN	Plasminogen activator inhibitor 1 OS=Homo sapiens OX=9606 GN=SERPINE1 PE=1 SV=1	0.961259	0.005027
Q9NZT2	OGFR_HUMAN	Opioid growth factor receptor OS=Homo sapiens OX=9606 GN=OGFR PE=1 SV=3	0.961203	3.78E-05
Q13753	LAMC2_HUMAN	Laminin subunit gamma-2 OS=Homo sapiens OX=9606 GN=LAMC2 PE=1 SV=2	0.961131	2.56E-05
Q9GZT4	SRR_HUMAN	Serine racemase OS=Homo sapiens OX=9606 GN=SRR PE=1 SV=1	0.960992	2.13E-05
P84095	RHOG_HUMAN	Rho-related GTP-binding protein RhoG OS=Homo sapiens OX=9606 GN=RHOG PE=1 SV=1	0.96041	2.14E-05
Q9NQT5	EXOS3_HUMAN	Exosome complex component RRP40 OS=Homo sapiens OX=9606 GN=EXOSC3 PE=1 SV=3	0.960216	2.14E-05
O96005	CLPT1_HUMAN	Cleft lip and palate transmembrane protein 1 OS=Homo sapiens OX=9606 GN=CLPTM1 PE=1 SV=1	0.960144	2.14E-05
P56945	BCAR1_HUMAN	Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens OX=9606 GN=BCAR1 PE=1 SV=2	0.959657	9.13E-05
Q7LBC6	KDM3B_HUMAN	Lysine-specific demethylase 3B OS=Homo sapiens OX=9606 GN=KDM3B PE=1 SV=2	0.959589	2.19E-05
Q8IYB1	M21D2_HUMAN	Protein MB21D2 OS=Homo sapiens OX=9606 GN=MB21D2 PE=1 SV=3	0.959358	9.59E-04
Q9BTE7	DCNL5_HUMAN	DCN1-like protein 5 OS=Homo sapiens OX=9606 GN=DCUN1D5 PE=1 SV=1	0.959149	2.87E-05
Q15067	ACOX1_HUMAN	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens OX=9606 GN=ACOX1 PE=1 SV=3	0.958649	1.11E-06
Q9BW04	SARG_HUMAN	Specifically androgen-regulated gene protein OS=Homo sapiens OX=9606 GN=SARG PE=1 SV=2	0.95818	2.16E-05
Q6P1N0	C2D1A_HUMAN	Coiled-coil and C2 domain-containing protein 1A OS=Homo sapiens OX=9606 GN=CC2D1A PE=1 SV=1	0.95751	4.32E-05
P55210	CASP7_HUMAN	Caspase-7 OS=Homo sapiens OX=9606 GN=CASP7 PE=1 SV=1	0.957348	2.28E-05
Q8TDB6	DTX3L_HUMAN	E3 ubiquitin-protein ligase DTX3L OS=Homo sapiens OX=9606 GN=DTX3L PE=1 SV=1	0.956673	2.25E-05
Q9UN86	G3BP2_HUMAN	Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens OX=9606 GN=G3BP2 PE=1 SV=2	0.956008	2.27E-05
P63220	RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens OX=9606 GN=RPS21 PE=1 SV=1	0.955716	3.38E-05
O43823	AKAP8_HUMAN	A-kinase anchor protein 8 OS=Homo sapiens OX=9606 GN=AKAP8 PE=1 SV=1	0.955331	2.33E-05
Q8NFU3	TSTD1_HUMAN	Thiosulfate:glutathione sulfurtransferase OS=Homo sapiens OX=9606 GN=TSTD1 PE=1 SV=3	0.955276	2.37E-05
Q12824	SNF5_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens OX=9606 GN=SMARCB1 PE=1 SV=2	0.955076	9.60E-06
O15031	PLXB2_HUMAN	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	0.955061	2.14E-05
Q96S66	CLCC1_HUMAN	Chloride channel CLIC-like protein 1 OS=Homo sapiens OX=9606 GN=CLCC1 PE=1 SV=1	0.955055	2.35E-05
Q9BXY0	MAK16_HUMAN	Protein MAK16 homolog OS=Homo sapiens OX=9606 GN=MAK16 PE=1 SV=2	0.954871	2.46E-05
Q9Y5Q9	TF3C3_HUMAN	General transcription factor 3C polypeptide 3 OS=Homo sapiens OX=9606 GN=GTF3C3 PE=1 SV=1	0.954377	2.30E-05
Q9BVL2	NUP58_HUMAN	Nucleoporin p58/p45 OS=Homo sapiens OX=9606 GN=NUP58 PE=1 SV=1	0.954105	2.31E-05
Q9H0A0	NAT10_HUMAN	RNA cytidine acetyltransferase OS=Homo sapiens OX=9606 GN=NAT10 PE=1 SV=2	0.954012	2.49E-05
O14908	GIPC1_HUMAN	PDZ domain-containing protein GIPC1 OS=Homo sapiens OX=9606 GN=GIPC1 PE=1 SV=2	0.952975	6.04E-04
Q15007	FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP OS=Homo sapiens OX=9606 GN=WTAP PE=1 SV=2	0.952918	3.10E-04
Q92520	FAM3C_HUMAN	Protein FAM3C OS=Homo sapiens OX=9606 GN=FAM3C PE=1 SV=1	0.95231	2.51E-05
Q9NNW7	TRXR2_HUMAN	Thioredoxin reductase 2 mitochondrial OS=Homo sapiens OX=9606 GN=TXNRD2 PE=1 SV=3	0.951544	2.51E-05
Q9Y6K5	OAS3_HUMAN	2'-5'-oligoadenylate synthase 3 OS=Homo sapiens OX=9606 GN=OAS3 PE=1 SV=3	0.950485	2.55E-05
Q9BV86	NTM1A_HUMAN	N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens OX=9606 GN=NTMT1 PE=1 SV=3	0.95038	2.55E-05
Q7Z417	NUFP2_HUMAN	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens OX=9606 GN=NUFIP2 PE=1 SV=1	0.949374	7.56E-05
P62195	PR58_HUMAN	26S proteasome regulatory subunit 8 OS=Homo sapiens OX=9606 GN=PSMC5 PE=1 SV=1	0.949087	1.44E-04

P09914	IFIT1_HUMAN	Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens OX=9606 GN=IFIT1 PE=1 SV=2	0.949082	7.48E-05
Q9Y223	GLCNE_HUMAN	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Homo sapiens OX=9606 GN=GNE PE=1 SV=1	0.948589	2.10E-04
Q9NRZ9	HELLS_HUMAN	Lymphoid-specific helicase OS=Homo sapiens OX=9606 GN=HELLS PE=1 SV=1	0.948299	2.71E-05
P24821	TENA_HUMAN	Tenascin OS=Homo sapiens OX=9606 GN=TNC PE=1 SV=3	0.948267	7.75E-05
P78330	SERB_HUMAN	Phosphoserine phosphatase OS=Homo sapiens OX=9606 GN=PSPH PE=1 SV=2	0.948261	2.55E-05
Q9Y676	RT18B_HUMAN	28S ribosomal protein S18b mitochondrial OS=Homo sapiens OX=9606 GN=MRPS18B PE=1 SV=1	0.94812	2.57E-05
Q9Y3D0	CIA2B_HUMAN	Cytosolic iron-sulfur assembly component 2B OS=Homo sapiens OX=9606 GN=CIAO2B PE=1 SV=1	0.947024	0.001595
Q13057	COASY_HUMAN	Bifunctional coenzyme A synthase OS=Homo sapiens OX=9606 GN=COASY PE=1 SV=4	0.946816	2.24E-05
Q8WWQ0	PHIP_HUMAN	PH-interacting protein OS=Homo sapiens OX=9606 GN=PHIP PE=1 SV=2	0.946484	2.71E-05
Q7Z7L1	SLN11_HUMAN	Schlafen family member 11 OS=Homo sapiens OX=9606 GN=SLFN11 PE=1 SV=2	0.946281	7.22E-06
P82673	RT35_HUMAN	28S ribosomal protein S35 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS35 PE=1 SV=1	0.944648	2.75E-05
O75792	RNH2A_HUMAN	Ribonuclease H2 subunit A OS=Homo sapiens OX=9606 GN=RNASEH2A PE=1 SV=2	0.943252	2.83E-05
Q9H993	ARMT1_HUMAN	Damage-control phosphatase ARMT1 OS=Homo sapiens OX=9606 GN=ARMT1 PE=1 SV=1	0.943028	3.09E-05
Q9Y2A7	NCKP1_HUMAN	Nck-associated protein 1 OS=Homo sapiens OX=9606 GN=NCKAP1 PE=1 SV=1	0.940264	3.46E-05
Q00535	CDK5_HUMAN	Cyclin-dependent-like kinase 5 OS=Homo sapiens OX=9606 GN=CDK5 PE=1 SV=3	0.940194	1.99E-04
Q9NP61	ARFG3_HUMAN	ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens OX=9606 GN=ARFGAP3 PE=1 SV=1	0.940175	1.31E-05
P57735	RAB25_HUMAN	Ras-related protein Rab-25 OS=Homo sapiens OX=9606 GN=RAB25 PE=1 SV=2	0.939922	6.22E-04
Q8ND56	LS14A_HUMAN	Protein LSM14 homolog A OS=Homo sapiens OX=9606 GN=LSM14A PE=1 SV=3	0.93985	3.09E-05
P46199	IF2M_HUMAN	Translation initiation factor IF-2 mitochondrial OS=Homo sapiens OX=9606 GN=MTIF2 PE=1 SV=2	0.939669	3.17E-05
Q96FV9	THOC1_HUMAN	THO complex subunit 1 OS=Homo sapiens OX=9606 GN=THOC1 PE=1 SV=1	0.939627	3.18E-05
P20337	RAB3B_HUMAN	Ras-related protein Rab-3B OS=Homo sapiens OX=9606 GN=RAB3B PE=1 SV=2	0.939425	3.18E-05
P28070	PSB4_HUMAN	Proteasome subunit beta type-4 OS=Homo sapiens OX=9606 GN=PSMB4 PE=1 SV=4	0.939124	2.30E-05
P46934	NEDD4_HUMAN	E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens OX=9606 GN=NEDD4 PE=1 SV=4	0.939029	2.14E-06
P52434	RPAB3_HUMAN	DNA-directed RNA polymerases I II and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H PE=1 SV=4	0.938091	3.22E-05
P63167	DYL1_HUMAN	Dynein light chain 1 cytoplasmic OS=Homo sapiens OX=9606 GN=DYNLL1 PE=1 SV=1	0.937669	3.17E-05
Q15750	TAB1_HUMAN	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens OX=9606 GN=TAB1 PE=1 SV=1	0.937393	7.67E-06
Q12802	AKP13_HUMAN	A-kinase anchor protein 13 OS=Homo sapiens OX=9606 GN=AKAP13 PE=1 SV=2	0.935951	3.35E-05
Q16881	TRXR1_HUMAN	Thioredoxin reductase 1 cytoplasmic OS=Homo sapiens OX=9606 GN=TXNRD1 PE=1 SV=3	0.935561	1.18E-04
Q9GZL7	WDR12_HUMAN	Ribosome biogenesis protein WDR12 OS=Homo sapiens OX=9606 GN=WDR12 PE=1 SV=2	0.935083	3.35E-05
P13010	XRCC5_HUMAN	X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1 SV=3	0.935061	7.33E-06
Q70J99	UN13D_HUMAN	Protein unc-13 homolog D OS=Homo sapiens OX=9606 GN=UNC13D PE=1 SV=1	0.934946	5.53E-04
Q9Y3C6	PPIL1_HUMAN	Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens OX=9606 GN=PPIL1 PE=1 SV=1	0.934905	3.38E-05
Q9UNH7	SNX6_HUMAN	Sorting nexin-6 OS=Homo sapiens OX=9606 GN=SNX6 PE=1 SV=1	0.934594	3.68E-05
O15264	MK13_HUMAN	Mitogen-activated protein kinase 13 OS=Homo sapiens OX=9606 GN=MAPK13 PE=1 SV=1	0.934254	3.58E-05
P50281	MMP14_HUMAN	Matrix metalloproteinase-14 OS=Homo sapiens OX=9606 GN=MMP14 PE=1 SV=3	0.93424	3.35E-05
O43396	TXNL1_HUMAN	Thioredoxin-like protein 1 OS=Homo sapiens OX=9606 GN=TXNL1 PE=1 SV=3	0.933182	3.38E-05
Q8N6T3	ARFG1_HUMAN	ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=ARFGAP1 PE=1 SV=2	0.933135	1.15E-05

P37235	HPCL1_HUMAN	Hippocalcin-like protein 1 OS=Homo sapiens OX=9606 GN=HPCL1 PE=1 SV=3	0.932886	8.24E-04
P82909	RT36_HUMAN	28S ribosomal protein S36 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS36 PE=1 SV=2	0.932388	3.46E-05
Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP] mitochondrial OS=Homo sapiens OX=9606 GN=PCK2 PE=1 SV=4	0.932286	0.001476
P08779	K1C16_HUMAN	Keratin type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4	0.932215	5.20E-05
Q9BW27	NUP85_HUMAN	Nuclear pore complex protein Nup85 OS=Homo sapiens OX=9606 GN=NUP85 PE=1 SV=1	0.93217	2.15E-06
Q9BTD8	RBM42_HUMAN	RNA-binding protein 42 OS=Homo sapiens OX=9606 GN=RBM42 PE=1 SV=1	0.931575	1.83E-05
Q16222	UAP1_HUMAN	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens OX=9606 GN=UAP1 PE=1 SV=3	0.930545	3.53E-05
Q8IZP0	ABI1_HUMAN	Abl interactor 1 OS=Homo sapiens OX=9606 GN=ABI1 PE=1 SV=4	0.930278	3.83E-05
Q9BQE5	APOL2_HUMAN	Apolipoprotein L2 OS=Homo sapiens OX=9606 GN=APOL2 PE=1 SV=1	0.929611	3.71E-05
P61289	PSME3_HUMAN	Proteasome activator complex subunit 3 OS=Homo sapiens OX=9606 GN=PSME3 PE=1 SV=1	0.928917	0.001806
O43847	NRDC_HUMAN	Nardilysin OS=Homo sapiens OX=9606 GN=NRDC PE=1 SV=3	0.928628	3.47E-04
Q01780	EXOSX_HUMAN	Exosome component 10 OS=Homo sapiens OX=9606 GN=EXOSC10 PE=1 SV=2	0.928447	4.76E-04
Q01650	LAT1_HUMAN	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens OX=9606 GN=SLC7A5 PE=1 SV=2	0.928187	3.83E-05
O43251	RFOX2_HUMAN	RNA binding protein fox-1 homolog 2 OS=Homo sapiens OX=9606 GN=RBOX2 PE=1 SV=3	0.927675	0.005383
P48147	PPCE_HUMAN	Prolyl endopeptidase OS=Homo sapiens OX=9606 GN=PREP PE=1 SV=2	0.927621	2.37E-05
Q86YS6	RAB43_HUMAN	Ras-related protein Rab-43 OS=Homo sapiens OX=9606 GN=RAB43 PE=1 SV=1	0.92753	3.71E-05
P18615	NELFE_HUMAN	Negative elongation factor E OS=Homo sapiens OX=9606 GN=NELFE PE=1 SV=3	0.926501	8.19E-05
Q5JPE7	NOMO2_HUMAN	Nodal modulator 2 OS=Homo sapiens OX=9606 GN=NOMO2 PE=1 SV=1	0.92619	2.88E-04
O15355	PPM1G_HUMAN	Protein phosphatase 1G OS=Homo sapiens OX=9606 GN=PPM1G PE=1 SV=1	0.925999	1.06E-04
P52292	IMA1_HUMAN	Importin subunit alpha-1 OS=Homo sapiens OX=9606 GN=KPNA2 PE=1 SV=1	0.925769	2.24E-05
Q9H074	PAIP1_HUMAN	Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens OX=9606 GN=PAIP1 PE=1 SV=1	0.925472	2.09E-04
O15344	TRI18_HUMAN	E3 ubiquitin-protein ligase Midline-1 OS=Homo sapiens OX=9606 GN=MID1 PE=1 SV=1	0.925469	3.80E-05
Q96CN7	ISOC1_HUMAN	Isochorismatase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ISOC1 PE=1 SV=3	0.925165	3.83E-05
P32004	L1CAM_HUMAN	Neural cell adhesion molecule L1 OS=Homo sapiens OX=9606 GN=L1CAM PE=1 SV=2	0.92508	3.74E-05
Q14232	EI2BA_HUMAN	Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens OX=9606 GN=EIF2B1 PE=1 SV=1	0.924754	4.01E-05
O00743	PPP6_HUMAN	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens OX=9606 GN=PPP6C PE=1 SV=1	0.924158	1.82E-05
Q13131	AAPK1_HUMAN	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens OX=9606 GN=PRKAA1 PE=1 SV=4	0.923996	1.45E-04
Q8TC07	TBC15_HUMAN	TBC1 domain family member 15 OS=Homo sapiens OX=9606 GN=TBC1D15 PE=1 SV=2	0.923691	1.17E-05
P49354	FNTA_HUMAN	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens OX=9606 GN=FNTA PE=1 SV=1	0.923552	2.61E-04
Q8TEX9	IPO4_HUMAN	Importin-4 OS=Homo sapiens OX=9606 GN=IPO4 PE=1 SV=2	0.923288	9.01E-04
Q08378	GOGA3_HUMAN	Golgin subfamily A member 3 OS=Homo sapiens OX=9606 GN=GOLGA3 PE=1 SV=2	0.923166	2.13E-05
Q16787	LAMA3_HUMAN	Laminin subunit alpha-3 OS=Homo sapiens OX=9606 GN=LAMA3 PE=1 SV=2	0.922807	0.00736
Q7Z3T8	ZFY16_HUMAN	Zinc finger FYVE domain-containing protein 16 OS=Homo sapiens OX=9606 GN=ZFYVE16 PE=1 SV=3	0.922447	4.15E-05
Q13045	FLII_HUMAN	Protein flightless-1 homolog OS=Homo sapiens OX=9606 GN=FLII PE=1 SV=2	0.922363	1.41E-04
Q8NBJ7	SUMF2_HUMAN	Inactive C-alpha-formylglycine-generating enzyme 2 OS=Homo sapiens OX=9606 GN=SUMF2 PE=1 SV=2	0.922156	7.75E-05
O95218	ZRAB2_HUMAN	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ZRANB2 PE=1 SV=2	0.922033	8.13E-05
O75116	ROCK2_HUMAN	Rho-associated protein kinase 2 OS=Homo sapiens OX=9606 GN=ROCK2 PE=1 SV=4	0.921443	4.19E-05
Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9 mitochondrial OS=Homo sapiens OX=9606 GN=ACOT9 PE=1 SV=2	0.921228	3.54E-05

Q86SF2	GALT7_HUMAN	N-acetylgalactosaminyltransferase 7 OS=Homo sapiens OX=9606 GN=GALNT7 PE=1 SV=1	0.920948	4.49E-05
P25788	PSA3_HUMAN	Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=2	0.92039	4.15E-05
P07942	LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens OX=9606 GN=LAMB1 PE=1 SV=2	0.91974	6.75E-05
P36551	HEM6_HUMAN	Oxygen-dependent coproporphyrinogen-III oxidase mitochondrial OS=Homo sapiens OX=9606 GN=CPOX PE=1 SV=3	0.919658	1.83E-04
P46778	RL21_HUMAN	60S ribosomal protein L21 OS=Homo sapiens OX=9606 GN=RPL21 PE=1 SV=2	0.918953	1.98E-05
Q14558	KPRA_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens OX=9606 GN=PRPSAP1 PE=1 SV=2	0.918919	9.50E-05
Q96PC5	MIA2_HUMAN	Melanoma inhibitory activity protein 2 OS=Homo sapiens OX=9606 GN=MIA2 PE=1 SV=4	0.918804	4.60E-05
O43592	XPOT_HUMAN	Exportin-T OS=Homo sapiens OX=9606 GN=XPOT PE=1 SV=2	0.918645	1.49E-04
Q02127	PYRD_HUMAN	Dihydroorotate dehydrogenase (quinone) mitochondrial OS=Homo sapiens OX=9606 GN=DHODH PE=1 SV=3	0.918432	0.009441
Q9Y5M8	SRPRB_HUMAN	Signal recognition particle receptor subunit beta OS=Homo sapiens OX=9606 GN=SRPRB PE=1 SV=3	0.918336	8.88E-04
Q13751	LAMB3_HUMAN	Laminin subunit beta-3 OS=Homo sapiens OX=9606 GN=LAMB3 PE=1 SV=1	0.917994	7.44E-05
O75410	TACC1_HUMAN	Transforming acidic coiled-coil-containing protein 1 OS=Homo sapiens OX=9606 GN=TACC1 PE=1 SV=2	0.917984	1.57E-04
Q9BUL8	PDC10_HUMAN	Programmed cell death protein 10 OS=Homo sapiens OX=9606 GN=PDCD10 PE=1 SV=1	0.91747	4.48E-05
Q9GZP4	PITH1_HUMAN	PITH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PITHD1 PE=1 SV=1	0.916992	4.46E-05
P23588	IF4B_HUMAN	Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=2	0.916766	1.29E-05
Q8WUD1	RAB2B_HUMAN	Ras-related protein Rab-2B OS=Homo sapiens OX=9606 GN=RAB2B PE=1 SV=1	0.916693	4.08E-04
P35637	FUS_HUMAN	RNA-binding protein FUS OS=Homo sapiens OX=9606 GN=FUS PE=1 SV=1	0.916549	1.65E-05
Q8TDD1	DDX54_HUMAN	ATP-dependent RNA helicase DDX54 OS=Homo sapiens OX=9606 GN=DDX54 PE=1 SV=2	0.915557	4.60E-05
Q7Z2Z2	EFL1_HUMAN	Elongation factor-like GTPase 1 OS=Homo sapiens OX=9606 GN=EFL1 PE=1 SV=2	0.91507	0.001348
Q9UNS2	CSN3_HUMAN	COP9 signalosome complex subunit 3 OS=Homo sapiens OX=9606 GN=COPS3 PE=1 SV=3	0.915025	7.33E-06
Q9UFC0	LRWD1_HUMAN	Leucine-rich repeat and WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=LRWD1 PE=1 SV=2	0.914908	4.56E-05
Q6ZXV5	TMTC3_HUMAN	Protein O-mannosyl-transferase TMTC3 OS=Homo sapiens OX=9606 GN=TMTC3 PE=1 SV=2	0.914783	4.48E-05
Q92597	NDRG1_HUMAN	Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1	0.91472	4.74E-05
P32320	CDD_HUMAN	Cytidine deaminase OS=Homo sapiens OX=9606 GN=CDA PE=1 SV=2	0.914418	4.62E-05
Q8N7H5	PAF1_HUMAN	RNA polymerase II-associated factor 1 homolog OS=Homo sapiens OX=9606 GN=PAF1 PE=1 SV=2	0.914187	5.72E-04
Q32P44	EMAL3_HUMAN	Echinoderm microtubule-associated protein-like 3 OS=Homo sapiens OX=9606 GN=EML3 PE=1 SV=1	0.913945	1.54E-05
Q96RQ3	MCCA_HUMAN	Methylcrotonoyl-CoA carboxylase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=MCCC1 PE=1 SV=3	0.913888	6.29E-05
Q9Y4X5	ARI1_HUMAN	E3 ubiquitin-protein ligase ARIH1 OS=Homo sapiens OX=9606 GN=ARIH1 PE=1 SV=2	0.913663	4.67E-05
P20020	AT2B1_HUMAN	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens OX=9606 GN=ATP2B1 PE=1 SV=4	0.913648	4.67E-05
Q96B54	ZN428_HUMAN	Zinc finger protein 428 OS=Homo sapiens OX=9606 GN=ZNF428 PE=1 SV=2	0.913585	4.62E-05
Q86XL3	ANKL2_HUMAN	Ankyrin repeat and LEM domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ANKLE2 PE=1 SV=4	0.913166	4.67E-05
Q6PGP7	TTC37_HUMAN	Tetratricopeptide repeat protein 37 OS=Homo sapiens OX=9606 GN=TTC37 PE=1 SV=1	0.913017	4.60E-05
Q01085	TIAR_HUMAN	Nucleolysin TIAR OS=Homo sapiens OX=9606 GN=TIAL1 PE=1 SV=1	0.9128	4.49E-05
Q15642	CIP4_HUMAN	Cdc42-interacting protein 4 OS=Homo sapiens OX=9606 GN=TRIP10 PE=1 SV=3	0.912257	3.78E-06
Q92538	GBF1_HUMAN	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=GBF1 PE=1 SV=2	0.91222	2.11E-04
Q9Y5X1	SNX9_HUMAN	Sorting nexin-9 OS=Homo sapiens OX=9606 GN=SNX9 PE=1 SV=1	0.912052	7.97E-05
Q96A33	CCD47_HUMAN	Coiled-coil domain-containing protein 47 OS=Homo sapiens OX=9606 GN=CCDC47 PE=1 SV=1	0.91184	1.06E-04
Q8WU90	ZC3HF_HUMAN	Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens OX=9606 GN=ZC3H15 PE=1 SV=1	0.911665	4.67E-05

Q9UBB4	ATX10_HUMAN	Ataxin-10 OS=Homo sapiens OX=9606 GN=ATXN10 PE=1 SV=1	0.911636	4.60E-05
Q9BQ52	RNZ2_HUMAN	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens OX=9606 GN=ELAC2 PE=1 SV=2	0.911296	1.31E-05
Q9BYG3	MK67I_HUMAN	MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens OX=9606 GN=NIFK PE=1 SV=1	0.90991	1.34E-04
Q5JTH9	RRP12_HUMAN	RRP12-like protein OS=Homo sapiens OX=9606 GN=RRP12 PE=1 SV=2	0.909749	5.01E-05
P42285	MTREX_HUMAN	Exosome RNA helicase MTR4 OS=Homo sapiens OX=9606 GN=MTREX PE=1 SV=3	0.909689	5.08E-04
Q8IWE2	NXP20_HUMAN	Protein NOXP20 OS=Homo sapiens OX=9606 GN=FAM114A1 PE=1 SV=2	0.909337	1.76E-04
Q9H9A6	LRC40_HUMAN	Leucine-rich repeat-containing protein 40 OS=Homo sapiens OX=9606 GN=LRRC40 PE=1 SV=1	0.908934	8.46E-05
O00469	PLOD2_HUMAN	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens OX=9606 GN=PLOD2 PE=1 SV=2	0.908836	1.29E-04
Q13951	PEBB_HUMAN	Core-binding factor subunit beta OS=Homo sapiens OX=9606 GN=CBFB PE=1 SV=2	0.908761	5.00E-05
Q14166	TTL12_HUMAN	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens OX=9606 GN=TTL12 PE=1 SV=2	0.907924	7.22E-06
O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=IDH3B PE=1 SV=2	0.907716	0.00374
P05120	PAI2_HUMAN	Plasminogen activator inhibitor 2 OS=Homo sapiens OX=9606 GN=SERPINB2 PE=1 SV=2	0.907629	9.69E-05
Q06124	PTN11_HUMAN	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 PE=1 SV=3	0.907405	3.29E-04
P32321	DCTD_HUMAN	Deoxycytidylate deaminase OS=Homo sapiens OX=9606 GN=DCTD PE=1 SV=2	0.907088	0.002435
Q15738	NSDHL_HUMAN	Sterol-4-alpha-carboxylate 3-dehydrogenase decarboxylating OS=Homo sapiens OX=9606 GN=NSDHL PE=1 SV=2	0.90653	1.01E-04
Q16625	OCLN_HUMAN	Occludin OS=Homo sapiens OX=9606 GN=OCLN PE=1 SV=1	0.906497	1.13E-04
Q9BYD6	RM01_HUMAN	39S ribosomal protein L1 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL1 PE=1 SV=2	0.906328	5.52E-05
Q7L1Q6	BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=BZW1 PE=1 SV=1	0.905574	2.94E-06
Q99543	DNJC2_HUMAN	DnaJ homolog subfamily C member 2 OS=Homo sapiens OX=9606 GN=DNAJC2 PE=1 SV=4	0.905394	3.26E-04
Q9HAV4	XPO5_HUMAN	Exportin-5 OS=Homo sapiens OX=9606 GN=XPO5 PE=1 SV=1	0.905052	3.80E-05
Q96ST3	SIN3A_HUMAN	Paired amphipathic helix protein Sin3a OS=Homo sapiens OX=9606 GN=SIN3A PE=1 SV=2	0.904964	5.45E-05
P42892	ECE1_HUMAN	Endothelin-converting enzyme 1 OS=Homo sapiens OX=9606 GN=ECE1 PE=1 SV=2	0.904885	1.67E-04
Q9Y4P1	ATG4B_HUMAN	Cysteine protease ATG4B OS=Homo sapiens OX=9606 GN=ATG4B PE=1 SV=2	0.904673	1.08E-04
Q9NUQ7	UFSP2_HUMAN	Ufm1-specific protease 2 OS=Homo sapiens OX=9606 GN=UFSP2 PE=1 SV=3	0.90446	5.42E-05
Q13795	ARFRP_HUMAN	ADP-ribosylation factor-related protein 1 OS=Homo sapiens OX=9606 GN=ARFRP1 PE=1 SV=1	0.90392	2.48E-04
Q9UJZ1	STML2_HUMAN	Stomatin-like protein 2 mitochondrial OS=Homo sapiens OX=9606 GN=STOML2 PE=1 SV=1	0.903722	6.77E-04
Q96GG9	DCN1_HUMAN	DCN1-like protein 1 OS=Homo sapiens OX=9606 GN=DCUN1D1 PE=1 SV=1	0.90354	5.84E-05
P61586	RHOA_HUMAN	Transforming protein RhoA OS=Homo sapiens OX=9606 GN=RHOA PE=1 SV=1	0.903124	5.67E-05
A8MXV4	NUD19_HUMAN	Nucleoside diphosphate-linked moiety X motif 19 OS=Homo sapiens OX=9606 GN=NUDT19 PE=1 SV=1	0.902984	5.67E-05
Q66K74	MAP1S_HUMAN	Microtubule-associated protein 1S OS=Homo sapiens OX=9606 GN=MAP1S PE=1 SV=2	0.902911	1.09E-04
P09110	THIK_HUMAN	3-ketoacyl-CoA thiolase peroxisomal OS=Homo sapiens OX=9606 GN=ACAA1 PE=1 SV=2	0.902615	5.84E-05
Q96J02	ITCH_HUMAN	E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens OX=9606 GN=ITCH PE=1 SV=2	0.90259	6.51E-05
O60684	IMA7_HUMAN	Importin subunit alpha-7 OS=Homo sapiens OX=9606 GN=KPNA6 PE=1 SV=1	0.902185	5.64E-06
Q9BTE1	DCTN5_HUMAN	Dynactin subunit 5 OS=Homo sapiens OX=9606 GN=DCTN5 PE=1 SV=1	0.902013	1.18E-04
Q9BTX1	NDC1_HUMAN	Nucleoporin NDC1 OS=Homo sapiens OX=9606 GN=NDC1 PE=1 SV=2	0.901979	5.90E-05
P14735	IDE_HUMAN	Insulin-degrading enzyme OS=Homo sapiens OX=9606 GN=IDE PE=1 SV=4	0.901886	6.01E-05
Q8WXF1	PSPC1_HUMAN	Paraspeckle component 1 OS=Homo sapiens OX=9606 GN=PSPC1 PE=1 SV=1	0.901691	0.001076
Q96KG9	SCYL1_HUMAN	N-terminal kinase-like protein OS=Homo sapiens OX=9606 GN=SCYL1 PE=1 SV=1	0.901574	1.34E-06

Q5TDH0	DDI2_HUMAN	Protein DDI1 homolog 2 OS=Homo sapiens OX=9606 GN=DDI2 PE=1 SV=1	0.901217	5.67E-05
Q8N766	EMC1_HUMAN	ER membrane protein complex subunit 1 OS=Homo sapiens OX=9606 GN=EMC1 PE=1 SV=1	0.901114	1.17E-04
Q9BR76	COR1B_HUMAN	Coronin-1B OS=Homo sapiens OX=9606 GN=CORO1B PE=1 SV=1	0.900931	2.81E-05
P46777	RL5_HUMAN	60S ribosomal protein L5 OS=Homo sapiens OX=9606 GN=RPL5 PE=1 SV=3	0.900691	2.60E-04
O76071	CIAO1_HUMAN	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens OX=9606 GN=CIAO1 PE=1 SV=1	0.900529	9.18E-05
P20290	BTF3_HUMAN	Transcription factor BTF3 OS=Homo sapiens OX=9606 GN=BTF3 PE=1 SV=1	0.900411	7.75E-05
O95865	DDAH2_HUMAN	N(G) N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens OX=9606 GN=DDAH2 PE=1 SV=1	0.900341	8.46E-05
P68400	CSK21_HUMAN	Casein kinase II subunit alpha OS=Homo sapiens OX=9606 GN=CSNK2A1 PE=1 SV=1	0.900087	1.99E-04
Q86XP3	DDX42_HUMAN	ATP-dependent RNA helicase DDX42 OS=Homo sapiens OX=9606 GN=DDX42 PE=1 SV=1	0.899896	8.63E-04
P60033	CD81_HUMAN	CD81 antigen OS=Homo sapiens OX=9606 GN=CD81 PE=1 SV=1	0.899643	5.67E-05
P61225	RAP2B_HUMAN	Ras-related protein Rap-2b OS=Homo sapiens OX=9606 GN=RAP2B PE=1 SV=1	0.899071	5.83E-05
P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=3	0.898938	1.30E-05
P61011	SRP54_HUMAN	Signal recognition particle 54 kDa protein OS=Homo sapiens OX=9606 GN=SRP54 PE=1 SV=1	0.898893	5.70E-06
Q8NFZ8	CADM4_HUMAN	Cell adhesion molecule 4 OS=Homo sapiens OX=9606 GN=CADM4 PE=1 SV=1	0.898807	6.41E-05
Q71RC2	LARP4_HUMAN	La-related protein 4 OS=Homo sapiens OX=9606 GN=LARP4 PE=1 SV=3	0.898763	7.75E-05
O43447	PPIH_HUMAN	Peptidyl-prolyl cis-trans isomerase H OS=Homo sapiens OX=9606 GN=PPIH PE=1 SV=1	0.898429	5.66E-05
P23368	MAOM_HUMAN	NAD-dependent malic enzyme mitochondrial OS=Homo sapiens OX=9606 GN=ME2 PE=1 SV=1	0.898419	6.13E-05
Q96HY6	DDR GK_HUMAN	DDR GK domain-containing protein 1 OS=Homo sapiens OX=9606 GN=DDR GK1 PE=1 SV=2	0.898305	2.85E-04
P56537	IF6_HUMAN	Eukaryotic translation initiation factor 6 OS=Homo sapiens OX=9606 GN=EIF6 PE=1 SV=1	0.898191	5.51E-04
Q9H9Q2	CSN7B_HUMAN	COP9 signalosome complex subunit 7b OS=Homo sapiens OX=9606 GN=COPS7B PE=1 SV=1	0.897022	5.69E-05
Q5H9R7	PP6R3_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=2	0.896616	8.31E-04
Q8IX12	CCAR1_HUMAN	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens OX=9606 GN=CCAR1 PE=1 SV=2	0.89642	2.99E-04
Q13523	PRP4B_HUMAN	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3	0.8962	6.37E-05
Q9UBS4	DJB11_HUMAN	DnaJ homolog subfamily B member 11 OS=Homo sapiens OX=9606 GN=DNAJB11 PE=1 SV=1	0.895852	3.03E-06
Q92692	NECT2_HUMAN	Nectin-2 OS=Homo sapiens OX=9606 GN=NECTIN2 PE=1 SV=1	0.895534	6.41E-05
P00749	UROK_HUMAN	Urokinase-type plasminogen activator OS=Homo sapiens OX=9606 GN=PLAU PE=1 SV=2	0.895411	7.02E-05
Q9Y2T3	GUAD_HUMAN	Guanine deaminase OS=Homo sapiens OX=9606 GN=GDA PE=1 SV=1	0.895395	6.41E-05
P50402	EMD_HUMAN	Emerin OS=Homo sapiens OX=9606 GN=EMD PE=1 SV=1	0.895204	7.97E-05
Q9Y4R8	TELO2_HUMAN	Telomere length regulation protein TEL2 homolog OS=Homo sapiens OX=9606 GN=TELO2 PE=1 SV=2	0.894835	6.56E-05
Q8IWZ3	ANKH1_HUMAN	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ANKHD1 PE=1 SV=1	0.894658	3.82E-04
Q8NCW5	NNRE_HUMAN	NAD(P)H-hydrate epimerase OS=Homo sapiens OX=9606 GN=NAXE PE=1 SV=2	0.894611	9.81E-05
Q7L5D6	GET4_HUMAN	Golgi to ER traffic protein 4 homolog OS=Homo sapiens OX=9606 GN=GET4 PE=1 SV=1	0.894556	6.51E-05
Q99961	SH3G1_HUMAN	Endophilin-A2 OS=Homo sapiens OX=9606 GN=SH3GL1 PE=1 SV=1	0.894205	3.65E-04
Q5UIP0	RIF1_HUMAN	Telomere-associated protein RIF1 OS=Homo sapiens OX=9606 GN=RIF1 PE=1 SV=2	0.893987	8.90E-04
Q96EK5	KBP_HUMAN	KIF-binding protein OS=Homo sapiens OX=9606 GN=KIFBP PE=1 SV=1	0.89376	5.55E-04
Q8N684	CPSF7_HUMAN	Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens OX=9606 GN=CPSF7 PE=1 SV=1	0.893452	2.44E-05
Q5GLZ8	HERC4_HUMAN	Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens OX=9606 GN=HERC4 PE=1 SV=1	0.893419	6.66E-05
P57737	CORO7_HUMAN	Coronin-7 OS=Homo sapiens OX=9606 GN=CORO7 PE=1 SV=2	0.892982	6.72E-05

P31949	S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens OX=9606 GN=S100A11 PE=1 SV=2	0.892831	7.41E-05
Q92665	RT31_HUMAN	28S ribosomal protein S31 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS31 PE=1 SV=3	0.892715	1.51E-04
P05187	PPB1_HUMAN	Alkaline phosphatase placental type OS=Homo sapiens OX=9606 GN=ALPP PE=1 SV=2	0.89269	0.001159
Q14651	PLS1_HUMAN	Plastin-1 OS=Homo sapiens OX=9606 GN=PLS1 PE=1 SV=2	0.892191	9.05E-05
Q969G3	SMCE1_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606 GN=SMARCE1 PE=1 SV=2	0.892171	1.02E-05
P49023	PAXI_HUMAN	Paxillin OS=Homo sapiens OX=9606 GN=PXN PE=1 SV=3	0.892085	0.005459
Q13136	LIPA1_HUMAN	Liprin-alpha-1 OS=Homo sapiens OX=9606 GN=PPFIA1 PE=1 SV=1	0.892047	0.001835
P19387	RPB3_HUMAN	DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens OX=9606 GN=POLR2C PE=1 SV=2	0.891827	3.85E-06
O75175	CNOT3_HUMAN	CCR4-NOT transcription complex subunit 3 OS=Homo sapiens OX=9606 GN=CNOT3 PE=1 SV=1	0.891276	6.77E-05
Q8TEM1	PO210_HUMAN	Nuclear pore membrane glycoprotein 210 OS=Homo sapiens OX=9606 GN=NUP210 PE=1 SV=3	0.891078	1.98E-05
P36543	VATE1_HUMAN	V-type proton ATPase subunit E 1 OS=Homo sapiens OX=9606 GN=ATP6V1E1 PE=1 SV=1	0.890722	6.75E-05
P0DP24	CALM2_HUMAN	Calmodulin-2 OS=Homo sapiens OX=9606 GN=CALM2 PE=1 SV=1	0.890404	1.54E-04
P0DP23	CALM1_HUMAN	Calmodulin-1 OS=Homo sapiens OX=9606 GN=CALM1 PE=1 SV=1	0.890404	1.54E-04
P0DP25	CALM3_HUMAN	Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1	0.890404	1.54E-04
O43681	ASNA_HUMAN	ATPase ASNA1 OS=Homo sapiens OX=9606 GN=ASNA1 PE=1 SV=2	0.890394	7.02E-05
Q13185	CBX3_HUMAN	Chromobox protein homolog 3 OS=Homo sapiens OX=9606 GN=CBX3 PE=1 SV=4	0.889206	5.79E-05
P53350	PLK1_HUMAN	Serine/threonine-protein kinase PLK1 OS=Homo sapiens OX=9606 GN=PLK1 PE=1 SV=1	0.889056	7.02E-05
P23921	RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens OX=9606 GN=RRM1 PE=1 SV=1	0.889026	1.81E-04
Q9UGP8	SEC63_HUMAN	Translocation protein SEC63 homolog OS=Homo sapiens OX=9606 GN=SEC63 PE=1 SV=2	0.887766	2.30E-04
Q86Y56	DAAF5_HUMAN	Dynein assembly factor 5 axonemal OS=Homo sapiens OX=9606 GN=DAAF5 PE=1 SV=4	0.887586	3.85E-05
Q99614	TTC1_HUMAN	Tetratricopeptide repeat protein 1 OS=Homo sapiens OX=9606 GN=TTC1 PE=1 SV=1	0.887106	1.15E-04
Q9UNW1	MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens OX=9606 GN=MINPP1 PE=1 SV=1	0.8866	7.44E-05
P43243	MATR3_HUMAN	Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=2	0.886343	4.68E-05
P51151	RAB9A_HUMAN	Ras-related protein Rab-9A OS=Homo sapiens OX=9606 GN=RAB9A PE=1 SV=1	0.886148	0.003258
Q9NXW2	DJB12_HUMAN	DnaJ homolog subfamily B member 12 OS=Homo sapiens OX=9606 GN=DNAJB12 PE=1 SV=5	0.885426	7.48E-05
P51114	FXR1_HUMAN	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens OX=9606 GN=FXR1 PE=1 SV=3	0.885288	0.005192
P61457	PHS_HUMAN	Pterin-4-alpha-carbinolamine dehydratase OS=Homo sapiens OX=9606 GN=PCBD1 PE=1 SV=2	0.88509	1.71E-04
Q07065	CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2	0.885064	9.50E-07
Q99986	VRK1_HUMAN	Serine/threonine-protein kinase VRK1 OS=Homo sapiens OX=9606 GN=VRK1 PE=1 SV=1	0.884344	7.75E-05
Q99590	SCAFB_HUMAN	Protein SCAF11 OS=Homo sapiens OX=9606 GN=SCAF11 PE=1 SV=2	0.884331	7.56E-05
P06865	HEXA_HUMAN	Beta-hexosaminidase subunit alpha OS=Homo sapiens OX=9606 GN=HEXA PE=1 SV=2	0.882746	7.75E-05
P39687	AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32A PE=1 SV=1	0.88243	7.75E-05
Q7Z4Q2	HEAT3_HUMAN	HEAT repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=HEATR3 PE=1 SV=2	0.88242	7.89E-05
Q96CS3	FAF2_HUMAN	FAS-associated factor 2 OS=Homo sapiens OX=9606 GN=FAF2 PE=1 SV=2	0.882385	9.29E-05
Q13190	STX5_HUMAN	Syntaxin-5 OS=Homo sapiens OX=9606 GN=STX5 PE=1 SV=2	0.881501	7.97E-05
P21589	5NTD_HUMAN	5'-nucleotidase OS=Homo sapiens OX=9606 GN=NT5E PE=1 SV=1	0.881403	1.50E-04
Q96EE3	SEH1_HUMAN	Nucleoporin SEH1 OS=Homo sapiens OX=9606 GN=SEH1L PE=1 SV=3	0.880563	8.19E-05
Q9H0S4	DDX47_HUMAN	Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens OX=9606 GN=DDX47 PE=1 SV=1	0.879844	1.09E-04
Q13162	PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapiens OX=9606 GN=PRDX4 PE=1 SV=1	0.879834	7.99E-05

O75400	PR40A_HUMAN	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens OX=9606 GN=PRPF40A PE=1 SV=2	0.879635	0.004857
Q99447	PCY2_HUMAN	Ethanolamine-phosphate cytidyltransferase OS=Homo sapiens OX=9606 GN=PCYT2 PE=1 SV=1	0.879343	7.97E-05
O75477	ERL1_HUMAN	Erlin-1 OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=2	0.879267	8.09E-05
Q9H944	MED20_HUMAN	Mediator of RNA polymerase II transcription subunit 20 OS=Homo sapiens OX=9606 GN=MED20 PE=1 SV=1	0.879064	8.11E-05
Q9Y508	RN114_HUMAN	E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens OX=9606 GN=RNF114 PE=1 SV=1	0.879042	8.39E-05
P28072	PSB6_HUMAN	Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 SV=4	0.878932	9.19E-05
P53582	MAP11_HUMAN	Methionine aminopeptidase 1 OS=Homo sapiens OX=9606 GN=METAP1 PE=1 SV=2	0.878864	6.27E-05
Q8TF05	PP4R1_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP4R1 PE=1 SV=1	0.878762	8.66E-05
P29083	T2EA_HUMAN	General transcription factor IIE subunit 1 OS=Homo sapiens OX=9606 GN=GTF2E1 PE=1 SV=2	0.878214	8.46E-05
Q96PU5	NED4L_HUMAN	E3 ubiquitin-protein ligase NEDD4-like OS=Homo sapiens OX=9606 GN=NEDD4L PE=1 SV=2	0.877338	8.39E-05
P60660	MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens OX=9606 GN=MYL6 PE=1 SV=2	0.877185	1.99E-04
Q15050	RRS1_HUMAN	Ribosome biogenesis regulatory protein homolog OS=Homo sapiens OX=9606 GN=RRS1 PE=1 SV=2	0.876729	1.63E-04
P20700	LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2	0.876391	2.10E-04
Q32P28	P3H1_HUMAN	Prolyl 3-hydroxylase 1 OS=Homo sapiens OX=9606 GN=P3H1 PE=1 SV=2	0.876033	0.002008
Q13641	TPBG_HUMAN	Trophoblast glycoprotein OS=Homo sapiens OX=9606 GN=TPBG PE=1 SV=1	0.876005	2.67E-04
P10155	RO60_HUMAN	60 kDa S5-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=RO60 PE=1 SV=2	0.875839	1.68E-04
Q5JTD0	TJAP1_HUMAN	Tight junction-associated protein 1 OS=Homo sapiens OX=9606 GN=TJAP1 PE=1 SV=1	0.875404	0.006642
P09758	TACD2_HUMAN	Tumor-associated calcium signal transducer 2 OS=Homo sapiens OX=9606 GN=TACSTD2 PE=1 SV=3	0.875387	6.90E-05
Q96QR8	PURB_HUMAN	Transcriptional activator protein Pur-beta OS=Homo sapiens OX=9606 GN=PURB PE=1 SV=3	0.875291	5.92E-04
Q5VV41	ARHGG_HUMAN	Rho guanine nucleotide exchange factor 16 OS=Homo sapiens OX=9606 GN=ARHGEF16 PE=1 SV=1	0.875245	6.74E-04
O75828	CBR3_HUMAN	Carbonyl reductase [NADPH] 3 OS=Homo sapiens OX=9606 GN=CBR3 PE=1 SV=3	0.875182	8.46E-05
Q96SB4	SRPK1_HUMAN	SRSF protein kinase 1 OS=Homo sapiens OX=9606 GN=SRPK1 PE=1 SV=2	0.875137	8.63E-05
Q9H9E3	COG4_HUMAN	Conserved oligomeric Golgi complex subunit 4 OS=Homo sapiens OX=9606 GN=COG4 PE=1 SV=3	0.874709	8.74E-05
P82933	RT09_HUMAN	28S ribosomal protein S9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS9 PE=1 SV=2	0.874415	3.42E-04
P33121	ACSL1_HUMAN	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens OX=9606 GN=ACSL1 PE=1 SV=1	0.874199	8.66E-05
Q9Y5K5	UCHL5_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens OX=9606 GN=UCHL5 PE=1 SV=3	0.873927	8.74E-05
Q92871	PMM1_HUMAN	Phosphomannomutase 1 OS=Homo sapiens OX=9606 GN=PMM1 PE=1 SV=2	0.873876	8.60E-05
P54709	AT1B3_HUMAN	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens OX=9606 GN=ATP1B3 PE=1 SV=1	0.873719	1.85E-04
Q12797	ASPH_HUMAN	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3	0.873532	8.65E-05
Q9Y5K8	VATD_HUMAN	V-type proton ATPase subunit D OS=Homo sapiens OX=9606 GN=ATP6V1D PE=1 SV=1	0.873436	8.66E-05
Q969X6	UTP4_HUMAN	U3 small nucleolar RNA-associated protein 4 homolog OS=Homo sapiens OX=9606 GN=UTP4 PE=1 SV=1	0.873394	3.63E-04
P08648	ITA5_HUMAN	Integrin alpha-5 OS=Homo sapiens OX=9606 GN=ITGA5 PE=1 SV=2	0.873296	9.13E-05
Q14966	ZNF638_HUMAN	Zinc finger protein 638 OS=Homo sapiens OX=9606 GN=ZNF638 PE=1 SV=2	0.872888	4.67E-04
Q9NRW7	VPS45_HUMAN	Vacuolar protein sorting-associated protein 45 OS=Homo sapiens OX=9606 GN=VPS45 PE=1 SV=1	0.872836	8.87E-05
Q01844	EWS_HUMAN	RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1	0.872702	8.74E-05
Q02809	PLOD1_HUMAN	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens OX=9606 GN=PLOD1 PE=1 SV=2	0.87261	1.02E-04
Q9BXJ9	NAA15_HUMAN	N-alpha-acetyltransferase 15 NatA auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA15 PE=1 SV=1	0.872412	1.02E-04
Q9NR12	PDLI7_HUMAN	PDZ and LIM domain protein 7 OS=Homo sapiens OX=9606 GN=PDLIM7 PE=1 SV=1	0.872133	7.13E-04

O75886	STAM2_HUMAN	Signal transducing adapter molecule 2 OS=Homo sapiens OX=9606 GN=STAM2 PE=1 SV=1	0.872067	8.65E-05
P16070	CD44_HUMAN	CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=3	0.872064	1.14E-04
Q13685	AAMP_HUMAN	Angio-associated migratory cell protein OS=Homo sapiens OX=9606 GN=AAMP PE=1 SV=2	0.872061	8.73E-05
P09486	SPRC_HUMAN	SPARC OS=Homo sapiens OX=9606 GN=SPARC PE=1 SV=1	0.871774	8.74E-05
P16435	NCPR_HUMAN	NADPH--cytochrome P450 reductase OS=Homo sapiens OX=9606 GN=POR PE=1 SV=2	0.871746	7.97E-05
P63261	ACTG_HUMAN	Actin cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1	0.871285	9.17E-05
P29353	SHC1_HUMAN	SHC-transforming protein 1 OS=Homo sapiens OX=9606 GN=SHC1 PE=1 SV=4	0.87109	8.63E-05
Q13619	CUL4A_HUMAN	Cullin-4A OS=Homo sapiens OX=9606 GN=CUL4A PE=1 SV=3	0.870814	4.63E-04
Q07812	BAX_HUMAN	Apoptosis regulator BAX OS=Homo sapiens OX=9606 GN=BAX PE=1 SV=1	0.870791	9.11E-05
P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=PDHB PE=1 SV=3	0.870596	4.63E-04
Q9BST9	RTKN_HUMAN	Rhotekin OS=Homo sapiens OX=9606 GN=RTKN PE=1 SV=2	0.870579	9.26E-05
Q99615	DNJC7_HUMAN	DnaJ homolog subfamily C member 7 OS=Homo sapiens OX=9606 GN=DNAJC7 PE=1 SV=2	0.870104	1.36E-04
Q9Y394	DHRS7_HUMAN	Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 PE=1 SV=1	0.869939	9.18E-05
Q04760	LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapiens OX=9606 GN=GLO1 PE=1 SV=4	0.869621	9.29E-05
Q9UJH6	SHPK_HUMAN	Sedoheptulokinase OS=Homo sapiens OX=9606 GN=SHPK PE=1 SV=3	0.869587	2.10E-04
O00567	NOP56_HUMAN	Nucleolar protein 56 OS=Homo sapiens OX=9606 GN=NOP56 PE=1 SV=4	0.869582	4.16E-04
Q15526	SURF1_HUMAN	Surfeit locus protein 1 OS=Homo sapiens OX=9606 GN=SURF1 PE=1 SV=1	0.869577	0.00625
Q9NT62	ATG3_HUMAN	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens OX=9606 GN=ATG3 PE=1 SV=1	0.868877	9.19E-05
Q9UPN9	TRI33_HUMAN	E3 ubiquitin-protein ligase TRIM33 OS=Homo sapiens OX=9606 GN=TRIM33 PE=1 SV=3	0.868105	9.69E-05
Q12788	TBL3_HUMAN	Transducin beta-like protein 3 OS=Homo sapiens OX=9606 GN=TBL3 PE=1 SV=2	0.86787	8.23E-05
P21399	ACOC_HUMAN	Cytoplasmic aconitate hydratase OS=Homo sapiens OX=9606 GN=ACO1 PE=1 SV=3	0.867741	4.83E-04
Q86VS8	HOOK3_HUMAN	Protein Hook homolog 3 OS=Homo sapiens OX=9606 GN=HOOK3 PE=1 SV=2	0.867713	8.46E-05
O00629	IMA3_HUMAN	Importin subunit alpha-3 OS=Homo sapiens OX=9606 GN=KPNA4 PE=1 SV=1	0.867406	1.46E-04
Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=OGDH PE=1 SV=3	0.867354	2.01E-08
Q3ZCW2	LEGL_HUMAN	Galectin-related protein OS=Homo sapiens OX=9606 GN=LGALS1 PE=1 SV=2	0.867324	0.005836
P63172	DYLT1_HUMAN	Dynein light chain Tctex-type 1 OS=Homo sapiens OX=9606 GN=DYNLT1 PE=1 SV=1	0.867286	1.31E-04
O14672	ADA10_HUMAN	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	0.866821	4.93E-04
Q9BZE1	RM37_HUMAN	39S ribosomal protein L37 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL37 PE=1 SV=2	0.866718	9.49E-05
Q14376	GALE_HUMAN	UDP-glucose 4-epimerase OS=Homo sapiens OX=9606 GN=GALE PE=1 SV=2	0.866634	5.45E-04
Q96E11	RRFM_HUMAN	Ribosome-recycling factor mitochondrial OS=Homo sapiens OX=9606 GN=MRRF PE=1 SV=1	0.86662	9.78E-05
Q9NYL9	TMOD3_HUMAN	Tropomodulin-3 OS=Homo sapiens OX=9606 GN=TMOD3 PE=1 SV=1	0.866517	2.83E-04
Q9NRG0	CHRC1_HUMAN	Chromatin accessibility complex protein 1 OS=Homo sapiens OX=9606 GN=CHRC1 PE=1 SV=1	0.86649	3.29E-04
P24752	THIL_HUMAN	Acetyl-CoA acetyltransferase mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 PE=1 SV=1	0.866115	6.60E-04
P09543	CN37_HUMAN	2' 3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens OX=9606 GN=CNP PE=1 SV=2	0.8658	2.39E-04
O94888	UBXN7_HUMAN	UBX domain-containing protein 7 OS=Homo sapiens OX=9606 GN=UBXN7 PE=1 SV=2	0.86555	1.50E-04
Q14690	RRP5_HUMAN	Protein RRP5 homolog OS=Homo sapiens OX=9606 GN=PDCD11 PE=1 SV=3	0.865141	1.85E-04
O95104	SCAF4_HUMAN	SR-related and CTD-associated factor 4 OS=Homo sapiens OX=9606 GN=SCAF4 PE=1 SV=3	0.864997	8.66E-05
Q8TE68	ES8L1_HUMAN	Epidermal growth factor receptor kinase substrate 8-like protein 1 OS=Homo sapiens OX=9606 GN=EPS8L1 PE=1 SV=3	0.864813	6.72E-05

Q96C36	P5CR2_HUMAN	Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens OX=9606 GN=PYCR2 PE=1 SV=1	0.864811	9.68E-05
Q9H2M9	RBGPR_HUMAN	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens OX=9606 GN=RAB3GAP2 PE=1 SV=1	0.864769	7.34E-04
Q15293	RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens OX=9606 GN=RCN1 PE=1 SV=1	0.864648	1.02E-04
Q86X29	LSR_HUMAN	Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens OX=9606 GN=LSR PE=1 SV=4	0.864345	5.00E-04
A1L0T0	ILVBL_HUMAN	Acetolactate synthase-like protein OS=Homo sapiens OX=9606 GN=ILVBL PE=1 SV=2	0.864213	1.63E-04
Q7RTV0	PHF5A_HUMAN	PHD finger-like domain-containing protein 5A OS=Homo sapiens OX=9606 GN=PHF5A PE=1 SV=1	0.863777	1.02E-04
O75694	NU155_HUMAN	Nuclear pore complex protein Nup155 OS=Homo sapiens OX=9606 GN=NUP155 PE=1 SV=1	0.863723	5.34E-04
Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosomes protein 3 OS=Homo sapiens OX=9606 GN=SMC3 PE=1 SV=2	0.863622	1.41E-04
Q86X55	CARM1_HUMAN	Histone-arginine methyltransferase CARM1 OS=Homo sapiens OX=9606 GN=CARM1 PE=1 SV=3	0.863353	1.06E-04
P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 PE=1 SV=2	0.863149	5.74E-05
Q9P2R7	SUCB1_HUMAN	Succinate--CoA ligase [ADP-forming] subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=SUCLA2 PE=1 SV=3	0.862496	1.07E-04
P24928	RPB1_HUMAN	DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens OX=9606 GN=POLR2A PE=1 SV=2	0.862496	6.04E-05
Q8IWS0	PHF6_HUMAN	PHD finger protein 6 OS=Homo sapiens OX=9606 GN=PHF6 PE=1 SV=1	0.862496	1.05E-04
Q9Y282	ERGI3_HUMAN	Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Homo sapiens OX=9606 GN=ERGIC3 PE=1 SV=1	0.862234	1.02E-04
Q8TBA6	GOGA5_HUMAN	Golgin subfamily A member 5 OS=Homo sapiens OX=9606 GN=GOLGA5 PE=1 SV=3	0.862225	1.31E-04
P31937	3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=HIBADH PE=1 SV=2	0.862121	4.60E-05
P52701	MSH6_HUMAN	DNA mismatch repair protein Msh6 OS=Homo sapiens OX=9606 GN=MSH6 PE=1 SV=2	0.862079	1.04E-04
Q15434	RBMS2_HUMAN	RNA-binding motif single-stranded-interacting protein 2 OS=Homo sapiens OX=9606 GN=RBMS2 PE=1 SV=1	0.861426	1.02E-04
P60983	GMFB_HUMAN	Glia maturation factor beta OS=Homo sapiens OX=9606 GN=GMFB PE=1 SV=2	0.861294	1.07E-04
Q9UI30	TR112_HUMAN	Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens OX=9606 GN=TRMT112 PE=1 SV=1	0.86101	2.41E-04
Q9Y5S9	RBM8A_HUMAN	RNA-binding protein 8A OS=Homo sapiens OX=9606 GN=RBM8A PE=1 SV=1	0.860749	0.00442
Q01628	IFM3_HUMAN	Interferon-induced transmembrane protein 3 OS=Homo sapiens OX=9606 GN=IFITM3 PE=1 SV=2	0.860718	1.07E-04
P04439	HLAA_HUMAN	HLA class I histocompatibility antigen A alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2	0.860484	1.07E-04
Q9UBF2	COPG2_HUMAN	Coatomer subunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 PE=1 SV=1	0.859915	1.15E-04
Q969V3	NCLN_HUMAN	Nicalin OS=Homo sapiens OX=9606 GN=NCLN PE=1 SV=2	0.859693	1.12E-04
Q5T6F2	UBAP2_HUMAN	Ubiquitin-associated protein 2 OS=Homo sapiens OX=9606 GN=UBAP2 PE=1 SV=1	0.859519	2.20E-04
Q96FX7	TRM61_HUMAN	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens OX=9606 GN=TRMT61A PE=1 SV=1	0.859418	1.07E-04
Q13177	PAK2_HUMAN	Serine/threonine-protein kinase PAK 2 OS=Homo sapiens OX=9606 GN=PAK2 PE=1 SV=3	0.859347	0.008486
P25789	PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1	0.858774	1.09E-04
P37198	NUP62_HUMAN	Nuclear pore glycoprotein p62 OS=Homo sapiens OX=9606 GN=NUP62 PE=1 SV=3	0.858528	8.82E-06
Q05639	EF1A2_HUMAN	Elongation factor 1-alpha 2 OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1	0.858514	2.21E-05
Q00796	DHSO_HUMAN	Sorbitol dehydrogenase OS=Homo sapiens OX=9606 GN=SORD PE=1 SV=4	0.858319	1.93E-04
Q96KR1	ZFR_HUMAN	Zinc finger RNA-binding protein OS=Homo sapiens OX=9606 GN=ZFR PE=1 SV=2	0.858217	1.16E-04
P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit mitochondrial OS=Homo sapiens OX=9606 GN=SDHA PE=1 SV=2	0.857981	9.13E-05
P53602	MVD1_HUMAN	Diphosphomevalonate decarboxylase OS=Homo sapiens OX=9606 GN=MVD PE=1 SV=1	0.85717	2.81E-04
P02649	APOE_HUMAN	Apolipoprotein E OS=Homo sapiens OX=9606 GN=APOE PE=1 SV=1	0.856653	2.25E-04
Q9H078	CLPB_HUMAN	Caseinolytic peptidase B protein homolog OS=Homo sapiens OX=9606 GN=CLPB PE=1 SV=1	0.856553	1.67E-04
P22223	CADH3_HUMAN	Cadherin-3 OS=Homo sapiens OX=9606 GN=CDH3 PE=1 SV=2	0.85633	1.62E-04

P04818	TYSY_HUMAN	Thymidylate synthase OS=Homo sapiens OX=9606 GN=TYMS PE=1 SV=3	0.856278	1.39E-04
Q13492	PICAL_HUMAN	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens OX=9606 GN=PICALM PE=1 SV=2	0.855934	3.35E-04
P16144	ITB4_HUMAN	Integrin beta-4 OS=Homo sapiens OX=9606 GN=ITGB4 PE=1 SV=5	0.855371	6.12E-05
P52735	VAV2_HUMAN	Guanine nucleotide exchange factor VAV2 OS=Homo sapiens OX=9606 GN=VAV2 PE=1 SV=2	0.855056	1.15E-04
P29590	PML_HUMAN	Protein PML OS=Homo sapiens OX=9606 GN=PML PE=1 SV=3	0.854995	3.86E-05
O60256	KPRB_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens OX=9606 GN=PRPSAP2 PE=1 SV=1	0.854724	1.24E-04
P42166	LAP2A_HUMAN	Lamina-associated polypeptide 2 isoform alpha OS=Homo sapiens OX=9606 GN=TMPO PE=1 SV=2	0.854717	2.41E-04
Q92615	LAR4B_HUMAN	La-related protein 4B OS=Homo sapiens OX=9606 GN=LARP4B PE=1 SV=3	0.854512	2.67E-04
O75190	DNJB6_HUMAN	DnaJ homolog subfamily B member 6 OS=Homo sapiens OX=9606 GN=DNAJB6 PE=1 SV=2	0.854462	1.17E-04
Q86Y82	STX12_HUMAN	Syntaxin-12 OS=Homo sapiens OX=9606 GN=STX12 PE=1 SV=1	0.854459	1.54E-04
P24539	AT5F1_HUMAN	ATP synthase F(0) complex subunit B1 mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PB PE=1 SV=2	0.854056	1.39E-04
Q92785	REQU_HUMAN	Zinc finger protein ubi-d4 OS=Homo sapiens OX=9606 GN=DPF2 PE=1 SV=2	0.853891	1.18E-04
P14927	QCR7_HUMAN	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens OX=9606 GN=UQCRB PE=1 SV=2	0.853799	1.18E-04
O43719	HTSF1_HUMAN	HIV Tat-specific factor 1 OS=Homo sapiens OX=9606 GN=HTATSF1 PE=1 SV=1	0.853743	1.17E-04
Q8N1P7	CRBG2_HUMAN	Beta/gamma crystallin domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CRYBG2 PE=2 SV=2	0.85356	1.17E-04
Q8WX92	NELFB_HUMAN	Negative elongation factor B OS=Homo sapiens OX=9606 GN=NELFB PE=1 SV=1	0.853532	1.20E-04
Q9Y520	PRC2C_HUMAN	Protein PRRC2C OS=Homo sapiens OX=9606 GN=PRRC2C PE=1 SV=4	0.853052	0.001107
Q9Y6M5	ZNT1_HUMAN	Zinc transporter 1 OS=Homo sapiens OX=9606 GN=SLC30A1 PE=1 SV=3	0.85272	1.21E-04
Q8N4X5	AF1L2_HUMAN	Actin filament-associated protein 1-like 2 OS=Homo sapiens OX=9606 GN=AFAP1L2 PE=1 SV=1	0.85271	5.27E-04
P10644	KAPO_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR1A PE=1 SV=1	0.852687	1.22E-04
Q9Y446	PKP3_HUMAN	Plakophilin-3 OS=Homo sapiens OX=9606 GN=PKP3 PE=1 SV=1	0.852333	4.27E-05
O00186	STXB3_HUMAN	Syntaxin-binding protein 3 OS=Homo sapiens OX=9606 GN=STXBP3 PE=1 SV=2	0.851642	1.20E-04
P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens OX=9606 GN=GNB2 PE=1 SV=3	0.851618	1.20E-04
O43583	DENR_HUMAN	Density-regulated protein OS=Homo sapiens OX=9606 GN=DENR PE=1 SV=2	0.851477	1.20E-04
P35914	HMGCL_HUMAN	Hydroxymethylglutaryl-CoA lyase mitochondrial OS=Homo sapiens OX=9606 GN=HMGCL PE=1 SV=2	0.850997	1.23E-04
P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens OX=9606 GN=PGAM1 PE=1 SV=2	0.850105	1.26E-04
P22061	PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens OX=9606 GN=PCMT1 PE=1 SV=4	0.850099	0.007738
Q09161	NCBP1_HUMAN	Nuclear cap-binding protein subunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1	0.849999	4.98E-04
Q9BU23	LMF2_HUMAN	Lipase maturation factor 2 OS=Homo sapiens OX=9606 GN=LMF2 PE=1 SV=2	0.84999	1.29E-04
O60568	PLOD3_HUMAN	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	0.849402	1.52E-04
P49407	ARRB1_HUMAN	Beta-arrestin-1 OS=Homo sapiens OX=9606 GN=ARRB1 PE=1 SV=2	0.849315	1.23E-04
Q14534	ERG1_HUMAN	Squalene monooxygenase OS=Homo sapiens OX=9606 GN=SQLE PE=1 SV=3	0.849232	0.007008
P36404	ARL2_HUMAN	ADP-ribosylation factor-like protein 2 OS=Homo sapiens OX=9606 GN=ARL2 PE=1 SV=4	0.848861	1.27E-04
P00491	PNPH_HUMAN	Purine nucleoside phosphorylase OS=Homo sapiens OX=9606 GN=PNP PE=1 SV=2	0.848804	1.91E-04
P08754	GNAI3_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha OS=Homo sapiens OX=9606 GN=GNAI3 PE=1 SV=3	0.848151	2.25E-04
Q00059	TFAM_HUMAN	Transcription factor A mitochondrial OS=Homo sapiens OX=9606 GN=TFAM PE=1 SV=1	0.848109	1.27E-04
P41743	KPCI_HUMAN	Protein kinase C iota type OS=Homo sapiens OX=9606 GN=PRKCI PE=1 SV=2	0.847802	1.28E-04
Q99598	TSNAX_HUMAN	Translin-associated protein X OS=Homo sapiens OX=9606 GN=TSNAX PE=1 SV=1	0.847748	4.63E-04

Q9Y6M1	IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2 PE=1 SV=2	0.847664	6.77E-05
O75832	PSD10_HUMAN	26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens OX=9606 GN=PSMD10 PE=1 SV=1	0.847543	1.31E-04
Q9UK41	VPS28_HUMAN	Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens OX=9606 GN=VPS28 PE=1 SV=1	0.847326	1.11E-04
O00273	DFFA_HUMAN	DNA fragmentation factor subunit alpha OS=Homo sapiens OX=9606 GN=DFFA PE=1 SV=1	0.847307	4.97E-04
P35611	ADDA_HUMAN	Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=2	0.846637	1.31E-04
P53041	PPP5_HUMAN	Serine/threonine-protein phosphatase 5 OS=Homo sapiens OX=9606 GN=PPP5C PE=1 SV=1	0.846017	1.50E-04
O14776	TCRG1_HUMAN	Transcription elongation regulator 1 OS=Homo sapiens OX=9606 GN=TCERG1 PE=1 SV=2	0.846013	1.32E-04
P30530	UFO_HUMAN	Tyrosine-protein kinase receptor UFO OS=Homo sapiens OX=9606 GN=AXL PE=1 SV=4	0.845797	9.33E-04
Q9NPD8	UBE2T_HUMAN	Ubiquitin-conjugating enzyme E2 T OS=Homo sapiens OX=9606 GN=UBE2T PE=1 SV=1	0.84545	1.26E-04
P46782	RS5_HUMAN	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=4	0.845294	9.49E-05
Q9UBC2	EP15R_HUMAN	Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens OX=9606 GN=EPS15L1 PE=1 SV=1	0.845134	1.21E-04
Q15398	DLGP5_HUMAN	Disks large-associated protein 5 OS=Homo sapiens OX=9606 GN=DLGAP5 PE=1 SV=2	0.844759	1.37E-04
P10412	H14_HUMAN	Histone H1.4 OS=Homo sapiens OX=9606 GN=H1-4 PE=1 SV=2	0.844722	1.39E-04
Q8TDN6	BRX1_HUMAN	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRX1 PE=1 SV=2	0.844562	2.55E-05
Q9Y3D7	TIM16_HUMAN	Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens OX=9606 GN=PAM16 PE=1 SV=2	0.844349	1.37E-04
O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens OX=9606 GN=ARPC3 PE=1 SV=3	0.844293	0.004664
Q02790	FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens OX=9606 GN=FKBP4 PE=1 SV=3	0.844255	3.07E-04
Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 PE=1 SV=1	0.843854	1.07E-04
Q01658	NC2B_HUMAN	Protein Dr1 OS=Homo sapiens OX=9606 GN=DR1 PE=1 SV=1	0.843748	1.47E-04
P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNP3 PE=1 SV=2	0.843679	1.09E-04
Q15785	TOM34_HUMAN	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens OX=9606 GN=TOMM34 PE=1 SV=2	0.843274	5.05E-05
Q9H223	EHD4_HUMAN	EH domain-containing protein 4 OS=Homo sapiens OX=9606 GN=EHD4 PE=1 SV=1	0.843179	6.63E-04
Q9C0C2	TB182_HUMAN	182 kDa tankyrase-1-binding protein OS=Homo sapiens OX=9606 GN=TNKS1BP1 PE=1 SV=4	0.842319	8.18E-04
P27707	DCK_HUMAN	Deoxycytidine kinase OS=Homo sapiens OX=9606 GN=DCK PE=1 SV=1	0.84184	1.43E-04
Q6WKZ4	RFIP1_HUMAN	Rab11 family-interacting protein 1 OS=Homo sapiens OX=9606 GN=RAB11FIP1 PE=1 SV=3	0.841824	2.88E-04
Q9BRR6	ADPGK_HUMAN	ADP-dependent glucokinase OS=Homo sapiens OX=9606 GN=ADPGK PE=1 SV=1	0.841738	1.46E-04
Q9H9J2	RM44_HUMAN	39S ribosomal protein L44 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL44 PE=1 SV=1	0.841424	1.44E-04
Q15334	L2GL1_HUMAN	Lethal(2) giant larvae protein homolog 1 OS=Homo sapiens OX=9606 GN=LLGL1 PE=1 SV=3	0.841346	1.46E-04
Q05048	CSTF1_HUMAN	Cleavage stimulation factor subunit 1 OS=Homo sapiens OX=9606 GN=CSTF1 PE=1 SV=1	0.84085	1.47E-04
P51553	IDH3G_HUMAN	Isocitrate dehydrogenase [NAD] subunit gamma mitochondrial OS=Homo sapiens OX=9606 GN=IDH3G PE=1 SV=1	0.840707	8.74E-05
A0AVT1	UBA6_HUMAN	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens OX=9606 GN=UBA6 PE=1 SV=1	0.840436	0.003361
P54725	RD23A_HUMAN	UV excision repair protein RAD23 homolog A OS=Homo sapiens OX=9606 GN=RAD23A PE=1 SV=1	0.840059	1.46E-04
P48449	ERG7_HUMAN	Lanosterol synthase OS=Homo sapiens OX=9606 GN=LSS PE=1 SV=1	0.839827	6.65E-04
O60313	OPA1_HUMAN	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=3	0.839717	1.34E-04
Q8WXI9	P66B_HUMAN	Transcriptional repressor p66-beta OS=Homo sapiens OX=9606 GN=GATAD2B PE=1 SV=1	0.839663	1.47E-04
P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI2 PE=1 SV=3	0.839658	3.85E-04
Q9P2J5	SYLC_HUMAN	Leucine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=LARS1 PE=1 SV=2	0.839443	2.10E-04
P62633	CNBP_HUMAN	Cellular nucleic acid-binding protein OS=Homo sapiens OX=9606 GN=CNBP PE=1 SV=1	0.839367	1.49E-04

Q9NYU2	UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens OX=9606 GN=UGGT1 PE=1 SV=3	0.839312	0.002197
Q99653	CHP1_HUMAN	Calcineurin B homologous protein 1 OS=Homo sapiens OX=9606 GN=CHP1 PE=1 SV=3	0.839167	1.23E-04
P62820	RAB1A_HUMAN	Ras-related protein Rab-1A OS=Homo sapiens OX=9606 GN=RAB1A PE=1 SV=3	0.839008	4.24E-04
P37268	FDFT_HUMAN	Squalene synthase OS=Homo sapiens OX=9606 GN=FDFT1 PE=1 SV=1	0.83881	1.66E-04
Q7Z739	YTHD3_HUMAN	YTH domain-containing family protein 3 OS=Homo sapiens OX=9606 GN=YTHDF3 PE=1 SV=1	0.83868	7.44E-05
Q9NR50	EI2BG_HUMAN	Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens OX=9606 GN=EIF2B3 PE=1 SV=1	0.83829	1.87E-04
Q13618	CUL3_HUMAN	Cullin-3 OS=Homo sapiens OX=9606 GN=CUL3 PE=1 SV=2	0.837864	1.98E-05
P62330	ARF6_HUMAN	ADP-ribosylation factor 6 OS=Homo sapiens OX=9606 GN=ARF6 PE=1 SV=2	0.837816	1.24E-04
P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1	0.837783	7.69E-04
O15382	BCAT2_HUMAN	Branched-chain-amino-acid aminotransferase mitochondrial OS=Homo sapiens OX=9606 GN=BCAT2 PE=1 SV=2	0.837469	1.52E-04
Q9UJU6	DBNL_HUMAN	Drebrin-like protein OS=Homo sapiens OX=9606 GN=DBNL PE=1 SV=1	0.836994	8.98E-05
Q9H3P7	GCP60_HUMAN	Golgi resident protein GCP60 OS=Homo sapiens OX=9606 GN=ACBD3 PE=1 SV=4	0.836783	1.35E-04
Q13907	IDI1_HUMAN	Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens OX=9606 GN=IDI1 PE=1 SV=2	0.836637	1.52E-04
Q9Y385	UB2J1_HUMAN	Ubiquitin-conjugating enzyme E2 J1 OS=Homo sapiens OX=9606 GN=UBE2J1 PE=1 SV=2	0.836623	0.005671
Q9BY32	ITPA_HUMAN	Inosine triphosphate pyrophosphatase OS=Homo sapiens OX=9606 GN=ITPA PE=1 SV=2	0.836143	2.18E-04
Q16512	PKN1_HUMAN	Serine/threonine-protein kinase N1 OS=Homo sapiens OX=9606 GN=PKN1 PE=1 SV=2	0.835798	1.55E-04
Q9UJX2	CDC23_HUMAN	Cell division cycle protein 23 homolog OS=Homo sapiens OX=9606 GN=CDC23 PE=1 SV=3	0.835497	1.57E-04
P09913	IFIT2_HUMAN	Interferon-induced protein with tetratricopeptide repeats 2 OS=Homo sapiens OX=9606 GN=IFIT2 PE=1 SV=1	0.835296	6.04E-05
O00505	IMA4_HUMAN	Importin subunit alpha-4 OS=Homo sapiens OX=9606 GN=KPNA3 PE=1 SV=2	0.835195	1.60E-04
O94905	ERLN2_HUMAN	Erlin-2 OS=Homo sapiens OX=9606 GN=ERLIN2 PE=1 SV=1	0.835151	1.83E-04
Q9H3U1	UN45A_HUMAN	Protein unc-45 homolog A OS=Homo sapiens OX=9606 GN=UNC45A PE=1 SV=1	0.834982	2.06E-04
Q9NTJ3	SMC4_HUMAN	Structural maintenance of chromosomes protein 4 OS=Homo sapiens OX=9606 GN=SMC4 PE=1 SV=2	0.834877	5.00E-05
Q8NBN3	TM87A_HUMAN	Transmembrane protein 87A OS=Homo sapiens OX=9606 GN=TMEM87A PE=1 SV=3	0.834875	1.54E-04
O15027	SC16A_HUMAN	Protein transport protein Sec16A OS=Homo sapiens OX=9606 GN=SEC16A PE=1 SV=4	0.834581	9.72E-04
P17480	UBF1_HUMAN	Nucleolar transcription factor 1 OS=Homo sapiens OX=9606 GN=UBTF PE=1 SV=1	0.834269	1.53E-04
Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1	0.834088	1.28E-04
Q9P265	DIP2B_HUMAN	Disco-interacting protein 2 homolog B OS=Homo sapiens OX=9606 GN=DIP2B PE=1 SV=3	0.833955	1.59E-04
Q86VM9	ZCH18_HUMAN	Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18 PE=1 SV=2	0.833309	1.55E-04
O00560	SDCB1_HUMAN	Syntenin-1 OS=Homo sapiens OX=9606 GN=SDCBP PE=1 SV=1	0.833246	4.50E-04
Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=5	0.833062	3.00E-04
Q8TEQ6	GEMI5_HUMAN	Gem-associated protein 5 OS=Homo sapiens OX=9606 GN=GEMIN5 PE=1 SV=3	0.832764	6.75E-05
Q16539	MK14_HUMAN	Mitogen-activated protein kinase 14 OS=Homo sapiens OX=9606 GN=MAPK14 PE=1 SV=3	0.832364	1.62E-04
Q9Y2U8	MAN1_HUMAN	Inner nuclear membrane protein Man1 OS=Homo sapiens OX=9606 GN=LEMD3 PE=1 SV=2	0.832354	6.41E-05
O60828	PQBP1_HUMAN	Polyglutamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PQBP1 PE=1 SV=1	0.832344	1.65E-04
Q8TED0	UTP15_HUMAN	U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens OX=9606 GN=UTP15 PE=1 SV=3	0.832329	1.63E-04
Q6NYC8	PPR18_HUMAN	Phostensin OS=Homo sapiens OX=9606 GN=PPP1R18 PE=1 SV=1	0.83229	1.62E-04
P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 OS=Homo sapiens OX=9606 GN=AK1 PE=1 SV=3	0.832211	2.88E-04
Q9H0W9	CK054_HUMAN	Ester hydrolase C11orf54 OS=Homo sapiens OX=9606 GN=C11orf54 PE=1 SV=1	0.831851	2.68E-04

O00217	NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS8 PE=1 SV=1	0.831803	1.66E-04
Q86Y39	NDUAB_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens OX=9606 GN=NDUFA11 PE=1 SV=3	0.831789	1.64E-04
P23229	ITA6_HUMAN	Integrin alpha-6 OS=Homo sapiens OX=9606 GN=ITGA6 PE=1 SV=5	0.831715	7.37E-04
Q9NUQ3	TXLNG_HUMAN	Gamma-taxilin OS=Homo sapiens OX=9606 GN=TXLNG PE=1 SV=2	0.831486	1.62E-04
Q14165	MLEC_HUMAN	Malectin OS=Homo sapiens OX=9606 GN=MLEC PE=1 SV=1	0.831478	2.97E-04
Q92973	TNPO1_HUMAN	Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 PE=1 SV=2	0.831002	1.67E-04
O00625	PIR_HUMAN	Pirin OS=Homo sapiens OX=9606 GN=PIR PE=1 SV=1	0.830971	1.69E-04
Q99805	TM9S2_HUMAN	Transmembrane 9 superfamily member 2 OS=Homo sapiens OX=9606 GN=TM9SF2 PE=1 SV=1	0.830953	2.49E-04
Q96RS6	NUDC1_HUMAN	NudC domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NUDC1 PE=1 SV=2	0.830226	0.001665
P11047	LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3	0.829888	3.85E-05
Q96FQ6	S10AG_HUMAN	Protein S100-A16 OS=Homo sapiens OX=9606 GN=S100A16 PE=1 SV=1	0.829872	1.72E-04
Q7L0Y3	TM10C_HUMAN	tRNA methyltransferase 10 homolog C OS=Homo sapiens OX=9606 GN=TRMT10C PE=1 SV=2	0.829618	6.41E-05
Q16718	NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=3	0.829159	5.27E-04
Q9Y376	CAB39_HUMAN	Calcium-binding protein 39 OS=Homo sapiens OX=9606 GN=CAB39 PE=1 SV=1	0.828802	0.001577
O15160	RPAC1_HUMAN	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens OX=9606 GN=POLR1C PE=1 SV=1	0.828612	1.46E-04
Q8NBX0	SCPDL_HUMAN	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens OX=9606 GN=SCCPDH PE=1 SV=1	0.828447	6.95E-04
P07339	CATD_HUMAN	Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1	0.828426	4.45E-04
P11498	PYC_HUMAN	Pyruvate carboxylase mitochondrial OS=Homo sapiens OX=9606 GN=PC PE=1 SV=2	0.828373	2.39E-04
O15498	YKT6_HUMAN	Synaptobrevin homolog YKT6 OS=Homo sapiens OX=9606 GN=YKT6 PE=1 SV=1	0.827866	1.69E-04
P78406	RAE1L_HUMAN	mRNA export factor OS=Homo sapiens OX=9606 GN=RAE1 PE=1 SV=1	0.827819	2.16E-04
Q9BYJ9	YTHD1_HUMAN	YTH domain-containing family protein 1 OS=Homo sapiens OX=9606 GN=YTHDF1 PE=1 SV=1	0.827705	1.62E-04
Q96BP3	PPWD1_HUMAN	Peptidylprolyl isomerase domain and WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=PPWD1 PE=1 SV=1	0.82741	1.73E-04
Q9HCS7	SYF1_HUMAN	Pre-mRNA-splicing factor SYF1 OS=Homo sapiens OX=9606 GN=XAB2 PE=1 SV=2	0.827405	1.67E-04
Q96JY6	PDLI2_HUMAN	PDZ and LIM domain protein 2 OS=Homo sapiens OX=9606 GN=PDLIM2 PE=1 SV=1	0.827262	2.83E-04
Q9UBQ7	GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens OX=9606 GN=GRHPR PE=1 SV=1	0.827163	6.35E-04
Q9GZT8	NIF3L_HUMAN	NIF3-like protein 1 OS=Homo sapiens OX=9606 GN=NIF3L1 PE=1 SV=2	0.826866	2.52E-04
O94855	SC24D_HUMAN	Protein transport protein Sec24D OS=Homo sapiens OX=9606 GN=SEC24D PE=1 SV=2	0.826609	2.22E-04
P05556	ITB1_HUMAN	Integrin beta-1 OS=Homo sapiens OX=9606 GN=ITGB1 PE=1 SV=2	0.826551	5.21E-04
Q8NBJ4	GOLM1_HUMAN	Golgi membrane protein 1 OS=Homo sapiens OX=9606 GN=GOLM1 PE=1 SV=1	0.826548	0.001127
Q86YP4	P66A_HUMAN	Transcriptional repressor p66-alpha OS=Homo sapiens OX=9606 GN=GATAD2A PE=1 SV=1	0.826312	8.31E-04
Q9Y263	PLAP_HUMAN	Phospholipase A-2-activating protein OS=Homo sapiens OX=9606 GN=PLAA PE=1 SV=2	0.826216	4.28E-05
Q99661	KIF2C_HUMAN	Kinesin-like protein KIF2C OS=Homo sapiens OX=9606 GN=KIF2C PE=1 SV=2	0.825992	1.77E-04
Q9NY93	DDX56_HUMAN	Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens OX=9606 GN=DDX56 PE=1 SV=1	0.825837	1.78E-04
Q9Y333	LSM2_HUMAN	U6 snRNA-associated Sm-like protein LSM2 OS=Homo sapiens OX=9606 GN=LSM2 PE=1 SV=1	0.82567	1.79E-04
Q9UQ80	PA2G4_HUMAN	Proliferation-associated protein 2G4 OS=Homo sapiens OX=9606 GN=PA2G4 PE=1 SV=3	0.82556	3.09E-04
P61966	AP1S1_HUMAN	AP-1 complex subunit sigma-1A OS=Homo sapiens OX=9606 GN=AP1S1 PE=1 SV=1	0.825321	1.77E-04
Q9NYF8	BCLF1_HUMAN	Bcl-2-associated transcription factor 1 OS=Homo sapiens OX=9606 GN=BCLAF1 PE=1 SV=2	0.825081	6.55E-04
O60271	JIP4_HUMAN	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens OX=9606 GN=SPAG9 PE=1 SV=4	0.825074	3.71E-04
Q9BYT8	NEUL_HUMAN	Neurolysin mitochondrial OS=Homo sapiens OX=9606 GN=NLN PE=1 SV=1	0.825074	6.99E-04

Q9UHD2	TBK1_HUMAN	Serine/threonine-protein kinase TBK1 OS=Homo sapiens OX=9606 GN=TBK1 PE=1 SV=1	0.825008	1.81E-04
Q9BSJ2	GCP2_HUMAN	Gamma-tubulin complex component 2 OS=Homo sapiens OX=9606 GN=TUBGCP2 PE=1 SV=2	0.824737	1.82E-04
P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=5	0.824698	1.77E-04
Q96TC7	RMD3_HUMAN	Regulator of microtubule dynamics protein 3 OS=Homo sapiens OX=9606 GN=RMDN3 PE=1 SV=2	0.824595	1.83E-04
O75915	PRAF3_HUMAN	PRA1 family protein 3 OS=Homo sapiens OX=9606 GN=ARL6IP5 PE=1 SV=1	0.824473	1.84E-04
P61923	COPZ1_HUMAN	Coatamer subunit zeta-1 OS=Homo sapiens OX=9606 GN=COPZ1 PE=1 SV=1	0.823931	0.0012
P61086	UBE2K_HUMAN	Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens OX=9606 GN=UBE2K PE=1 SV=3	0.823785	3.92E-04
Q52LJ0	FA98B_HUMAN	Protein FAM98B OS=Homo sapiens OX=9606 GN=FAM98B PE=1 SV=2	0.823374	1.83E-04
P29558	RBMS1_HUMAN	RNA-binding motif single-stranded-interacting protein 1 OS=Homo sapiens OX=9606 GN=RBMS1 PE=1 SV=3	0.823347	1.92E-04
Q6UN15	FIP1_HUMAN	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens OX=9606 GN=FIP1L1 PE=1 SV=1	0.823122	3.29E-04
P30153	2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=4	0.823122	3.65E-04
P04632	CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 SV=1	0.823122	9.87E-04
Q8TAQ2	SMRC2_HUMAN	SWI/SNF complex subunit SMARCC2 OS=Homo sapiens OX=9606 GN=SMARCC2 PE=1 SV=1	0.823046	9.28E-05
O00232	PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens OX=9606 GN=PSMD12 PE=1 SV=3	0.822934	4.79E-04
Q13564	ULA1_HUMAN	NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens OX=9606 GN=NAE1 PE=1 SV=1	0.82276	0.002044
P22033	MUTA_HUMAN	Methylmalonyl-CoA mutase mitochondrial OS=Homo sapiens OX=9606 GN=MMUT PE=1 SV=4	0.822687	1.87E-04
P22059	OSBP1_HUMAN	Oxysterol-binding protein 1 OS=Homo sapiens OX=9606 GN=OSBP PE=1 SV=1	0.822334	6.95E-04
Q15646	OASL_HUMAN	2'-5'-oligoadenylate synthase-like protein OS=Homo sapiens OX=9606 GN=OASL PE=1 SV=2	0.822097	1.87E-04
Q13443	ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens OX=9606 GN=ADAM9 PE=1 SV=1	0.822063	1.99E-04
P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 OS=Homo sapiens OX=9606 GN=PSMA1 PE=1 SV=1	0.821938	1.88E-04
O43399	TPD54_HUMAN	Tumor protein D54 OS=Homo sapiens OX=9606 GN=TPD52L2 PE=1 SV=2	0.821617	0.001901
P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606 GN=PRKAR2A PE=1 SV=2	0.821406	2.88E-04
P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5	0.821141	1.50E-04
Q8TC12	RDH11_HUMAN	Retinol dehydrogenase 11 OS=Homo sapiens OX=9606 GN=RDH11 PE=1 SV=2	0.820941	8.41E-04
P41236	IPP2_HUMAN	Protein phosphatase inhibitor 2 OS=Homo sapiens OX=9606 GN=PPP1R2 PE=1 SV=2	0.820935	1.96E-04
Q96P70	IPO9_HUMAN	Importin-9 OS=Homo sapiens OX=9606 GN=IPO9 PE=1 SV=3	0.820867	2.48E-04
Q15437	SC23B_HUMAN	Protein transport protein Sec23B OS=Homo sapiens OX=9606 GN=SEC23B PE=1 SV=2	0.820557	3.08E-04
P55081	MFAP1_HUMAN	Microfibrillar-associated protein 1 OS=Homo sapiens OX=9606 GN=MFAP1 PE=1 SV=2	0.820422	2.03E-04
Q9NQW7	XPP1_HUMAN	Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1 PE=1 SV=3	0.819846	2.19E-04
Q8N1G4	LRC47_HUMAN	Leucine-rich repeat-containing protein 47 OS=Homo sapiens OX=9606 GN=LRRC47 PE=1 SV=1	0.819562	7.41E-06
O00487	PSDE_HUMAN	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens OX=9606 GN=PSMD14 PE=1 SV=1	0.819512	2.10E-04
P49750	YLPM1_HUMAN	YLP motif-containing protein 1 OS=Homo sapiens OX=9606 GN=YLPM1 PE=1 SV=4	0.819392	1.94E-04
Q9UHB9	SRP68_HUMAN	Signal recognition particle subunit SRP68 OS=Homo sapiens OX=9606 GN=SRP68 PE=1 SV=2	0.819132	5.40E-04
Q9BWU0	NADAP_HUMAN	Kanadaptn OS=Homo sapiens OX=9606 GN=SLC4A1AP PE=1 SV=1	0.819002	6.19E-04
Q01130	SRSF2_HUMAN	Serine/arginine-rich splicing factor 2 OS=Homo sapiens OX=9606 GN=SRSF2 PE=1 SV=4	0.818718	2.10E-04
Q53GQ0	DHB12_HUMAN	Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens OX=9606 GN=HSD17B12 PE=1 SV=2	0.8186	4.19E-05
Q9HCY8	S10AE_HUMAN	Protein S100-A14 OS=Homo sapiens OX=9606 GN=S100A14 PE=1 SV=1	0.818516	2.05E-04

O14646	CHD1_HUMAN	Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=CHD1 PE=1 SV=2	0.818422	0.006599
O95433	AHSA1_HUMAN	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens OX=9606 GN=AHSA1 PE=1 SV=1	0.81835	7.39E-04
Q9Y696	CLIC4_HUMAN	Chloride intracellular channel protein 4 OS=Homo sapiens OX=9606 GN=CLIC4 PE=1 SV=4	0.818303	2.50E-04
Q96I20	PAWR_HUMAN	PRKC apoptosis WT1 regulator protein OS=Homo sapiens OX=9606 GN=PAWR PE=1 SV=1	0.818254	1.63E-04
O95757	HS74L_HUMAN	Heat shock 70 kDa protein 4L OS=Homo sapiens OX=9606 GN=HSPA4L PE=1 SV=3	0.817479	4.28E-05
Q12849	GRSF1_HUMAN	G-rich sequence factor 1 OS=Homo sapiens OX=9606 GN=GRSF1 PE=1 SV=3	0.817136	2.89E-04
Q9BXK5	B2L13_HUMAN	Bcl-2-like protein 13 OS=Homo sapiens OX=9606 GN=BCL2L13 PE=1 SV=1	0.817025	3.71E-04
Q9NRF9	DPOE3_HUMAN	DNA polymerase epsilon subunit 3 OS=Homo sapiens OX=9606 GN=POLE3 PE=1 SV=1	0.81697	2.03E-04
Q2TAY7	SMU1_HUMAN	WD40 repeat-containing protein SMU1 OS=Homo sapiens OX=9606 GN=SMU1 PE=1 SV=2	0.816729	9.81E-05
Q16186	ADRM1_HUMAN	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens OX=9606 GN=ADRM1 PE=1 SV=2	0.816725	1.13E-04
Q13033	STRN3_HUMAN	Striatin-3 OS=Homo sapiens OX=9606 GN=STRN3 PE=1 SV=3	0.816619	2.10E-04
Q13501	SQSTM_HUMAN	Sequestosome-1 OS=Homo sapiens OX=9606 GN=SQSTM1 PE=1 SV=1	0.815874	4.97E-04
Q14C86	GAPD1_HUMAN	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=GAPVD1 PE=1 SV=2	0.815696	0.002283
Q6NZY4	ZCHC8_HUMAN	Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens OX=9606 GN=ZCHC8 PE=1 SV=2	0.815519	4.38E-05
Q9Y3X0	CCDC9_HUMAN	Coiled-coil domain-containing protein 9 OS=Homo sapiens OX=9606 GN=CCDC9 PE=1 SV=1	0.81535	2.10E-04
O94906	PRP6_HUMAN	Pre-mRNA-processing factor 6 OS=Homo sapiens OX=9606 GN=PRPF6 PE=1 SV=1	0.815289	8.60E-05
Q9Y262	EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1	0.814885	4.04E-05
Q9P0V9	SEP10_HUMAN	Septin-10 OS=Homo sapiens OX=9606 GN=SEPTIN10 PE=1 SV=2	0.814758	2.06E-04
P42566	EPS15_HUMAN	Epidermal growth factor receptor substrate 15 OS=Homo sapiens OX=9606 GN=EPS15 PE=1 SV=2	0.814577	8.37E-05
P50851	LRBA_HUMAN	Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens OX=9606 GN=LRBA PE=1 SV=4	0.81455	0.002527
Q16850	CP51A_HUMAN	Lanosterol 14-alpha demethylase OS=Homo sapiens OX=9606 GN=CYP51A1 PE=1 SV=3	0.814343	8.19E-05
Q9BRJ6	CG050_HUMAN	Uncharacterized protein C7orf50 OS=Homo sapiens OX=9606 GN=C7orf50 PE=1 SV=1	0.814312	3.29E-04
Q9NPL8	TIDC1_HUMAN	Complex I assembly factor TIMMDC1 mitochondrial OS=Homo sapiens OX=9606 GN=TIMMDC1 PE=1 SV=2	0.814032	2.11E-04
P20073	ANXA7_HUMAN	Annexin A7 OS=Homo sapiens OX=9606 GN=ANXA7 PE=1 SV=3	0.813496	0.005647
P61204	ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=2	0.813457	1.65E-04
P84077	ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapiens OX=9606 GN=ARF1 PE=1 SV=2	0.813457	1.65E-04
Q96BJ3	AIDA_HUMAN	Axin interactor dorsalization-associated protein OS=Homo sapiens OX=9606 GN=AIDA PE=1 SV=1	0.813103	2.11E-04
O60231	DHX16_HUMAN	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 OS=Homo sapiens OX=9606 GN=DHX16 PE=1 SV=2	0.812721	2.14E-04
O15258	RER1_HUMAN	Protein RER1 OS=Homo sapiens OX=9606 GN=RER1 PE=1 SV=1	0.812422	2.06E-04
O15294	OGT1_HUMAN	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens OX=9606 GN=OGT PE=1 SV=3	0.812421	1.31E-05
P55265	DSRAD_HUMAN	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=4	0.812304	4.60E-05
P34932	HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=4	0.811842	0.007555
Q08209	PP2BA_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens OX=9606 GN=PPP3CA PE=1 SV=1	0.811733	2.17E-04
Q5RKV6	EXOS6_HUMAN	Exosome complex component MTR3 OS=Homo sapiens OX=9606 GN=EXOSC6 PE=1 SV=1	0.811584	2.28E-04
P30622	CLIP1_HUMAN	CAP-Gly domain-containing linker protein 1 OS=Homo sapiens OX=9606 GN=CLIP1 PE=1 SV=2	0.811351	0.001467
O95470	SGPL1_HUMAN	Sphingosine-1-phosphate lyase 1 OS=Homo sapiens OX=9606 GN=SGPL1 PE=1 SV=3	0.811174	0.00104
O95219	SNX4_HUMAN	Sorting nexin-4 OS=Homo sapiens OX=9606 GN=SNX4 PE=1 SV=1	0.811097	2.25E-04
P31146	COR1A_HUMAN	Coronin-1A OS=Homo sapiens OX=9606 GN=CORO1A PE=1 SV=4	0.810987	2.25E-04

P42785	PCP_HUMAN	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens OX=9606 GN=PRCP PE=1 SV=1	0.810661	0.002536
P22234	PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo sapiens OX=9606 GN=PAICS PE=1 SV=3	0.810312	6.12E-04
P36915	GNL1_HUMAN	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens OX=9606 GN=GNL1 PE=1 SV=2	0.809778	1.34E-04
Q96RP9	EFGM_HUMAN	Elongation factor G mitochondrial OS=Homo sapiens OX=9606 GN=GFM1 PE=1 SV=2	0.809766	2.59E-04
Q96AY3	FKB10_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens OX=9606 GN=FKBP10 PE=1 SV=1	0.8095	0.001461
Q14739	LBR_HUMAN	Delta(14)-sterol reductase LBR OS=Homo sapiens OX=9606 GN=LBR PE=1 SV=2	0.809456	2.17E-04
P37108	SRP14_HUMAN	Signal recognition particle 14 kDa protein OS=Homo sapiens OX=9606 GN=SRP14 PE=1 SV=2	0.809316	2.17E-04
P06756	ITAV_HUMAN	Integrin alpha-V OS=Homo sapiens OX=9606 GN=ITGAV PE=1 SV=2	0.808963	4.67E-05
P52888	THOP1_HUMAN	Thimet oligopeptidase OS=Homo sapiens OX=9606 GN=THOP1 PE=1 SV=2	0.808795	2.28E-04
Q12888	TP53B_HUMAN	TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2	0.808497	3.29E-04
Q5TFE4	NT5D1_HUMAN	5'-nucleotidase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NT5DC1 PE=1 SV=1	0.808392	2.46E-04
O60493	SNX3_HUMAN	Sorting nexin-3 OS=Homo sapiens OX=9606 GN=SNX3 PE=1 SV=3	0.808187	0.001433
Q13555	KCC2G_HUMAN	Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Homo sapiens OX=9606 GN=CAMK2G PE=1 SV=4	0.808018	1.82E-04
Q9UDY2	ZO2_HUMAN	Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=2	0.807813	0.002256
Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6	0.807798	0.003892
P48163	MAOX_HUMAN	NADP-dependent malic enzyme OS=Homo sapiens OX=9606 GN=ME1 PE=1 SV=1	0.807756	2.21E-04
Q14738	2A5D_HUMAN	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens OX=9606 GN=PPP2R5D PE=1 SV=1	0.807355	2.48E-04
Q9H8H0	NOL11_HUMAN	Nucleolar protein 11 OS=Homo sapiens OX=9606 GN=NOL11 PE=1 SV=1	0.807355	0.001092
Q8IYI6	EXOC8_HUMAN	Exocyst complex component 8 OS=Homo sapiens OX=9606 GN=EXOC8 PE=1 SV=2	0.807168	0.009867
O95373	IPO7_HUMAN	Importin-7 OS=Homo sapiens OX=9606 GN=IPO7 PE=1 SV=1	0.807161	9.90E-04
Q8N983	RM43_HUMAN	39S ribosomal protein L43 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL43 PE=1 SV=1	0.806925	2.37E-04
Q9Y512	SAM50_HUMAN	Sorting and assembly machinery component 50 homolog OS=Homo sapiens OX=9606 GN=SAMM50 PE=1 SV=3	0.806872	5.12E-04
P62917	RL8_HUMAN	60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=2	0.806571	2.32E-04
P61026	RAB10_HUMAN	Ras-related protein Rab-10 OS=Homo sapiens OX=9606 GN=RAB10 PE=1 SV=1	0.806483	0.00149
Q99439	CNN2_HUMAN	Calponin-2 OS=Homo sapiens OX=9606 GN=CNN2 PE=1 SV=4	0.806218	2.38E-04
P35241	RADI_HUMAN	Radixin OS=Homo sapiens OX=9606 GN=RDYX PE=1 SV=1	0.80612	2.10E-04
Q9UIA9	XPO7_HUMAN	Exportin-7 OS=Homo sapiens OX=9606 GN=XPO7 PE=1 SV=3	0.805832	0.001868
Q9Y295	DRG1_HUMAN	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=DRG1 PE=1 SV=1	0.8056	1.02E-04
P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1 PE=1 SV=3	0.805442	7.14E-04
O75489	NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS3 PE=1 SV=1	0.80525	1.77E-04
Q92888	ARHG1_HUMAN	Rho guanine nucleotide exchange factor 1 OS=Homo sapiens OX=9606 GN=ARHGEF1 PE=1 SV=2	0.804975	2.68E-04
Q8IVT2	MISP_HUMAN	Mitotic interactor and substrate of PLK1 OS=Homo sapiens OX=9606 GN=MISP PE=1 SV=1	0.80471	0.004027
Q9NYL4	FKB11_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP11 OS=Homo sapiens OX=9606 GN=FKBP11 PE=1 SV=1	0.804629	2.41E-04
Q5BKZ1	ZN326_HUMAN	DBIRD complex subunit ZNF326 OS=Homo sapiens OX=9606 GN=ZNF326 PE=1 SV=2	0.804604	1.71E-04
Q92896	GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sapiens OX=9606 GN=GLG1 PE=1 SV=2	0.804484	5.67E-05
P27797	CALR_HUMAN	Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1	0.80433	2.63E-04
P51452	DUS3_HUMAN	Dual specificity protein phosphatase 3 OS=Homo sapiens OX=9606 GN=DUSP3 PE=1 SV=1	0.804306	3.62E-04
P11802	CDK4_HUMAN	Cyclin-dependent kinase 4 OS=Homo sapiens OX=9606 GN=CDK4 PE=1 SV=2	0.804109	2.45E-04

P33176	KINH_HUMAN	Kinesin-1 heavy chain OS=Homo sapiens OX=9606 GN=KIF5B PE=1 SV=1	0.804019	4.06E-04
Q16630	CPSF6_HUMAN	Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens OX=9606 GN=CPSF6 PE=1 SV=2	0.803777	0.00199
Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a OS=Homo sapiens OX=9606 GN=SAR1A PE=1 SV=1	0.803692	0.00224
O60762	DPM1_HUMAN	Dolichol-phosphate mannosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=DPM1 PE=1 SV=1	0.803616	2.49E-04
P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein OS=Homo sapiens OX=9606 GN=VASP PE=1 SV=3	0.803131	2.99E-04
P19338	NUCL_HUMAN	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	0.802808	0.005449
A6NHR9	SMHD1_HUMAN	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SMCHD1 PE=1 SV=2	0.802481	1.50E-04
Q01581	HMCS1_HUMAN	Hydroxymethylglutaryl-CoA synthase cytoplasmic OS=Homo sapiens OX=9606 GN=HMGS1 PE=1 SV=2	0.802432	0.003191
Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 OS=Homo sapiens OX=9606 GN=ERP44 PE=1 SV=1	0.802354	4.33E-04
O00410	IPO5_HUMAN	Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4	0.802219	0.003348
Q9Y2Q3	GSTK1_HUMAN	Glutathione S-transferase kappa 1 OS=Homo sapiens OX=9606 GN=GSTK1 PE=1 SV=3	0.802018	9.73E-04
O43809	CPSF5_HUMAN	Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens OX=9606 GN=NUDT21 PE=1 SV=1	0.8019	7.75E-05
P62081	RS7_HUMAN	40S ribosomal protein S7 OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1	0.801748	2.46E-04
Q13586	STIM1_HUMAN	Stromal interaction molecule 1 OS=Homo sapiens OX=9606 GN=STIM1 PE=1 SV=3	0.801631	1.68E-04
Q9UJC3	HOOK1_HUMAN	Protein Hook homolog 1 OS=Homo sapiens OX=9606 GN=HOOK1 PE=1 SV=2	0.801316	2.75E-04
Q9Y6W5	WASF2_HUMAN	Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens OX=9606 GN=WASF2 PE=1 SV=3	0.801215	2.50E-04
Q99829	CPNE1_HUMAN	Copine-1 OS=Homo sapiens OX=9606 GN=CPNE1 PE=1 SV=1	0.801185	3.33E-04
P16278	BGAL_HUMAN	Beta-galactosidase OS=Homo sapiens OX=9606 GN=GLB1 PE=1 SV=2	0.800978	2.59E-04
P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSMC2 PE=1 SV=3	0.800946	3.13E-04
P43307	SSRA_HUMAN	Translocon-associated protein subunit alpha OS=Homo sapiens OX=9606 GN=SSR1 PE=1 SV=3	0.800753	2.63E-04
Q5K651	SAMD9_HUMAN	Sterile alpha motif domain-containing protein 9 OS=Homo sapiens OX=9606 GN=SAMD9 PE=1 SV=1	0.800672	2.67E-04
Q9Y3L3	3BP1_HUMAN	SH3 domain-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3BP1 PE=1 SV=3	0.800338	2.63E-04
P55957	BID_HUMAN	BH3-interacting domain death agonist OS=Homo sapiens OX=9606 GN=BID PE=1 SV=1	0.800256	2.59E-04
P21912	SDHB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit mitochondrial OS=Homo sapiens OX=9606 GN=SDHB PE=1 SV=3	0.800244	6.71E-04
O75439	MPPB_HUMAN	Mitochondrial-processing peptidase subunit beta OS=Homo sapiens OX=9606 GN=PMPCB PE=1 SV=2	0.800041	4.12E-04
Q9GZZ9	UBA5_HUMAN	Ubiquitin-like modifier-activating enzyme 5 OS=Homo sapiens OX=9606 GN=UBA5 PE=1 SV=1	0.800024	2.53E-04
Q3KQU3	MA7D1_HUMAN	MAP7 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MAP7D1 PE=1 SV=1	0.798991	5.61E-04
Q8TCA0	LRC20_HUMAN	Leucine-rich repeat-containing protein 20 OS=Homo sapiens OX=9606 GN=LRR20 PE=1 SV=1	0.798907	0.001299
P11310	ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ACADM PE=1 SV=1	0.798709	1.09E-04
Q14289	FAK2_HUMAN	Protein-tyrosine kinase 2-beta OS=Homo sapiens OX=9606 GN=PTK2B PE=1 SV=2	0.798112	2.70E-04
P17301	ITA2_HUMAN	Integrin alpha-2 OS=Homo sapiens OX=9606 GN=ITGA2 PE=1 SV=1	0.798092	0.001371
P00533	EGFR_HUMAN	Epidermal growth factor receptor OS=Homo sapiens OX=9606 GN=EGFR PE=1 SV=2	0.79802	8.98E-05
P46379	BAG6_HUMAN	Large proline-rich protein BAG6 OS=Homo sapiens OX=9606 GN=BAG6 PE=1 SV=2	0.797811	0.002023
Q13572	ITPK1_HUMAN	Inositol-tetrakisphosphate 1-kinase OS=Homo sapiens OX=9606 GN=ITPK1 PE=1 SV=2	0.797803	2.70E-04
P25490	TYY1_HUMAN	Transcriptional repressor protein YY1 OS=Homo sapiens OX=9606 GN=YY1 PE=1 SV=2	0.797714	2.80E-04
Q15165	PON2_HUMAN	Serum paraoxonase/arylesterase 2 OS=Homo sapiens OX=9606 GN=PON2 PE=1 SV=4	0.797433	2.82E-04
Q06210	GFPT1_HUMAN	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens OX=9606 GN=GFPT1 PE=1 SV=3	0.797278	0.001921

Q9HCE1	MOV10_HUMAN	Helicase MOV-10 OS=Homo sapiens OX=9606 GN=MOV10 PE=1 SV=2	0.797148	0.001643
Q96HE7	ERO1A_HUMAN	ERO1-like protein alpha OS=Homo sapiens OX=9606 GN=ERO1A PE=1 SV=2	0.79704	6.89E-04
Q93050	VPP1_HUMAN	V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens OX=9606 GN=ATP6V0A1 PE=1 SV=3	0.797013	2.75E-04
Q9NZ08	ERAP1_HUMAN	Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens OX=9606 GN=ERAP1 PE=1 SV=3	0.796566	2.43E-04
Q92485	ASM3B_HUMAN	Acid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens OX=9606 GN=SMPDL3B PE=1 SV=2	0.796467	2.88E-04
Q5T8P6	RBM26_HUMAN	RNA-binding protein 26 OS=Homo sapiens OX=9606 GN=RBM26 PE=1 SV=3	0.796387	1.87E-04
Q8N1F7	NUP93_HUMAN	Nuclear pore complex protein Nup93 OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=2	0.796344	4.35E-04
Q01469	FABP5_HUMAN	Fatty acid-binding protein 5 OS=Homo sapiens OX=9606 GN=FABP5 PE=1 SV=3	0.79628	2.77E-04
Q96B36	AKT51_HUMAN	Proline-rich AKT1 substrate 1 OS=Homo sapiens OX=9606 GN=AKT1S1 PE=1 SV=1	0.796213	0.002238
P17655	CAN2_HUMAN	Calpain-2 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN2 PE=1 SV=6	0.795611	3.55E-04
Q9NRX4	PHP14_HUMAN	14 kDa phosphohistidine phosphatase OS=Homo sapiens OX=9606 GN=PHPT1 PE=1 SV=1	0.795503	2.88E-04
Q27J81	INF2_HUMAN	Inverted formin-2 OS=Homo sapiens OX=9606 GN=INF2 PE=1 SV=2	0.795451	2.96E-04
Q969N2	PIGT_HUMAN	GPI transamidase component PIG-T OS=Homo sapiens OX=9606 GN=PIGT PE=1 SV=1	0.795341	2.90E-04
O60232	ZNRD2_HUMAN	Protein ZNRD2 OS=Homo sapiens OX=9606 GN=ZNRD2 PE=1 SV=1	0.794927	3.00E-04
Q5W111	SPRY7_HUMAN	SPRY domain-containing protein 7 OS=Homo sapiens OX=9606 GN=SPRYD7 PE=1 SV=2	0.794628	0.004454
Q8IYB5	SMAP1_HUMAN	Stromal membrane-associated protein 1 OS=Homo sapiens OX=9606 GN=SMAP1 PE=1 SV=2	0.794518	2.85E-04
Q9BZG1	RAB34_HUMAN	Ras-related protein Rab-34 OS=Homo sapiens OX=9606 GN=RAB34 PE=1 SV=1	0.793966	2.89E-04
Q6PI48	SYDM_HUMAN	Aspartate--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1	0.793946	0.007555
O75351	VPS4B_HUMAN	Vacuolar protein sorting-associated protein 4B OS=Homo sapiens OX=9606 GN=VPS4B PE=1 SV=2	0.793858	2.89E-04
P27816	MAP4_HUMAN	Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=3	0.793444	8.95E-04
O75940	SPF30_HUMAN	Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens OX=9606 GN=SMNDC1 PE=1 SV=1	0.793234	1.50E-04
Q8TCS8	PNPT1_HUMAN	Polyribonucleotide nucleotidyltransferase 1 mitochondrial OS=Homo sapiens OX=9606 GN=PNPT1 PE=1 SV=2	0.792794	4.85E-04
Q14789	GOLGB1_HUMAN	Golgin subfamily B member 1 OS=Homo sapiens OX=9606 GN=GOLGB1 PE=1 SV=2	0.792767	0.001084
Q96DB5	RMD1_HUMAN	Regulator of microtubule dynamics protein 1 OS=Homo sapiens OX=9606 GN=RMDN1 PE=1 SV=1	0.792739	0.002723
O75396	SEC22B_HUMAN	Vesicle-trafficking protein SEC22b OS=Homo sapiens OX=9606 GN=SEC22B PE=1 SV=4	0.792113	4.08E-04
Q08379	GOLGA2_HUMAN	Golgin subfamily A member 2 OS=Homo sapiens OX=9606 GN=GOLGA2 PE=1 SV=3	0.791899	4.46E-04
O14896	IRF6_HUMAN	Interferon regulatory factor 6 OS=Homo sapiens OX=9606 GN=IRF6 PE=1 SV=1	0.791865	3.10E-04
Q9NP81	SYSM_HUMAN	Serine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=SARS2 PE=1 SV=1	0.79106	2.98E-04
P78318	IGBP1_HUMAN	Immunoglobulin-binding protein 1 OS=Homo sapiens OX=9606 GN=IGBP1 PE=1 SV=1	0.791005	0.001795
Q16740	CLPP_HUMAN	ATP-dependent Clp protease proteolytic subunit mitochondrial OS=Homo sapiens OX=9606 GN=CLPP PE=1 SV=1	0.790547	3.09E-04
P32969	RL9_HUMAN	60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1	0.790194	3.09E-04
Q14157	UBP2L_HUMAN	Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 GN=UBAP2L PE=1 SV=2	0.790146	0.001773
Q9NR30	DDX21_HUMAN	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5	0.789914	3.13E-04
Q9Y679	AUP1_HUMAN	Ancient ubiquitous protein 1 OS=Homo sapiens OX=9606 GN=AUP1 PE=1 SV=2	0.789797	2.96E-04
P35251	RFC1_HUMAN	Replication factor C subunit 1 OS=Homo sapiens OX=9606 GN=RFC1 PE=1 SV=4	0.789713	1.31E-04
Q10570	CPSF1_HUMAN	Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens OX=9606 GN=CPSF1 PE=1 SV=2	0.789671	3.81E-04
Q9UBQ5	EIF3K_HUMAN	Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens OX=9606 GN=EIF3K PE=1 SV=1	0.789081	8.31E-04

Q14684	RRP1B_HUMAN	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens OX=9606 GN=RRP1B PE=1 SV=3	0.788642	6.04E-05
Q9NR45	SIAS_HUMAN	Sialic acid synthase OS=Homo sapiens OX=9606 GN=NANS PE=1 SV=2	0.78855	1.49E-04
P25325	THTM_HUMAN	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens OX=9606 GN=MPST PE=1 SV=3	0.788391	3.09E-04
Q9NRL3	STRN4_HUMAN	Striatin-4 OS=Homo sapiens OX=9606 GN=STRN4 PE=1 SV=2	0.78838	3.13E-04
P36871	PGM1_HUMAN	Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=3	0.788064	2.96E-04
Q92598	HS105_HUMAN	Heat shock protein 105 kDa OS=Homo sapiens OX=9606 GN=HSPH1 PE=1 SV=1	0.787839	5.51E-04
P62263	RS14_HUMAN	40S ribosomal protein S14 OS=Homo sapiens OX=9606 GN=RPS14 PE=1 SV=3	0.787669	3.34E-04
Q8NHV4	NEDD1_HUMAN	Protein NEDD1 OS=Homo sapiens OX=9606 GN=NEDD1 PE=1 SV=1	0.787279	0.001522
Q9Y3Z3	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens OX=9606 GN=SAMHD1 PE=1 SV=2	0.78722	8.71E-04
O94826	TOM70_HUMAN	Mitochondrial import receptor subunit TOM70 OS=Homo sapiens OX=9606 GN=TOMM70 PE=1 SV=1	0.787197	0.001499
Q86U38	NOP9_HUMAN	Nucleolar protein 9 OS=Homo sapiens OX=9606 GN=NOP9 PE=1 SV=1	0.787055	0.007287
O95833	CLIC3_HUMAN	Chloride intracellular channel protein 3 OS=Homo sapiens OX=9606 GN=CLIC3 PE=1 SV=2	0.786965	1.86E-04
Q10471	GALT2_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens OX=9606 GN=GALNT2 PE=1 SV=1	0.786866	4.52E-04
Q6P1L8	RM14_HUMAN	39S ribosomal protein L14 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL14 PE=1 SV=1	0.7868	3.35E-04
P43304	GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=GPDM2 PE=1 SV=3	0.786797	9.00E-06
Q9H2U2	IPYR2_HUMAN	Inorganic pyrophosphatase 2 mitochondrial OS=Homo sapiens OX=9606 GN=PPA2 PE=1 SV=2	0.786555	1.50E-04
P30519	HMOX2_HUMAN	Heme oxygenase 2 OS=Homo sapiens OX=9606 GN=HMOX2 PE=1 SV=2	0.785994	0.001204
P18754	RCC1_HUMAN	Regulator of chromosome condensation OS=Homo sapiens OX=9606 GN=RCC1 PE=1 SV=1	0.785975	1.66E-04
Q9UNZ2	NSFL1C_HUMAN	NSFL1 cofactor p47 OS=Homo sapiens OX=9606 GN=NSFL1C PE=1 SV=2	0.785674	0.001498
Q13505	MTX1_HUMAN	Metaxin-1 OS=Homo sapiens OX=9606 GN=MTX1 PE=1 SV=3	0.785556	5.65E-04
Q8NBF2	NHL2_HUMAN	NHL repeat-containing protein 2 OS=Homo sapiens OX=9606 GN=NHLRC2 PE=1 SV=1	0.785191	4.98E-04
O00425	IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP3 PE=1 SV=2	0.785154	3.13E-04
P54687	BCAT1_HUMAN	Branched-chain-amino-acid aminotransferase cytosolic OS=Homo sapiens OX=9606 GN=BCAT1 PE=1 SV=3	0.785143	2.21E-04
Q14203	DCTN1_HUMAN	Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=1 SV=3	0.784699	9.89E-04
Q14807	KIF22_HUMAN	Kinesin-like protein KIF22 OS=Homo sapiens OX=9606 GN=KIF22 PE=1 SV=5	0.784688	3.31E-04
Q9BY77	PDIP3_HUMAN	Polymerase delta-interacting protein 3 OS=Homo sapiens OX=9606 GN=POLDIP3 PE=1 SV=2	0.784391	2.41E-04
Q9NTX5	ECHD1_HUMAN	Ethylmalonyl-CoA decarboxylase OS=Homo sapiens OX=9606 GN=ECHDC1 PE=1 SV=2	0.784005	6.19E-04
P09525	ANXA4_HUMAN	Annexin A4 OS=Homo sapiens OX=9606 GN=ANXA4 PE=1 SV=4	0.783825	0.005159
Q92541	RTF1_HUMAN	RNA polymerase-associated protein RTF1 homolog OS=Homo sapiens OX=9606 GN=RTF1 PE=1 SV=4	0.783736	3.37E-04
Q14574	DSC3_HUMAN	Desmocollin-3 OS=Homo sapiens OX=9606 GN=DSC3 PE=1 SV=3	0.783726	3.33E-04
P78344	IF4G2_HUMAN	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1	0.783606	1.71E-04
Q15643	TRIPB_HUMAN	Thyroid receptor-interacting protein 11 OS=Homo sapiens OX=9606 GN=TRIP11 PE=1 SV=3	0.783508	0.004019
P53396	ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens OX=9606 GN=ACLY PE=1 SV=3	0.783385	8.19E-05
O00764	PDXK_HUMAN	Pyridoxal kinase OS=Homo sapiens OX=9606 GN=PDXK PE=1 SV=1	0.783139	0.00625
P04083	ANXA1_HUMAN	Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2	0.783099	1.92E-04
Q6IN85	P4R3A_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 3A OS=Homo sapiens OX=9606 GN=PPP4R3A PE=1 SV=1	0.782802	3.43E-04
Q9UBQ0	VPS29_HUMAN	Vacuolar protein sorting-associated protein 29 OS=Homo sapiens OX=9606 GN=VPS29 PE=1 SV=1	0.782643	0.00257
Q9UKL0	RCOR1_HUMAN	REST corepressor 1 OS=Homo sapiens OX=9606 GN=RCOR1 PE=1 SV=2	0.782579	3.35E-04
O75312	ZPR1_HUMAN	Zinc finger protein ZPR1 OS=Homo sapiens OX=9606 GN=ZPR1 PE=1 SV=1	0.782552	3.39E-04

O75223	GGCT_HUMAN	Gamma-glutamylcyclotransferase OS=Homo sapiens OX=9606 GN=GGCT PE=1 SV=1	0.782376	0.001139
Q6PD74	AAGAB_HUMAN	Alpha- and gamma-adaptin-binding protein p34 OS=Homo sapiens OX=9606 GN=AAGAB PE=1 SV=1	0.781477	5.46E-04
Q86UE4	LYRIC_HUMAN	Protein LYRIC OS=Homo sapiens OX=9606 GN=MTDH PE=1 SV=2	0.781331	0.001269
P29317	EPHA2_HUMAN	Ephrin type-A receptor 2 OS=Homo sapiens OX=9606 GN=EPHA2 PE=1 SV=2	0.78108	3.30E-04
O43291	SPIT2_HUMAN	Kunitz-type protease inhibitor 2 OS=Homo sapiens OX=9606 GN=SPINT2 PE=1 SV=2	0.78099	3.64E-04
Q9BV20	MTNA_HUMAN	Methylthioribose-1-phosphate isomerase OS=Homo sapiens OX=9606 GN=MRI1 PE=1 SV=1	0.780668	3.35E-04
Q9P0I2	EMC3_HUMAN	ER membrane protein complex subunit 3 OS=Homo sapiens OX=9606 GN=EMC3 PE=1 SV=3	0.780601	3.44E-04
Q14573	ITPR3_HUMAN	Inositol 1 4 5-trisphosphate receptor type 3 OS=Homo sapiens OX=9606 GN=ITPR3 PE=1 SV=2	0.780555	0.003045
P00367	DHE3_HUMAN	Glutamate dehydrogenase 1 mitochondrial OS=Homo sapiens OX=9606 GN=GLUD1 PE=1 SV=2	0.780484	2.93E-04
O75131	CPNE3_HUMAN	Copine-3 OS=Homo sapiens OX=9606 GN=CPNE3 PE=1 SV=1	0.78004	0.001421
Q96P48	ARAP1_HUMAN	Arf-GAP with Rho-GAP domain ANK repeat and PH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ARAP1 PE=1 SV=3	0.779742	3.57E-04
Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 OS=Homo sapiens OX=9606 GN=SCARB2 PE=1 SV=2	0.779734	3.52E-04
P43897	EFTS_HUMAN	Elongation factor Ts mitochondrial OS=Homo sapiens OX=9606 GN=TSFM PE=1 SV=2	0.779542	8.91E-05
Q13561	DCTN2_HUMAN	Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=4	0.779347	4.86E-04
P29144	TPP2_HUMAN	Tripeptidyl-peptidase 2 OS=Homo sapiens OX=9606 GN=TPP2 PE=1 SV=4	0.779329	4.04E-05
Q9Y4K1	CRBG1_HUMAN	Beta/gamma crystallin domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CRYBG1 PE=1 SV=3	0.779191	6.96E-04
P61758	PFD3_HUMAN	Prefoldin subunit 3 OS=Homo sapiens OX=9606 GN=VBP1 PE=1 SV=4	0.779113	3.62E-04
P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 OS=Homo sapiens OX=9606 GN=PDIA4 PE=1 SV=2	0.779091	0.001914
O60763	USO1_HUMAN	General vesicular transport factor p115 OS=Homo sapiens OX=9606 GN=USO1 PE=1 SV=2	0.778986	0.001143
Q8IV48	ERI1_HUMAN	3'-5' exoribonuclease 1 OS=Homo sapiens OX=9606 GN=ERI1 PE=1 SV=3	0.778967	3.62E-04
Q7L576	CYFP1_HUMAN	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1	0.778914	6.41E-05
Q9UHY7	ENOPH_HUMAN	Enolase-phosphatase E1 OS=Homo sapiens OX=9606 GN=ENOPH1 PE=1 SV=1	0.778327	7.34E-04
P30085	KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens OX=9606 GN=CMKP1 PE=1 SV=3	0.778192	0.004977
Q8NE71	ABCF1_HUMAN	ATP-binding cassette sub-family F member 1 OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 SV=2	0.778169	2.11E-04
Q9Y2B0	CNPY2_HUMAN	Protein canopy homolog 2 OS=Homo sapiens OX=9606 GN=CNPY2 PE=1 SV=1	0.777816	3.70E-04
P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=2	0.777608	0.001184
P38432	COIL_HUMAN	Coilin OS=Homo sapiens OX=9606 GN=COIL PE=1 SV=1	0.776739	1.07E-04
O43776	SYNC_HUMAN	Asparagine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=NARS1 PE=1 SV=1	0.776514	0.001893
O75340	PDCD6_HUMAN	Programmed cell death protein 6 OS=Homo sapiens OX=9606 GN=PDCD6 PE=1 SV=1	0.776507	1.09E-04
P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=2	0.776462	5.55E-04
Q6UB35	C1TM_HUMAN	Monofunctional C1-tetrahydrofolate synthase mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD1L PE=1 SV=1	0.776355	3.44E-04
Q13637	RAB32_HUMAN	Ras-related protein Rab-32 OS=Homo sapiens OX=9606 GN=RAB32 PE=1 SV=3	0.776176	3.79E-04
P39023	RL3_HUMAN	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2	0.776167	2.01E-04
O75381	PEX14_HUMAN	Peroxisomal membrane protein PEX14 OS=Homo sapiens OX=9606 GN=PEX14 PE=1 SV=1	0.776145	1.99E-04
Q9NQG5	RPR1B_HUMAN	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens OX=9606 GN=RPRD1B PE=1 SV=1	0.77594	0.00376
Q9NZZ3	CHMP5_HUMAN	Charged multivesicular body protein 5 OS=Homo sapiens OX=9606 GN=CHMP5 PE=1 SV=1	0.775248	3.78E-04
P49588	SYAC_HUMAN	Alanine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=AARS1 PE=1 SV=2	0.774773	0.003688

P51784	UBP11_HUMAN	Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens OX=9606 GN=USP11 PE=1 SV=3	0.774675	3.75E-04
Q96LJ7	DHRS1_HUMAN	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens OX=9606 GN=DHRS1 PE=1 SV=1	0.774255	3.89E-04
Q9Y2Z0	SGT1_HUMAN	Protein SGT1 homolog OS=Homo sapiens OX=9606 GN=SUGT1 PE=1 SV=3	0.774217	0.001185
P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Homo sapiens OX=9606 GN=PSMA2 PE=1 SV=2	0.774213	0.002129
Q16643	DREB_HUMAN	Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4	0.774211	4.99E-04
Q92900	RENT1_HUMAN	Regulator of nonsense transcripts 1 OS=Homo sapiens OX=9606 GN=UPF1 PE=1 SV=2	0.774111	9.13E-05
Q9Y673	ALG5_HUMAN	Dolichyl-phosphate beta-glucosyltransferase OS=Homo sapiens OX=9606 GN=ALG5 PE=1 SV=1	0.773802	3.85E-04
P05386	RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Homo sapiens OX=9606 GN=RPLP1 PE=1 SV=1	0.773749	3.99E-04
Q9NVH2	INT7_HUMAN	Integrator complex subunit 7 OS=Homo sapiens OX=9606 GN=INTS7 PE=1 SV=1	0.773611	4.36E-04
O00429	DNM1L_HUMAN	Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=2	0.773434	2.77E-04
Q8TCJ2	STT3B_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens OX=9606 GN=STT3B PE=1 SV=1	0.773248	3.92E-04
Q86SX6	GLRX5_HUMAN	Glutaredoxin-related protein 5 mitochondrial OS=Homo sapiens OX=9606 GN=GLRX5 PE=1 SV=2	0.772867	3.91E-04
Q04637	IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=4	0.772847	3.00E-04
Q9HD45	TM9S3_HUMAN	Transmembrane 9 superfamily member 3 OS=Homo sapiens OX=9606 GN=TM9SF3 PE=1 SV=2	0.772795	2.17E-04
P47914	RL29_HUMAN	60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=1 SV=2	0.772787	3.91E-04
P22102	PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens OX=9606 GN=GART PE=1 SV=1	0.77265	6.66E-04
Q9UID3	VPS51_HUMAN	Vacuolar protein sorting-associated protein 51 homolog OS=Homo sapiens OX=9606 GN=VPS51 PE=1 SV=2	0.77254	6.99E-04
Q15008	PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens OX=9606 GN=PSMD6 PE=1 SV=1	0.772453	8.93E-05
Q8WX93	PALLD_HUMAN	Palladin OS=Homo sapiens OX=9606 GN=PALLD PE=1 SV=3	0.772438	0.001555
O95155	UBE4B_HUMAN	Ubiquitin conjugation factor E4 B OS=Homo sapiens OX=9606 GN=UBE4B PE=1 SV=1	0.772056	7.56E-05
P10515	ODP2_HUMAN	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex mitochondrial OS=Homo sapiens OX=9606 GN=DLAT PE=1 SV=3	0.771862	6.51E-04
Q14566	MCM6_HUMAN	DNA replication licensing factor MCM6 OS=Homo sapiens OX=9606 GN=MCM6 PE=1 SV=1	0.771854	2.11E-04
P48047	ATPO_HUMAN	ATP synthase subunit O mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PO PE=1 SV=1	0.771792	0.001901
P06493	CDK1_HUMAN	Cyclin-dependent kinase 1 OS=Homo sapiens OX=9606 GN=CDK1 PE=1 SV=3	0.771731	7.98E-04
Q14126	DSG2_HUMAN	Desmoglein-2 OS=Homo sapiens OX=9606 GN=DSG2 PE=1 SV=2	0.771731	0.002212
Q8NFAQ	TOIP2_HUMAN	Torsin-1A-interacting protein 2 OS=Homo sapiens OX=9606 GN=TOR1AIP2 PE=1 SV=1	0.771629	0.000439
P23743	DGKA_HUMAN	Diacylglycerol kinase alpha OS=Homo sapiens OX=9606 GN=DGKA PE=1 SV=3	0.771454	7.39E-04
O14976	GAK_HUMAN	Cyclin-G-associated kinase OS=Homo sapiens OX=9606 GN=GAK PE=1 SV=2	0.771424	4.30E-04
Q9H4L5	OSBL3_HUMAN	Oxysterol-binding protein-related protein 3 OS=Homo sapiens OX=9606 GN=OSBPL3 PE=1 SV=1	0.771395	0.003045
P10586	PTPRF_HUMAN	Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens OX=9606 GN=PTPRF PE=1 SV=2	0.771235	1.82E-04
Q9NRR5	UBQL4_HUMAN	Ubiquilin-4 OS=Homo sapiens OX=9606 GN=UBQLN4 PE=1 SV=2	0.771102	4.08E-04
P13797	PLST_HUMAN	Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4	0.770957	7.45E-04
Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB PE=1 SV=4	0.770816	4.33E-04
P35221	CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1	0.770813	1.39E-04
Q13283	G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=1	0.770813	3.79E-04
O95084	PRS23_HUMAN	Serine protease 23 OS=Homo sapiens OX=9606 GN=PRSS23 PE=1 SV=1	0.770633	4.21E-04
Q9Y3E5	PTH2_HUMAN	Peptidyl-tRNA hydrolase 2 mitochondrial OS=Homo sapiens OX=9606 GN=PTRH2 PE=1 SV=1	0.770533	4.07E-04
Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase AK3 mitochondrial OS=Homo sapiens OX=9606 GN=AK3 PE=1 SV=4	0.770418	4.93E-04

Q13232	NDK3_HUMAN	Nucleoside diphosphate kinase 3 OS=Homo sapiens OX=9606 GN=NME3 PE=1 SV=2	0.770383	0.00208
Q07866	KLC1_HUMAN	Kinesin light chain 1 OS=Homo sapiens OX=9606 GN=KLC1 PE=1 SV=2	0.770213	5.55E-04
P13073	COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1 mitochondrial OS=Homo sapiens OX=9606 GN=COX41 PE=1 SV=1	0.770177	4.10E-04
P62834	RAP1A_HUMAN	Ras-related protein Rap-1A OS=Homo sapiens OX=9606 GN=RAP1A PE=1 SV=1	0.770062	3.99E-04
Q9UKF6	CPSF3_HUMAN	Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens OX=9606 GN=CPSF3 PE=1 SV=1	0.769943	4.07E-04
Q9NWS0	PIHD1_HUMAN	PIH1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PIHD1 PE=1 SV=1	0.769885	4.08E-04
Q9NZB2	F120A_HUMAN	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A PE=1 SV=2	0.769723	0.004696
P19784	CSK22_HUMAN	Casein kinase II subunit alpha' OS=Homo sapiens OX=9606 GN=CSNK2A2 PE=1 SV=1	0.769417	5.76E-04
Q96CM8	ACSF2_HUMAN	Medium-chain acyl-CoA ligase ACSF2 mitochondrial OS=Homo sapiens OX=9606 GN=ACSF2 PE=1 SV=2	0.769387	4.15E-04
P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha OS=Homo sapiens OX=9606 GN=GDI1 PE=1 SV=2	0.76882	3.31E-04
Q14696	MESD_HUMAN	LRP chaperone MESD OS=Homo sapiens OX=9606 GN=MESD PE=1 SV=2	0.768634	0.00405
P61160	ARP2_HUMAN	Actin-related protein 2 OS=Homo sapiens OX=9606 GN=ACTR2 PE=1 SV=1	0.768562	8.58E-04
Q9NQR4	NIT2_HUMAN	Omega-amidase NIT2 OS=Homo sapiens OX=9606 GN=NIT2 PE=1 SV=1	0.768436	1.25E-04
Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NONO PE=1 SV=4	0.768053	0.008475
Q8TE77	SSH3_HUMAN	Protein phosphatase Slingshot homolog 3 OS=Homo sapiens OX=9606 GN=SSH3 PE=1 SV=2	0.767682	2.00E-04
Q9BYD2	RM09_HUMAN	39S ribosomal protein L9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL9 PE=1 SV=2	0.767324	4.33E-04
P18827	SDC1_HUMAN	Syndecan-1 OS=Homo sapiens OX=9606 GN=SDC1 PE=1 SV=3	0.767302	4.81E-04
P63208	SKP1_HUMAN	S-phase kinase-associated protein 1 OS=Homo sapiens OX=9606 GN=SKP1 PE=1 SV=2	0.767184	0.003258
O95831	AIFM1_HUMAN	Apoptosis-inducing factor 1 mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 PE=1 SV=1	0.767035	6.36E-04
Q9Y5Z4	HEBP2_HUMAN	Heme-binding protein 2 OS=Homo sapiens OX=9606 GN=HEBP2 PE=1 SV=1	0.766701	9.90E-04
P18858	DNL1_HUMAN	DNA ligase 1 OS=Homo sapiens OX=9606 GN=LIG1 PE=1 SV=1	0.766669	2.38E-04
Q15019	SEPT2_HUMAN	Septin-2 OS=Homo sapiens OX=9606 GN=SEPTIN2 PE=1 SV=1	0.766569	0.001522
Q9BSJ8	ESYT1_HUMAN	Extended synaptotagmin-1 OS=Homo sapiens OX=9606 GN=ESYT1 PE=1 SV=1	0.766409	6.20E-04
Q03252	LMNB2_HUMAN	Lamin-B2 OS=Homo sapiens OX=9606 GN=LMNB2 PE=1 SV=4	0.766358	0.001269
Q8TDB8	GTR14_HUMAN	Solute carrier family 2 facilitated glucose transporter member 14 OS=Homo sapiens OX=9606 GN=SLC2A14 PE=1 SV=1	0.766018	8.44E-04
P11169	GTR3_HUMAN	Solute carrier family 2 facilitated glucose transporter member 3 OS=Homo sapiens OX=9606 GN=SLC2A3 PE=1 SV=1	0.766018	8.44E-04
O14929	HAT1_HUMAN	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens OX=9606 GN=HAT1 PE=1 SV=1	0.765794	1.95E-04
P50748	KNTC1_HUMAN	Kinetochore-associated protein 1 OS=Homo sapiens OX=9606 GN=KNTC1 PE=1 SV=1	0.765751	4.48E-04
P19404	NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFV2 PE=1 SV=2	0.765738	4.24E-04
Q9H2U1	DHX36_HUMAN	ATP-dependent DNA/RNA helicase DHX36 OS=Homo sapiens OX=9606 GN=DHX36 PE=1 SV=2	0.765635	4.50E-04
P00374	DYR_HUMAN	Dihydrofolate reductase OS=Homo sapiens OX=9606 GN=DHFR PE=1 SV=2	0.765535	3.92E-04
O43617	TPPC3_HUMAN	Trafficking protein particle complex subunit 3 OS=Homo sapiens OX=9606 GN=TRAPPC3 PE=1 SV=1	0.765438	4.40E-04
Q9H8T0	AKTIP_HUMAN	AKT-interacting protein OS=Homo sapiens OX=9606 GN=AKTIP PE=1 SV=1	0.765363	4.50E-04
Q08380	LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens OX=9606 GN=LGALS3BP PE=1 SV=1	0.765064	3.92E-04
P08708	RS17_HUMAN	40S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=2	0.765058	0.003097
Q04917	1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens OX=9606 GN=YWHAH PE=1 SV=4	0.76498	0.002028
P49841	GSK3B_HUMAN	Glycogen synthase kinase-3 beta OS=Homo sapiens OX=9606 GN=GSK3B PE=1 SV=2	0.764711	4.51E-04
Q92599	SEPT8_HUMAN	Septin-8 OS=Homo sapiens OX=9606 GN=SEPTIN8 PE=1 SV=4	0.764698	0.001093

Q9H2P0	ADNP_HUMAN	Activity-dependent neuroprotector homeobox protein OS=Homo sapiens OX=9606 GN=ADNP PE=1 SV=1	0.764437	4.50E-04
Q9NVD7	PARVA_HUMAN	Alpha-parvin OS=Homo sapiens OX=9606 GN=PARVA PE=1 SV=1	0.764027	4.47E-04
Q9UHD1	CHRD1_HUMAN	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CHORDC1 PE=1 SV=2	0.763851	2.31E-04
Q6PIU2	NCEH1_HUMAN	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens OX=9606 GN=NCEH1 PE=1 SV=3	0.76371	4.03E-04
Q9Y2K7	KDM2A_HUMAN	Lysine-specific demethylase 2A OS=Homo sapiens OX=9606 GN=KDM2A PE=1 SV=3	0.763657	4.64E-04
P40121	CAPG_HUMAN	Macrophage-capping protein OS=Homo sapiens OX=9606 GN=CAPG PE=1 SV=2	0.763409	8.34E-04
O43765	SGTA_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens OX=9606 GN=SGTA PE=1 SV=1	0.763265	4.66E-04
Q9Y2T2	AP3M1_HUMAN	AP-3 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP3M1 PE=1 SV=1	0.763174	2.83E-04
Q9ULZ3	ASC_HUMAN	Apoptosis-associated speck-like protein containing a CARD OS=Homo sapiens OX=9606 GN=PYCARD PE=1 SV=2	0.763045	2.19E-04
O00515	LAD1_HUMAN	Ladinin-1 OS=Homo sapiens OX=9606 GN=LAD1 PE=1 SV=2	0.763042	1.99E-04
O75934	SPF27_HUMAN	Pre-mRNA-splicing factor SPF27 OS=Homo sapiens OX=9606 GN=BCAS2 PE=1 SV=1	0.762917	8.23E-04
Q13868	EXOS2_HUMAN	Exosome complex component RRP4 OS=Homo sapiens OX=9606 GN=EXOSC2 PE=1 SV=2	0.762894	0.005211
Q13085	ACACA_HUMAN	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACACA PE=1 SV=2	0.762844	6.93E-05
P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B OS=Homo sapiens OX=9606 GN=RAD23B PE=1 SV=1	0.762671	7.62E-04
P06454	PTMA_HUMAN	Prothymosin alpha OS=Homo sapiens OX=9606 GN=PTMA PE=1 SV=2	0.762501	4.77E-04
Q9NS69	TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens OX=9606 GN=TOMM22 PE=1 SV=3	0.762501	0.001078
Q15819	UB2V2_HUMAN	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens OX=9606 GN=UBE2V2 PE=1 SV=4	0.762249	4.73E-04
Q15021	CND1_HUMAN	Condensin complex subunit 1 OS=Homo sapiens OX=9606 GN=NCAPD2 PE=1 SV=3	0.762143	1.80E-04
Q9BQE3	TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1	0.761942	4.13E-04
P49915	GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=GMPS PE=1 SV=1	0.761886	0.006498
Q3LXA3	TKFC_HUMAN	Triokinase/FMN cyclase OS=Homo sapiens OX=9606 GN=TKFC PE=1 SV=2	0.76184	6.41E-05
Q96FW1	OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 OS=Homo sapiens OX=9606 GN=OTUB1 PE=1 SV=2	0.76184	6.87E-04
Q01804	OTUD4_HUMAN	OTU domain-containing protein 4 OS=Homo sapiens OX=9606 GN=OTUD4 PE=1 SV=4	0.761789	0.001918
P36952	SPB5_HUMAN	Serpin B5 OS=Homo sapiens OX=9606 GN=SERPINB5 PE=1 SV=2	0.761611	3.29E-04
O00566	MPP10_HUMAN	U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens OX=9606 GN=MPHOSPH10 PE=1 SV=2	0.761481	4.71E-04
Q12996	CSTF3_HUMAN	Cleavage stimulation factor subunit 3 OS=Homo sapiens OX=9606 GN=CSTF3 PE=1 SV=1	0.761435	4.93E-04
Q99426	TBCB_HUMAN	Tubulin-folding cofactor B OS=Homo sapiens OX=9606 GN=TBCB PE=1 SV=2	0.761307	3.10E-04
P35579	MYH9_HUMAN	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4	0.761213	0.001204
Q9UBL3	ASH2L_HUMAN	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens OX=9606 GN=ASH2L PE=1 SV=1	0.761131	4.71E-04
O75165	DJC13_HUMAN	DnaJ homolog subfamily C member 13 OS=Homo sapiens OX=9606 GN=DNAJC13 PE=1 SV=5	0.761002	7.25E-04
P57764	GSDMD_HUMAN	Gasdermin-D OS=Homo sapiens OX=9606 GN=GSDMD PE=1 SV=1	0.76088	4.88E-04
Q9UPN7	PP6R1_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP6R1 PE=1 SV=5	0.760837	4.78E-04
P35580	MYH10_HUMAN	Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3	0.760425	1.24E-04
P12236	ADT3_HUMAN	ADP/ATP translocase 3 OS=Homo sapiens OX=9606 GN=SLC25A6 PE=1 SV=4	0.760195	0.001144
Q13404	UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens OX=9606 GN=UBE2V1 PE=1 SV=2	0.75998	4.88E-04
Q12972	PP1R8_HUMAN	Nuclear inhibitor of protein phosphatase 1 OS=Homo sapiens OX=9606 GN=PPP1R8 PE=1 SV=2	0.759522	4.61E-04
Q9NUQ9	FA49B_HUMAN	Protein FAM49B OS=Homo sapiens OX=9606 GN=FAM49B PE=1 SV=1	0.759406	2.57E-04
Q96D71	REPS1_HUMAN	RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens OX=9606 GN=REPS1 PE=1 SV=3	0.759258	4.78E-04

P23381	SYWC_HUMAN	Tryptophan--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=WARS1 PE=1 SV=2	0.759196	0.002113
O95782	AP2A1_HUMAN	AP-2 complex subunit alpha-1 OS=Homo sapiens OX=9606 GN=AP2A1 PE=1 SV=3	0.75909	0.001557
Q92817	EVPL_HUMAN	Envoplakin OS=Homo sapiens OX=9606 GN=EVPL PE=1 SV=3	0.758797	2.12E-04
Q92890	UFD1_HUMAN	Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Homo sapiens OX=9606 GN=UFD1 PE=1 SV=3	0.758772	6.54E-04
P48730	KC1D_HUMAN	Casein kinase I isoform delta OS=Homo sapiens OX=9606 GN=CSNK1D PE=1 SV=2	0.758707	4.93E-04
Q8WWC4	MAIP1_HUMAN	m-AAA protease-interacting protein 1 mitochondrial OS=Homo sapiens OX=9606 GN=MAIP1 PE=1 SV=1	0.758676	4.93E-04
P51153	RAB13_HUMAN	Ras-related protein Rab-13 OS=Homo sapiens OX=9606 GN=RAB13 PE=1 SV=1	0.758588	4.79E-04
Q15813	TBCE_HUMAN	Tubulin-specific chaperone E OS=Homo sapiens OX=9606 GN=TBCE PE=1 SV=1	0.758556	1.63E-04
Q9BW83	IFT27_HUMAN	Intraflagellar transport protein 27 homolog OS=Homo sapiens OX=9606 GN=IFT27 PE=1 SV=1	0.758547	4.92E-04
Q14839	CHD4_HUMAN	Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens OX=9606 GN=CHD4 PE=1 SV=2	0.758445	0.005105
Q9NZI8	IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=1 SV=2	0.758414	8.86E-04
O60869	EDF1_HUMAN	Endothelial differentiation-related factor 1 OS=Homo sapiens OX=9606 GN=EDF1 PE=1 SV=1	0.758321	1.79E-04
Q15382	RHEB_HUMAN	GTP-binding protein Rheb OS=Homo sapiens OX=9606 GN=RHEB PE=1 SV=1	0.757962	4.73E-04
P34897	GLYM_HUMAN	Serine hydroxymethyltransferase mitochondrial OS=Homo sapiens OX=9606 GN=SHMT2 PE=1 SV=3	0.757799	0.002259
Q2TAA2	IAH1_HUMAN	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens OX=9606 GN=IAH1 PE=1 SV=1	0.757627	4.93E-04
P17980	PRS6A_HUMAN	26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=3	0.757336	1.67E-04
Q01082	SPTB2_HUMAN	Spectrin beta chain non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTBN1 PE=1 SV=2	0.757278	0.001227
P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 PE=1 SV=1	0.757216	5.02E-04
O95425	SVIL_HUMAN	Supervillin OS=Homo sapiens OX=9606 GN=SVIL PE=1 SV=2	0.757097	5.66E-04
Q16851	UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens OX=9606 GN=UGP2 PE=1 SV=5	0.757044	8.45E-04
Q14315	FLNC_HUMAN	Filamin-C OS=Homo sapiens OX=9606 GN=FLNC PE=1 SV=3	0.756957	0.001228
P13647	K2C5_HUMAN	Keratin type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3	0.756828	4.98E-04
P04183	KITH_HUMAN	Thymidine kinase cytosolic OS=Homo sapiens OX=9606 GN=TK1 PE=1 SV=2	0.756729	2.49E-04
P05026	AT1B1_HUMAN	Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens OX=9606 GN=ATP1B1 PE=1 SV=1	0.756399	7.24E-04
Q96BW5	PTER_HUMAN	Phosphotriesterase-related protein OS=Homo sapiens OX=9606 GN=PTER PE=1 SV=1	0.756353	8.11E-05
Q13123	RED_HUMAN	Protein Red OS=Homo sapiens OX=9606 GN=IK PE=1 SV=3	0.756297	0.001076
P49327	FAS_HUMAN	Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3	0.756213	1.43E-04
Q6PKG0	LARP1_HUMAN	La-related protein 1 OS=Homo sapiens OX=9606 GN=LARP1 PE=1 SV=2	0.756027	1.12E-05
Q92882	OSTF1_HUMAN	Osteoclast-stimulating factor 1 OS=Homo sapiens OX=9606 GN=OSTF1 PE=1 SV=2	0.755963	4.11E-04
P11233	RALA_HUMAN	Ras-related protein Ral-A OS=Homo sapiens OX=9606 GN=RALA PE=1 SV=1	0.75586	5.01E-04
P50416	CPT1A_HUMAN	Carnitine O-palmitoyltransferase 1 liver isoform OS=Homo sapiens OX=9606 GN=CPT1A PE=1 SV=2	0.755819	1.83E-04
Q96AT9	RPE_HUMAN	Ribulose-phosphate 3-epimerase OS=Homo sapiens OX=9606 GN=RPE PE=1 SV=1	0.755647	5.04E-04
O95396	MOCS3_HUMAN	Adenylyltransferase and sulfurtransferase MOCS3 OS=Homo sapiens OX=9606 GN=MOCS3 PE=1 SV=1	0.755644	5.10E-04
Q08J23	NSUN2_HUMAN	RNA cytosine C(5)-methyltransferase NSUN2 OS=Homo sapiens OX=9606 GN=NSUN2 PE=1 SV=2	0.755459	7.39E-04
P20340	RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens OX=9606 GN=RAB6A PE=1 SV=3	0.755378	0.006018
Q9NXV6	CARF_HUMAN	CDKN2A-interacting protein OS=Homo sapiens OX=9606 GN=CDKN2AIP PE=1 SV=3	0.755336	5.44E-04
P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=4	0.755253	0.001547
Q9GZS3	WDR61_HUMAN	WD repeat-containing protein 61 OS=Homo sapiens OX=9606 GN=WDR61 PE=1 SV=1	0.755142	3.96E-04

Q13126	MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase OS=Homo sapiens OX=9606 GN=MTAP PE=1 SV=2	0.755031	5.18E-04
P0DMM9	ST1A3_HUMAN	Sulfotransferase 1A3 OS=Homo sapiens OX=9606 GN=SULT1A3 PE=1 SV=1	0.754962	4.98E-04
P0DMM0	ST1A4_HUMAN	Sulfotransferase 1A4 OS=Homo sapiens OX=9606 GN=SULT1A4 PE=1 SV=1	0.754962	4.98E-04
P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III OS=Homo sapiens OX=9606 GN=EIF4A3 PE=1 SV=4	0.754939	4.48E-04
Q8IWA5	CTL2_HUMAN	Choline transporter-like protein 2 OS=Homo sapiens OX=9606 GN=SLC44A2 PE=1 SV=3	0.754888	4.93E-04
Q07157	ZO1_HUMAN	Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=3	0.754888	6.81E-04
Q04206	TF65_HUMAN	Transcription factor p65 OS=Homo sapiens OX=9606 GN=RELA PE=1 SV=2	0.754348	5.64E-04
Q14435	GALT3_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 3 OS=Homo sapiens OX=9606 GN=GALNT3 PE=1 SV=2	0.754149	5.04E-04
Q86V81	THOC4_HUMAN	THO complex subunit 4 OS=Homo sapiens OX=9606 GN=ALYREF PE=1 SV=3	0.75411	5.09E-04
Q9NUJ1	ABHDA_HUMAN	Mycophenolic acid acyl-glucuronide esterase mitochondrial OS=Homo sapiens OX=9606 GN=ABHD10 PE=1 SV=1	0.753956	8.89E-04
O60306	AQR_HUMAN	RNA helicase aquarius OS=Homo sapiens OX=9606 GN=AQR PE=1 SV=4	0.753706	5.20E-04
O15212	PFD6_HUMAN	Prefoldin subunit 6 OS=Homo sapiens OX=9606 GN=PFDN6 PE=1 SV=1	0.753603	1.88E-04
Q12965	MYO1E_HUMAN	Unconventional myosin-le OS=Homo sapiens OX=9606 GN=MYO1E PE=1 SV=2	0.753304	7.34E-04
Q7L014	DDX46_HUMAN	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens OX=9606 GN=DDX46 PE=1 SV=2	0.753238	3.35E-04
Q9BXS6	NUSAP_HUMAN	Nucleolar and spindle-associated protein 1 OS=Homo sapiens OX=9606 GN=NUSAP1 PE=1 SV=1	0.753007	5.08E-04
O00442	RTCA_HUMAN	RNA 3'-terminal phosphate cyclase OS=Homo sapiens OX=9606 GN=RTCA PE=1 SV=1	0.752907	6.87E-04
P61201	CSN2_HUMAN	COP9 signalosome complex subunit 2 OS=Homo sapiens OX=9606 GN=COPS2 PE=1 SV=1	0.752857	1.90E-04
O75718	CRTAP_HUMAN	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	0.752808	5.42E-04
P30050	RL12_HUMAN	60S ribosomal protein L12 OS=Homo sapiens OX=9606 GN=RPL12 PE=1 SV=1	0.75269	5.36E-04
Q8WYA6	CTBL1_HUMAN	Beta-catenin-like protein 1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1	0.75269	0.002673
P48444	COPD_HUMAN	Coatmer subunit delta OS=Homo sapiens OX=9606 GN=ARCN1 PE=1 SV=1	0.75185	0.001521
Q9UI09	NDUAC_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Homo sapiens OX=9606 GN=NDUFA12 PE=1 SV=1	0.751759	5.36E-04
P34896	GLYC_HUMAN	Serine hydroxymethyltransferase cytosolic OS=Homo sapiens OX=9606 GN=SHMT1 PE=1 SV=1	0.751661	0.002416
O00204	ST2B1_HUMAN	Sulfotransferase 2B1 OS=Homo sapiens OX=9606 GN=SULT2B1 PE=1 SV=2	0.751589	3.29E-04
P28838	AMPL_HUMAN	Cytosol aminopeptidase OS=Homo sapiens OX=9606 GN=LAP3 PE=1 SV=3	0.751536	3.01E-04
P07954	FUMH_HUMAN	Fumarate hydratase mitochondrial OS=Homo sapiens OX=9606 GN=FH PE=1 SV=3	0.751282	0.001168
P18887	XRCC1_HUMAN	DNA repair protein XRCC1 OS=Homo sapiens OX=9606 GN=XRCC1 PE=1 SV=2	0.751179	9.77E-04
O95721	SNP29_HUMAN	Synaptosomal-associated protein 29 OS=Homo sapiens OX=9606 GN=SNAP29 PE=1 SV=1	0.751156	0.006216
Q13813	SPTN1_HUMAN	Spectrin alpha chain non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=3	0.751063	0.001448
P41227	NAA10_HUMAN	N-alpha-acetyltransferase 10 OS=Homo sapiens OX=9606 GN=NAA10 PE=1 SV=1	0.751046	5.46E-04
Q9Y450	HBS1L_HUMAN	HBS1-like protein OS=Homo sapiens OX=9606 GN=HBS1L PE=1 SV=1	0.750795	3.37E-04
P15121	ALDR_HUMAN	Aldo-keto reductase family 1 member B1 OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1 SV=3	0.750739	5.47E-04
O95336	6PGL_HUMAN	6-phosphogluconolactonase OS=Homo sapiens OX=9606 GN=PGLS PE=1 SV=2	0.750727	2.97E-04
Q8N6H7	ARFG2_HUMAN	ADP-ribosylation factor GTPase-activating protein 2 OS=Homo sapiens OX=9606 GN=ARFGAP2 PE=1 SV=1	0.750496	6.80E-04
P30419	NMT1_HUMAN	Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens OX=9606 GN=NMT1 PE=1 SV=2	0.75048	8.73E-05
Q13526	PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens OX=9606 GN=PIN1 PE=1 SV=1	0.750238	5.47E-04
Q13257	MD2L1_HUMAN	Mitotic spindle assembly checkpoint protein MAD2A OS=Homo sapiens OX=9606 GN=MAD2L1 PE=1 SV=1	0.750022	5.55E-04

Q9ULA0	DNPEP_HUMAN	Aspartyl aminopeptidase OS=Homo sapiens OX=9606 GN=DNPEP PE=1 SV=1	0.750022	5.66E-04
P63010	AP2B1_HUMAN	AP-2 complex subunit beta OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1	0.749651	0.001025
Q12931	TRAP1_HUMAN	Heat shock protein 75 kDa mitochondrial OS=Homo sapiens OX=9606 GN=TRAP1 PE=1 SV=3	0.749566	0.001366
Q00169	PIPNA_HUMAN	Phosphatidylinositol transfer protein alpha isoform OS=Homo sapiens OX=9606 GN=PITPNA PE=1 SV=2	0.74942	5.55E-04
P40763	STAT3_HUMAN	Signal transducer and activator of transcription 3 OS=Homo sapiens OX=9606 GN=STAT3 PE=1 SV=2	0.749418	8.50E-04
Q13895	BYST_HUMAN	Bystin OS=Homo sapiens OX=9606 GN=BYSL PE=1 SV=3	0.749217	5.66E-04
O75044	SRGP2_HUMAN	SLIT-ROBO Rho GTPase-activating protein 2 OS=Homo sapiens OX=9606 GN=SRGAP2 PE=1 SV=3	0.749178	0.001233
P20618	PSB1_HUMAN	Proteasome subunit beta type-1 OS=Homo sapiens OX=9606 GN=PSMB1 PE=1 SV=2	0.749038	0.009231
Q16763	UBE2S_HUMAN	Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens OX=9606 GN=UBE2S PE=1 SV=2	0.748911	5.56E-04
P67870	CSK2B_HUMAN	Casein kinase II subunit beta OS=Homo sapiens OX=9606 GN=CSNK2B PE=1 SV=1	0.748775	6.10E-04
O15511	ARPC5_HUMAN	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens OX=9606 GN=ARPC5 PE=1 SV=3	0.748461	3.56E-04
Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H OS=Homo sapiens OX=9606 GN=EIF4H PE=1 SV=5	0.748461	4.38E-04
O43815	STRN_HUMAN	Striatin OS=Homo sapiens OX=9606 GN=STRN PE=1 SV=4	0.748299	5.47E-04
Q00403	TF2B_HUMAN	Transcription initiation factor IIB OS=Homo sapiens OX=9606 GN=GTF2B PE=1 SV=1	0.748188	5.63E-04
Q15717	ELAV1_HUMAN	ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=2	0.748175	6.22E-04
A0AV96	RBM47_HUMAN	RNA-binding protein 47 OS=Homo sapiens OX=9606 GN=RBM47 PE=1 SV=2	0.747918	3.13E-04
Q8IXI1	MIRO2_HUMAN	Mitochondrial Rho GTPase 2 OS=Homo sapiens OX=9606 GN=RHOT2 PE=1 SV=2	0.74789	8.41E-04
O14818	PSA7_HUMAN	Proteasome subunit alpha type-7 OS=Homo sapiens OX=9606 GN=PSMA7 PE=1 SV=1	0.747654	6.94E-04
P22570	ADRO_HUMAN	NADPH:adrenodoxin oxidoreductase mitochondrial OS=Homo sapiens OX=9606 GN=FDXR PE=1 SV=3	0.747649	6.77E-05
Q9NR46	SHLB2_HUMAN	Endophilin-B2 OS=Homo sapiens OX=9606 GN=SH3GLB2 PE=1 SV=1	0.747329	8.81E-04
Q8NFW8	NEUA_HUMAN	N-acylneuraminate cytidyltransferase OS=Homo sapiens OX=9606 GN=CMAS PE=1 SV=2	0.747325	4.89E-04
P50995	ANX11_HUMAN	Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1 SV=1	0.747316	0.004696
P19623	SPEE_HUMAN	Spermidine synthase OS=Homo sapiens OX=9606 GN=SRM PE=1 SV=1	0.747254	0.002156
Q9UIQ6	LCAP_HUMAN	Leucyl-cystinyl aminopeptidase OS=Homo sapiens OX=9606 GN=LNPEP PE=1 SV=3	0.747168	4.67E-04
Q9UNQ2	DIM1_HUMAN	Probable dimethyladenosine transferase OS=Homo sapiens OX=9606 GN=DIMT1 PE=1 SV=1	0.747123	5.72E-04
Q8NEU8	DP13B_HUMAN	DCC-interacting protein 13-beta OS=Homo sapiens OX=9606 GN=APPL2 PE=1 SV=3	0.746991	6.01E-04
O00148	DX39A_HUMAN	ATP-dependent RNA helicase DDX39A OS=Homo sapiens OX=9606 GN=DDX39A PE=1 SV=2	0.746881	0.002809
Q9Y2R9	RT07_HUMAN	28S ribosomal protein S7 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS7 PE=1 SV=2	0.746548	6.07E-04
P42126	ECI1_HUMAN	Enoyl-CoA delta isomerase 1 mitochondrial OS=Homo sapiens OX=9606 GN=ECI1 PE=1 SV=1	0.745987	5.74E-04
Q6Y7W6	GGYF2_HUMAN	GRB10-interacting GYF protein 2 OS=Homo sapiens OX=9606 GN=GIGYF2 PE=1 SV=1	0.745776	3.29E-04
Q96B97	SH3K1_HUMAN	SH3 domain-containing kinase-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3KBP1 PE=1 SV=2	0.745749	0.002295
Q86T12	DPP9_HUMAN	Dipeptidyl peptidase 9 OS=Homo sapiens OX=9606 GN=DPP9 PE=1 SV=3	0.745736	0.002052
O75821	EIF3G_HUMAN	Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens OX=9606 GN=EIF3G PE=1 SV=2	0.745683	7.13E-04
P13693	TCTP_HUMAN	Translationally-controlled tumor protein OS=Homo sapiens OX=9606 GN=TPT1 PE=1 SV=1	0.745495	1.83E-04
P62258	1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1	0.745233	7.35E-04
Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=2	0.745108	8.55E-04
P57081	WDR4_HUMAN	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4 OS=Homo sapiens OX=9606 GN=WDR4 PE=1 SV=2	0.745031	0.003056
Q99798	ACON_HUMAN	Aconitate hydratase mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=2	0.744441	9.77E-04

Q99459	CDC5L_HUMAN	Cell division cycle 5-like protein OS=Homo sapiens OX=9606 GN=CDC5L PE=1 SV=2	0.744265	4.79E-04
Q96EK6	GNA1_HUMAN	Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens OX=9606 GN=GNPNAT1 PE=1 SV=1	0.744239	9.69E-04
P30084	ECHM_HUMAN	Enoyl-CoA hydratase mitochondrial OS=Homo sapiens OX=9606 GN=ECHS1 PE=1 SV=4	0.74413	4.66E-04
P05787	K2C8_HUMAN	Keratin type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7	0.744088	0.001184
P35250	RFC2_HUMAN	Replication factor C subunit 2 OS=Homo sapiens OX=9606 GN=RFC2 PE=1 SV=3	0.743882	6.09E-04
Q96T88	UHRF1_HUMAN	E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens OX=9606 GN=UHRF1 PE=1 SV=1	0.743486	0.002387
O75534	CSDE1_HUMAN	Cold shock domain-containing protein E1 OS=Homo sapiens OX=9606 GN=CSDE1 PE=1 SV=2	0.74336	3.18E-05
P43487	RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens OX=9606 GN=RANBP1 PE=1 SV=1	0.742974	6.19E-04
Q92905	CSN5_HUMAN	COP9 signalosome complex subunit 5 OS=Homo sapiens OX=9606 GN=COPSS PE=1 SV=4	0.742878	8.31E-04
P46459	NSF_HUMAN	Vesicle-fusing ATPase OS=Homo sapiens OX=9606 GN=NSF PE=1 SV=3	0.742866	0.001343
Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens OX=9606 GN=MAPRE1 PE=1 SV=3	0.742771	0.001114
Q9H2J4	PDCL3_HUMAN	Phosducin-like protein 3 OS=Homo sapiens OX=9606 GN=PDCL3 PE=1 SV=1	0.742739	4.33E-04
O94925	GLSK_HUMAN	Glutaminase kidney isoform mitochondrial OS=Homo sapiens OX=9606 GN=GLS PE=1 SV=1	0.742734	0.001582
P11172	UMPS_HUMAN	Uridine 5'-monophosphate synthase OS=Homo sapiens OX=9606 GN=UMPS PE=1 SV=1	0.742431	0.003682
P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens OX=9606 GN=PEBP1 PE=1 SV=3	0.742425	5.10E-04
Q12800	TFCP2_HUMAN	Alpha-globin transcription factor CP2 OS=Homo sapiens OX=9606 GN=TFCP2 PE=1 SV=2	0.742353	0.00167
Q9BZH6	WDR11_HUMAN	WD repeat-containing protein 11 OS=Homo sapiens OX=9606 GN=WDR11 PE=1 SV=1	0.742163	0.001059
O14974	MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1	0.742037	6.20E-04
Q15599	NHRF2_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens OX=9606 GN=SLC9A3R2 PE=1 SV=2	0.741989	6.56E-04
Q9BY43	CHM4A_HUMAN	Charged multivesicular body protein 4a OS=Homo sapiens OX=9606 GN=CHMP4A PE=1 SV=3	0.741802	6.25E-04
O00159	MYO1C_HUMAN	Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4	0.741747	8.90E-04
Q9BPX3	CND3_HUMAN	Condensin complex subunit 3 OS=Homo sapiens OX=9606 GN=NCAPG PE=1 SV=1	0.741617	1.85E-04
Q9H0W8	SMG9_HUMAN	Protein SMG9 OS=Homo sapiens OX=9606 GN=SMG9 PE=1 SV=1	0.741575	6.28E-04
Q16795	NDUA9_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9 mitochondrial OS=Homo sapiens OX=9606 GN=NDUFA9 PE=1 SV=2	0.741478	0.009231
Q7LGA3	HS2ST_HUMAN	Heparan sulfate 2-O-sulfotransferase 1 OS=Homo sapiens OX=9606 GN=HS2ST1 PE=1 SV=1	0.741393	6.18E-04
P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=2	0.741307	0.006721
Q9HAB8	PPCS_HUMAN	Phosphopantothenate--cysteine ligase OS=Homo sapiens OX=9606 GN=PPCS PE=1 SV=2	0.740841	6.61E-04
P21281	VATB2_HUMAN	V-type proton ATPase subunit B brain isoform OS=Homo sapiens OX=9606 GN=ATP6V1B2 PE=1 SV=3	0.740622	0.001129
Q9BZE4	NOG1_HUMAN	Nucleolar GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP4 PE=1 SV=3	0.740532	6.20E-04
P78371	TCPB_HUMAN	T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=4	0.740508	3.13E-04
Q15154	PCM1_HUMAN	Pericentriolar material 1 protein OS=Homo sapiens OX=9606 GN=PCM1 PE=1 SV=5	0.740332	6.43E-04
Q7Z406	MYH14_HUMAN	Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=2	0.740241	2.99E-04
O15460	P4HA2_HUMAN	Prolyl 4-hydroxylase subunit alpha-2 OS=Homo sapiens OX=9606 GN=P4HA2 PE=1 SV=1	0.740187	0.001082
Q86WQ0	NR2CA_HUMAN	Nuclear receptor 2C2-associated protein OS=Homo sapiens OX=9606 GN=NR2C2AP PE=1 SV=1	0.739732	6.60E-04
O43660	PLRG1_HUMAN	Pleiotropic regulator 1 OS=Homo sapiens OX=9606 GN=PLRG1 PE=1 SV=1	0.739685	0.001387
Q9UPN3	MACF1_HUMAN	Microtubule-actin cross-linking factor 1 isoforms 1/2/3/5 OS=Homo sapiens OX=9606 GN=MACF1 PE=1 SV=4	0.73966	8.97E-04
Q9Y6Q5	AP1M2_HUMAN	AP-1 complex subunit mu-2 OS=Homo sapiens OX=9606 GN=AP1M2 PE=1 SV=4	0.739574	6.67E-04

O75347	TBCA_HUMAN	Tubulin-specific chaperone A OS=Homo sapiens OX=9606 GN=TBCA PE=1 SV=3	0.739526	6.40E-04
Q86VR2	RETR3_HUMAN	Reticulophagy regulator 3 OS=Homo sapiens OX=9606 GN=RETREG3 PE=1 SV=1	0.73865	6.56E-04
P62995	TRA2B_HUMAN	Transformer-2 protein homolog beta OS=Homo sapiens OX=9606 GN=TRA2B PE=1 SV=1	0.738642	0.003861
P53621	COPA_HUMAN	Coatomer subunit alpha OS=Homo sapiens OX=9606 GN=COPA PE=1 SV=2	0.738597	7.97E-05
Q9UJA5	TRM6_HUMAN	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens OX=9606 GN=TRMT6 PE=1 SV=1	0.738513	6.43E-04
Q9P2R3	ANFY1_HUMAN	Rabankyrin-5 OS=Homo sapiens OX=9606 GN=ANKFY1 PE=1 SV=2	0.738243	0.003628
Q9UMX0	UBQL1_HUMAN	Ubiquilin-1 OS=Homo sapiens OX=9606 GN=UBQLN1 PE=1 SV=2	0.738153	9.85E-04
O43143	DHX15_HUMAN	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens OX=9606 GN=DHX15 PE=1 SV=2	0.738148	0.001475
Q96KA5	CLP1L_HUMAN	Cleft lip and palate transmembrane protein 1-like protein OS=Homo sapiens OX=9606 GN=CLPTM1L PE=1 SV=1	0.738084	6.60E-04
Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein mitochondrial OS=Homo sapiens OX=9606 GN=SSBP1 PE=1 SV=1	0.738064	0.003934
Q5JWF2	GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens OX=9606 GN=GNAS PE=1 SV=2	0.737829	2.35E-04
Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=4	0.737547	2.53E-04
P56134	ATPK_HUMAN	ATP synthase subunit f mitochondrial OS=Homo sapiens OX=9606 GN=ATP5MF PE=1 SV=3	0.737544	6.63E-04
Q13616	CUL1_HUMAN	Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=2	0.737517	3.58E-04
P19388	RPAB1_HUMAN	DNA-directed RNA polymerases I II and III subunit RPABC1 OS=Homo sapiens OX=9606 GN=POLR2E PE=1 SV=4	0.737376	6.76E-04
Q9UKX7	NUP50_HUMAN	Nuclear pore complex protein Nup50 OS=Homo sapiens OX=9606 GN=NUP50 PE=1 SV=2	0.737267	0.002842
Q8IY81	SPB1_HUMAN	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 OS=Homo sapiens OX=9606 GN=FTSJ3 PE=1 SV=2	0.737262	0.001416
Q96S44	PRPK_HUMAN	EKC/KEOPS complex subunit TP53RK OS=Homo sapiens OX=9606 GN=TP53RK PE=1 SV=2	0.736479	6.53E-04
Q9UBW8	CSN7A_HUMAN	COP9 signalosome complex subunit 7a OS=Homo sapiens OX=9606 GN=COPS7A PE=1 SV=1	0.736405	0.001309
Q9UHD8	SEPT9_HUMAN	Septin-9 OS=Homo sapiens OX=9606 GN=SEPTIN9 PE=1 SV=2	0.736275	0.001692
Q13409	DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=3	0.736173	1.60E-04
Q9BVG4	PBDC1_HUMAN	Protein PBDC1 OS=Homo sapiens OX=9606 GN=PBDC1 PE=1 SV=1	0.736104	0.00149
Q96T37	RBM15_HUMAN	RNA-binding protein 15 OS=Homo sapiens OX=9606 GN=RBM15 PE=1 SV=2	0.735987	3.78E-04
O95340	PAPS2_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens OX=9606 GN=PAPS2 PE=1 SV=2	0.735597	6.83E-04
P50991	TCPD_HUMAN	T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4	0.735537	7.23E-04
Q68EM7	RHG17_HUMAN	Rho GTPase-activating protein 17 OS=Homo sapiens OX=9606 GN=ARHGAP17 PE=1 SV=1	0.735442	0.001141
Q9BTE3	MCMBP_HUMAN	Mini-chromosome maintenance complex-binding protein OS=Homo sapiens OX=9606 GN=MCMBP PE=1 SV=2	0.735362	2.80E-04
Q01970	PLCB3_HUMAN	1-phosphatidylinositol 4 5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens OX=9606 GN=PLCB3 PE=1 SV=2	0.735267	2.10E-04
P78347	GTF2I_HUMAN	General transcription factor II-I OS=Homo sapiens OX=9606 GN=GTF2I PE=1 SV=2	0.735252	3.18E-04
Q13620	CUL4B_HUMAN	Cullin-4B OS=Homo sapiens OX=9606 GN=CUL4B PE=1 SV=4	0.73515	7.01E-04
Q9UI10	EI2BD_HUMAN	Translation initiation factor eIF-2B subunit delta OS=Homo sapiens OX=9606 GN=EIF2B4 PE=1 SV=2	0.735138	0.004729
Q32MZ4	LRRF1_HUMAN	Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens OX=9606 GN=LRRFIP1 PE=1 SV=2	0.735088	0.005694
Q6P2E9	EDC4_HUMAN	Enhancer of mRNA-decapping protein 4 OS=Homo sapiens OX=9606 GN=EDC4 PE=1 SV=1	0.734988	1.17E-04
Q6NUK1	SCMC1_HUMAN	Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens OX=9606 GN=SLC25A24 PE=1 SV=2	0.734515	0.003807
Q9H9B4	SFXN1_HUMAN	Sideroflexin-1 OS=Homo sapiens OX=9606 GN=SFXN1 PE=1 SV=4	0.734335	0.001579
P61158	ARP3_HUMAN	Actin-related protein 3 OS=Homo sapiens OX=9606 GN=ACTR3 PE=1 SV=3	0.734156	0.001144
O15270	SPTC2_HUMAN	Serine palmitoyltransferase 2 OS=Homo sapiens OX=9606 GN=SPTLC2 PE=1 SV=1	0.734106	6.84E-04
P55735	SEC13_HUMAN	Protein SEC13 homolog OS=Homo sapiens OX=9606 GN=SEC13 PE=1 SV=3	0.734052	2.75E-04
P08243	ASNS_HUMAN	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=ASNS PE=1 SV=4	0.733788	7.09E-04

Q8WVJ2	NUDC2_HUMAN	NudC domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NUDCD2 PE=1 SV=1	0.733554	7.00E-04
Q9Y678	COPG1_HUMAN	Coatamer subunit gamma-1 OS=Homo sapiens OX=9606 GN=COPG1 PE=1 SV=1	0.733455	9.16E-04
P25685	DNJB1_HUMAN	DnaJ homolog subfamily B member 1 OS=Homo sapiens OX=9606 GN=DNAJB1 PE=1 SV=4	0.733425	4.55E-04
P40937	RFC5_HUMAN	Replication factor C subunit 5 OS=Homo sapiens OX=9606 GN=RFC5 PE=1 SV=1	0.733147	3.82E-04
Q15369	ELOC_HUMAN	Elongin-C OS=Homo sapiens OX=9606 GN=ELOC PE=1 SV=1	0.733061	0.001146
O43678	NDUA2_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens OX=9606 GN=NDUFA2 PE=1 SV=3	0.732554	7.34E-04
Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=SUCLG2 PE=1 SV=2	0.73252	0.003708
Q9UNX4	WDR3_HUMAN	WD repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=WDR3 PE=1 SV=1	0.732436	0.001362
Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A OS=Homo sapiens OX=9606 GN=SMC1A PE=1 SV=2	0.732415	7.08E-04
Q6P2Q9	PRP8_HUMAN	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens OX=9606 GN=PRPF8 PE=1 SV=2	0.732403	0.004221
P29373	RABP2_HUMAN	Cellular retinoic acid-binding protein 2 OS=Homo sapiens OX=9606 GN=CRABP2 PE=1 SV=2	0.732368	0.009424
Q8IWX8	CHERP_HUMAN	Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens OX=9606 GN=CHERP PE=1 SV=3	0.732327	6.98E-04
P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta mitochondrial OS=Homo sapiens OX=9606 GN=HADHB PE=1 SV=3	0.732102	0.003241
Q9NX58	LYAR_HUMAN	Cell growth-regulating nucleolar protein OS=Homo sapiens OX=9606 GN=LYAR PE=1 SV=2	0.73192	0.001963
Q9UI12	VATH_HUMAN	V-type proton ATPase subunit H OS=Homo sapiens OX=9606 GN=ATP6V1H PE=1 SV=1	0.731918	7.22E-04
O43290	SNUT1_HUMAN	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens OX=9606 GN=SART1 PE=1 SV=1	0.731779	5.88E-04
P18031	PTN1_HUMAN	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens OX=9606 GN=PTPN1 PE=1 SV=1	0.731667	2.58E-04
P49643	PRI2_HUMAN	DNA primase large subunit OS=Homo sapiens OX=9606 GN=PRIM2 PE=1 SV=2	0.73149	0.001603
Q8WVB6	CTF18_HUMAN	Chromosome transmission fidelity protein 18 homolog OS=Homo sapiens OX=9606 GN=CTF18 PE=1 SV=1	0.731454	0.002659
O14744	ANM5_HUMAN	Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=4	0.731312	7.08E-04
P07814	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens OX=9606 GN=EPRS1 PE=1 SV=5	0.731089	0.001973
P09429	HMGB1_HUMAN	High mobility group protein B1 OS=Homo sapiens OX=9606 GN=HMGB1 PE=1 SV=3	0.731077	7.15E-04
Q9Y265	RUVB1_HUMAN	RuvB-like 1 OS=Homo sapiens OX=9606 GN=RUVBL1 PE=1 SV=1	0.731065	0.004518
Q15029	U5S1_HUMAN	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=EFTUD2 PE=1 SV=1	0.730474	0.004454
P52566	GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens OX=9606 GN=ARHGDI2 PE=1 SV=3	0.730434	0.002153
Q96QK1	VPS35_HUMAN	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV=2	0.730279	6.74E-04
P23434	GCSH_HUMAN	Glycine cleavage system H protein mitochondrial OS=Homo sapiens OX=9606 GN=GCSH PE=1 SV=2	0.730279	0.006749
Q15075	EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens OX=9606 GN=EEA1 PE=1 SV=2	0.730182	0.002645
Q8NFH3	NUP43_HUMAN	Nucleoporin Nup43 OS=Homo sapiens OX=9606 GN=NUP43 PE=1 SV=1	0.730179	4.86E-04
Q96EY1	DNJA3_HUMAN	DnaJ homolog subfamily A member 3 mitochondrial OS=Homo sapiens OX=9606 GN=DNAJA3 PE=1 SV=2	0.729954	0.002562
O95684	FR1OP_HUMAN	FGFR1 oncogene partner OS=Homo sapiens OX=9606 GN=FGFR1OP PE=1 SV=1	0.729653	7.21E-04
Q86TU7	SETD3_HUMAN	Actin-histidine N-methyltransferase OS=Homo sapiens OX=9606 GN=SETD3 PE=1 SV=1	0.729449	1.16E-04
Q9BQG0	MBB1A_HUMAN	Myb-binding protein 1A OS=Homo sapiens OX=9606 GN=MYBBP1A PE=1 SV=2	0.729386	0.003708
Q29RF7	PDS5A_HUMAN	Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens OX=9606 GN=PDS5A PE=1 SV=1	0.729321	7.38E-04
P39748	FEN1_HUMAN	Flap endonuclease 1 OS=Homo sapiens OX=9606 GN=FEN1 PE=1 SV=1	0.729259	6.17E-04
Q9C0B5	ZDHC5_HUMAN	Palmitoyltransferase ZDHC5 OS=Homo sapiens OX=9606 GN=ZDHC5 PE=1 SV=2	0.729183	0.001204
Q92878	RAD50_HUMAN	DNA repair protein RAD50 OS=Homo sapiens OX=9606 GN=RAD50 PE=1 SV=1	0.728981	3.12E-04

P54105	ICLN_HUMAN	Methylosome subunit pICln OS=Homo sapiens OX=9606 GN=CLNS1A PE=1 SV=1	0.728486	0.001343
P61019	RAB2A_HUMAN	Ras-related protein Rab-2A OS=Homo sapiens OX=9606 GN=RAB2A PE=1 SV=1	0.728459	7.75E-04
P13807	GYS1_HUMAN	Glycogen [starch] synthase muscle OS=Homo sapiens OX=9606 GN=GYS1 PE=1 SV=2	0.728087	0.007752
Q9NX02	NALP2_HUMAN	NACHT LRR and PYD domains-containing protein 2 OS=Homo sapiens OX=9606 GN=NLRP2 PE=1 SV=1	0.72806	0.001853
Q13427	PPIG_HUMAN	Peptidyl-prolyl cis-trans isomerase G OS=Homo sapiens OX=9606 GN=PPIG PE=1 SV=2	0.727691	9.78E-04
Q9H9P8	L2HDH_HUMAN	L-2-hydroxyglutarate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=L2HGDH PE=1 SV=3	0.727593	2.53E-05
Q96C86	DCPS_HUMAN	m7GpppX diphosphatase OS=Homo sapiens OX=9606 GN=DCPS PE=1 SV=2	0.727493	7.62E-04
P07858	CATB_HUMAN	Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3	0.726152	9.78E-04
P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=ACADVL PE=1 SV=1	0.725959	0.001431
Q09028	RBBP4_HUMAN	Histone-binding protein RBBP4 OS=Homo sapiens OX=9606 GN=RBBP4 PE=1 SV=3	0.725619	0.009025
Q13363	CTBP1_HUMAN	C-terminal-binding protein 1 OS=Homo sapiens OX=9606 GN=CTBP1 PE=1 SV=2	0.72535	3.51E-04
Q13405	RM49_HUMAN	39S ribosomal protein L49 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL49 PE=1 SV=1	0.72522	7.86E-04
Q99848	EBP2_HUMAN	Probable rRNA-processing protein EBP2 OS=Homo sapiens OX=9606 GN=EBNA1BP2 PE=1 SV=2	0.725071	7.62E-04
P11388	TOP2A_HUMAN	DNA topoisomerase 2-alpha OS=Homo sapiens OX=9606 GN=TOP2A PE=1 SV=3	0.724802	0.002274
P04637	P53_HUMAN	Cellular tumor antigen p53 OS=Homo sapiens OX=9606 GN=TP53 PE=1 SV=4	0.724745	7.98E-04
Q9NZL4	HPBP1_HUMAN	Hsp70-binding protein 1 OS=Homo sapiens OX=9606 GN=HSPBP1 PE=1 SV=2	0.724614	0.001479
Q13287	NMI_HUMAN	N-myc-interactor OS=Homo sapiens OX=9606 GN=NMI PE=1 SV=2	0.724468	8.05E-04
P23246	SFPQ_HUMAN	Splicing factor proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2	0.724391	0.008628
P49419	AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=5	0.724237	3.38E-04
Q9BT78	CSN4_HUMAN	COP9 signalosome complex subunit 4 OS=Homo sapiens OX=9606 GN=COPS4 PE=1 SV=1	0.724156	0.001976
P24666	PPAC_HUMAN	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=ACP1 PE=1 SV=3	0.724045	7.62E-04
Q7Z2K6	ERMP1_HUMAN	Endoplasmic reticulum metalloproteinase 1 OS=Homo sapiens OX=9606 GN=ERMP1 PE=1 SV=2	0.72383	0.00147
P13489	RINI_HUMAN	Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNH1 PE=1 SV=2	0.723784	0.001973
Q96CW1	AP2M1_HUMAN	AP-2 complex subunit mu OS=Homo sapiens OX=9606 GN=AP2M1 PE=1 SV=2	0.723751	4.40E-04
P07737	PROF1_HUMAN	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2	0.723638	0.001795
Q7Z4W1	DCXR_HUMAN	L-xylulose reductase OS=Homo sapiens OX=9606 GN=DCXR PE=1 SV=2	0.723602	0.001633
Q86V21	AACS_HUMAN	Acetoacetyl-CoA synthetase OS=Homo sapiens OX=9606 GN=AACS PE=1 SV=1	0.723563	8.38E-04
Q9Y5B9	SP16H_HUMAN	FACT complex subunit SPT16 OS=Homo sapiens OX=9606 GN=SUPT16H PE=1 SV=1	0.723535	7.98E-04
O14617	AP3D1_HUMAN	AP-3 complex subunit delta-1 OS=Homo sapiens OX=9606 GN=AP3D1 PE=1 SV=1	0.723513	0.002921
Q9UKK9	NUDT5_HUMAN	ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1	0.723313	8.33E-04
O14562	UBFD1_HUMAN	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens OX=9606 GN=UBFD1 PE=1 SV=2	0.723078	8.54E-04
Q9H788	SH24A_HUMAN	SH2 domain-containing protein 4A OS=Homo sapiens OX=9606 GN=SH2D4A PE=1 SV=1	0.72306	7.82E-04
O75436	VP26A_HUMAN	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens OX=9606 GN=VPS26A PE=1 SV=2	0.722934	4.62E-05
P35268	RL22_HUMAN	60S ribosomal protein L22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=2	0.722808	0.001165
P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=2	0.722395	1.91E-04
Q9NX46	ARHL2_HUMAN	ADP-ribose glycohydrolase ARH3 OS=Homo sapiens OX=9606 GN=ADPRHL2 PE=1 SV=1	0.722147	0.007738
P68371	TBB4B_HUMAN	Tubulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1	0.722105	0.006599
Q3MHD2	LSM12_HUMAN	Protein LSM12 homolog OS=Homo sapiens OX=9606 GN=LSM12 PE=1 SV=2	0.721996	8.31E-04

O43252	PAPS1_HUMAN	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens OX=9606 GN=PAPSS1 PE=1 SV=2	0.72148	7.45E-04
P20936	RASA1_HUMAN	Ras GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RASA1 PE=1 SV=1	0.721451	8.54E-04
Q9H0D6	XRN2_HUMAN	5'-3' exoribonuclease 2 OS=Homo sapiens OX=9606 GN=XRN2 PE=1 SV=1	0.721446	0.001916
P07741	APT_HUMAN	Adenine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=2	0.721369	0.001928
P30040	ERP29_HUMAN	Endoplasmic reticulum resident protein 29 OS=Homo sapiens OX=9606 GN=ERP29 PE=1 SV=4	0.721363	4.15E-04
P00441	SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo sapiens OX=9606 GN=SOD1 PE=1 SV=2	0.721024	8.34E-04
P63000	RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens OX=9606 GN=RAC1 PE=1 SV=1	0.721024	0.004333
Q96PU8	QKI_HUMAN	Protein quaking OS=Homo sapiens OX=9606 GN=QKI PE=1 SV=1	0.720894	8.34E-04
Q8TF74	WIPF2_HUMAN	WAS/WASL-interacting protein family member 2 OS=Homo sapiens OX=9606 GN=WIPF2 PE=1 SV=1	0.720866	8.63E-04
P62873	GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens OX=9606 GN=GNB1 PE=1 SV=3	0.720846	0.001598
Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=3	0.720814	0.002362
Q6PJT7	ZC3HE_HUMAN	Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens OX=9606 GN=ZC3H14 PE=1 SV=1	0.720716	5.53E-04
Q9ULW0	TPX2_HUMAN	Targeting protein for Xklp2 OS=Homo sapiens OX=9606 GN=TPX2 PE=1 SV=2	0.720477	8.45E-04
P06737	PYGL_HUMAN	Glycogen phosphorylase liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4	0.720248	2.76E-04
Q9NR19	ACSA_HUMAN	Acetyl-coenzyme A synthetase cytoplasmic OS=Homo sapiens OX=9606 GN=ACSS2 PE=1 SV=1	0.720128	0.001038
Q8NBU5	ATAD1_HUMAN	ATPase family AAA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ATAD1 PE=1 SV=1	0.719734	8.96E-04
P21333	FLNA_HUMAN	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4	0.719694	0.003662
P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1	0.719639	8.44E-04
P0DMV9	HS71B_HUMAN	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1	0.719639	8.44E-04
Q96H79	ZCCHL_HUMAN	Zinc finger CCCH-type antiviral protein 1-like OS=Homo sapiens OX=9606 GN=ZC3HAV1L PE=1 SV=2	0.719584	8.90E-04
Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SND1 PE=1 SV=1	0.719478	0.002984
Q14764	MVP_HUMAN	Major vault protein OS=Homo sapiens OX=9606 GN=MVP PE=1 SV=4	0.719234	0.002636
O95571	ETHE1_HUMAN	Persulfide dioxygenase ETHE1 mitochondrial OS=Homo sapiens OX=9606 GN=ETHE1 PE=1 SV=2	0.71922	0.002772
O43488	ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens OX=9606 GN=AKR7A2 PE=1 SV=3	0.719128	5.49E-04
Q14137	BOP1_HUMAN	Ribosome biogenesis protein BOP1 OS=Homo sapiens OX=9606 GN=BOP1 PE=1 SV=2	0.719084	0.001816
O60264	SMCA5_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 SV=1	0.719001	1.63E-04
Q99613	EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens OX=9606 GN=EIF3C PE=1 SV=1	0.718768	0.00381
P49590	SYHM_HUMAN	Histidine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=HARS2 PE=1 SV=1	0.718697	8.79E-04
Q96EY7	PTCD3_HUMAN	Pentatricopeptide repeat domain-containing protein 3 mitochondrial OS=Homo sapiens OX=9606 GN=PTCD3 PE=1 SV=3	0.718521	9.03E-04
P46109	CRKL_HUMAN	Crk-like protein OS=Homo sapiens OX=9606 GN=CRKL PE=1 SV=1	0.718386	4.33E-04
P09960	LKHA4_HUMAN	Leukotriene A-4 hydrolase OS=Homo sapiens OX=9606 GN=LTA4H PE=1 SV=2	0.718276	8.72E-04
Q9GZZ1	NAA50_HUMAN	N-alpha-acetyltransferase 50 OS=Homo sapiens OX=9606 GN=NAA50 PE=1 SV=1	0.718107	0.001157
P20810	ICAL_HUMAN	Calpastatin OS=Homo sapiens OX=9606 GN=CAST PE=1 SV=4	0.718033	0.001261
Q9UNL2	SSRG_HUMAN	Translocon-associated protein subunit gamma OS=Homo sapiens OX=9606 GN=SSR3 PE=1 SV=1	0.717979	8.97E-04
Q96MW1	CCD43_HUMAN	Coiled-coil domain-containing protein 43 OS=Homo sapiens OX=9606 GN=CCDC43 PE=1 SV=2	0.717938	8.75E-04
P09104	ENOG_HUMAN	Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=3	0.717837	9.05E-04
Q9NPH2	INO1_HUMAN	Inositol-3-phosphate synthase 1 OS=Homo sapiens OX=9606 GN=ISYNA1 PE=1 SV=1	0.717784	0.00101
Q9BV57	MTND_HUMAN	1 2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Homo sapiens OX=9606 GN=ADI1 PE=1 SV=1	0.7176	9.12E-04

Q14CX7	NAA25_HUMAN	N-alpha-acetyltransferase 25 NatB auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA25 PE=1 SV=1	0.717491	3.60E-04
Q9Y5A9	YTHD2_HUMAN	YTH domain-containing family protein 2 OS=Homo sapiens OX=9606 GN=YTHDF2 PE=1 SV=2	0.717486	0.0098
P42574	CASP3_HUMAN	Caspase-3 OS=Homo sapiens OX=9606 GN=CASP3 PE=1 SV=2	0.71727	0.001206
P30876	RPB2_HUMAN	DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=1	0.716977	9.42E-04
P49006	MRP_HUMAN	MARCKS-related protein OS=Homo sapiens OX=9606 GN=MARCKSL1 PE=1 SV=2	0.716905	9.45E-04
O95486	SC24A_HUMAN	Protein transport protein Sec24A OS=Homo sapiens OX=9606 GN=SEC24A PE=1 SV=2	0.716301	8.87E-04
O00571	DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=3	0.716228	8.63E-04
P29966	MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens OX=9606 GN=MARCKS PE=1 SV=4	0.716207	0.002008
P54136	SYRC_HUMAN	Arginine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=RARS1 PE=1 SV=2	0.716088	5.33E-04
P0C0S5	H2AZ_HUMAN	Histone H2A.Z OS=Homo sapiens OX=9606 GN=H2AZ1 PE=1 SV=2	0.716008	0.00381
Q71UI9	H2AV_HUMAN	Histone H2A.V OS=Homo sapiens OX=9606 GN=H2AFV PE=1 SV=3	0.716008	0.00381
P35249	RFC4_HUMAN	Replication factor C subunit 4 OS=Homo sapiens OX=9606 GN=RFC4 PE=1 SV=2	0.715847	7.32E-04
O43242	PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PSMD3 PE=1 SV=2	0.715635	0.001196
P51531	SMCA2_HUMAN	Probable global transcription activator SNF2L2 OS=Homo sapiens OX=9606 GN=SMARCA2 PE=1 SV=2	0.715575	9.28E-04
Q9BVP2	GNL3_HUMAN	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens OX=9606 GN=GNL3 PE=1 SV=2	0.71556	0.002316
Q9H3K6	BOLA2_HUMAN	Bola-like protein 2 OS=Homo sapiens OX=9606 GN=BOLA2 PE=1 SV=1	0.715488	6.65E-04
Q16204	CCDC6_HUMAN	Coiled-coil domain-containing protein 6 OS=Homo sapiens OX=9606 GN=CCDC6 PE=1 SV=2	0.715305	0.001093
P10321	HLAC_HUMAN	HLA class I histocompatibility antigen C alpha chain OS=Homo sapiens OX=9606 GN=HLA-C PE=1 SV=3	0.715286	0.001046
P36507	MP2K2_HUMAN	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens OX=9606 GN=MAP2K2 PE=1 SV=1	0.715161	0.005573
P98175	RBM10_HUMAN	RNA-binding protein 10 OS=Homo sapiens OX=9606 GN=RBM10 PE=1 SV=3	0.714846	0.001963
Q15427	SF3B4_HUMAN	Splicing factor 3B subunit 4 OS=Homo sapiens OX=9606 GN=SF3B4 PE=1 SV=1	0.714784	9.33E-04
Q13867	BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens OX=9606 GN=BLMH PE=1 SV=1	0.714649	9.16E-04
O14964	HGS_HUMAN	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens OX=9606 GN=HGS PE=1 SV=1	0.714649	9.55E-04
P54652	HSP72_HUMAN	Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1	0.714598	0.005741
P22087	FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens OX=9606 GN=FBL PE=1 SV=2	0.714452	0.002274
Q9NYK5	RM39_HUMAN	39S ribosomal protein L39 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL39 PE=1 SV=3	0.714419	9.72E-04
Q9H6S3	ES8L2_HUMAN	Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens OX=9606 GN=EPS8L2 PE=1 SV=2	0.714375	6.39E-04
P15880	RS2_HUMAN	40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2	0.714297	8.85E-04
Q99460	PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PSMD1 PE=1 SV=2	0.714145	0.003144
Q13242	SRSF9_HUMAN	Serine/arginine-rich splicing factor 9 OS=Homo sapiens OX=9606 GN=SRSF9 PE=1 SV=1	0.713875	8.18E-04
P18085	ARF4_HUMAN	ADP-ribosylation factor 4 OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=3	0.713654	7.48E-04
P31948	STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1	0.713467	0.001354
Q9UGV2	NDRG3_HUMAN	Protein NDRG3 OS=Homo sapiens OX=9606 GN=NDRG3 PE=1 SV=2	0.713269	0.001689
P13674	P4HA1_HUMAN	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens OX=9606 GN=P4HA1 PE=1 SV=2	0.713062	0.001071
Q9BRX8	PXL2A_HUMAN	Peroxisome-like 2A OS=Homo sapiens OX=9606 GN=PRXL2A PE=1 SV=3	0.71289	9.63E-04
Q96HC4	PDLI5_HUMAN	PDZ and LIM domain protein 5 OS=Homo sapiens OX=9606 GN=PDLIM5 PE=1 SV=5	0.712104	0.001878
Q9Y2S7	PDIP2_HUMAN	Polymerase delta-interacting protein 2 OS=Homo sapiens OX=9606 GN=POLDIP2 PE=1 SV=1	0.711947	8.57E-04
O75663	TIPRL_HUMAN	TIP41-like protein OS=Homo sapiens OX=9606 GN=TIPRL PE=1 SV=2	0.71192	9.42E-04

Q9NUU7	DD19A_HUMAN	ATP-dependent RNA helicase DDX19A OS=Homo sapiens OX=9606 GN=DDX19A PE=1 SV=1	0.711569	9.52E-04
P07355	ANXA2_HUMAN	Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2	0.711414	0.001384
Q6NUQ4	TM214_HUMAN	Transmembrane protein 214 OS=Homo sapiens OX=9606 GN=TMEM214 PE=1 SV=2	0.711258	0.001983
P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens OX=9606 GN=RPS27A PE=1 SV=2	0.711104	9.77E-04
P28288	ABCD3_HUMAN	ATP-binding cassette sub-family D member 3 OS=Homo sapiens OX=9606 GN=ABCD3 PE=1 SV=1	0.710734	0.001248
Q15637	SF01_HUMAN	Splicing factor 1 OS=Homo sapiens OX=9606 GN=SF1 PE=1 SV=4	0.71067	4.93E-04
Q96IJ6	GMPPA_HUMAN	Mannose-1-phosphate guanyltrtransferase alpha OS=Homo sapiens OX=9606 GN=GMPPA PE=1 SV=1	0.710622	9.72E-04
Q92621	NU205_HUMAN	Nuclear pore complex protein Nup205 OS=Homo sapiens OX=9606 GN=NUP205 PE=1 SV=3	0.710416	1.56E-05
P54886	P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens OX=9606 GN=ALDH18A1 PE=1 SV=2	0.710359	4.64E-04
P09874	PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4	0.710256	0.001354
Q14997	PSME4_HUMAN	Proteasome activator complex subunit 4 OS=Homo sapiens OX=9606 GN=PSME4 PE=1 SV=2	0.710251	9.77E-04
Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2	0.709844	0.001424
P52758	RIDA_HUMAN	2-iminobutanoate/2-iminopropanoate deaminase OS=Homo sapiens OX=9606 GN=RIDA PE=1 SV=1	0.709729	0.001017
P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens OX=9606 GN=TPM4 PE=1 SV=3	0.709728	0.002129
P41214	EIF2D_HUMAN	Eukaryotic translation initiation factor 2D OS=Homo sapiens OX=9606 GN=EIF2D PE=1 SV=3	0.709053	9.89E-04
Q9UHB6	LIMA1_HUMAN	LIM domain and actin-binding protein 1 OS=Homo sapiens OX=9606 GN=LIMA1 PE=1 SV=1	0.70858	0.007177
Q9UGI8	TES_HUMAN	Testin OS=Homo sapiens OX=9606 GN=TES PE=1 SV=1	0.708287	0.00113
Q9UG63	ABCF2_HUMAN	ATP-binding cassette sub-family F member 2 OS=Homo sapiens OX=9606 GN=ABCF2 PE=1 SV=2	0.708111	2.76E-04
P05198	IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens OX=9606 GN=EIF2S1 PE=1 SV=3	0.708091	0.001737
O75717	WDHD1_HUMAN	WD repeat and HMG-box DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=WDHD1 PE=1 SV=1	0.707939	5.10E-04
O14618	CCS_HUMAN	Copper chaperone for superoxide dismutase OS=Homo sapiens OX=9606 GN=CCS PE=1 SV=1	0.707747	9.94E-04
P09622	DLDH_HUMAN	Dihydrolipoyl dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=DLD PE=1 SV=2	0.707735	9.48E-04
P14625	ENPL_HUMAN	Endoplasmic reticulum protein OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1	0.707659	0.001032
P35270	SPRE_HUMAN	Sepiapterin reductase OS=Homo sapiens OX=9606 GN=SPR PE=1 SV=1	0.707416	9.70E-04
P06733	ENOA_HUMAN	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2	0.707397	9.08E-04
P15924	DESP_HUMAN	Desmoplakin OS=Homo sapiens OX=9606 GN=DSP PE=1 SV=3	0.707142	0.002169
Q9Y3F4	STRAP_HUMAN	Serine-threonine kinase receptor-associated protein OS=Homo sapiens OX=9606 GN=STRAP PE=1 SV=1	0.706828	0.003202
Q99471	PFD5_HUMAN	Prefoldin subunit 5 OS=Homo sapiens OX=9606 GN=PFDN5 PE=1 SV=2	0.706751	0.001028
Q96JB5	CK5P3_HUMAN	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens OX=9606 GN=CDK5RAP3 PE=1 SV=2	0.706527	4.89E-04
Q13188	STK3_HUMAN	Serine/threonine-protein kinase 3 OS=Homo sapiens OX=9606 GN=STK3 PE=1 SV=2	0.706269	0.00984
P15374	UCHL3_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens OX=9606 GN=UCHL3 PE=1 SV=1	0.706168	1.63E-04
Q9Y2W2	WBP11_HUMAN	WW domain-binding protein 11 OS=Homo sapiens OX=9606 GN=WBP11 PE=1 SV=1	0.70596	4.67E-04
P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1	0.705884	0.001842
P27708	PYR1_HUMAN	CAD protein OS=Homo sapiens OX=9606 GN=CAD PE=1 SV=3	0.705316	0.001021
O43707	ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2	0.705056	8.38E-04
P15559	NQO1_HUMAN	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens OX=9606 GN=NQO1 PE=1 SV=1	0.705009	4.30E-04
O75475	PSIP1_HUMAN	PC4 and SFRS1-interacting protein OS=Homo sapiens OX=9606 GN=PSIP1 PE=1 SV=1	0.704923	0.001408
Q8NHH9	ATLA2_HUMAN	Atlastin-2 OS=Homo sapiens OX=9606 GN=ATL2 PE=1 SV=2	0.704652	5.19E-05
Q9NQW6	ANLN_HUMAN	Anillin OS=Homo sapiens OX=9606 GN=ANLN PE=1 SV=2	0.704652	0.005266

Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=2	0.704413	0.001269
Q9Y5X3	SNX5_HUMAN	Sorting nexin-5 OS=Homo sapiens OX=9606 GN=SNX5 PE=1 SV=1	0.704328	2.06E-04
P53618	COPB_HUMAN	Coatomer subunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3	0.704298	0.001764
Q7L5N7	PCAT2_HUMAN	Lysophosphatidylcholine acyltransferase 2 OS=Homo sapiens OX=9606 GN=LPCAT2 PE=1 SV=1	0.703844	0.001076
P04080	CYTB_HUMAN	Cystatin-B OS=Homo sapiens OX=9606 GN=CSTB PE=1 SV=2	0.703759	0.001051
Q9UHV9	PFD2_HUMAN	Prefoldin subunit 2 OS=Homo sapiens OX=9606 GN=PFDN2 PE=1 SV=1	0.703607	0.001087
Q8NFH5	NUP35_HUMAN	Nucleoporin NUP35 OS=Homo sapiens OX=9606 GN=NUP35 PE=1 SV=1	0.703607	0.001111
Q9HD26	GOPC_HUMAN	Golgi-associated PDZ and coiled-coil motif-containing protein OS=Homo sapiens OX=9606 GN=GOPC PE=1 SV=1	0.703591	0.001076
Q7Z2W4	ZCCHV_HUMAN	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens OX=9606 GN=ZC3HAV1 PE=1 SV=3	0.703589	0.00354
Q9Y490	TLN1_HUMAN	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3	0.703383	0.007545
P19838	NFKB1_HUMAN	Nuclear factor NF-kappa-B p105 subunit OS=Homo sapiens OX=9606 GN=NFKB1 PE=1 SV=2	0.703319	0.001524
P25398	RS12_HUMAN	40S ribosomal protein S12 OS=Homo sapiens OX=9606 GN=RPS12 PE=1 SV=3	0.703018	0.001035
P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1	0.702971	1.38E-04
Q13573	SNW1_HUMAN	SNW domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SNW1 PE=1 SV=1	0.70286	0.005276
P78316	NOP14_HUMAN	Nucleolar protein 14 OS=Homo sapiens OX=9606 GN=NOP14 PE=1 SV=3	0.702857	0.001104
Q86UP2	KTN1_HUMAN	Kinectin OS=Homo sapiens OX=9606 GN=KTN1 PE=1 SV=1	0.702785	0.005847
Q15459	SF3A1_HUMAN	Splicing factor 3A subunit 1 OS=Homo sapiens OX=9606 GN=SF3A1 PE=1 SV=1	0.702552	0.002439
Q9BW19	KIFC1_HUMAN	Kinesin-like protein KIFC1 OS=Homo sapiens OX=9606 GN=KIFC1 PE=1 SV=2	0.702495	0.001086
P49903	SPS1_HUMAN	Selenide water dikinase 1 OS=Homo sapiens OX=9606 GN=SEPHS1 PE=1 SV=2	0.702168	2.82E-04
Q9Y5P6	GMPPB_HUMAN	Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens OX=9606 GN=GMPPB PE=1 SV=2	0.701858	0.001127
Q5T4S7	UBR4_HUMAN	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens OX=9606 GN=UBR4 PE=1 SV=1	0.701852	0.002156
Q9UNF1	MAGD2_HUMAN	Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGED2 PE=1 SV=2	0.701715	0.001132
P41091	IF2G_HUMAN	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens OX=9606 GN=EIF2S3 PE=1 SV=3	0.701607	5.44E-04
O00461	GOLI4_HUMAN	Golgi integral membrane protein 4 OS=Homo sapiens OX=9606 GN=GOLIM4 PE=1 SV=1	0.701349	0.001126
Q9BVJ6	UT14A_HUMAN	U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens OX=9606 GN=UTP14A PE=1 SV=1	0.701276	0.00116
O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 OS=Homo sapiens OX=9606 GN=PGRMC2 PE=1 SV=1	0.701055	0.00113
P62266	RS23_HUMAN	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3	0.700832	0.001202
P68366	TBA4A_HUMAN	Tubulin alpha-4A chain OS=Homo sapiens OX=9606 GN=TUBA4A PE=1 SV=1	0.70077	0.00116
Q6YP21	KAT3_HUMAN	Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens OX=9606 GN=KYAT3 PE=1 SV=1	0.70064	7.15E-04
Q8TAT6	NPL4_HUMAN	Nuclear protein localization protein 4 homolog OS=Homo sapiens OX=9606 GN=NPLOC4 PE=1 SV=3	0.700592	6.87E-04
Q9HAV7	GRPE1_HUMAN	GrpE protein homolog 1 mitochondrial OS=Homo sapiens OX=9606 GN=GRPEL1 PE=1 SV=2	0.70027	0.001198
P53634	CATC_HUMAN	Dipeptidyl peptidase 1 OS=Homo sapiens OX=9606 GN=CTSC PE=1 SV=2	0.699919	0.001075
P80217	IN35_HUMAN	Interferon-induced 35 kDa protein OS=Homo sapiens OX=9606 GN=IFI35 PE=1 SV=5	0.699652	0.00149
Q92979	NEP1_HUMAN	Ribosomal RNA small subunit methyltransferase NEP1 OS=Homo sapiens OX=9606 GN=EMG1 PE=1 SV=4	0.699436	0.003301
P49321	NASP_HUMAN	Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=2	0.699421	0.006599
O60841	IF2P_HUMAN	Eukaryotic translation initiation factor 5B OS=Homo sapiens OX=9606 GN=EIF5B PE=1 SV=4	0.699181	0.002366
P62826	RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=3	0.699167	0.001246
P49790	NU153_HUMAN	Nuclear pore complex protein Nup153 OS=Homo sapiens OX=9606 GN=NUP153 PE=1 SV=2	0.699164	7.33E-06

Q9H488	OFUT1_HUMAN	GDP-fucose protein O-fucosyltransferase 1 OS=Homo sapiens OX=9606 GN=POFUT1 PE=1 SV=1	0.698907	4.93E-04
P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1	0.698849	0.002138
Q92499	DDX1_HUMAN	ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=2	0.698585	0.001608
Q9Y6H1	CHCH2_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CHCHD2 PE=1 SV=1	0.69829	0.001187
P31946	1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=3	0.698233	0.002549
Q96KB5	TOPK_HUMAN	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens OX=9606 GN=PBK PE=1 SV=3	0.698065	0.001166
P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 GN=ARHGDI1 PE=1 SV=3	0.698056	0.001129
Q14258	TRIM25_HUMAN	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens OX=9606 GN=TRIM25 PE=1 SV=2	0.697562	0.001129
O75822	EIF3J_HUMAN	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens OX=9606 GN=EIF3J PE=1 SV=2	0.697477	0.002036
Q14254	FLOT2_HUMAN	Flotillin-2 OS=Homo sapiens OX=9606 GN=FLOT2 PE=1 SV=2	0.697341	0.001204
P11387	TOP1_HUMAN	DNA topoisomerase 1 OS=Homo sapiens OX=9606 GN=TOP1 PE=1 SV=2	0.697291	4.57E-04
O94842	TOX4_HUMAN	TOX high mobility group box family member 4 OS=Homo sapiens OX=9606 GN=TOX4 PE=1 SV=1	0.697265	0.001177
Q6XQN6	PNCB_HUMAN	Nicotinate phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=NAPRT PE=1 SV=2	0.697239	0.002505
Q96SU4	OSBL9_HUMAN	Oxysterol-binding protein-related protein 9 OS=Homo sapiens OX=9606 GN=OSBPL9 PE=1 SV=2	0.697068	9.16E-04
O95747	OXSRI_HUMAN	Serine/threonine-protein kinase OSR1 OS=Homo sapiens OX=9606 GN=OXSRI PE=1 SV=1	0.69701	0.002113
Q9Y3B9	RRP15_HUMAN	RRP15-like protein OS=Homo sapiens OX=9606 GN=RRP15 PE=1 SV=2	0.696952	0.001188
Q9BUJ2	HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=2	0.696389	0.00495
P54920	SNAA_HUMAN	Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=3	0.69637	0.001595
P40855	PEX19_HUMAN	Peroxisomal biogenesis factor 19 OS=Homo sapiens OX=9606 GN=PEX19 PE=1 SV=1	0.696367	0.001207
P55036	PSMD4_HUMAN	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens OX=9606 GN=PSMD4 PE=1 SV=1	0.696284	0.001426
Q9UBX3	DIC_HUMAN	Mitochondrial dicarboxylate carrier OS=Homo sapiens OX=9606 GN=SLC25A10 PE=1 SV=2	0.696141	0.001259
O95292	VAPB_HUMAN	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens OX=9606 GN=VAPB PE=1 SV=3	0.695796	0.001716
O15400	STX7_HUMAN	Syntaxin-7 OS=Homo sapiens OX=9606 GN=STX7 PE=1 SV=4	0.695521	0.001166
O95817	BAG3_HUMAN	BAG family molecular chaperone regulator 3 OS=Homo sapiens OX=9606 GN=BAG3 PE=1 SV=3	0.695296	9.66E-05
Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=2	0.69524	7.13E-04
Q96TA2	YME1L1_HUMAN	ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens OX=9606 GN=YME1L1 PE=1 SV=2	0.695183	0.001393
P06396	GELS_HUMAN	Gelsolin OS=Homo sapiens OX=9606 GN=GSLN PE=1 SV=1	0.695145	0.001097
P55884	EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens OX=9606 GN=EIF3B PE=1 SV=3	0.695145	0.009931
Q15054	DPOD3_HUMAN	DNA polymerase delta subunit 3 OS=Homo sapiens OX=9606 GN=POLD3 PE=1 SV=2	0.695026	0.001227
P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=2	0.694623	0.002347
O95861	BPNT1_HUMAN	3'(2') 5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1	0.694343	0.009308
Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=2	0.694123	5.31E-04
Q9NQC3	RTN4_HUMAN	Reticulon-4 OS=Homo sapiens OX=9606 GN=RTN4 PE=1 SV=2	0.693897	0.001157
P11766	ADHX_HUMAN	Alcohol dehydrogenase class-3 OS=Homo sapiens OX=9606 GN=ADH5 PE=1 SV=4	0.693766	7.34E-04
Q13630	FCL_HUMAN	GDP-L-fucose synthase OS=Homo sapiens OX=9606 GN=TSTA3 PE=1 SV=1	0.693596	0.001387
O43684	BUB3_HUMAN	Mitotic checkpoint protein BUB3 OS=Homo sapiens OX=9606 GN=BUB3 PE=1 SV=1	0.69345	0.002748
O60832	DKC1_HUMAN	H/ACA ribonucleoprotein complex subunit DKC1 OS=Homo sapiens OX=9606 GN=DKC1 PE=1 SV=3	0.693434	0.001185
O14907	TX1B3_HUMAN	Tax1-binding protein 3 OS=Homo sapiens OX=9606 GN=TAX1BP3 PE=1 SV=2	0.693236	0.001277

P18206	VINC_HUMAN	Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=4	0.693187	0.005018
P38606	VATA_HUMAN	V-type proton ATPase catalytic subunit A OS=Homo sapiens OX=9606 GN=ATP6V1A PE=1 SV=2	0.693093	1.54E-04
Q9Y5Q8	TF3C5_HUMAN	General transcription factor 3C polypeptide 5 OS=Homo sapiens OX=9606 GN=GTF3C5 PE=1 SV=2	0.692413	0.001263
Q9P015	RM15_HUMAN	39S ribosomal protein L15 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL15 PE=1 SV=1	0.692134	0.003435
P49736	MCM2_HUMAN	DNA replication licensing factor MCM2 OS=Homo sapiens OX=9606 GN=MCM2 PE=1 SV=4	0.692002	0.007802
P58107	EPIPL_HUMAN	Epiplakin OS=Homo sapiens OX=9606 GN=EPPK1 PE=1 SV=3	0.691878	4.60E-04
P42704	LPPRC_HUMAN	Leucine-rich PPR motif-containing protein mitochondrial OS=Homo sapiens OX=9606 GN=LRPPRC PE=1 SV=3	0.691878	0.009849
Q05D32	CTSL2_HUMAN	CTD small phosphatase-like protein 2 OS=Homo sapiens OX=9606 GN=CTDSPL2 PE=1 SV=2	0.691586	0.001321
P53597	SUCA_HUMAN	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=SUCLG1 PE=1 SV=4	0.69151	0.001331
Q96LD4	TRI47_HUMAN	E3 ubiquitin-protein ligase TRIM47 OS=Homo sapiens OX=9606 GN=TRIM47 PE=1 SV=2	0.691492	0.001304
P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4	0.691459	0.00117
P32929	CGL_HUMAN	Cystathionine gamma-lyase OS=Homo sapiens OX=9606 GN=CTH PE=1 SV=3	0.691228	0.002813
P51648	AL3A2_HUMAN	Aldehyde dehydrogenase family 3 member A2 OS=Homo sapiens OX=9606 GN=ALDH3A2 PE=1 SV=1	0.691104	0.001509
P61106	RAB14_HUMAN	Ras-related protein Rab-14 OS=Homo sapiens OX=9606 GN=RAB14 PE=1 SV=4	0.690813	0.002718
O60884	DNJA2_HUMAN	DnaJ homolog subfamily A member 2 OS=Homo sapiens OX=9606 GN=DNAJA2 PE=1 SV=1	0.690599	0.002027
Q96CW5	GCP3_HUMAN	Gamma-tubulin complex component 3 OS=Homo sapiens OX=9606 GN=TUBGCP3 PE=1 SV=2	0.690456	0.00206
P61224	RAP1B_HUMAN	Ras-related protein Rap-1b OS=Homo sapiens OX=9606 GN=RAP1B PE=1 SV=1	0.690171	9.23E-04
P60900	PSA6_HUMAN	Proteasome subunit alpha type-6 OS=Homo sapiens OX=9606 GN=PSMA6 PE=1 SV=1	0.68977	0.002141
P62495	ERF1_HUMAN	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens OX=9606 GN=ETF1 PE=1 SV=3	0.688964	0.001553
Q14318	FKBP8_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens OX=9606 GN=FKBP8 PE=1 SV=2	0.68896	1.04E-04
P15586	GNS_HUMAN	N-acetylglucosamine-6-sulfatase OS=Homo sapiens OX=9606 GN=GNS PE=1 SV=3	0.688652	0.001348
O14497	ARI1A_HUMAN	AT-rich interactive domain-containing protein 1A OS=Homo sapiens OX=9606 GN=ARID1A PE=1 SV=3	0.688595	0.001356
Q15006	EMC2_HUMAN	ER membrane protein complex subunit 2 OS=Homo sapiens OX=9606 GN=EMC2 PE=1 SV=1	0.6885	0.001331
Q16513	PKN2_HUMAN	Serine/threonine-protein kinase N2 OS=Homo sapiens OX=9606 GN=PKN2 PE=1 SV=1	0.688359	0.007531
O00499	BIN1_HUMAN	Myc box-dependent-interacting protein 1 OS=Homo sapiens OX=9606 GN=BIN1 PE=1 SV=1	0.688225	8.63E-04
P48643	TCPE_HUMAN	T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1	0.687597	0.002916
P23497	SP100_HUMAN	Nuclear autoantigen Sp-100 OS=Homo sapiens OX=9606 GN=SP100 PE=1 SV=3	0.687497	6.51E-04
P60953	CDC42_HUMAN	Cell division control protein 42 homolog OS=Homo sapiens OX=9606 GN=CDC42 PE=1 SV=2	0.68731	0.001369
Q13243	SRSF5_HUMAN	Serine/arginine-rich splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 PE=1 SV=1	0.687238	0.001311
P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase mitochondrial OS=Homo sapiens OX=9606 GN=PRDX3 PE=1 SV=3	0.686737	0.001524
O76003	GLRX3_HUMAN	Glutaredoxin-3 OS=Homo sapiens OX=9606 GN=GLRX3 PE=1 SV=2	0.686682	3.29E-04
P56182	RRP1_HUMAN	Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens OX=9606 GN=RRP1 PE=1 SV=1	0.686662	0.002026
P55263	ADK_HUMAN	Adenosine kinase OS=Homo sapiens OX=9606 GN=ADK PE=1 SV=2	0.686561	0.003747
P18583	SON_HUMAN	Protein SON OS=Homo sapiens OX=9606 GN=SON PE=1 SV=4	0.686483	0.002601
O15067	PUR4_HUMAN	Phosphoribosylformylglycinamide synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1 SV=4	0.68602	0.003754
P51610	HCFC1_HUMAN	Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCFC1 PE=1 SV=2	0.685891	2.20E-04
Q96PZ0	PUS7_HUMAN	Pseudouridylate synthase 7 homolog OS=Homo sapiens OX=9606 GN=PUS7 PE=1 SV=2	0.685812	9.27E-04
O95347	SMC2_HUMAN	Structural maintenance of chromosomes protein 2 OS=Homo sapiens OX=9606 GN=SMC2 PE=1 SV=2	0.685795	5.78E-04

Q00688	FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens OX=9606 GN=FKBP3 PE=1 SV=1	0.685749	0.001416
Q7Z7H5	TMED4_HUMAN	Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens OX=9606 GN=TMED4 PE=1 SV=1	0.685023	0.00147
Q6FI81	CPIN1_HUMAN	Anamorsin OS=Homo sapiens OX=9606 GN=CIAPIN1 PE=1 SV=2	0.684958	0.001851
Q14694	UBP10_HUMAN	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens OX=9606 GN=USP10 PE=1 SV=2	0.684946	9.79E-04
Q9BRX5	PSF3_HUMAN	DNA replication complex GINS protein PSF3 OS=Homo sapiens OX=9606 GN=GINS3 PE=1 SV=1	0.684774	0.001526
P62851	RS25_HUMAN	40S ribosomal protein S25 OS=Homo sapiens OX=9606 GN=RPS25 PE=1 SV=1	0.684682	0.001475
P62888	RL30_HUMAN	60S ribosomal protein L30 OS=Homo sapiens OX=9606 GN=RPL30 PE=1 SV=2	0.684679	0.008195
P48739	PIPNB_HUMAN	Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens OX=9606 GN=PITPNB PE=1 SV=2	0.684569	0.001386
P05362	ICAM1_HUMAN	Intercellular adhesion molecule 1 OS=Homo sapiens OX=9606 GN=ICAM1 PE=1 SV=2	0.684498	0.002558
P21127	CD11B_HUMAN	Cyclin-dependent kinase 11B OS=Homo sapiens OX=9606 GN=CDK11B PE=1 SV=4	0.684445	0.001384
P31930	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1 mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC1 PE=1 SV=3	0.683907	0.00204
Q13617	CUL2_HUMAN	Cullin-2 OS=Homo sapiens OX=9606 GN=CUL2 PE=1 SV=2	0.683681	0.001456
P16989	YBOX3_HUMAN	Y-box-binding protein 3 OS=Homo sapiens OX=9606 GN=YBX3 PE=1 SV=4	0.683511	6.64E-04
Q7Z4V5	HDGR2_HUMAN	Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens OX=9606 GN=HDGFL2 PE=1 SV=1	0.683436	0.001495
O95881	TXD12_HUMAN	Thioredoxin domain-containing protein 12 OS=Homo sapiens OX=9606 GN=TXNDC12 PE=1 SV=1	0.683355	0.001469
P11908	PRPS2_HUMAN	Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens OX=9606 GN=PRPS2 PE=1 SV=2	0.683328	0.00145
P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3	0.68331	0.001424
Q96C19	EFHD2_HUMAN	EF-hand domain-containing protein D2 OS=Homo sapiens OX=9606 GN=EFHD2 PE=1 SV=1	0.683176	0.001428
Q9NP72	RAB18_HUMAN	Ras-related protein Rab-18 OS=Homo sapiens OX=9606 GN=RAB18 PE=1 SV=1	0.683143	0.001228
Q12792	TWF1_HUMAN	Twinfilin-1 OS=Homo sapiens OX=9606 GN=TWF1 PE=1 SV=3	0.68291	0.001469
P52732	KIF11_HUMAN	Kinesin-like protein KIF11 OS=Homo sapiens OX=9606 GN=KIF11 PE=1 SV=2	0.682771	0.001076
Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase mitochondrial OS=Homo sapiens OX=9606 GN=SQOR PE=1 SV=1	0.682754	7.30E-04
Q9P035	HACD3_HUMAN	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=2	0.682638	0.002201
Q9BXP5	SRRT_HUMAN	Serrate RNA effector molecule homolog OS=Homo sapiens OX=9606 GN=SRRT PE=1 SV=1	0.682439	0.00167
Q9BWF3	RBM4_HUMAN	RNA-binding protein 4 OS=Homo sapiens OX=9606 GN=RBM4 PE=1 SV=1	0.68235	0.001542
P50213	IDH3A_HUMAN	Isocitrate dehydrogenase [NAD] subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=IDH3A PE=1 SV=1	0.68228	0.00149
P12429	ANXA3_HUMAN	Annexin A3 OS=Homo sapiens OX=9606 GN=ANXA3 PE=1 SV=3	0.682272	0.00818
Q8WWM7	ATX2L_HUMAN	Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=2	0.681625	0.002149
Q9NUQ6	SPS2L_HUMAN	SPATS2-like protein OS=Homo sapiens OX=9606 GN=SPATS2L PE=1 SV=2	0.681531	0.001499
Q9UBT2	SAE2_HUMAN	SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 GN=UBA2 PE=1 SV=2	0.68137	0.001112
O43278	SPIT1_HUMAN	Kunitz-type protease inhibitor 1 OS=Homo sapiens OX=9606 GN=SPINT1 PE=1 SV=2	0.681349	0.004866
P40938	RFC3_HUMAN	Replication factor C subunit 3 OS=Homo sapiens OX=9606 GN=RFC3 PE=1 SV=2	0.681334	7.58E-04
Q3ZCQ8	TIM50_HUMAN	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens OX=9606 GN=TIMM50 PE=1 SV=2	0.681281	0.00149
Q9P287	BCCIP_HUMAN	BRCA2 and CDKN1A-interacting protein OS=Homo sapiens OX=9606 GN=BCCIP PE=1 SV=1	0.681025	0.002274
P27694	RFA1_HUMAN	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2	0.680917	0.001366
Q9Y365	STA10_HUMAN	START domain-containing protein 10 OS=Homo sapiens OX=9606 GN=STARD10 PE=1 SV=2	0.680823	0.001485
P50895	BCAM_HUMAN	Basal cell adhesion molecule OS=Homo sapiens OX=9606 GN=BCAM PE=1 SV=2	0.680574	0.002274
Q96ME1	FXL18_HUMAN	F-box/LRR-repeat protein 18 OS=Homo sapiens OX=9606 GN=FBXL18 PE=1 SV=2	0.680297	0.001495

P33991	MCM4_HUMAN	DNA replication licensing factor MCM4 OS=Homo sapiens OX=9606 GN=MCM4 PE=1 SV=5	0.680243	0.001994
Q15185	TEBP_HUMAN	Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 PE=1 SV=1	0.679984	0.001577
P49720	PSB3_HUMAN	Proteasome subunit beta type-3 OS=Homo sapiens OX=9606 GN=PSMB3 PE=1 SV=2	0.679695	0.007164
Q9UJW0	DCTN4_HUMAN	Dynactin subunit 4 OS=Homo sapiens OX=9606 GN=DCTN4 PE=1 SV=1	0.679667	0.006007
Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3	0.67939	6.60E-04
Q16543	CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1	0.67921	0.00177
P08758	ANXA5_HUMAN	Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2	0.678926	4.72E-04
Q8WUM4	PDC6I_HUMAN	Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 GN=PDCD6IP PE=1 SV=1	0.678863	0.003283
Q9H0H5	RGAP1_HUMAN	Rac GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RACGAP1 PE=1 SV=1	0.678854	0.001587
Q9NR56	MBNL1_HUMAN	Muscleblind-like protein 1 OS=Homo sapiens OX=9606 GN=MBNL1 PE=1 SV=2	0.678441	0.002598
Q9Y624	JAM1_HUMAN	Junctional adhesion molecule A OS=Homo sapiens OX=9606 GN=F11R PE=1 SV=1	0.678418	0.002673
Q96J01	THOC3_HUMAN	THO complex subunit 3 OS=Homo sapiens OX=9606 GN=THOC3 PE=1 SV=1	0.678072	7.45E-04
O60814	H2B1K_HUMAN	Histone H2B type 1-K OS=Homo sapiens OX=9606 GN=H2BC12 PE=1 SV=3	0.678072	0.001521
P62807	H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens OX=9606 GN=H2BC4 PE=1 SV=4	0.678072	0.001521
Q99879	H2B1M_HUMAN	Histone H2B type 1-M OS=Homo sapiens OX=9606 GN=H2BC14 PE=1 SV=3	0.678072	0.001521
Q99877	H2B1N_HUMAN	Histone H2B type 1-N OS=Homo sapiens OX=9606 GN=H2BC15 PE=1 SV=3	0.678072	0.001521
Q93079	H2B1H_HUMAN	Histone H2B type 1-H OS=Homo sapiens OX=9606 GN=HIST1H2BH PE=1 SV=3	0.678072	0.001521
P58876	H2B1D_HUMAN	Histone H2B type 1-D OS=Homo sapiens OX=9606 GN=HIST1H2BD PE=1 SV=2	0.678072	0.001521
Q5QNW6	H2B2F_HUMAN	Histone H2B type 2-F OS=Homo sapiens OX=9606 GN=HIST2H2BF PE=1 SV=3	0.678072	0.001521
O94760	DDAH1_HUMAN	N(G) N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens OX=9606 GN=DDAH1 PE=1 SV=3	0.677916	7.98E-04
P31350	RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens OX=9606 GN=RRM2 PE=1 SV=1	0.677443	0.004959
Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	0.677438	0.003277
Q13442	HAP28_HUMAN	28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens OX=9606 GN=PDAP1 PE=1 SV=1	0.677424	0.004755
O60701	UGDH_HUMAN	UDP-glucose 6-dehydrogenase OS=Homo sapiens OX=9606 GN=UGDH PE=1 SV=1	0.677169	4.61E-04
P14868	SYDC_HUMAN	Aspartate--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=DARS1 PE=1 SV=2	0.677132	0.001319
Q96C90	PP14B_HUMAN	Protein phosphatase 1 regulatory subunit 14B OS=Homo sapiens OX=9606 GN=PPP1R14B PE=1 SV=3	0.676904	0.001851
P62993	GRB2_HUMAN	Growth factor receptor-bound protein 2 OS=Homo sapiens OX=9606 GN=GRB2 PE=1 SV=1	0.676828	0.001631
Q9Y3B7	RM11_HUMAN	39S ribosomal protein L11 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL11 PE=1 SV=1	0.676684	0.001529
P21283	VATC1_HUMAN	V-type proton ATPase subunit C 1 OS=Homo sapiens OX=9606 GN=ATP6V1C1 PE=1 SV=4	0.676433	4.05E-04
P62899	RL31_HUMAN	60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1	0.676368	0.001555
P48729	KC1A_HUMAN	Casein kinase I isoform alpha OS=Homo sapiens OX=9606 GN=CSNK1A1 PE=1 SV=2	0.676258	0.002837
P40222	TXLNA_HUMAN	Alpha-taxilin OS=Homo sapiens OX=9606 GN=TXLNA PE=1 SV=3	0.67615	0.002546
Q8WUM0	NU133_HUMAN	Nuclear pore complex protein Nup133 OS=Homo sapiens OX=9606 GN=NUP133 PE=1 SV=2	0.676137	0.004384
P35269	T2FA_HUMAN	General transcription factor IIF subunit 1 OS=Homo sapiens OX=9606 GN=GTF2F1 PE=1 SV=2	0.676037	4.10E-04
Q96552	PIGS_HUMAN	GPI transamidase component PIG-S OS=Homo sapiens OX=9606 GN=PIGS PE=1 SV=3	0.675599	0.002955
P13804	ETFA_HUMAN	Electron transfer flavoprotein subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=ETFA PE=1 SV=1	0.675253	2.87E-04
P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta OS=Homo sapiens OX=9606 GN=HEXB PE=1 SV=3	0.675147	0.006486

O94973	AP2A2_HUMAN	AP-2 complex subunit alpha-2 OS=Homo sapiens OX=9606 GN=AP2A2 PE=1 SV=2	0.674886	0.001643
Q9H3R5	CENPH_HUMAN	Centromere protein H OS=Homo sapiens OX=9606 GN=CENPH PE=1 SV=1	0.674708	0.001618
Q8IWZ8	SUGP1_HUMAN	SURP and G-patch domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUGP1 PE=1 SV=2	0.674694	0.001594
Q6KB66	K2C80_HUMAN	Keratin type II cytoskeletal 80 OS=Homo sapiens OX=9606 GN=KRT80 PE=1 SV=2	0.674548	0.002343
Q14498	RBM39_HUMAN	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2	0.674458	9.45E-04
P35658	NU214_HUMAN	Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=2	0.674399	0.001337
Q5VW32	BROX_HUMAN	BRO1 domain-containing protein BROX OS=Homo sapiens OX=9606 GN=BROX PE=1 SV=1	0.674188	0.004749
P02786	TFR1_HUMAN	Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2	0.673928	0.00447
Q13510	ASAH1_HUMAN	Acid ceramidase OS=Homo sapiens OX=9606 GN=ASAH1 PE=1 SV=5	0.673864	0.001567
O00116	ADAS_HUMAN	Alkylldihydroxyacetonephosphate synthase peroxisomal OS=Homo sapiens OX=9606 GN=AGPS PE=1 SV=1	0.673729	0.003553
O76021	RL1D1_HUMAN	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RSL1D1 PE=1 SV=3	0.673705	0.001226
O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens OX=9606 GN=CLIC1 PE=1 SV=4	0.673551	4.63E-04
P12270	TPR_HUMAN	Nucleoprotein TPR OS=Homo sapiens OX=9606 GN=TPR PE=1 SV=3	0.673415	0.001476
Q02878	RL6_HUMAN	60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3	0.673255	0.002328
Q96G03	PGM2_HUMAN	Phosphoglucosyltransferase-2 OS=Homo sapiens OX=9606 GN=PGM2 PE=1 SV=4	0.67319	0.003318
O75153	CLU_HUMAN	Clustered mitochondria protein homolog OS=Homo sapiens OX=9606 GN=CLUH PE=1 SV=2	0.673145	0.004837
P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens OX=9606 GN=APEX1 PE=1 SV=2	0.673019	0.005968
P61964	WDR5_HUMAN	WD repeat-containing protein 5 OS=Homo sapiens OX=9606 GN=WDR5 PE=1 SV=1	0.672336	9.42E-04
Q15102	PA1B3_HUMAN	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens OX=9606 GN=PAFAH1B3 PE=1 SV=1	0.672079	0.001737
Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1 PE=1 SV=2	0.671781	0.002734
P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1	0.671748	0.003682
P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=3	0.671674	0.003547
Q15126	PMVK_HUMAN	Phosphomevalonate kinase OS=Homo sapiens OX=9606 GN=PMVK PE=1 SV=3	0.671636	0.001689
P33993	MCM7_HUMAN	DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=1 SV=4	0.671629	0.00261
O75521	ECI2_HUMAN	Enoyl-CoA delta isomerase 2 mitochondrial OS=Homo sapiens OX=9606 GN=ECI2 PE=1 SV=4	0.671513	0.001767
P53990	IST1_HUMAN	IST1 homolog OS=Homo sapiens OX=9606 GN=IST1 PE=1 SV=1	0.671272	0.001719
Q8WUA2	PPIL4_HUMAN	Peptidyl-prolyl cis-trans isomerase-like 4 OS=Homo sapiens OX=9606 GN=PPIL4 PE=1 SV=1	0.670863	0.001695
Q15654	TRIP6_HUMAN	Thyroid receptor-interacting protein 6 OS=Homo sapiens OX=9606 GN=TRIP6 PE=1 SV=3	0.670301	0.001621
Q9NTI5	PDS5B_HUMAN	Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens OX=9606 GN=PDS5B PE=1 SV=1	0.670295	0.007442
P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=2	0.669851	0.001856
P26196	DDX6_HUMAN	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens OX=9606 GN=DDX6 PE=1 SV=2	0.669606	0.002673
P61247	RS3A_HUMAN	40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=2	0.669221	0.003504
Q16891	MIC60_HUMAN	MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=1	0.668959	9.73E-04
Q9NX40	OCAD1_HUMAN	OCIA domain-containing protein 1 OS=Homo sapiens OX=9606 GN=OCAD1 PE=1 SV=1	0.668515	0.001282
O00203	AP3B1_HUMAN	AP-3 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP3B1 PE=1 SV=3	0.668486	0.001311
P06753	TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=2	0.668336	0.001849
P00390	GSHR_HUMAN	Glutathione reductase mitochondrial OS=Homo sapiens OX=9606 GN=GSR PE=1 SV=2	0.668253	0.005906

Q92542	NICA_HUMAN	Nicastrin OS=Homo sapiens OX=9606 GN=NCSTN PE=1 SV=2	0.66821	0.003922
P19525	E2AK2_HUMAN	Interferon-induced double-stranded RNA-activated protein kinase OS=Homo sapiens OX=9606 GN=EIF2AK2 PE=1 SV=2	0.668145	0.004721
O14579	COPE_HUMAN	Coatomer subunit epsilon OS=Homo sapiens OX=9606 GN=COPE PE=1 SV=3	0.667998	0.001874
Q9NRG9	AAAS_HUMAN	Aladin OS=Homo sapiens OX=9606 GN=AAAS PE=1 SV=1	0.667691	0.003165
P60981	DEST_HUMAN	Destrin OS=Homo sapiens OX=9606 GN=DSTN PE=1 SV=3	0.667667	0.001813
Q9NV06	DCA13_HUMAN	DDB1- and CUL4-associated factor 13 OS=Homo sapiens OX=9606 GN=DCAF13 PE=1 SV=2	0.667381	0.001853
P25205	MCM3_HUMAN	DNA replication licensing factor MCM3 OS=Homo sapiens OX=9606 GN=MCM3 PE=1 SV=3	0.667164	0.003017
Q9Y3A3	PHOCN_HUMAN	MOB-like protein phocein OS=Homo sapiens OX=9606 GN=MOB4 PE=1 SV=1	0.667053	0.001934
Q12933	TRAF2_HUMAN	TNF receptor-associated factor 2 OS=Homo sapiens OX=9606 GN=TRAF2 PE=1 SV=2	0.666998	0.001874
Q9Y3I0	RTCB_HUMAN	RNA-splicing ligase RtcB homolog OS=Homo sapiens OX=9606 GN=RTCB PE=1 SV=1	0.66684	0.00264
P28331	NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS1 PE=1 SV=3	0.666283	2.53E-04
Q16576	RBBP7_HUMAN	Histone-binding protein RBBP7 OS=Homo sapiens OX=9606 GN=RBBP7 PE=1 SV=1	0.666244	0.005482
P30154	2AAB_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=3	0.666206	0.001911
Q9P1F3	ABRAL_HUMAN	Costars family protein ABRACL OS=Homo sapiens OX=9606 GN=ABRACL PE=1 SV=1	0.666186	0.003504
O14828	SCAM3_HUMAN	Secretory carrier-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=SCAMP3 PE=1 SV=3	0.665462	0.002101
Q9Y285	SYFA_HUMAN	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=3	0.665441	0.003196
Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASP1 PE=1 SV=2	0.665163	0.001705
P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2	0.664897	0.001545
Q9BWM7	SFXN3_HUMAN	Sideroflexin-3 OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=3	0.664539	0.001903
P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1	0.664514	0.001928
Q9NVH1	DJC11_HUMAN	DnaJ homolog subfamily C member 11 OS=Homo sapiens OX=9606 GN=DNAJC11 PE=1 SV=2	0.664507	0.001947
P49642	PRI1_HUMAN	DNA primase small subunit OS=Homo sapiens OX=9606 GN=PRIM1 PE=1 SV=1	0.664213	0.001895
O75947	ATP5H_HUMAN	ATP synthase subunit d mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PD PE=1 SV=3	0.663674	0.001934
P48634	PRC2A_HUMAN	Protein PRRC2A OS=Homo sapiens OX=9606 GN=PRRC2A PE=1 SV=3	0.663637	0.002462
Q9BRA2	TXD17_HUMAN	Thioredoxin domain-containing protein 17 OS=Homo sapiens OX=9606 GN=TXNDC17 PE=1 SV=1	0.663323	0.001973
P51148	RAB5C_HUMAN	Ras-related protein Rab-5C OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=2	0.663191	0.003342
P37837	TALDO_HUMAN	Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=1 SV=2	0.662999	0.001916
Q02978	M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens OX=9606 GN=SLC25A11 PE=1 SV=3	0.662918	0.001017
P26641	EF1G_HUMAN	Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EEF1G PE=1 SV=3	0.662884	0.00359
P23526	SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=AHCY PE=1 SV=4	0.662668	0.003022
P62310	LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSM3 OS=Homo sapiens OX=9606 GN=LSM3 PE=1 SV=2	0.662583	0.002028
Q9NRF8	PYRG2_HUMAN	CTP synthase 2 OS=Homo sapiens OX=9606 GN=CTPS2 PE=1 SV=1	0.662419	0.001903
P61020	RAB5B_HUMAN	Ras-related protein Rab-5B OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1	0.662419	0.002015
Q9UHY1	NRBP_HUMAN	Nuclear receptor-binding protein OS=Homo sapiens OX=9606 GN=NRBP1 PE=1 SV=1	0.662157	0.004761
Q13098	CSN1_HUMAN	COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=4	0.662064	0.004333
P28340	DPOD1_HUMAN	DNA polymerase delta catalytic subunit OS=Homo sapiens OX=9606 GN=POLD1 PE=1 SV=2	0.661611	0.002452
Q9P0M6	H2AW_HUMAN	Core histone macro-H2A.2 OS=Homo sapiens OX=9606 GN=H2AFY2 PE=1 SV=3	0.661573	0.002008
P05387	RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1	0.661513	0.003491

P62910	RL32_HUMAN	60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=2	0.661402	0.001107
Q8TD16	BICD2_HUMAN	Protein bicaudal D homolog 2 OS=Homo sapiens OX=9606 GN=BICD2 PE=1 SV=1	0.660911	0.001976
Q8N0X7	SPART_HUMAN	Spartin OS=Homo sapiens OX=9606 GN=SPART PE=1 SV=1	0.660715	1.13E-04
P12004	PCNA_HUMAN	Proliferating cell nuclear antigen OS=Homo sapiens OX=9606 GN=PCNA PE=1 SV=1	0.660599	0.003161
Q8WVM8	SCFD1_HUMAN	Sec1 family domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SCFD1 PE=1 SV=4	0.66032	0.008857
O94874	UFL1_HUMAN	E3 UFM1-protein ligase 1 OS=Homo sapiens OX=9606 GN=UFL1 PE=1 SV=2	0.660251	5.64E-04
P01024	CO3_HUMAN	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2	0.660241	0.002028
O00233	PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens OX=9606 GN=PSMD9 PE=1 SV=3	0.66015	0.001987
P36578	RL4_HUMAN	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5	0.659892	0.002027
P24941	CDK2_HUMAN	Cyclin-dependent kinase 2 OS=Homo sapiens OX=9606 GN=CDK2 PE=1 SV=2	0.659857	8.12E-04
O95573	ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens OX=9606 GN=ACSL3 PE=1 SV=3	0.659771	0.002984
Q9H4A4	AMPB_HUMAN	Aminopeptidase B OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=2	0.659629	0.004091
Q9HCN8	SDF2L_HUMAN	Stromal cell-derived factor 2-like protein 1 OS=Homo sapiens OX=9606 GN=SDF2L1 PE=1 SV=2	0.659158	0.002084
Q9H4A6	GOLP3_HUMAN	Golgi phosphoprotein 3 OS=Homo sapiens OX=9606 GN=GOLPH3 PE=1 SV=1	0.658787	0.001963
Q8WWY3	PRP31_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens OX=9606 GN=PRPF31 PE=1 SV=2	0.658719	0.003161
Q96AG4	LRC59_HUMAN	Leucine-rich repeat-containing protein 59 OS=Homo sapiens OX=9606 GN=LRRCS9 PE=1 SV=1	0.658693	0.00269
Q9NQ88	TIGAR_HUMAN	Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens OX=9606 GN=TIGAR PE=1 SV=1	0.658585	0.00204
Q15436	SC23A_HUMAN	Protein transport protein Sec23A OS=Homo sapiens OX=9606 GN=SEC23A PE=1 SV=2	0.658443	3.18E-04
P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens OX=9606 GN=PPP1CB PE=1 SV=3	0.658329	0.002097
Q07666	KHDR1_HUMAN	KH domain-containing RNA-binding signal transduction-associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRBS1 PE=1 SV=1	0.658247	0.001885
Q9UJ70	NAGK_HUMAN	N-acetyl-D-glucosamine kinase OS=Homo sapiens OX=9606 GN=NAGK PE=1 SV=4	0.657859	0.00495
P31689	DNJA1_HUMAN	DnaJ homolog subfamily A member 1 OS=Homo sapiens OX=9606 GN=DNAJA1 PE=1 SV=2	0.657643	0.001949
P05783	K1C18_HUMAN	Keratin type I cytoskeletal 18 OS=Homo sapiens OX=9606 GN=KRT18 PE=1 SV=2	0.657112	0.001585
P31947	1433S_HUMAN	14-3-3 protein sigma OS=Homo sapiens OX=9606 GN=SFN PE=1 SV=1	0.657013	0.003485
P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E OS=Homo sapiens OX=9606 GN=SNRPE PE=1 SV=1	0.656836	0.002039
Q9NPF4	OSGEP_HUMAN	Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens OX=9606 GN=OSGEP PE=1 SV=1	0.656516	0.002904
Q92990	GLMN_HUMAN	Glomulin OS=Homo sapiens OX=9606 GN=GLMN PE=1 SV=2	0.656116	0.0038
Q14331	FRG1_HUMAN	Protein FRG1 OS=Homo sapiens OX=9606 GN=FRG1 PE=1 SV=1	0.656097	0.002131
Q9Y371	SHLB1_HUMAN	Endophilin-B1 OS=Homo sapiens OX=9606 GN=SH3GLB1 PE=1 SV=1	0.656062	7.49E-04
Q9BQ39	DDX50_HUMAN	ATP-dependent RNA helicase DDX50 OS=Homo sapiens OX=9606 GN=DDX50 PE=1 SV=1	0.655892	0.002135
O60610	DIAP1_HUMAN	Protein diaphanous homolog 1 OS=Homo sapiens OX=9606 GN=DIAPH1 PE=1 SV=2	0.655865	9.00E-04
Q9HCC0	MCCB_HUMAN	Methylcrotonyl-CoA carboxylase beta chain mitochondrial OS=Homo sapiens OX=9606 GN=MCC2C PE=1 SV=1	0.655736	8.18E-04
Q96N66	MBOA7_HUMAN	Lysophospholipid acyltransferase 7 OS=Homo sapiens OX=9606 GN=MBOAT7 PE=1 SV=2	0.655501	0.002131
P60510	PP4C_HUMAN	Serine/threonine-protein phosphatase 4 catalytic subunit OS=Homo sapiens OX=9606 GN=PPP4C PE=1 SV=1	0.655352	0.001207
Q9UHQ9	NB5R1_HUMAN	NADH-cytochrome b5 reductase 1 OS=Homo sapiens OX=9606 GN=CYB5R1 PE=1 SV=1	0.655299	0.002212
O95487	SC24B_HUMAN	Protein transport protein Sec24B OS=Homo sapiens OX=9606 GN=SEC24B PE=1 SV=2	0.655166	0.002141
P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=4	0.65491	0.003139

P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens OX=9606 GN=SNRPD3 PE=1 SV=1	0.654865	0.003228
Q9Y224	RTRAF_HUMAN	RNA transcription translation and transport factor protein OS=Homo sapiens OX=9606 GN=RTRAF PE=1 SV=1	0.654774	0.004084
Q96K17	BT3L4_HUMAN	Transcription factor BTF3 homolog 4 OS=Homo sapiens OX=9606 GN=BTF3L4 PE=1 SV=1	0.654613	0.002212
O95295	SNAPN_HUMAN	SNARE-associated protein Snapin OS=Homo sapiens OX=9606 GN=SNAPIN PE=1 SV=1	0.654478	0.002249
Q01105	SET_HUMAN	Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=3	0.654131	0.002225
O60826	CCD22_HUMAN	Coiled-coil domain-containing protein 22 OS=Homo sapiens OX=9606 GN=CCDC22 PE=1 SV=1	0.653917	0.002197
P31153	METK2_HUMAN	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens OX=9606 GN=MAT2A PE=1 SV=1	0.653795	0.005211
P54577	SYYC_HUMAN	Tyrosine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=YARS1 PE=1 SV=4	0.652533	0.001021
O43148	MCES_HUMAN	mRNA cap guanine-N7 methyltransferase OS=Homo sapiens OX=9606 GN=RNMT PE=1 SV=1	0.6525	0.002252
P67809	YBOX1_HUMAN	Y-box-binding protein 1 OS=Homo sapiens OX=9606 GN=YBX1 PE=1 SV=3	0.652281	0.00224
P04792	HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2	0.652188	0.002026
P28065	PSB9_HUMAN	Proteasome subunit beta type-9 OS=Homo sapiens OX=9606 GN=PSMB9 PE=1 SV=2	0.652077	0.002252
P33992	MCM5_HUMAN	DNA replication licensing factor MCM5 OS=Homo sapiens OX=9606 GN=MCM5 PE=1 SV=5	0.651785	0.001421
O75643	U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens OX=9606 GN=SNRNP200 PE=1 SV=2	0.6516	0.001949
P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens OX=9606 GN=VDAC1 PE=1 SV=2	0.651305	0.002299
O00178	GTPB1_HUMAN	GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP1 PE=1 SV=3	0.651099	0.002328
P35606	COPB2_HUMAN	Coatomer subunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2	0.650898	8.31E-04
Q9NW13	RBM28_HUMAN	RNA-binding protein 28 OS=Homo sapiens OX=9606 GN=RBM28 PE=1 SV=3	0.650746	0.00232
P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 OS=Homo sapiens OX=9606 GN=AKR1A1 PE=1 SV=3	0.650654	0.002804
P49005	DPOD2_HUMAN	DNA polymerase delta subunit 2 OS=Homo sapiens OX=9606 GN=POLD2 PE=1 SV=1	0.650639	0.002295
Q16181	SEPT7_HUMAN	Septin-7 OS=Homo sapiens OX=9606 GN=SEPTIN7 PE=1 SV=2	0.649814	0.003429
Q12979	ABR_HUMAN	Active breakpoint cluster region-related protein OS=Homo sapiens OX=9606 GN=ABR PE=1 SV=2	0.649435	0.002301
P68036	UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens OX=9606 GN=UBE2L3 PE=1 SV=1	0.649178	0.002387
Q9NWH9	SLTM_HUMAN	SAFB-like transcription modulator OS=Homo sapiens OX=9606 GN=SLTM PE=1 SV=2	0.648778	0.002387
Q9BRT2	UQCC2_HUMAN	Ubiquinol-cytochrome-c reductase complex assembly factor 2 OS=Homo sapiens OX=9606 GN=UQCC2 PE=1 SV=1	0.648269	0.002391
Q13153	PAK1_HUMAN	Serine/threonine-protein kinase PAK 1 OS=Homo sapiens OX=9606 GN=PAK1 PE=1 SV=2	0.648208	0.00237
Q8N5A5	ZGPAT_HUMAN	Zinc finger CCCH-type with G patch domain-containing protein OS=Homo sapiens OX=9606 GN=ZGPAT PE=1 SV=3	0.648197	0.0024
Q8IXB1	DJC10_HUMAN	DnaJ homolog subfamily C member 10 OS=Homo sapiens OX=9606 GN=DNAJC10 PE=1 SV=2	0.648165	0.002225
P22676	CALB2_HUMAN	Calretinin OS=Homo sapiens OX=9606 GN=CALB2 PE=2 SV=2	0.647813	0.002295
Q13435	SF3B2_HUMAN	Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=2	0.647809	0.003228
Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=5	0.647124	0.003922
Q86W42	THOC6_HUMAN	THO complex subunit 6 homolog OS=Homo sapiens OX=9606 GN=THOC6 PE=1 SV=1	0.64689	0.001342
Q9Y3B3	TMED7_HUMAN	Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens OX=9606 GN=TMED7 PE=1 SV=2	0.646746	0.002478
Q8TCG1	CIP2A_HUMAN	Protein CIP2A OS=Homo sapiens OX=9606 GN=CIP2A PE=1 SV=2	0.646265	0.003641
O43324	MCA3_HUMAN	Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens OX=9606 GN=EEF1E1 PE=1 SV=1	0.646259	0.002512
Q92620	PRP16_HUMAN	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 OS=Homo sapiens OX=9606 GN=DHX38 PE=1 SV=2	0.64625	0.002448
O95202	LETM1_HUMAN	Mitochondrial proton/calcium exchanger protein OS=Homo sapiens OX=9606 GN=LETM1 PE=1 SV=1	0.646214	0.003892
Q86X76	NIT1_HUMAN	Deaminated glutathione amidase OS=Homo sapiens OX=9606 GN=NIT1 PE=1 SV=2	0.645764	0.009197

O75955	FLOT1_HUMAN	Flotillin-1 OS=Homo sapiens OX=9606 GN=FLOT1 PE=1 SV=3	0.644905	0.003264
Q02241	KIF23_HUMAN	Kinesin-like protein KIF23 OS=Homo sapiens OX=9606 GN=KIF23 PE=1 SV=3	0.644634	0.003135
Q9Y2H6	FND3A_HUMAN	Fibronectin type-III domain-containing protein 3A OS=Homo sapiens OX=9606 GN=FND3A PE=1 SV=4	0.644481	0.001577
Q5VTR2	BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens OX=9606 GN=RNF20 PE=1 SV=2	0.64427	0.001354
P40926	MDHM_HUMAN	Malate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3	0.644096	0.001798
Q9Y6M9	NDUB9_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens OX=9606 GN=NDUB9 PE=1 SV=3	0.644082	0.002527
Q13155	AIMP2_HUMAN	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens OX=9606 GN=AIMP2 PE=1 SV=2	0.643758	0.002553
O60749	SNX2_HUMAN	Sorting nexin-2 OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=2	0.643752	0.004696
Q969Z0	FAKD4_HUMAN	FAST kinase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=TBRG4 PE=1 SV=1	0.643604	0.002601
Q7Z6Z7	HUWE1_HUMAN	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens OX=9606 GN=HUWE1 PE=1 SV=3	0.643602	5.24E-04
Q9GZN8	CT027_HUMAN	UPF0687 protein C20orf27 OS=Homo sapiens OX=9606 GN=C20orf27 PE=1 SV=3	0.643578	0.002444
P23258	TBG1_HUMAN	Tubulin gamma-1 chain OS=Homo sapiens OX=9606 GN=TUBG1 PE=1 SV=2	0.643479	0.002117
Q92552	RT27_HUMAN	28S ribosomal protein S27 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS27 PE=1 SV=3	0.643418	0.00265
Q9Y6D5	BIG2_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens OX=9606 GN=ARFGF2 PE=1 SV=3	0.643175	0.002567
Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=4	0.642937	0.002615
Q9H8S9	MOB1A_HUMAN	MOB kinase activator 1A OS=Homo sapiens OX=9606 GN=MOB1A PE=1 SV=4	0.642044	0.002512
Q7L9L4	MOB1B_HUMAN	MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B PE=1 SV=3	0.642044	0.002512
P42771	CDN2A_HUMAN	Cyclin-dependent kinase inhibitor 2A OS=Homo sapiens OX=9606 GN=CDKN2A PE=1 SV=2	0.64201	0.004789
P05161	ISG15_HUMAN	Ubiquitin-like protein ISG15 OS=Homo sapiens OX=9606 GN=ISG15 PE=1 SV=5	0.641998	0.00257
Q9NTZ6	RBM12_HUMAN	RNA-binding protein 12 OS=Homo sapiens OX=9606 GN=RBM12 PE=1 SV=1	0.641939	0.00295
P60174	TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=3	0.641808	0.006947
O75348	VATG1_HUMAN	V-type proton ATPase subunit G 1 OS=Homo sapiens OX=9606 GN=ATP6V1G1 PE=1 SV=3	0.641594	0.00261
O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens OX=9606 GN=ARPC2 PE=1 SV=1	0.641038	0.005818
O75676	KS6A4_HUMAN	Ribosomal protein S6 kinase alpha-4 OS=Homo sapiens OX=9606 GN=RPS6KA4 PE=1 SV=1	0.64096	0.003312
P04843	RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1	0.640919	0.002012
P52294	IMA5_HUMAN	Importin subunit alpha-5 OS=Homo sapiens OX=9606 GN=KPNA1 PE=1 SV=3	0.639591	0.008459
P62837	UB2D2_HUMAN	Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens OX=9606 GN=UBE2D2 PE=1 SV=1	0.639377	0.002793
P61077	UB2D3_HUMAN	Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens OX=9606 GN=UBE2D3 PE=1 SV=1	0.639377	0.002793
Q92696	PGTA_HUMAN	Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens OX=9606 GN=RABGGTA PE=1 SV=2	0.639118	0.002274
O15213	WDR46_HUMAN	WD repeat-containing protein 46 OS=Homo sapiens OX=9606 GN=WDR46 PE=1 SV=3	0.638137	0.005881
O60936	NOL3_HUMAN	Nucleolar protein 3 OS=Homo sapiens OX=9606 GN=NOL3 PE=1 SV=2	0.637663	0.002783
Q8IXM2	BAP18_HUMAN	Chromatin complexes subunit BAP18 OS=Homo sapiens OX=9606 GN=BAP18 PE=1 SV=1	0.63743	0.002654
P46108	CRK_HUMAN	Adapter molecule crk OS=Homo sapiens OX=9606 GN=CRK PE=1 SV=2	0.637246	0.00286
O00762	UBE2C_HUMAN	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens OX=9606 GN=UBE2C PE=1 SV=1	0.63648	0.002864
Q9UMS4	PRP19_HUMAN	Pre-mRNA-processing factor 19 OS=Homo sapiens OX=9606 GN=PRPF19 PE=1 SV=1	0.636409	0.005304
Q05519	SRSF11_HUMAN	Serine/arginine-rich splicing factor 11 OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1	0.636362	0.002718
P23919	KTHY_HUMAN	Thymidylate kinase OS=Homo sapiens OX=9606 GN=DTYMK PE=1 SV=4	0.636275	0.002864

O75390	CISY_HUMAN	Citrate synthase mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=2	0.636125	0.002549
Q13428	TCOF_HUMAN	Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 PE=1 SV=3	0.635965	0.001673
P84098	RL19_HUMAN	60S ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1	0.635927	0.002743
Q9BUQ8	DDX23_HUMAN	Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens OX=9606 GN=DDX23 PE=1 SV=3	0.635844	0.003605
Q9Y570	PPME1_HUMAN	Protein phosphatase methylesterase 1 OS=Homo sapiens OX=9606 GN=PPME1 PE=1 SV=3	0.634802	0.003908
Q96A49	SYAP1_HUMAN	Synapse-associated protein 1 OS=Homo sapiens OX=9606 GN=SYAP1 PE=1 SV=1	0.634785	0.006157
Q13144	EI2BE_HUMAN	Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens OX=9606 GN=EIF2B5 PE=1 SV=3	0.634209	0.004328
P61421	VA0D1_HUMAN	V-type proton ATPase subunit d 1 OS=Homo sapiens OX=9606 GN=ATP6V0D1 PE=1 SV=1	0.634141	0.005414
P26640	SYVC_HUMAN	Valine--tRNA ligase OS=Homo sapiens OX=9606 GN=VAR51 PE=1 SV=4	0.63402	2.06E-04
Q15392	DHC24_HUMAN	Delta(24)-sterol reductase OS=Homo sapiens OX=9606 GN=DHCR24 PE=1 SV=2	0.633936	0.002904
Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=2	0.633872	0.002234
P09493	TPM1_HUMAN	Tropomyosin alpha-1 chain OS=Homo sapiens OX=9606 GN=TPM1 PE=1 SV=2	0.633872	0.002926
Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=5	0.632977	0.006793
P05023	AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 PE=1 SV=1	0.632791	0.001605
Q9NVE7	PANK4_HUMAN	4'-phosphopantetheine phosphatase OS=Homo sapiens OX=9606 GN=PANK4 PE=1 SV=1	0.632217	0.003042
Q9H773	DCTP1_HUMAN	dCTP pyrophosphatase 1 OS=Homo sapiens OX=9606 GN=DCTPP1 PE=1 SV=1	0.632072	0.002374
O15020	SPTN2_HUMAN	Spectrin beta chain non-erythrocytic 2 OS=Homo sapiens OX=9606 GN=SPTBN2 PE=1 SV=3	0.631806	1.89E-04
P33240	CSTF2_HUMAN	Cleavage stimulation factor subunit 2 OS=Homo sapiens OX=9606 GN=CSTF2 PE=1 SV=1	0.631716	0.005138
Q16401	PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens OX=9606 GN=PSMD5 PE=1 SV=3	0.631355	0.001028
O43395	PRPF3_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens OX=9606 GN=PRPF3 PE=1 SV=2	0.631133	0.002981
P08133	ANXA6_HUMAN	Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3	0.631064	1.48E-05
Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 OS=Homo sapiens OX=9606 GN=GCN1 PE=1 SV=6	0.630866	7.97E-05
Q99959	PKP2_HUMAN	Plakophilin-2 OS=Homo sapiens OX=9606 GN=PKP2 PE=1 SV=2	0.630581	0.008596
Q53EL6	PDCD4_HUMAN	Programmed cell death protein 4 OS=Homo sapiens OX=9606 GN=PDCD4 PE=1 SV=2	0.629993	0.003129
Q9P2M7	CING_HUMAN	Cingulin OS=Homo sapiens OX=9606 GN=CGN PE=1 SV=2	0.629659	0.005828
P78417	GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=Homo sapiens OX=9606 GN=GSTO1 PE=1 SV=2	0.629641	0.003191
P30740	ILEU_HUMAN	Leukocyte elastase inhibitor OS=Homo sapiens OX=9606 GN=SERPINB1 PE=1 SV=1	0.629382	0.002301
P99999	CYC_HUMAN	Cytochrome c OS=Homo sapiens OX=9606 GN=CYCS PE=1 SV=2	0.628851	0.005221
P07384	CAN1_HUMAN	Calpain-1 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN1 PE=1 SV=1	0.62861	0.002945
Q9H8Y8	GORS2_HUMAN	Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2 PE=1 SV=3	0.628357	5.38E-04
O94992	HEX11_HUMAN	Protein HEXIM1 OS=Homo sapiens OX=9606 GN=HEXIM1 PE=1 SV=1	0.627658	0.003258
O75569	PRKRA_HUMAN	Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens OX=9606 GN=PRKRA PE=1 SV=1	0.626666	0.003295
P11234	RALB_HUMAN	Ras-related protein Ral-B OS=Homo sapiens OX=9606 GN=RALB PE=1 SV=1	0.626637	0.003295
Q9UMS0	NFU1_HUMAN	NFU1 iron-sulfur cluster scaffold homolog mitochondrial OS=Homo sapiens OX=9606 GN=NFU1 PE=1 SV=2	0.626407	0.002027
Q08257	QOR_HUMAN	Quinone oxidoreductase OS=Homo sapiens OX=9606 GN=CRYZ PE=1 SV=1	0.626185	0.00204
P55145	MANF_HUMAN	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens OX=9606 GN=MANF PE=1 SV=3	0.626056	0.002625
P82979	SARNP_HUMAN	SAP domain-containing ribonucleoprotein OS=Homo sapiens OX=9606 GN=SARNP PE=1 SV=3	0.626017	0.006242
O95758	PTBP3_HUMAN	Polypyrimidine tract-binding protein 3 OS=Homo sapiens OX=9606 GN=PTBP3 PE=1 SV=2	0.625789	0.003324

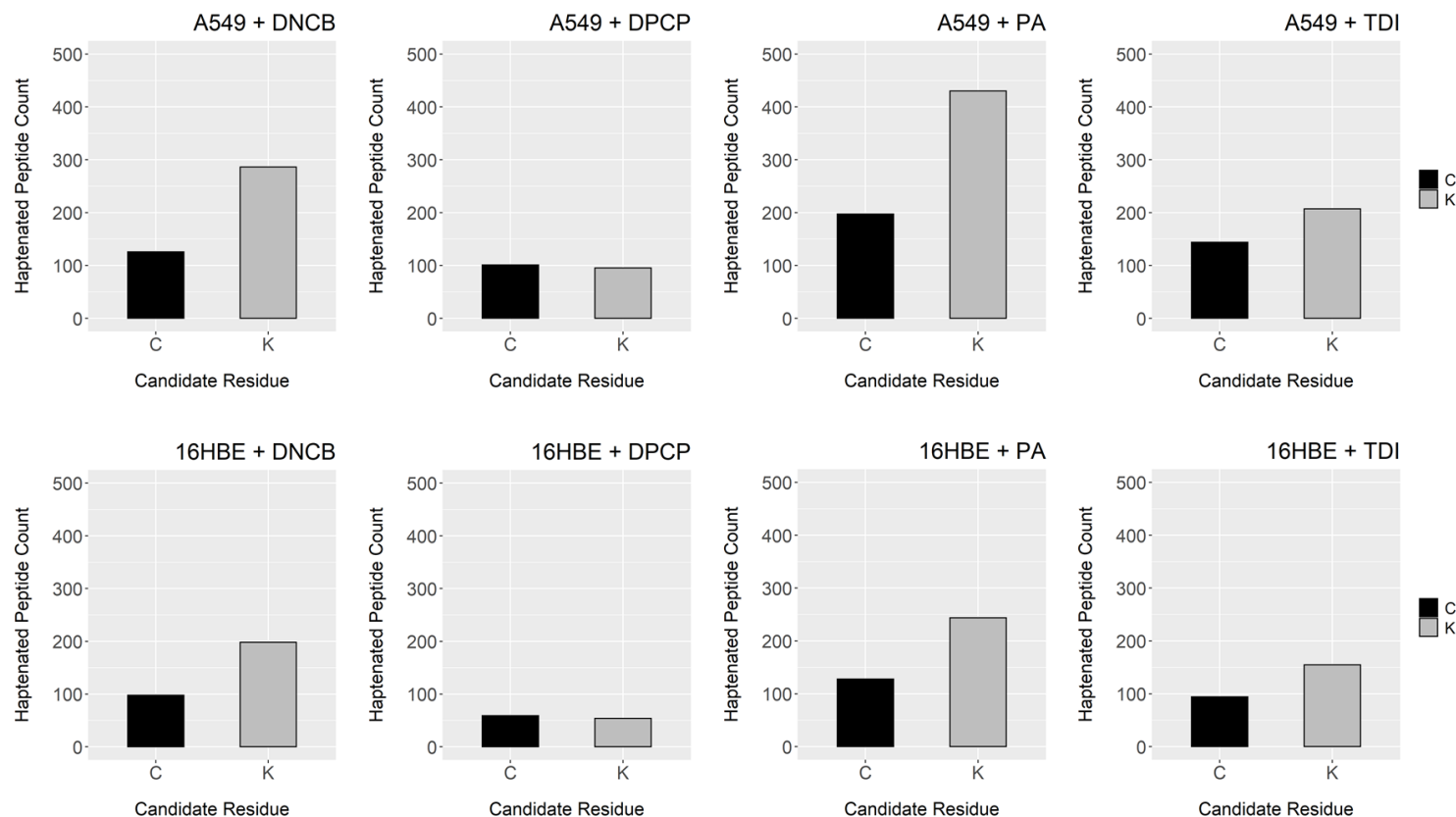
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Q6DD88	ATLA3_HUMAN	Atlastin-3 OS=Homo sapiens OX=9606 GN=ATL3 PE=1 SV=1	0.624473	2.75E-05
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Q53H82	LACB2_HUMAN	Endoribonuclease LACTB2 OS=Homo sapiens OX=9606 GN=LACTB2 PE=1 SV=2	0.624179	0.004694
Q9NRV9	HEBP1_HUMAN	Heme-binding protein 1 OS=Homo sapiens OX=9606 GN=HEBP1 PE=1 SV=1	0.624108	0.003336
Q6IAA8	LTOR1_HUMAN	Ragulator complex protein LAMTOR1 OS=Homo sapiens OX=9606 GN=LAMTOR1 PE=1 SV=2	0.624082	0.00536
P41250	GARS_HUMAN	Glycine--tRNA ligase OS=Homo sapiens OX=9606 GN=GARS1 PE=1 SV=3	0.623728	0.00405
O00541	PESC_HUMAN	Pescadillo homolog OS=Homo sapiens OX=9606 GN=PES1 PE=1 SV=1	0.623695	0.002739
P17812	PYRG1_HUMAN	CTP synthase 1 OS=Homo sapiens OX=9606 GN=CTPS1 PE=1 SV=2	0.623638	0.003139
Q9H330	TM245_HUMAN	Transmembrane protein 245 OS=Homo sapiens OX=9606 GN=TMEM245 PE=1 SV=3	0.623528	0.003479
Q9Y6E2	BZW2_HUMAN	Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606 GN=BZW2 PE=1 SV=1	0.623127	0.006599
Q93008	USP9X_HUMAN	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens OX=9606 GN=USP9X PE=1 SV=3	0.622831	9.29E-05
Q8N5K1	CISD2_HUMAN	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens OX=9606 GN=CISD2 PE=1 SV=1	0.622413	0.003387
Q9H6Z4	RANB3_HUMAN	Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=1	0.622372	0.002077
Q15435	PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PPP1R7 PE=1 SV=1	0.62017	0.005717
Q9Y289	SC5A6_HUMAN	Sodium-dependent multivitamin transporter OS=Homo sapiens OX=9606 GN=SLC5A6 PE=2 SV=2	0.619782	0.003479
P08865	RSSA_HUMAN	40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=4	0.619085	0.003415
Q9H6F5	CCD86_HUMAN	Coiled-coil domain-containing protein 86 OS=Homo sapiens OX=9606 GN=CCDC86 PE=1 SV=1	0.618769	0.003656
Q00653	NFKB2_HUMAN	Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens OX=9606 GN=NFKB2 PE=1 SV=4	0.618659	9.05E-04
P17858	PFKAL_HUMAN	ATP-dependent 6-phosphofructokinase liver type OS=Homo sapiens OX=9606 GN=PFKL PE=1 SV=6	0.618544	0.009723
Q9ULR0	ISY1_HUMAN	Pre-mRNA-splicing factor ISY1 homolog OS=Homo sapiens OX=9606 GN=ISY1 PE=1 SV=3	0.618425	0.003641
P62253	UB2G1_HUMAN	Ubiquitin-conjugating enzyme E2 G1 OS=Homo sapiens OX=9606 GN=UBE2G1 PE=1 SV=3	0.617834	0.003576
Q96B26	EXOS8_HUMAN	Exosome complex component RRP43 OS=Homo sapiens OX=9606 GN=EXOSC8 PE=1 SV=1	0.617419	0.003669
P42025	ACTY_HUMAN	Beta-actin OS=Homo sapiens OX=9606 GN=ACTR1B PE=1 SV=1	0.617217	0.008263
P51812	KS6A3_HUMAN	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens OX=9606 GN=RPS6KA3 PE=1 SV=1	0.615857	4.61E-04
Q13308	PTK7_HUMAN	Inactive tyrosine-protein kinase 7 OS=Homo sapiens OX=9606 GN=PTK7 PE=1 SV=2	0.615681	0.003695
P55196	AFAD_HUMAN	Afadin OS=Homo sapiens OX=9606 GN=AFDN PE=1 SV=3	0.614955	2.11E-04
P52630	STAT2_HUMAN	Signal transducer and activator of transcription 2 OS=Homo sapiens OX=9606 GN=STAT2 PE=1 SV=1	0.614883	0.003987
Q9Y320	TMX2_HUMAN	Thioredoxin-related transmembrane protein 2 OS=Homo sapiens OX=9606 GN=TMX2 PE=1 SV=1	0.614257	0.004915
P51398	RT29_HUMAN	28S ribosomal protein S29 mitochondrial OS=Homo sapiens OX=9606 GN=DAP3 PE=1 SV=1	0.613165	0.0098
Q15003	CND2_HUMAN	Condensin complex subunit 2 OS=Homo sapiens OX=9606 GN=NCAPH PE=1 SV=3	0.612977	4.12E-04
Q14141	SEPT6_HUMAN	Septin-6 OS=Homo sapiens OX=9606 GN=SEPTIN6 PE=1 SV=4	0.611962	0.006418
Q7Z3B4	NUP54_HUMAN	Nucleoporin p54 OS=Homo sapiens OX=9606 GN=NUP54 PE=1 SV=2	0.610348	0.003051
Q9UMY4	SNX12_HUMAN	Sorting nexin-12 OS=Homo sapiens OX=9606 GN=SNX12 PE=1 SV=4	0.610053	0.003387
P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens OX=9606 GN=PRKDC PE=1 SV=3	0.609735	0.001035
Q9H910	JUPI2_HUMAN	Jupiter microtubule associated homolog 2 OS=Homo sapiens OX=9606 GN=JPT2 PE=1 SV=1	0.609549	0.004712

Q9Y3D9	RT23_HUMAN	28S ribosomal protein S23 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS23 PE=1 SV=2	0.608855	0.004243
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Q9HB07	MYG1_HUMAN	UPF0160 protein MYG1 mitochondrial OS=Homo sapiens OX=9606 GN=C12orf10 PE=1 SV=2	0.6075	0.006193
Q9BRJ2	RM45_HUMAN	39S ribosomal protein L45 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL45 PE=1 SV=2	0.607443	0.004359
Q9BZX2	UCK2_HUMAN	Uridine-cytidine kinase 2 OS=Homo sapiens OX=9606 GN=UCK2 PE=1 SV=1	0.607357	0.00442
P35573	GDE_HUMAN	Glycogen debranching enzyme OS=Homo sapiens OX=9606 GN=AGL PE=1 SV=3	0.60733	0.003934
P11216	PYGB_HUMAN	Glycogen phosphorylase brain form OS=Homo sapiens OX=9606 GN=PYGB PE=1 SV=5	0.607234	0.004837
O95400	CD2B2_HUMAN	CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens OX=9606 GN=CD2BP2 PE=1 SV=1	0.606826	0.004228
Q9Y3P9	RBGP1_HUMAN	Rab GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RABGAP1 PE=1 SV=3	0.606523	0.008057
Q15149	PLEC_HUMAN	Plectin OS=Homo sapiens OX=9606 GN=PLEC PE=1 SV=3	0.606255	9.22E-04
P51580	TPMT_HUMAN	Thiopurine S-methyltransferase OS=Homo sapiens OX=9606 GN=TPMT PE=1 SV=1	0.605932	0.004359
Q6P3X3	TTC27_HUMAN	Tetratricopeptide repeat protein 27 OS=Homo sapiens OX=9606 GN=TTC27 PE=1 SV=1	0.60546	0.00893
P46060	RAGP1_HUMAN	Ran GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RANGAP1 PE=1 SV=1	0.60544	8.81E-04
P27361	MK03_HUMAN	Mitogen-activated protein kinase 3 OS=Homo sapiens OX=9606 GN=MAPK3 PE=1 SV=4	0.605074	0.004454
Q9NY12	GAR1_HUMAN	H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens OX=9606 GN=GAR1 PE=1 SV=1	0.604132	0.004462
Q9UBR2	CATZ_HUMAN	Cathepsin Z OS=Homo sapiens OX=9606 GN=CTSZ PE=1 SV=1	0.603428	0.004584
P50502	F10A1_HUMAN	Hsc70-interacting protein OS=Homo sapiens OX=9606 GN=ST13 PE=1 SV=2	0.603405	0.009346
P36873	PP1G_HUMAN	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens OX=9606 GN=PPP1CC PE=1 SV=1	0.602616	0.004603
P62753	RS6_HUMAN	40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1	0.602552	0.004536
O60934	NBN_HUMAN	Nibrin OS=Homo sapiens OX=9606 GN=NBN PE=1 SV=1	0.602127	0.004696
P57678	GEMI4_HUMAN	Gem-associated protein 4 OS=Homo sapiens OX=9606 GN=GEMIN4 PE=1 SV=2	0.602036	0.004944
P36957	ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex mitochondrial OS=Homo sapiens OX=9606 GN=DLST PE=1 SV=4	0.601324	0.006028
P48506	GSH1_HUMAN	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens OX=9606 GN=GCLC PE=1 SV=2	0.601294	0.004809
P16402	H13_HUMAN	Histone H1.3 OS=Homo sapiens OX=9606 GN=H1-3 PE=1 SV=2	0.600458	0.004761
Q9UBM7	DHCR7_HUMAN	7-dehydrocholesterol reductase OS=Homo sapiens OX=9606 GN=DHCR7 PE=1 SV=1	0.600297	0.004755
Q06203	PUR1_HUMAN	Amidophosphoribosyltransferase OS=Homo sapiens OX=9606 GN=PPAT PE=1 SV=1	0.600024	0.001379
P47813	IF1AX_HUMAN	Eukaryotic translation initiation factor 1A X-chromosomal OS=Homo sapiens OX=9606 GN=EIF1AX PE=1 SV=2	0.599795	0.007034
Q9Y5K6	CD2AP_HUMAN	CD2-associated protein OS=Homo sapiens OX=9606 GN=CD2AP PE=1 SV=1	0.599698	0.002425
Q9H444	CHM4B_HUMAN	Charged multivesicular body protein 4b OS=Homo sapiens OX=9606 GN=CHMP4B PE=1 SV=1	0.599216	0.004924
O94979	SC31A_HUMAN	Protein transport protein Sec31A OS=Homo sapiens OX=9606 GN=SEC31A PE=1 SV=3	0.59887	8.54E-04
P14618	KPYM_HUMAN	Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4	0.598795	0.008804
Q9H3N1	TMX1_HUMAN	Thioredoxin-related transmembrane protein 1 OS=Homo sapiens OX=9606 GN=TMX1 PE=1 SV=1	0.597769	0.004977
P62805	H4_HUMAN	Histone H4 OS=Homo sapiens OX=9606 GN=H4C1 PE=1 SV=2	0.597089	0.004915
Q9NV31	IMP3_HUMAN	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Homo sapiens OX=9606 GN=IMP3 PE=1 SV=1	0.596704	0.005105
P63104	1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1	0.596093	0.00427
Q96IX5	ATPMD_HUMAN	ATP synthase membrane subunit DAPIT mitochondrial OS=Homo sapiens OX=9606 GN=ATP5MD PE=1 SV=1	0.595158	0.005036
P11940	PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=2	0.594694	0.004908
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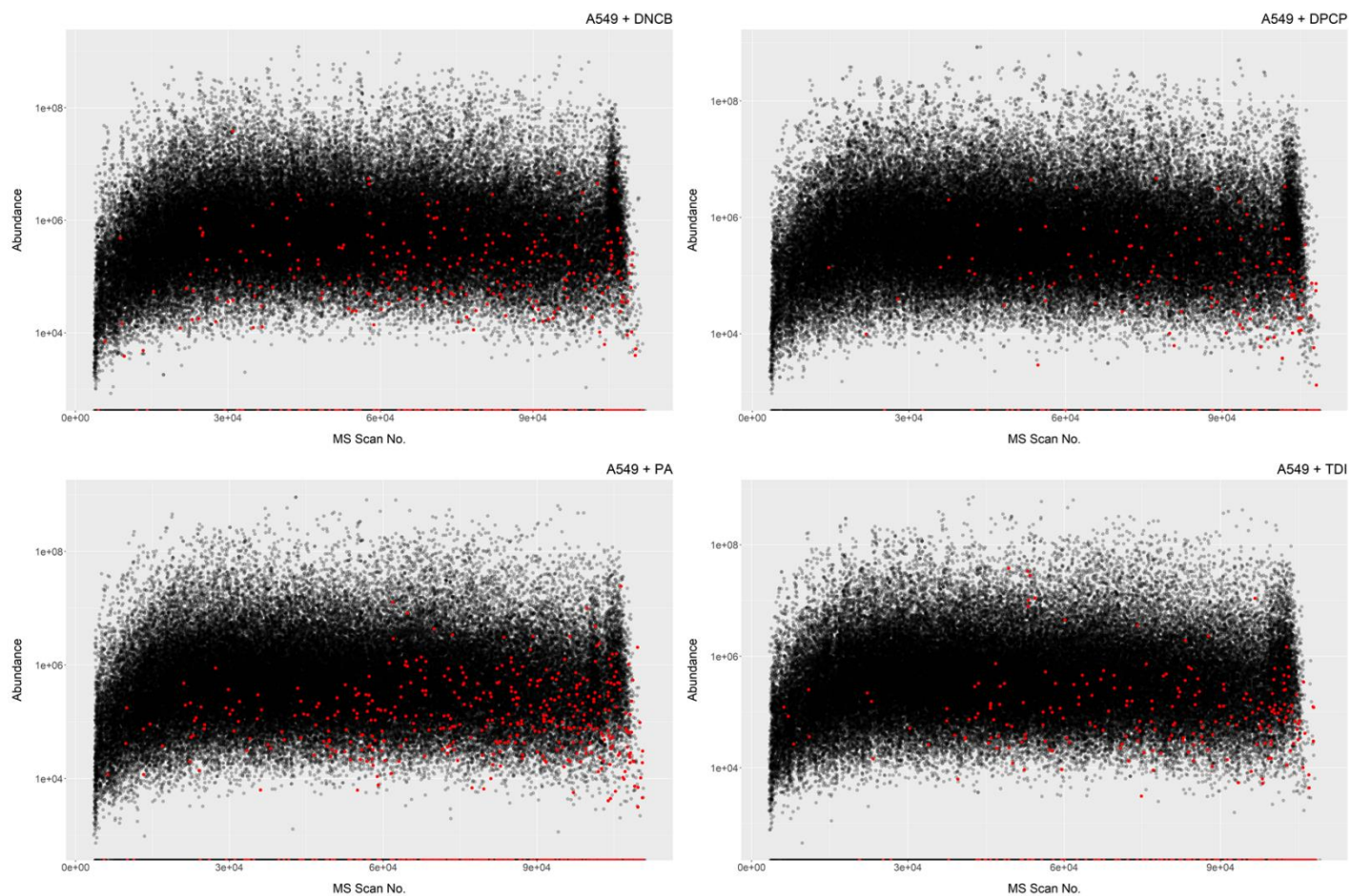
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O95197	RTN3_HUMAN	Reticulon-3 OS=Homo sapiens OX=9606 GN=RTN3 PE=1 SV=2	0.589221	0.005492
P41252	SYIC_HUMAN	Isoleucine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=IARS1 PE=1 SV=2	0.588931	0.003165
Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=2	0.588764	0.005511
P62942	FKBP1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens OX=9606 GN=FKBP1A PE=1 SV=2	0.588172	0.005836
O43264	ZW10_HUMAN	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens OX=9606 GN=ZW10 PE=1 SV=3	0.587885	0.004194
O43172	PRP4_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens OX=9606 GN=PRPF4 PE=1 SV=2	0.587465	0.003312
Q15907	RB11B_HUMAN	Ras-related protein Rab-11B OS=Homo sapiens OX=9606 GN=RAB11B PE=1 SV=4	0.58694	0.007738
P49458	SRP09_HUMAN	Signal recognition particle 9 kDa protein OS=Homo sapiens OX=9606 GN=SRP9 PE=1 SV=2	0.585894	0.007903
P53367	ARFP1_HUMAN	Arfaptin-1 OS=Homo sapiens OX=9606 GN=ARFIP1 PE=1 SV=2	0.584963	0.003934
Q9BRQ8	FSP1_HUMAN	Ferroptosis suppressor protein 1 OS=Homo sapiens OX=9606 GN=AIFM2 PE=1 SV=1	0.584963	0.005916
Q96I25	SPF45_HUMAN	Splicing factor 45 OS=Homo sapiens OX=9606 GN=RBM17 PE=1 SV=1	0.584963	0.006182
P62906	RL10A_HUMAN	60S ribosomal protein L10a OS=Homo sapiens OX=9606 GN=RPL10A PE=1 SV=2	0.584963	0.006302
Q9P206	K1522_HUMAN	Uncharacterized protein KIAA1522 OS=Homo sapiens OX=9606 GN=KIAA1522 PE=1 SV=2	0.584136	0.006205
Q86TX2	ACOT1_HUMAN	Acyl-coenzyme A thioesterase 1 OS=Homo sapiens OX=9606 GN=ACOT1 PE=1 SV=1	0.583518	0.006092
P46087	NOP2_HUMAN	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens OX=9606 GN=NOP2 PE=1 SV=2	0.58303	0.002882
Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens OX=9606 GN=HNRNPD PE=1 SV=1	0.582273	0.008147
Q9BSH4	TACO1_HUMAN	Translational activator of cytochrome c oxidase 1 OS=Homo sapiens OX=9606 GN=TACO1 PE=1 SV=1	0.580643	0.006342
Q9UBE0	SAE1_HUMAN	SUMO-activating enzyme subunit 1 OS=Homo sapiens OX=9606 GN=SAE1 PE=1 SV=1	0.58007	0.007347

Appendix Table 5: 16HBE14o⁻ global proteome changes following TDI exposure – Proteins with a significant difference in abundance are presented according to descending log2 fold change.

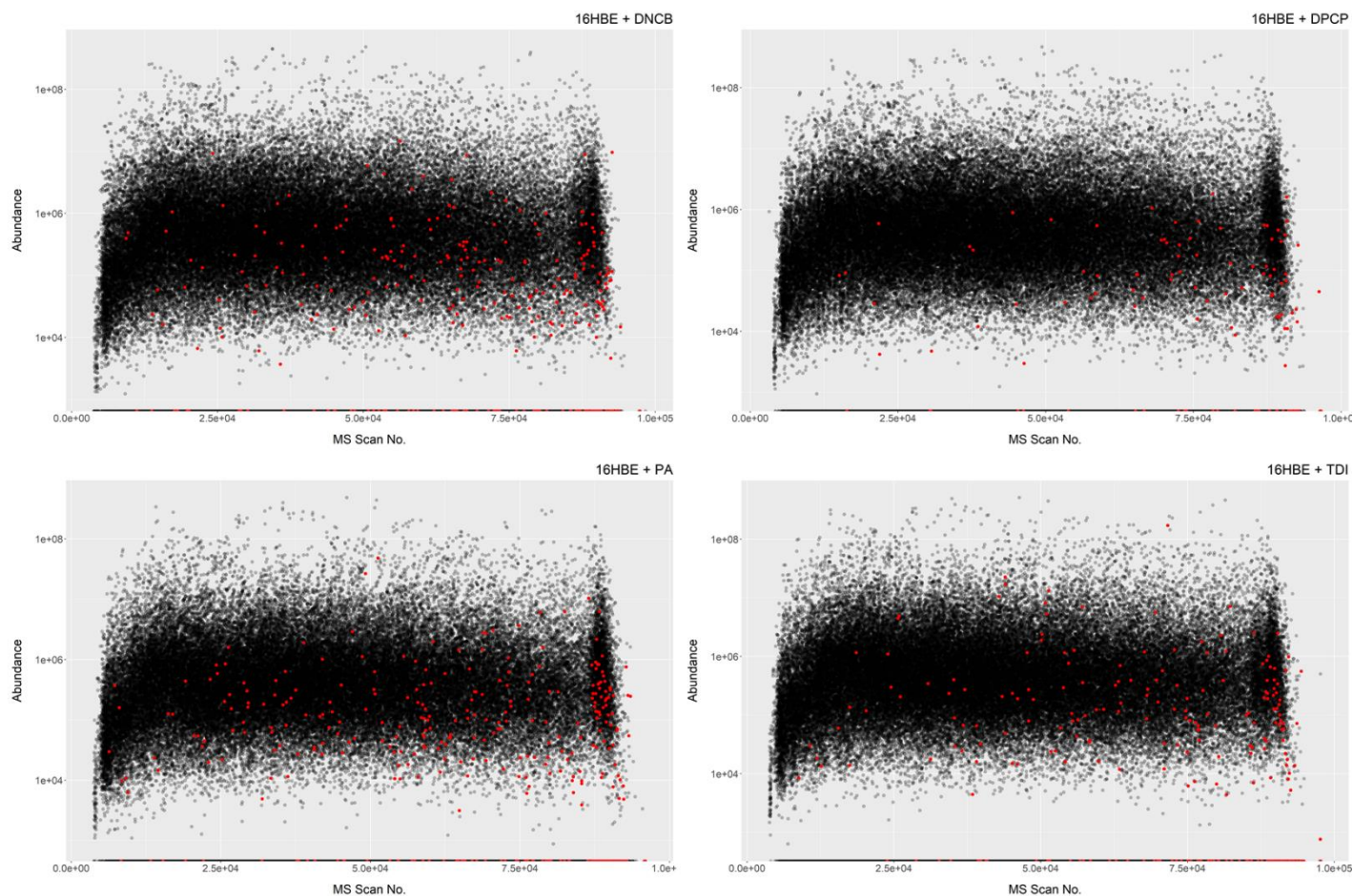
A.2.7 Candidate haptenome data



Appendix figure 3: Number of hapten modifications in the candidate haptenome for each cell line and sensitiser exposure – The number of cysteine and lysine residues in the global proteome data observed with an unvalidated hapten modification are presented. The results remain unvalidated until validation through inspection of the MS and MS/MS spectra associated with each peptide for doublet peptide m/z peaks and suitable coverage of y and b ions respectively.



Appendix figure 4: A549 candidate haptenome – The repertoire of peptides for each sensitiser exposure identified in human proteome database searches are presented according to their relative abundance and position within the total LC-MS separation gradient. Peptides identified with a hapten post-translational modification are highlighted.



Appendix figure 5: 16HBE14o⁻ candidate haptenome – The repertoire of peptides for each sensitiser exposure identified in human proteome database searches are presented according to their relative abundance and position within the total LC-MS separation gradient. Peptides identified with a hapten post-translational modification are highlighted.

A.2.8 Validated haptenome peptides

Appendix Table 6: Peptide repertoire of the A549 haptenome following DNCB exposure – Results are presented for peptides where satisfactory MS/MS spectrum validation was achieved.

Peptide	Accession	Uniprot ID	Protein Description	Replicate	Residue	Adduct
AVSTGVQAGIPMPC(+166.09)FTTALSFYDGYR	P52209	6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating	3	C	166
GLDGAVDMGARGAAAC(+166.09)DLVQR	Q8IZ83	A16A1_HUMAN	Aldehyde dehydrogenase family 16 member A1	3	C	166
LEPGSVCAVFLGGVGLAVIMGCK(+166.09)VAGASR	P11766	ADHX_HUMAN	Alcohol dehydrogenase class-3 (glutathione dehydrogenase)	2	K	166
EGISFHFTPVLVC(+166.09)KDPIR	Q9BRR6	ADPGK_HUMAN	ADP-dependent glucokinase	3	C	166
GDVDVSVPKVEGEMK(+166.09)VPDVEIK	Q09666	AHNK_HUMAN	Neuroblast differentiation-associated protein AHNK	3	K	166
KTFPTVNPSTGEVIC(+166.09)QVAEGDKEDVDK(+166.09)	P05091	ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial	2	K	166
KTFPTVNPSTGEVIC(+166.09)QVAEGDKEDVDK(+166.09)	P05091	ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial	2	C	166
MPILGLGTWK(+166.09)SPPGQVTEAVK	P15121	ALDR_HUMAN	Aldo-keto reductase family 1 member B1	1	K	166
AVAGDASESALLKCIELCC(+166.09)GSVK	P05023	AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 /K ATPase alpha-1 subunit)	1	C	166
KEDVGTVVGIDLGTTYSC(+166.09)VGVFK	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP	1	C	166
SLDGLSEAC(+166.09)GGAGSSGSAESGAGGGRR	Q96GS4	BORC6_HUMAN	BLOC-1-related complex subunit 6	3	C	166
RPGLLRPRGPCAC(+166.09)GCGCGSLHTDGDK	Q07021	C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial	2	C	166
DETVSDC(+166.09)SPHIANIGRLVEDMENK	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta	2	C	166
ISGGGGGKGGGGGGAGDGTEC(+166.09)RDIIAK(+166.09)	D6RIA3	CD054_HUMAN	Uncharacterized protein C4orf54	1	K	166
ISGGGGGKGGGGGGAGDGTEC(+166.09)RDIIAK(+166.09)	D6RIA3	CD054_HUMAN	Uncharacterized protein C4orf54	1	C	166
IPATTLMSTSATATETATK(+166.09)R	P16070	CD44_HUMAN	CD44 antigen	1	K	166
RSASQAGSKSQAVEKPPSEK(+166.09)PR	Q7Z7K6	CENPV_HUMAN	Centromere protein V	3	K	166

AGQSVIGLQMGTNKC(+166.09)ASQAGMTAYGTR	Q15417	CNN3_HUMAN	Calponin-3	1	C	166
VAGTGEGGLEEMVEELNSGKVMYAF(+166.09)RVK	Q9UJU6	DBNL_HUMAN	Drebrin-like protein	3	C	166
AAAPAPEEEMDEC(+166.09)EQALAAEPK	P26641	EF1G_HUMAN	Elongation factor 1-gamma	2	C	166
ISNGDVILVYGC(+166.09)SSLVSR	Q9UI10	EI2BD_HUMAN	Translation initiation factor eIF-2B subunit delta	2	C	166
ACLWGTGC(+166.09)VAGVLLQPSGAK	P58107	EPIPL_HUMAN	Epiplakin	2	C	166
SSPELLPSGVTDENEVTAVTEK(+166.09)VCSELDNNRHSK	P42566	EPS15_HUMAN	Epidermal growth factor receptor substrate 15	3	K	166
GTSFDAAATSGGSASSEK(+166.09)ASSTSPVEISEWLDQK	P13804	ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial	3	K	166
VVADGAGLPGEDWVFVSSK(+166.09)DADLTDTAQTR	Q13630	FCL_HUMAN	GDP-L-fucose synthase -binding protein)	2	K	166
ALGALVDSCAPGLCPDWDSWDASK(+166.09)PVTNAR	P21333	FLNA_HUMAN	Filamin-A	1	K	166
C(+166.09)SGPGLGAGVR	Q14315	FLNC_HUMAN	Filamin-C	2	C	166
WGPPLVDGGSPISC(+166.09)YSVEMSPIEK(+166.09)	Q9Y2H6	FND3A_HUMAN	Fibronectin type-III domain-containing protein 3A	1	K	166
WGPPLVDGGSPISC(+166.09)YSVEMSPIEK(+166.09)	Q9Y2H6	FND3A_HUMAN	Fibronectin type-III domain-containing protein 3A	1	C	166
LTLVC(+166.09)ESAPGPITMDLTGDLEALK	P52566	GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2	3	C	166
C(+166.09)SDAVPGGLFGFAAR	Q8TEQ6	GEMI5_HUMAN	Gem-associated protein 5	3	C	166
EAATLEVERPLPMEVEK(+166.09)NSTPSEPGSGR	P51858	HDGF_HUMAN	Hepatoma-derived growth factor	3	K	166
AFPQLGGRPGPEGEGLSPPPLQTQACPESSC(+166.09)LR	O94992	HEX1_HUMAN	Protein HEXIM1	3	C	166
EGEAAPGAAGASVGAAAATPGAEDWK(+166.09)K(+166.09)GAESP EK	A6NHT5	HMX3_HUMAN	Homeobox protein HMX3	3	K	166
EGEAAPGAAGASVGAAAATPGAEDWK(+166.09)K(+166.09)GAESP EK	A6NHT5	HMX3_HUMAN	Homeobox protein HMX3	3	K	166
KAEGGGGGGRPGAPAAGDGK(+166.09)TEQK	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	3	K	166
AGGIETIANEYDRCTPAC(+166.09)ISFGPK	P34932	HSP74_HUMAN	Heat shock 70 kDa protein 4	3	C	166
AGGIETIANEYDRCTPAC(+166.09)TPACISFGPK	P34932	HSP74_HUMAN	Heat shock 70 kDa protein 4	3	C	166
GK(+166.09)AGAAAGGPGVSGVCVCK	Q16270	IBP7_HUMAN	Insulin-like growth factor-binding protein 7	2	K	166
GKAGAAAGGPGVSGVC(+166.09)VCK	Q16270	IBP7_HUMAN	Insulin-like growth factor-binding protein 7	2	C	166
ELAQQIQKVILALGDYMGATC(+166.09)HACIGGTNVR	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II	2	C	166
AASLLLEILGLLC(+166.09)KSMGPKK	Q04637	IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	1	C	166
QEGIATSDNFMQAFLNVLDQC(+166.09)PK	P78344	IF4G2_HUMAN	Eukaryotic translation initiation factor 4 gamma 2	1	C	166

QTVADQVLVGSYC(+166.09)VFSNQGGVLVHPK(+166.09)	P56537	IF6_HUMAN	Eukaryotic translation initiation factor 6 GCN homolog))	2	K	166
QTVADQVLVGSYC(+166.09)VFSNQGGVLVHPK(+166.09)	P56537	IF6_HUMAN	Eukaryotic translation initiation factor 6 GCN homolog))	2	C	166
NPLMYLTGVQTDKAGDISC(+166.09)NADINPLK	P17301	ITA2_HUMAN	Integrin alpha-2	3	C	166
TGAVYLCPLTAHKDDC(+166.09)ERMNITVK	P26006	ITA3_HUMAN	Integrin alpha-3	1	C	166
ATTPASTANSDVATIPTDTPLK(+166.09)EENEGFVK	O60271	JIP4_HUMAN	C-Jun-amino-terminal kinase-interacting protein 4	3	K	166
SGGGGGGGFGRVSLAGAC(+166.09)GVGGYGSR	P13647	K2C5_HUMAN	Keratin, type II cytoskeletal 5	3	C	166
RSGSTPEAEGPSVGPSPC(+166.09)PSPTIPGLPTPSR	Q13554	KCC2B_HUMAN	Calcium/calmodulin-dependent protein kinase type II subunit beta	1	C	166
EAVSSPAVTSCVKG(+166.09)LFVIGGGPDDNTCS DK	Q6TFL4	KLH24_HUMAN	Kelch-like protein 24	1	K	166
LLEGEEQRLCEGIGAVNVC(+166.09)VSSSR	Q14533	KRT81_HUMAN	Keratin, type II cuticular Hb1	1	C	166
LVGGPVAGGDPNQ TIRGQYCDIC(+166.09)TAANSNK	O15230	LAMA5_HUMAN	Laminin subunit alpha-5	2	C	166
ALELK(+166.09)AKYESDMVTGGYAALINLCCR	P42704	LPPRC_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial	3	K	166
MAATASAGAGGIDGK(+166.09)PR	Q02978	M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein	3	K	166
QLC(+166.09)LEHDEKLVSYSLLR	Q9UPN3	MACF1_HUMAN	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/4/5	3	C	166
MVAAVAC(+166.09)AQVPK	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	2	C	166
EKSEDQDLQGLK(+166.09)DKPLK	P51608	MECP2_HUMAN	Methyl-CpG-binding protein 2	3	K	166
SLAPQAGTEPC(+166.09)PPEAAACLLGGSKPVNLGR	P11717	MPRI_HUMAN	Cation-independent mannose-6-phosphate receptor	3	C	166
VAVTSSSSSSSSSIPSAEK(+166.09)VPPTK	Q6WCQ1	MPRIIP_HUMAN	Myosin phosphatase Rho-interacting protein	1	K	166
TAGC(+166.09)VTGGEEIYLLCDK	P19838	NFKB1_HUMAN	Nuclear factor NF-kappa-B p105 subunit	2	C	166
C(+166.09)IACQAAKLSRDTAK	P49790	NU153_HUMAN	Nuclear pore complex protein Nup153	3	C	166
C(+166.09)SVLSNVEARR	P47712	PA24A_HUMAN	Cytosolic phospholipase A2	2	C	166
EGLLSEAAAEEDIADPFFAYC(+166.09)K	O94880	PHF14_HUMAN	PHD finger protein 14	3	C	166
ALDVSGSGILTACFARMVGC(+166.09)TGKVGIDHIK	P22061	PIMT_HUMAN	Protein-L-isoaspartate O-methyltransferase	2	C	166

TPTLTSIYCRGCSK(+166.09)PLCCSCALLDSSHSELK	P29590	PML_HUMAN	Protein PML	2	K	166
ISGADINSIC(+166.09)QESGMLAVR	P43686	PRS6B_HUMAN	26S proteasome regulatory subunit 6B	1	C	166
TALMLAC(+166.09)EIGSSNAVEALIKK	Q9P0K7	RAI14_HUMAN	Ankyrin	3	C	166
LLGVCCSVDNC(+166.09)RLFIGGIPKMK	A0AV96	RBM47_HUMAN	RNA-binding protein 47	2	C	166
C(+166.09)TGGEVGATSALAPKIGPLGLSPKK	P30050	RL12_HUMAN	60S ribosomal protein L12	2	C	166
ISLGLPVGAVINC(+166.09)ADNTGAKNLYIISVK	P62829	RL23_HUMAN	60S ribosomal protein L23	2	C	166
NLGKMTANSVLEPGNSEVSLVC(+166.09)EKLKNEK	P10155	RO60_HUMAN	RNA-binding protein RO60	1	C	166
KLLMMAGIDDC(+166.09)YTSARGCTATLGNFAK	P15880	RS2_HUMAN	40S ribosomal protein S2	1	C	166
THFGGGK(+166.09)TTGFGMIYDSLDAK	P62847	RS24_HUMAN	40S ribosomal protein S24	2	K	166
VASPK(+166.09)LMEEAPESYK	Q9Y3I0	RTCB_HUMAN	RNA-splicing ligase RtcB homolog	2	K	166
VPSGAAGGK(+166.09)MAEPCSPSGQQPPSPSPDELPANVK	Q14160	SCRIB_HUMAN	Protein scribble homolog	2	K	166
DEK(+166.09)QNLLSVGDYR	O60264	SMCA5_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	3	K	166
SAAGGGGSAGGGAGGAK(+166.09)TSK	P35716	SOX11_HUMAN	Transcription factor SOX-11	1	K	166
SGGSGGCSGAGGASNC(+166.09)GTGSGRSGLLDK	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2	1	C	166
SGGSGGC(+166.09)SGAGGASNCGTGSGR	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2	1	C	166
CDAC(+166.09)PEGAALPAALSCLSC(+166.09)LASFCPAHLGPHR	Q96LD4	TRI47_HUMAN	E3 ubiquitin-protein ligase TRIM47	3	C	166
SLVQEMVGSFGK(+166.09)R	O75643	U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa helicase	2	K	166
C(+166.09)ALSLFLMAVNIK	Q5T4S7	UBR4_HUMAN	E3 ubiquitin-protein ligase UBR4	2	C	166
GDASGACAAGALPVTGVC(+166.09)YK	Q9NYU2	UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1	2	C	166
KVTLSSYSKNLK(+166.09)PSSETK	Q9Y4E1	WAC2C_HUMAN	WASH complex subunit 2C	1	K	166
GAEEANVTGPGGVPVQGSK(+166.09)YAADR	P67809	YBOX1_HUMAN	Y-box-binding protein 1	1	K	166
SEAGHASSPDSEVTSCLQK(+166.09)EK	Q6NZY4	ZCHC8_HUMAN	Zinc finger CCHC domain-containing protein 8	3	K	166

Appendix Table 7: Peptide repertoire of the A549 haptenome following DPCP exposure – Results are presented for peptides where satisfactory MS/MS spectrum validation was achieved.

Peptide	Accession	Uniprot ID	Protein Description	Replicate	Residue	Adduct
NMGLSPPASSTSTSSTC(+206.22)RAEAPR	Q9HC52	CBX8_HUMAN	Chromobox protein homolog 8	1	C	206
NAGGTYNLDMVVSSAIGC(+206.22)QLGR	Q9BRF8	CPPED_HUMAN	Serine/threonine-protein phosphatase CPPED1	2	C	206
AADTIGYPVMIRSAYALGGLGSGIC(+224.26)PNR	P31327	CPSM_HUMAN	Carbamoyl-phosphate synthase , mitochondrial	1	C	224
RMPGTDAPGIPAALAFGPQVSDTLDC(+224.26)R	Q14203	DCTN1_HUMAN	Dynactin subunit 1	1	C	224
K(+224.26)PARLLEATAKPEPEEK	Q96KC8	DNJC1_HUMAN	DnaJ homolog subfamily C member 1	2	K	224
NIEGQMTYPYPVGMGNGTPC(+224.26)SLK	Q96DZ1	ERLEC_HUMAN	Endoplasmic reticulum lectin 1	1	C	224
AGGGGGGGGGGGGGGGGGAPVC(+222.24)GASGLCK	Q8TBJ5	FEZF2_HUMAN	Fez family zinc finger protein 2	3	C	222
SGGGGGRFSSC(+206.22)GGGGGSFGAGGGFGSR	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1	1	C	206
RPAGGRPPSPSAMGK(+206.22)RLSR	Q92615	LAR4B_HUMAN	La-related protein 4B	1	K	206
SDLDAVSMK(+206.22)CDSFLHQSPSSSVPTLR	Q9UPN3	MACF1_HUMAN	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/4/5	2	K	206
QAGLLAVMAQMGC(+206.22)YVPAEVC	P52701	MSH6_HUMAN	DNA mismatch repair protein Msh6	2	C	206
GAPTPPAATPPSPK(+224.26)GSPGTPPP(+206.22)GAPTPPAVTPPSK	E9PAV3	NACAM_HUMAN	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	3	K	206
GAPTPPAATPPSPK(+224.26)GSPGTPPP(+206.22)GAPTPPAVTPPSK	E9PAV3	NACAM_HUMAN	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	3	K	224
VTGTSLGGGTFLGLC(+206.22)SLLTGC(+206.22)ESFEEALEMASKGDSTQAD K	Q9H999	PANK3_HUMAN	Pantothenate kinase 3	3	C	206
QPTSEANC(+222.24)SAMFGKLMTIAKNLPDPGK	Q29RF7	PDS5A_HUMAN	Sister chromatid cohesion protein PDS5 homolog A	3	C	222
MNVSPDVNYEELARC(+224.26)TDDFNGAQCK	P17980	PRS6A_HUMAN	26S proteasome regulatory subunit 6A	1	C	224

RSGMYTVAMAYCGSGNNK(+224.26)AIR	Q99460	PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1	3	K	224
RLLEGDGGPNTGGMGAYC(+206.22)PAPQVSNDLLK	P22102	PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3	2	C	206
SGSGGGCSGAGGASNC(+224.26)GTGSGRSGLLDK	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2	2	C	224
LLGPGVNYSGCQITWAKFC(+206.22)K	P40763	STAT3_HUMAN	Signal transducer and activator of transcription 3	1	C	206
ESAVGQMGWSGGLSLRDMNLTGC(+206.22)LESGGSEEPGGIGVGEK	Q9C0C2	TB182_HUMAN	182 kDa tankyrase-1-binding protein	1	C	206
LRASKSVSNGTAK(+224.26)PATSENFDEDLK	Q96K49	TM87B_HUMAN	Transmembrane protein 87B	1	K	224
GDASGACAAGALPVTGVC(+222.24)YK	Q9NYU2	UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1	2	C	222
KGISGK(+206.22)GPGAGEGPGGAFAR	C4AMC7	WASH3_HUMAN:s p	Putative WAS protein family homolog 3	3	K	206
SEAGHASSPDSEVTSLCQK(+206.22)EK	Q6NZY4	ZCHC8_HUMAN	Zinc finger CCHC domain-containing protein 8	1	K	206

Appendix Table 8: Peptide repertoire of the A549 haptenome following PA exposure – Results are presented for peptides where satisfactory MS/MS spectrum validation was achieved.

Peptide	Accession	Uniprot ID	Protein Description	Replicate	Residue	Adduct
QAGEEEK(+148.12)VLK	Q8NE71	ABCF1_HUMAN	ATP-binding cassette sub-family F member 1	2	K	148
GEIVIGGQNISMGYFK(+130.10)NEEK(+148.12)TAEDYSVDENGQR	O60488	ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4	3	K	130
GEIVIGGQNISMGYFK(+130.10)NEEK(+148.12)TAEDYSVDENGQR	O60488	ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4	3	K	148
LLSRGPCSRDPCSNVTC(+148.12)SFGSTCAR	O00468	AGRIN_HUMAN	Agrin	1	C	148
HQGPCDQAPSPCLGVQCAFATC(+164.12)AVK	O00468	AGRIN_HUMAN	Agrin	3	C	164

ADIDVSGPK(+130.10)VDVECPDVNIEGPEGK	Q09666	AHNK_HUMAN	Neuroblast differentiation-associated protein AHNK	3	K	130
GPSLDIDTPDVNIEGPEGK(+148.12)LKGPK	Q09666	AHNK_HUMAN	Neuroblast differentiation-associated protein AHNK	1	K	148
GPSLDIDTPDVNIEGPEGK(+148.12)LKGPK	Q09666	AHNK_HUMAN	Neuroblast differentiation-associated protein AHNK	3	K	148
VDTSVSWEALICVGSSK(+130.10)K	Q02952	AKA12_HUMAN	A-kinase anchor protein 12	1	K	130
ASSEGGTAAGAGLSLHK(+130.10)NSVSQISVLSGGK	O15143	ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B	3	K	130
AVAGDASESALLKCIELCCGSVK(+130.10)EMR	P05023	AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 /K ATPase alpha-1 subunit)	2	K	130
AIAAK(+130.10)CGIIQPGEDFLCLEGK	Q16720	AT2B3_HUMAN	Plasma membrane calcium-transporting ATPase 3	2	K	130
K(+148.12)TTEEQVQASTPCPR	Q14137	BOP1_HUMAN	Ribosome biogenesis protein BOP1	1	K	148
QSVDK(+130.10)VTSPTKV	Q05682	CALD1_HUMAN	Caldesmon	1	K	130
GGGGGGGK(+130.10)SSSSSSASAAAAAASSSASCRR	Q07065	CKAP4_HUMAN	Cytoskeleton-associated protein 4	1	K	130
GDTGPPGPPGYGPAGPIGDK(+148.12)GQAGFPGGPGSPGLPGPK	P02462	CO4A1_HUMAN	Collagen alpha-1 chain	1	K	148
AYGEVYAAMNPINEYK(+130.10)DPENILHR	Q9Y2V7	COG6_HUMAN	Conserved oligomeric Golgi complex subunit 6	3	K	130
SADGPQGPPGLPGLKGDVPGVPLPGAK(+148.12)GEVGADGVPGFPLPGR	P39060	COIA1_HUMAN	Collagen alpha-1 chain	2	K	148
NAGGTYQNLDMMVSSAIGC(+148.12)QLGRDPHGLR	Q9BRF8	CPPED_HUMAN	Serine/threonine-protein phosphatase CPPED1	1	C	148
NGTAGLIPSELQEWVAC(+164.12)IAMEK	O14936	CSKP_HUMAN	Peripheral plasma membrane protein CASK	1	C	164
NNHGHIVTVASAAGHVSPFLAYCSSK(+148.12)FAAVGFHK	Q8NBQ5	DHB11_HUMAN	Estradiol 17-beta-dehydrogenase 11	1	K	148
AWTQVLLGQAEDK(+130.10)AEVDMDTDAPQVSHKPGGEPKIK	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1	3	K	130
SAVLSSKPGC(+164.12)FIAGADINMLAAC(+148.12)K(+130.10)	P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	2	K	130

SAVLISKPGC(+164.12)FIAGADINMLAAC(+148.12)K(+130.10)	P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	2	C	130
SAVLISKPGC(+164.12)FIAGADINMLAAC(+148.12)K(+130.10)	P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	2	K	148
SAVLISKPGC(+164.12)FIAGADINMLAAC(+148.12)K(+130.10)	P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	2	C	148
SAVLISKPGC(+164.12)FIAGADINMLAAC(+148.12)K(+130.10)	P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	2	K	164
SAVLISKPGC(+164.12)FIAGADINMLAAC(+148.12)K(+130.10)	P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	2	C	164
SGDAAIVEMVPGK(+130.10)PMCVESFSQYPPLGR	Q05639	EF1A2_HUMAN	Elongation factor 1-alpha 2	3	K	130
K(+130.10)ALGKYGPADVEDTTGSGATDSK(+148.12)	P24534	EF1B_HUMAN	Elongation factor 1-beta	2	K	130
K(+130.10)ALGKYGPADVEDTTGSGATDSK(+148.12)	P24534	EF1B_HUMAN	Elongation factor 1-beta	2	K	148
SNDLAVLDASNQISVYK(+130.10)C(+164.12)GDCPSADPTVK	O95163	ELP1_HUMAN	Elongator complex protein 1	3	K	130
SNDLAVLDASNQISVYK(+130.10)C(+164.12)GDCPSADPTVK	O95163	ELP1_HUMAN	ER membrane protein complex subunit 1	3	C	130
SNDLAVLDASNQISVYK(+130.10)C(+164.12)GDCPSADPTVK	O95163	ELP1_HUMAN	ER membrane protein complex subunit 1	3	K	164
SNDLAVLDASNQISVYK(+130.10)C(+164.12)GDCPSADPTVK	O95163	ELP1_HUMAN	ER membrane protein complex subunit 1	3	C	164
TVAAVMACRNEVQK(+148.12)SSSSEDGSMGSFSEK	Q8N766	EMC1_HUMAN	ER membrane protein complex subunit 1	2	K	148
SGETEDTFIADLVVGLC(+148.12)TGQIK(+130.10)TGAPCR	P06733	ENOA_HUMAN:sp	Alpha-enolase	3	K	130
SGETEDTFIADLVVGLC(+148.12)TGQIK(+130.10)TGAPCR	P06733	ENOA_HUMAN:sp	Alpha-enolase	3	C	130
SGETEDTFIADLVVGLC(+148.12)TGQIK(+130.10)TGAPCR	P06733	ENOA_HUMAN:sp	Alpha-enolase	3	K	148
SGETEDTFIADLVVGLC(+148.12)TGQIK(+130.10)TGAPCR	P06733	ENOA_HUMAN:sp	Alpha-enolase	3	C	148
MGSLSGLRLAAGSC(+148.12)FR	Q96A26	F162A_HUMAN	Protein FAM162A	2	C	148
VLTVLSICLSAVATATGAEGK(+148.12)R	P26885	FKBP2_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP2	3	K	148
VGEVCHITCK(+130.10)PEYAYGSAGSPPK	Q02790	FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP4	2	K	130
GVDLSGNDFKGGYFPENVK(+148.12)AMTSLR	Q13045	FLII_HUMAN	Protein flightless-1 homolog	2	K	148

AGPGTLSVTIEGPSK(+130.10)VKMDCQETPEGYK	O75369	FLNB_HUMAN	Filamin-B	2	K	130
VIGVKSEGEIARC(+164.12)K	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta	2	C	164
QLIC(+164.12)DPSYVKDR	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta	3	C	164
APESPPSADPALVAGPAEEAEC(+164.12)PPPR	Q6EEV4	GL1AD_HUMAN	DNA-directed RNA polymerase II subunit GRINL1A, isoforms 4/5	3	C	164
MSAGGPCPAAAGGGPGGASC(+164.12)SVGAPGGVSMFR	Q9HD26	GOPC_HUMAN	Golgi-associated PDZ and coiled-coil motif-containing protein	3	C	164
RDYASEAIK(+130.10)GAVVGIDLGTTNSCAVMEGK	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial	1	K	130
KDIC(+164.12)KGGNAVVDGCGK	P48506	GSH1_HUMAN	Glutamate--cysteine ligase catalytic subunit	2	C	164
SAGLAPDCEASATAETTVSSVGTC(+164.12)EAAGKSPEPK	Q9NQE9	HINT3_HUMAN	Adenosine 5'-monophosphoramidase HINT3	3	C	164
AEC(+148.12)EILMMVGLPAAGK	Q9BUJ2	HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1	2	C	148
AKAALNGADIYAGC(+164.12)CTLK	Q8WVV9	HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein L-like	2	C	164
SGAMVK(+148.12)MAAAGGGGGGGR	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	2	K	148
SGAMVK(+148.12)MAAAGGGGGGGRYGGGSEGGR	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	2	K	148
SGAMVK(+148.12)MAAAGGGGGGGGR	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	2	K	148
AEGGGGGGRPGAPAAGDGK(+130.10)TEQK	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	1	K	130
LSAASTWLEDEGVGATTVMLK(+130.10)EK	Q9Y4L1	HYOU1_HUMAN	Hypoxia up-regulated protein 1	3	K	130
CEPCDARALACAPPAVC(+164.12)AELVR	P17936	IBP3_HUMAN	Insulin-like growth factor-binding protein 3	1	C	164

SITILSTPEGTSAACK(+130.10)SILEIMHK	O00425	IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 3	3	K	130
SGVLGADGVCMTFMK(+130.10)QIAGGGDVTAK	Q68E01	INT3_HUMAN	Integrator complex subunit 3	2	K	130
HTGCCGDNDPIDVC(+148.12)EIGSKVCARGEIIGVK	Q15181	IPYR_HUMAN	Inorganic pyrophosphatase	2	C	148
SGGGGGGGGCGGGGGVSSLRISSSK(+130.10)GSLGGGFSSGGFSGGSFSR	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10	1	K	130
SGGGGGGGGCGGGGGVSSLRISSSK(+130.10)GSLGGGFSSGGFSGGSFSR	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10	3	K	130
SGGGGGGGGCGGGGGVSSLRISSSK(+148.12)GSLGGGFSSGGFSGGSFSR	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10	2	K	148
EGFGGLMC(+164.12)SAAAIR	Q13751	LAMB3_HUMAN	Laminin subunit beta-3	2	C	164
RAGVTCIVLPAENK(+148.12)K	P36776	LONM_HUMAN	Lon protease homolog, mitochondrial	2	K	148
K(+130.10)PTPIQLNPAPDGSANGTSSAETNLEALQK	Q02750	MP2K1_HUMAN	Dual specificity mitogen-activated protein kinase kinase 1	3	K	130
NKDAVNQMAVC(+148.12)PGNAVEPLPSNSENQNK	O75970	MPDZ_HUMAN	Multiple PDZ domain protein	1	C	148
DGGVCLLSGTK(+148.12)GASFGRLLQSMK	P11717	MPRI_HUMAN	Cation-independent mannose-6-phosphate receptor	1	K	148
GC(+164.12)PEDAAVCAVDKNGSK	P11717	MPRI_HUMAN	Cation-independent mannose-6-phosphate receptor	2	C	164
CPPEAPIFDEDK(+148.12)MQCVATCPTPLPPR	P98088	MUC5A_HUMAN	Mucin-5AC	2	K	148
EGPTPPAATPSHK(+130.10)GGPAMTPSPKR	E9PAV3	NACAM_HUMAN	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	2	K	130
GTDLEALLAIGK(+130.10)GADDGR	A2RRP1	NBAS_HUMAN	NBAS subunit of NRZ tethering complex	1	K	130
YGC(+164.12)EGPSHGGLPGASSEK	Q00653	NFKB2_HUMAN	Nuclear factor NF-kappa-B p100 subunit	2	C	164
GAGVAVLNGK(+130.10)LFVCGGFDGSHAISCVEMYDPTR	Q9Y6Y0	NS1BP_HUMAN	Influenza virus NS1A-binding protein	1	K	130
EGPNKTGTSCALDC(+164.12)GAGIGR	Q9BV86	NTM1A_HUMAN	N-terminal Xaa-Pro-Lys N-methyltransferase 1	3	C	164
SHLVHGSSPGVMGTSVATSASK(+130.10)IIPQGADSTMLATK	P35658	NU214_HUMAN	Nuclear pore complex protein Nup214	3	K	130

KEAGGGVGGPGAK(+130.10)SAAQAAQTNSNAAGK	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein	3	K	130
EAGGGVGGPGAK(+148.12)SAAQAAQTNSNAAGK	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein	3	K	148
MNGRTVGIVGNQPK(+130.10)VASGCLDINSSVK	P05166	PCCB_HUMAN	Propionyl-CoA carboxylase beta chain, mitochondrial	3	K	130
APDPGRLMAGCAAVGASLAAPGGGLC(+164.12)EQRGLEIEMQR	Q13563	PKD2_HUMAN	Polycystin-2	2	C	164
NQRPSSMVSETSTAGTASTLEAK(+148.12)PGPK	Q6IQ23	PKHA7_HUMAN	Pleckstrin homology domain-containing family A member 7	1	K	148
DVITHVVC(+148.12)TKTDFIITASHDGHVK	Q96BP3	PPWD1_HUMAN	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	1	C	148
EAPPPVLLTPK(+148.12)AVGTPGGGGGAVPGISAMSR	P48634	PRC2A_HUMAN	Protein PRRC2A	3	K	148
KIAELMPGASGAEVK(+130.10)GVCTEAGMYALR	P62195	PRS8_HUMAN	26S proteasome regulatory subunit 8	2	K	130
EDFASGTAAALAGGITMVC(+148.12)AMPNTRPPIIDAPALALAKLAEAGAR	P27708	PYR1_HUMAN	CAD protein	1	C	148
RMGPGATAGGAEK(+148.12)SNVK	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A	3	K	148
MGPGAASGGERPNLKIDSTPVKAGGGCC(+148.12)	Q9H0U4	RAB1B_HUMAN	Ras-related protein Rab-1B	3	C	148
MAAAGGGGGGAAAAAGRAYSFK(+148.12)VVLLGEGCVGK	Q9UL25	RAB21_HUMAN	Ras-related protein Rab-21	2	K	148
VFGALKGAVDGGLSIPHSTK(+148.12)R	P46777	RL5_HUMAN	60S ribosomal protein L5	3	K	148
CGIPVIIMGETGC(+164.12)GKTR	Q63HN8	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213	1	C	164
DAVPATLHLLPC(+164.12)EVAVDGPAPVGR	Q8TDP1	RNH2C_HUMAN	Ribonuclease H2 subunit C	2	C	164
RECPSDEC(+164.12)GAGVFMASHFDRHYCGK	P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a	1	C	164
RK(+130.10)DGGPATK	Q92922	SMRC1_HUMAN	SWI/SNF complex subunit SMARCC1	2	K	130
GFLGC(+148.12)FPDIIGTHKGAIEK	Q9Y5X1	SNX9_HUMAN	Sorting nexin-9	3	C	148
VELK(+130.10)MDLPGVSIADGETGMFSLSTIR	Q8IY81	SPB1_HUMAN	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3	1	K	130
WLPAAATFPVQDPASGAALGMVADC(+164.12)GVREAR	P51649	SSDH_HUMAN	Succinate-semialdehyde dehydrogenase, mitochondrial	1	C	164

			-dependent succinic semialdehyde dehydrogenase)			
SLRLATTAC(+148.12)TLGDGEAVGADSGTSSAVSLK	O94901	SUN1_HUMAN	SUN domain-containing protein 1	2	C	148
EAPCVLIYIPDGHTK(+130.10)EMPTSGSKEK	P07814	SYEP_HUMAN	Bifunctional glutamate/proline-tRNA ligase	1	K	130
GPGAAALATARSLWGTPRLPC(+148.12)SPGWQGATK	Q9NSE4	SYIM_HUMAN	Isoleucine--tRNA ligase, mitochondrial	2	C	148
EVDEQMLAIQSK(+130.10)NSSYFVEWIPNNVK	Q13509	TBB3_HUMAN:sp	Tubulin beta-3 chain	3	K	130
ENGTVTAANASTLNDGAAALVLMTADAAK(+148.12)R	P24752	THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial	2	K	148
MKPPAAC(+148.12)AGDMADAASPCSVVNDLR	P52888	THOP1_HUMAN	Thimet oligopeptidase	3	C	148
GITMATAKAVAAGNSC(+164.12)R	Q9Y490	TLN1_HUMAN:sp	Talin-1	1	C	164
EDPYGVAVGGTVGHC(+164.12)LCTGLAVIGGR	Q9HC07	TM165_HUMAN	Transmembrane protein 165	2	C	164
KNGSTAVAESVASPQK(+130.10)TMSVLSCICEAR	Q12888	TP53B_HUMAN	TP53-binding protein 1	1	K	130
QAQHLAETGSNMNDLK(+148.12)ELLEKSLHCLK(+130.10)	Q6PGP7	TTC37_HUMAN	SKI3 subunit of superkiller complex protein	1	K	130
QAQHLAETGSNMNDLK(+148.12)ELLEKSLHCLK(+130.10)	Q6PGP7	TTC37_HUMAN	SKI3 subunit of superkiller complex protein	1	K	148
EAAASGLPLMVIIHK(+130.10)SWCGACK	O95881	TXD12_HUMAN	Thioredoxin domain-containing protein 12	2	K	130
DAGGK(+148.12)SWCPDCVQAEPVVR	Q9BRA2	TXD17_HUMAN	Thioredoxin domain-containing protein 17	2	K	148
K(+130.10)VPTSNTGGWSCSLAEYIRHNDMPIYEAADK	Q5T4S7	UBR4_HUMAN	E3 ubiquitin-protein ligase UBR4	1	K	130
GVMGGQSAGPQHTEAETIQK(+130.10)LCDR	O60763	USO1_HUMAN	General vesicular transport factor p115	2	K	130
SC(+148.12)AVSLTTAAVAFGDEAK	O14607	UTY_HUMAN	Histone demethylase UTY demethylase UTY)	3	C	148
EAVKAASDELSK(+130.10)TISPMVMMDAK	P18206	VINC_HUMAN	Vinculin	1	K	130
ALHC(+148.12)CRGHAGSVDSIAVDGSGTK	Q9GZL7	WDR12_HUMAN	Ribosome biogenesis protein WDR12	3	C	148

Appendix Table 9: Peptide repertoire of the A549 haptenome following TDI exposure – Results are presented for peptides where satisfactory MS/MS spectrum validation was achieved.

Peptide	Accession	Uniprot ID	Protein Description	Replicate	Residue	Adduct
VETELQGVCDTVLGLLDShLIk(+148.16)EAGDAESR	P31947	1433S_HUMAN	14-3-3 protein sigma	3	K	148
MTEEPLMC(+174.16)AYCVTEPGAGSDVAGIK	P11310	ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	1	C	174
MDDDIaALVVDNGSGMC(+148.16)K(+148.16)AGFAGDDAPR	P60709	ACTB_HUMAN	Actin, cytoplasmic 1	2	K	148
MDDDIaALVVDNGSGMC(+148.16)K(+148.16)AGFAGDDAPR	P60709	ACTB_HUMAN	Actin, cytoplasmic 1	2	K	148
MDDDIaALVVDNGSGMC(+148.16)K(+148.16)AGFAGDDAPR	P60709	ACTB_HUMAN	Actin, cytoplasmic 1	2	C	148
MDDDIaALVVDNGSGMC(+148.16)K(+148.16)AGFAGDDAPR	P60709	ACTB_HUMAN	Actin, cytoplasmic 1	2	C	148
ENLLSLACQHqFCRSC(+148.16)WEQHCSVLVK(+148.16)	O95376	ARI2_HUMAN	E3 ubiquitin-protein ligase ARIH2	3	K	148
ENLLSLACQHqFCRSC(+148.16)WEQHCSVLVK(+148.16)	O95376	ARI2_HUMAN	E3 ubiquitin-protein ligase ARIH2	3	C	148
DAVDSLGEAVDMSIK(+148.16)GMYTLLAR	Q96GS4	BORC6_HUMAN	BLOC-1-related complex subunit 6	1	K	148
TSSEASVSSSVAK(+148.16)NSSSSGTSLLTPK	Q9NXV6	CARF_HUMAN	CDKN2A-interacting protein	1	K	148
SGSGNSGKGGNQLRC(+148.16)PK	O76031	CLPX_HUMAN	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	3	C	148
QPDAAATAGSLPTK(+148.16)GDSWVDPS	Q96D53	COQ8B_HUMAN	Atypical kinase COQ8B, mitochondrial	1	K	148
SVAVYGGGSMWEQAK(+148.16)ALQEGAEIVVCTPGR	Q86XP3	DDX42_HUMAN	ATP-dependent RNA helicase DDX42	3	K	148
EALCGC(+174.16)TVNVPTLDGRTIPVVK	P25685	DNJB1_HUMAN	DnaJ homolog subfamily B member 1	1	C	174
TAESQTPTPSATSFSGK(+148.16)SPVTTLLECMHK	P55265	DSRAD_HUMAN	Double-stranded RNA-specific adenosine deaminase	2	K	148

RSGVRAGEAEESSAVC(+174.16)QVDAEQR	Q8N3D4	EH1L1_HUMAN	EH domain-binding protein 1-like protein 1	1	C	174
AVIPMSCITNGSGANRK(+174.16)PSHTSAVSIAGK	Q9HC35	EMAL4_HUMAN	Echinoderm microtubule-associated protein-like 4	1	K	174
EVIIVSCGPAQC(+148.16)QETIRTALAMGADR	P38117	ETFB_HUMAN	Electron transfer flavoprotein subunit beta	2	C	148
VGEAGLLSVDC(+174.16)SEAGPGALGLEAVSDSGTKAEVSIQNNK	O75369	FLNB_HUMAN	Filamin-B	1	C	174
EAGAGGLSIAVEGPSK(+174.16)AEIAFEDRK	Q14315	FLNC_HUMAN	Filamin-C	1	K	174
WGDAGAEYVVESTGVFTTMEK(+174.16)AGAHLQGGAK	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	2	K	174
ESIDGK(+148.16)LPSTDQQESCSSTPGLEELFK	Q14789	GOGB1_HUMAN	Golgin subfamily B member 1	3	K	148
WVLGALLRGCGCNCSSC(+148.16)R	Q12849	GRSF1_HUMAN	G-rich sequence factor 1	2	C	148
KK(+174.16)AEGGGGGGRPGAPAAGDGK(+148.16)	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	1	K	148
AEGGGGGGRPGAPAAGDGK(+148.16)TEQKGGDK	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	2	K	148
KK(+174.16)AEGGGGGGRPGAPAAGDGK(+148.16)	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	1	K	174
GEGEPCGGGGAGRGYC(+174.16)APGMECVKSR	Q16270	IBP7_HUMAN	Insulin-like growth factor-binding protein 7	3	C	174
ENAGAAEKSITILSTPEGTSAACK(+174.16)SILEIMHK	O00425	IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 3	3	K	174
EALAK(+148.16)TEVSLTLTNKFDVPGDENAEMDAR	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1	1	K	148
SGGGGGGRFSSC(+148.16)GGGGGSFGAGGGFGSRSLVNLGGSK	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1	2	C	148
KPNSVPQELAATTEK(+148.16)TEPNSQEDK	Q9UPQ0	LIMC1_HUMAN	LIM and calponin homology domains-containing protein 1	3	K	148
EEQAEPDGTADVADK(+174.16)AGYLMGLNSAEMLK	Q9UKX3	MYH13_HUMAN	Myosin-13	1	K	174
NDGAAILAAVSSIAQK(+148.16)IR	P28331	NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	3	K	148
KEGDK(+174.16)INEGDLIAEVETDK	P10515	ODP2_HUMAN	Dihydrolipoyllysine-residue acetyltransferase component of	1	K	174

			pyruvate dehydrogenase complex, mitochondrial			
VASMP LISSTC(+174.16)DMVSAAYASTKESYPHIK	O60664	PLIN3_HUMAN	Perilipin-3	3	C	174
ALSGMCNIDTGLTFAAVHC(+148.16)LSGK(+148.16)	Q99575	POP1_HUMAN	Ribonucleases P/MRP protein subunit POP1	1	K	148
ALSGMCNIDTGLTFAAVHC(+148.16)LSGK(+148.16)	Q99575	POP1_HUMAN	Ribonucleases P/MRP protein subunit POP1	1	K	148
ALSGMCNIDTGLTFAAVHC(+148.16)LSGK(+148.16)	Q99575	POP1_HUMAN	Ribonucleases P/MRP protein subunit POP1	1	C	148
ALSGMCNIDTGLTFAAVHC(+148.16)LSGK(+148.16)	Q99575	POP1_HUMAN	Ribonucleases P/MRP protein subunit POP1	1	C	148
ALQLNELTMDDDTAVLVIDNGSGMC(+148.16)K	Q6S8J3	POTEE_HUMAN:sp	POTE ankyrin domain family member E	1	C	148
AVFPSIVGC(+148.16)PRQQGMMGGMHQKESYVGK	P0CG39	POTEJ_HUMAN	POTE ankyrin domain family member J	1	C	148
KVCAANFGDIC(+174.16)SVVGQQATEEMLLPR	Q8TF05	PP4R1_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 1	2	C	174
GFGYKGSCFHRIIPGFMC(+174.16)QGGDFTR	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A	3	C	174
SHLGVIESIAVSSEGALFC(+148.16)SVGDDK	Q96BP3	PPWD1_HUMAN	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	1	C	148
YGAAMALGICC(+174.16)AGTGK	Q99460	PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1	3	C	174
QMGPGAASGGERPNLKIDSTPVKPAGGGCC(+174.16)	Q92928	RAB1C_HUMAN	Putative Ras-related protein Rab-1C	1	C	174
GGEADNLDEFK(+174.16)EFENPEVPR	O60216	RAD21_HUMAN	Double-strand-break repair protein rad21 homolog	1	K	174
ITDFIK(+174.16)FDTGNLCMVTGGANLGR	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform	2	K	174
GVSEAAVLK(+174.16)PSEELPAEATSSVEPEKDSGSAAEAPR	O95104	SCAF4_HUMAN	SR-related and CTD-associated factor 4	1	K	174
ELALNTAQFAK(+174.16)SLAMLGSSSEDNTALSR	Q13596	SNX1_HUMAN	Sorting nexin-1	2	K	174

SGGSGGCSGAGGASNC(+148.16)GTGSGRSGLLDK(+174.16)	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2	2	K	148
SGGSGGCSGAGGASNC(+148.16)GTGSGRSGLLDK(+174.16)	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2	2	C	148
SGGSGGCSGAGGASNC(+148.16)GTGSGRSGLLDK(+174.16)	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2	2	K	174
SGGSGGCSGAGGASNC(+148.16)GTGSGRSGLLDK(+174.16)	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2	2	C	174
SAAPSTLDSSSTAPAQLGK(+148.16)K	Q9Y5M8	SRPRB_HUMAN	Signal recognition particle receptor subunit beta	3	K	148
KDGTVTAGNASGVADGAGAVIIASEDAVK(+174.16)K	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial	1	K	174
QAFTDVATGSLGQGLGAAC(+174.16)GMAYTGK	P29401	TKT_HUMAN	Transketolase	1	C	174
TPGAATASASGAAEDGACGC(+148.16)LPNPGTFEECHRK	O96008	TOM40_HUMAN	Mitochondrial import receptor subunit TOM40 homolog	3	C	148
EETVAEDVCIDLTC(+148.16)DSGSQAVPSPATR	Q12888	TP53B_HUMAN	TP53-binding protein 1	2	C	148
DPVSPASQK(+174.16)MVIQGPSSPQGEAMVTDVLEDQK	Q12888	TP53B_HUMAN	TP53-binding protein 1	1	K	174

A.3 Supplementary data for chapter 5

A.3.1 Immunopeptidome peptide repertoires

Appendix Table 10: Peptides observed in the immunopeptidome for A549 cells in the control group – individual peptide sequences are presented alongside the associated Uniprot protein accessions and IDs (where available).

Peptide	Accession	ID
GVIEKLLTSY	O75534	CSDE1_HUMAN
EVIGHYPGSSF	Q969W9	PMEPA_HUMAN
AAFLKAIGY	O75533	SF3B1_HUMAN
RNLDIRPTY	Q6PEY2	TBA3E_HUMAN
GVIDVITKTW	Q9H2D1	MFTC_HUMAN
EVFHPTHEW	Q9H173	SIL1_HUMAN
YAFVRPVIL	Q96S16	JMJD8_HUMAN
DVISTIGQAF	Q6S5L8	SHC4_HUMAN
ESFSDYPPLGRF	P68104	EF1A1_HUMAN
DVRPPYAEY	Q7Z4N8	P4HA3_HUMAN
DPVDIYKSW	P46940	IQGA1_HUMAN
YAAPHPLQSY	Q9ULL5	PRR12_HUMAN
FASGLIHRV	Q8N6L1	KTAP2_HUMAN
AVIGDVIRVY	Q9NR30	DDX21_HUMAN
SAYGSVKAY	P07355	ANXA2_HUMAN
DSFSDLYSSY	Q9BTX1	NDC1_HUMAN
DVKDYIQEY	Q63HN8	RN213_HUMAN
GTYENLIHVW	Q6Q0C0	TRAF7_HUMAN
EVAEVKISHF	Q8IZT6	ASPM_HUMAN
AANPHSFVF	Q9NQ55	SSF1_HUMAN
DTVVFVNQW	Q16678	CP1B1_HUMAN
HASDRIAL	P29401	TKT_HUMAN
AAQEAVKLY	O60506	HNRPQ_HUMAN
VATTRDYF	P06737	PYGL_HUMAN
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TSLDFLFHF	Q9Y334	VWA7_HUMAN
ISHIGKL	Q9P2W9	STX18_HUMAN
LGEHNIDVLEGNEQFINAAK	NA	NA
IANYRPTL	Q01082	SPTB2_HUMAN
EVVQEILQF	Q60437	PEPL_HUMAN
IAVAATPIP	P53634	CATC_HUMAN
NASPVISV	Q96T58	MINT_HUMAN
LSPPEPAPSPG	Q9Y261	FOXA2_HUMAN
SVPRGPAAQW	Q5SRD0	WAC2D_HUMAN
EQTPIHISW	Q16667	CDKN3_HUMAN
EVIKSQEVF	Q00463	TRAF5_HUMAN
VILPPRPPK	Q9BUA6	MYL10_HUMAN

DVVKEDAFYSW	Q04637	IF4G1_HUMAN
DVIGTLSGF	Q8N8Q9	NIPA2_HUMAN
EIQEQFLSY	Q86YQ8	CPNE8_HUMAN
VISPPTVPK	Q9H9Y6	RPA2_HUMAN
EVISGYEEL	Q7L576	CYFP1_HUMAN
GVAESIHLW	Q9BV38	WDR18_HUMAN
EAIGAVIHY	Q9UBB6	NCDN_HUMAN
EVLRGAIETY	Q12797	ASPH_HUMAN
AAVPSPIPV	Q2KHR2	RFX7_HUMAN
SAFPEVRSL	Q6YHU6	THADA_HUMAN
EAFEKSAATW	Q01082	SPTB2_HUMAN
EVYDPATETW	Q8IXQ5	KLHL7_HUMAN
EIEGYVPEHW	Q43674	NDUB5_HUMAN
ETIAKLIKY	Q94808	GFPT2_HUMAN
ASDFQPLRY	Q9BZE0	GLIS2_HUMAN
ILVVMFK	Q9NRD9	DUOX1_HUMAN
TVVGNPRSW	Q15321	TM9S1_HUMAN
PTALPAVPPP	A0A0B4J2F2	SIK1B_HUMAN
VAINHIVDF	P78346	RPP30_HUMAN
EPIEAIKF	Q75044	SRGP2_HUMAN
EVFDERAANF	P18206	VINC_HUMAN
QVADVVSRSW	P49327	FAS_HUMAN
EIAESVQAF	Q6PD74	AAGAB_HUMAN
LAKNFFNEL	Q15021	CND1_HUMAN
EVIERLIKS	Q00429	DNM1L_HUMAN
YTADPYHAL	Q43251	RFOX2_HUMAN
PLAAPFKR	Q5T890	ER6L2_HUMAN
SVVELINHY	Q92569	P55G_HUMAN
EVAEAITQF	Q9ULR3	PPM1H_HUMAN
EVIINTEIW	Q9Y4B6	DCAF1_HUMAN
SALEHVVEF	Q75581	LRP6_HUMAN
SVSVISRF	P61803	DAD1_HUMAN
DNTIFFTTY	Q99523	SORT_HUMAN
YAKDDPLEF	P06756	ITAV_HUMAN
EVNEVIQKVG	Q2LD37	K1109_HUMAN
NPPSTRSSF	Q8TC41	RN217_HUMAN
GPLGLPPKP	Q9P206	K1522_HUMAN
SDIDEIVLVGGSTR	P11021	BIP_HUMAN
EVIPALPRL	Q96Q05	TPPC9_HUMAN
GPALLPSPGP	Q5VWG9	TAF3_HUMAN
TIREPLGL	Q14683	P5I11_HUMAN
EVNELLQKF	Q9P0K7	RAI14_HUMAN
DIVGDFRGF	Q7L5Y1	ENO1_HUMAN
ETIPDGIGKL	Q9BTT6	LRRC1_HUMAN
GTADLVLSHW	Q5VWZ2	LYPL1_HUMAN
DTVTKELVSW	Q96DN5	TBC31_HUMAN
DVLSEEAALKW	Q9Y6E2	BZW2_HUMAN
DVASGQVVRKF	Q9BRX9	WDR83_HUMAN
DVIRLIMQY	Q2TAY7	SMU1_HUMAN
GVVDSDELPLNISR	P07900	HS90A_HUMAN

GVVDESDIPLNLSR	NA	NA
EEIAIIPSKKL	P08708	RS17_HUMAN
VATSFIRTIEL	Q9NWS1	PARI_HUMAN
IEEHLGKF	Q6DKI1	RL7L_HUMAN
ELIAKIPNFW	Q01105	SET_HUMAN
EVLDSLLAQY	Q9NZI8	IF2B1_HUMAN
NVFGDGPYSTF	Q5BJF6	ODFP2_HUMAN
GIIDSQIRQW	Q8NF91	SYNE1_HUMAN
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DVAEGDLIEHF	Q13151	ROA0_HUMAN
FSVDSPRIY	Q9Y2U8	MAN1_HUMAN
LAADFEIGHF	P55209	NP1L1_HUMAN
RWVELEKPLK	Q15678	PTN14_HUMAN
ETKEYFESW	Q16850	CP51A_HUMAN
EVFQTKIQEF	Q9Y6D9	MD1L1_HUMAN
DVVSGSEVLHW	Q9NQZ5	STAR7_HUMAN
EISELPVRTW	P11388	TOP2A_HUMAN
DVTDAVHEW	P61812	TGFB2_HUMAN
DILHSIFSSY	O00410	IPO5_HUMAN
FAIDPHLLLSV	Q29RF7	PDS5A_HUMAN
SAIEDVQLLSW	Q8IY22	CMIP_HUMAN
LEEPTVIKKY	Q9Y5X3	SNX5_HUMAN
ETIDTSRVSL	Q9BRR6	ADPGK_HUMAN
NAYSRIQA	O15230	LAMA5_HUMAN
EVIKKGYSW	P00338	LDHA_HUMAN
EVIDLMIKEY	Q8WUB8	PHF10_HUMAN
SVIDGRFEGF	O14672	ADA10_HUMAN
GVHPPAPGV	Q15428	SF3A2_HUMAN
EVYEGVWKY	P00519	ABL1_HUMAN
ETLDTLEKW	O43847	NRDC_HUMAN
ELIRYSEL	Q93008	USP9X_HUMAN
PDEVIKKW	P14735	IDE_HUMAN
NVIDKLAQF	Q8IWX8	CHERP_HUMAN
ENIEVYHSY	Q16881	TRXR1_HUMAN
DTISINHNW	Q9H9V9	JMJD4_HUMAN
YATGLLKQL	P51805	PLXA3_HUMAN
FSFVRVISL	Q9BVK2	ALG8_HUMAN
EVITNRPKGF	Q99996	AKAP9_HUMAN
EVTTHILSQF	Q9BR11	ZSWM1_HUMAN
IGVEHVVVY	P49411	EFTU_HUMAN
DAISAGKNW	Q8IWX8	CHERP_HUMAN
YTFPGILKW	Q9H7D0	DOCK5_HUMAN
GAYGKVFLV	O75676	KS6A4_HUMAN
EVIERDVVSGSEVLHW	Q9NQZ5	STAR7_HUMAN
TVAGLALIKKY	P43490	NAMPT_HUMAN
AEINNIKI	P11388	TOP2A_HUMAN
DVPAHLQNSW	Q96A33	CCD47_HUMAN
SAFPKEVKV	Q5TH69	BIG3_HUMAN
EVFIHKDKGF	Q15233	NONO_HUMAN

SAVGHVFSL	Q69YN4	VIR_HUMAN
RIKEEFQFL	Q04727	TLE4_HUMAN
DTKEGILQY	P05067	A4_HUMAN
EVAPVQGTA	Q96C23	GALM_HUMAN
DSRDGTPLSW	Q96NU0	CNT3B_HUMAN
VIDVITKTW	Q9H2D1	MFTC_HUMAN
DVLEFGNSW	P98088	MUC5A_HUMAN
EIIGPYASW	Q8N5B7	CERS5_HUMAN
EVVPAAVSGRW	Q8NE01	CNNM3_HUMAN
FIRDPLTL	P48506	GSH1_HUMAN
EVADYEATTF	Q9UNL2	SSRG_HUMAN
EVIRELAGI	Q9NXG2	THUM1_HUMAN
DLKEYFSTF	Q13148	TADBP_HUMAN
TILPGNLQSW	Q969J2	ZKSC4_HUMAN
TGVSSSTNPFPRQK	P63218	GBG5_HUMAN
TASPLVKSV	Q6P4F7	RHGBA_HUMAN
AAFEKALEV	Q13325	IFIT5_HUMAN
YIQDRIPSW	P07942	LAMB1_HUMAN
DSAADFFSHY	Q5JTW2	CEP78_HUMAN
EVFEGDIQQL	P20908	CO5A1_HUMAN
EVVSPSSW	Q9H490	PIGU_HUMAN
DTVDKIVVQKY	P51991	ROA3_HUMAN
SITDFHPDTW	Q8N2K1	UB2J2_HUMAN
RASLLKTY	Q86TU7	SETD3_HUMAN
EVVAEVQEF	Q9NRW7	VPS45_HUMAN
GTQPWFISK	Q15746	MYLK_HUMAN
DTLPQSLRSW	Q92887	MRP2_HUMAN
YSSPEILRV	Q2MV58	TECT1_HUMAN
KFLPFKVVEK	P11021	BIP_HUMAN
FAQGNVRLF	Q7L5A8	FA2H_HUMAN
PRLLKFW	Q9H0A0	NAT10_HUMAN
KTHLPPPAL	Q14159	SPIDR_HUMAN
SAYARLIDY	P34897	GLYM_HUMAN
YSALREIAF	O95260	ATE1_HUMAN
NIPGAIPHW	P17405	ASM_HUMAN
EVFTEILNY	Q8NAP3	ZBT38_HUMAN
SQYFPVTL	Q5R372	RBG1L_HUMAN
LVLSTLSGRPVK	Q9Y2P8	RCL1_HUMAN
EVVGEQVTSY	Q96KP4	CNDP2_HUMAN
DVIETINKY	O75038	PLCH2_HUMAN
YVQDRVPSY	Q9H992	MARH7_HUMAN
NTVDSIESF	Q2TAY7	SMU1_HUMAN
AASPFYRGY	P48506	GSH1_HUMAN
NATKLERVF	Q9NV06	DCA13_HUMAN
EVDHNLHEL	Q9NV31	IMP3_HUMAN
RLKDIGPEVVK	P51659	DHB4_HUMAN
GVYSALRALK	Q5SWA1	PR15B_HUMAN
YAAGVHSV	O43299	AP5Z1_HUMAN
KYKDIYTEL	Q6WCQ1	MPRIIP_HUMAN
EVIRLIANF	Q9UIA9	XPO7_HUMAN

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FTVPHTHVF	Q8NFZ0	FBH1_HUMAN
ETYEGWYRGY	Q14185	DOCK1_HUMAN
AETPDIKLF	P46782	RS5_HUMAN
FTPPIVKRL	P84022	SMAD3_HUMAN
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DVITIIDRSF	P46013	KI67_HUMAN
YAFNHPSI	Q9Y261	FOXA2_HUMAN
RVIDLKSELK	Q9NWH9	SLTM_HUMAN
AVIAIFKSY	Q9H490	PIGU_HUMAN
ETPRSVPGF	O95602	RPA1_HUMAN
KTKFTIENV	Q9NRX1	PNO1_HUMAN
LSVDLIKTY	Q9Y463	DYR1B_HUMAN
VSSVRWISY	Q8TF05	PP4R1_HUMAN
DIYNGKVTSI	Q14562	DHX8_HUMAN
MSADRVVAF	P24468	COT2_HUMAN
SVVAGFGHF	Q5RI15	COX20_HUMAN
NVIHNLATY	Q53FV1	ORML2_HUMAN
EVKLKVSDF	P61289	PSME3_HUMAN
EVHIQLSEW	Q5VW36	FOCAD_HUMAN
EVASVYQSY	Q7Z434	MAVS_HUMAN
YTVENSrvY	Q9H6W3	RIOX1_HUMAN
TAYPASIVH	Q9H2X6	HIPK2_HUMAN
HAAPFQNIL	Q7L576	CYFP1_HUMAN
NAIEHVIIP	Q9Y5K8	VATD_HUMAN
DLPDHLLSY	C9J710	UMAD1_HUMAN
DTKDKVLVF	Q8NCM8	DYHC2_HUMAN
EVTEVKVSSW	O95190	OAZ2_HUMAN
HVITGLLEHY	Q96FV2	SCRN2_HUMAN
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SAAERLLAA	Q15427	SF3B4_HUMAN
DVFRATYAAF	Q8TEP8	CE192_HUMAN
FTAGPDEVRAW	Q9NTK5	OLA1_HUMAN
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ELFPDRALSSW	Q9NZ71	RTel1_HUMAN
DTIPYLKKF	Q96PC5	MIA2_HUMAN
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AEVKISHF	Q8IZT6	ASPM_HUMAN
HTVGLIVQY	Q15327	INP4B_HUMAN
DVAPTQPRW	Q96RT7	GCP6_HUMAN
ETTRISLL	Q9NSG2	CA112_HUMAN
ISTEFHKL	Q8NAN2	MIGA1_HUMAN
SANTRFAL	P30740	ILEU_HUMAN

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FSAGEPRVL	Q9BRA0	LSMD1_HUMAN
DLKSALAKF	Q9H173	SIL1_HUMAN
EAIQDLWQW	P06748	NPM_HUMAN
GVYPGHRPGL	Q63HR2	TNS2_HUMAN
FVLDAVKGT	Q8NBS3	S4A11_HUMAN
DLYYNTITNF	Q14527	HLTF_HUMAN
YAKLIAEL	Q8NI27	THOC2_HUMAN
LVKDQVILK	O15228	GNPAT_HUMAN
YPGHRPGL	Q63HR2	TNS2_HUMAN
STFDSPAHW	P00533	EGFR_HUMAN
EVAAIQLAF	Q96ME1	FXL18_HUMAN
NLSQRVVS	Q8IY37	DHX37_HUMAN
PVHQPPPLP	O75909	CCNK_HUMAN
EVVCIRSTW	Q5VW36	FOCAD_HUMAN
YATTVIPRVY	Q9HC07	TM165_HUMAN
EVLTSKGDW	Q9BQ61	TRIR_HUMAN
DVLEQIQQF	Q9H0E9	BRD8_HUMAN
NTPEEIARF	Q99418	CYH2_HUMAN
EVPKKLTEW	Q92616	GCN1_HUMAN
NASPINRIV	Q9NWH9	SLTM_HUMAN
SVYAFSARPL	P07203	GPX1_HUMAN
DVIAEQSVSGY	Q6YI46	TMM64_HUMAN
TVLPGELQSW	O95125	ZN202_HUMAN
AYKNVKFVLK	Q9UNL2	SSRG_HUMAN
EIITSTTSNY	Q6P2Q9	PRP8_HUMAN
FHPTHEW	Q9H173	SIL1_HUMAN
LEGQPCFVV	Q8N135	LGI4_HUMAN
KAVGHFVI	O14980	XPO1_HUMAN
LGAPAKPPL	P42226	STAT6_HUMAN
SIDEPLFRSW	Q63HN8	RN213_HUMAN
SAFGAFGKPSSL	Q8IVT2	MISP_HUMAN
EVISTLHYF	Q8NEU8	DP13B_HUMAN
ETLPSKIQW	Q6UWW8	EST3_HUMAN
EVNASPLKHF	O95140	MFN2_HUMAN
DIILSTSPHC	Q14439	GP176_HUMAN
DTVTDVDKSW	Q969N2	PIGT_HUMAN
SVSPLQRIY	Q5HY98	ZN766_HUMAN
YAQIRTIAI	P53396	ACLY_HUMAN
AAIDHQIEV	Q9Y485	DMXL1_HUMAN
ETAGPWGQAAW	Q6ZRI6	CO039_HUMAN
KNSPTSLIY	Q6P9F0	CCD62_HUMAN
EVIQAYETL	Q92797	SYMPK_HUMAN
ISITLVSVPLIV	Q96KR6	F210B_HUMAN
FAYPAIRYL	P51398	RT29_HUMAN
DIIGGSFGRF	Q8NCM8	DYHC2_HUMAN
DLYNYINP	P23921	RIR1_HUMAN

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EVVGKIRSL	Q9H792	PEAK1_HUMAN
ASRPFASVNV	O75882	ATRN_HUMAN
KTLTLINV	Q9UBZ4	APEX2_HUMAN
SELDLYGNRY	P11413	G6PD_HUMAN
AVAAAGRLGW	Q8NE01	CNNM3_HUMAN
PFCLKVSK	NA	NA
SEFIDSQRVW	Q6P2Q9	PRP8_HUMAN
TVIEGYLHI	NA	NA
SENNIQTIF	P05556	ITB1_HUMAN
DLNTRVAYW	NA	NA
ETAVGAAIKSF	Q16851	UGPA_HUMAN
EIIAQINTL	NA	NA
EVYTEEDAASY	NA	NA
EIIGKRGIGY	NA	NA
EEVEVILQY	P05556	ITB1_HUMAN
TVVRTYAPY	NA	NA
HSAPFSWET	NA	NA
EVVESIEKI	NA	NA
KAEGHSSGSW	NA	NA
PWKHAGK	Q00978	IRF9_HUMAN
VELHVHLDGS	NA	NA
TTPSAVFRVW	NA	NA
DTKEAIANY	NA	NA
TVLPGEIQGW	NA	NA
DVKDLIGFF	NA	NA
VTSPIRASY	NA	NA
EVIQTLVEI	NA	NA
EVIRAFYSY	NA	NA
ESSDSLQSW	NA	NA
DAWEGKGVSY	NA	NA
IANAEEDVPIKLY	NA	NA
AVRPASLNL	NA	NA
MIRAAPPPL	NA	NA
EVIGKLKGL	NA	NA
FTINGITNW	NA	NA
EVYDPLSKRW	NA	NA
VISSIRNF	Q8N4H5	TOM5_HUMAN
RVYPQAVYF	NA	NA
VVPGKYVVT	NA	NA
PGTANGH	Q5XG87	PAPD7_HUMAN
ETIKDGVSRF	NA	NA
ATKSSYLNI	NA	NA
AIPDEVIKKW	P14735	IDE_HUMAN
SVKEWTITY	NA	NA
EVQSLYREI	NA	NA
VVYDGEHLGSF	NA	NA
LGGAPPVPS	NA	NA
FAADIPRIL	NA	NA
DVPEKSSLF	Q8NFH3	NUP43_HUMAN

SPASFKYAEY	O00410	IPO5_HUMAN
AVIAHDFLAF	NA	NA
SLPEHNLITW	NA	NA
AELGGLLY	NA	NA
PHRKKKPF	NA	NA
DVKDRVAIL	NA	NA
SGLIHRV	Q8N6L1	KTAP2_HUMAN
AAAVDVRTW	NA	NA
EVFRDSLHTY	NA	NA
HTIGCNAVSW	NA	NA
KFKEFVQSV	NA	NA
ELYTGTVSSF	NA	NA
EVIGSELKHW	NA	NA
VFPAHTTIAF	NA	NA
DVILGTRKTY	Q969N2	PIGT_HUMAN
EIAPGLTGSEW	NA	NA
SLNKMHHEDS	NA	NA
AVPGPPPLP	Q9ULL5	PRR12_HUMAN
IIRSVFLGK	NA	NA
GTKLPGLLK	NA	NA
FGVDRAILY	NA	NA
FVTEYTPRSW	NA	NA
DVIDTLTSL	NA	NA
EVVPAIEKL	NA	NA
PAAPALAAP	Q9P206	K1522_HUMAN
KLKNVFLAY	NA	NA
EVVDKKIEEF	O43847	NRDC_HUMAN
ETFGFRGEAL	NA	NA
ISGGKPLEV	Q8N9N2	ASCC1_HUMAN
GLPPPLAAVPVP	NA	NA
DIRSPAIW	NA	NA
TTIAKYAQY	NA	NA
VVTYRIVSY	NA	NA
TAFPHELEV	NA	NA
NVTDLTTSW	NA	NA
DLIGKLTSL	NA	NA
GSRPAAPLI	NA	NA
DILADDFHL	NA	NA
PPGFPGPK	NA	NA
LSAIHESTSV	NA	NA
FAFEHSEEY	NA	NA
YASDVQLIL	NA	NA
VTVPPPLPA	NA	NA
YTAQPTQGY	NA	NA
VASDLFVGGI	NA	NA
EIDIAGYRF	NA	NA
LISHECGLAAF	NA	NA
SAAEIYNEV	NA	NA
VFDEFKPLVEEPQNLK	P02768	ALBU_HUMAN
VLGAFSDGLAHLNLK	P68871	HBB_HUMAN

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VNVDEVGGGEALGR	P68871	HBB_HUMAN
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FYAPELLFFAK	P02768	ALBU_HUMAN
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YVIDPIKGL	NA	NA
SPDLPKLKPD	NA	NA
DVIADIQTI	NA	NA
QLVHLIYVI	NA	NA
LVNEVTEFAK	P02768	ALBU_HUMAN
SPLVAPPAAL	NA	NA
LVAASQAALGL	P02768	ALBU_HUMAN
LQGPKAIAHI	NA	NA
VAYKLGAAL	NA	NA
VGVGVPSP	NA	NA
QTALVELVK	P02768	ALBU_HUMAN
VGGHAAEYGAEALER	NA	NA
VRMLAKKPG	NA	NA
QDGQFSVLFTK	NA	NA
FQNALLVR	P02768	ALBU_HUMAN
FQNALIVR	NA	NA
KKHKKYVI	NA	NA
LGPVPPPG	NA	NA
EIFDGNVAHI	NA	NA
PGAPPKAVL	NA	NA
YLYEIAR	P02768	ALBU_HUMAN
YIYEIAR	NA	NA
RVIGPRHPI	NA	NA
IGLPPNSP	NA	NA
VVPQLKYKV	NA	NA
TLPPPFNII	NA	NA
PAKKRRSI	NA	NA
PEAEGPSPVGP	NA	NA
IGKMDSPI	NA	NA
VANQNPI	NA	NA
KHLSPIVH	NA	NA
LSCLDVHLD	NA	NA
VAPLGPKP	NA	NA
WLKPVRG	NA	NA
LLLLLLFAC	NA	NA
PGKIFKT	NA	NA
APLLGAYLGGI	NA	NA
VAIGFKTKL	NA	NA
THLAQQL	NA	NA
LGPLQTPL	NA	NA
LQGPLTPL	NA	NA
PALAYGN	NA	NA
RLDPKTSF	NA	NA

PGKLIIR	NA	NA
PGKLIIR	NA	NA
APGGVYAE	NA	NA
DLYLWLSY	NA	NA
PPFIATIT	NA	NA
APKAGPPGLVH	NA	NA
SWSSAPCPSL	NA	NA
PAGARVAPP	NA	NA
TPLLGVH	NA	NA
GNRSQPGI	NA	NA
FSALEVDETYVPK	P02768	ALBU_HUMAN
SSSSGFGA	NA	NA
KATFTTLL	NA	NA
GLPLPQPL	NA	NA
GIKLYHSI	NA	NA
AAAVMAARL	NA	NA
SPLKPAAP	NA	NA
VRLPHGRP	NA	NA
APLKRG	NA	NA
GLPAAPVPLP	NA	NA

Appendix Table 11: Peptides observed in the immunopeptidome for A549 cells exposed to DNCB – individual peptide sequences are presented alongside the associated Uniprot protein accessions and IDs (where available).

Peptide	Accession	ID
AAFLKAIGY	O75533	SF3B1_HUMAN
RNLDIRPTY	P68366	TBA4A_HUMAN
IANAEVDVPIKLY	P29323	EPHB2_HUMAN
YGYDNVKEY	Q96GN5	CDA7L_HUMAN
ESFSDYPLGRF	P68104	EF1A1_HUMAN
FASGLIHRV	Q8N6L1	KTAP2_HUMAN
EVIGHYPGSSF	Q969W9	PMEPA_HUMAN
GVIDVITKTW	Q9H2D1	MFTC_HUMAN
DVISTIGQAF	P29353	SHC1_HUMAN
AANPHSFVF	Q9NQ55	SSF1_HUMAN
GTYENLIHVW	Q6Q0C0	TRAF7_HUMAN
YQFTGIKKY	Q96IX5	ATPMD_HUMAN
DSFSDLYSSY	Q9BTX1	NDC1_HUMAN
DTSDIVHIW	Q71F23	CENPU_HUMAN
DPVDIYKSW	P46940	IQGA1_HUMAN
TTYEGIFKTL	Q8WWM7	ATX2L_HUMAN
DTAPRILFW	Q15904	VAS1_HUMAN
DVKDYIQEY	Q63HN8	RN213_HUMAN
EVAEVKISHF	Q8IZT6	ASPM_HUMAN
GVIEKLLTSY	O75534	CSDE1_HUMAN
GIYEGVFKTY	Q99700	ATX2_HUMAN
VATTRDYYF	P06737	PYGL_HUMAN

TYFQAKIRALK	O00391	QSOX1_HUMAN
DTVVFVNQW	Q16678	CP1B1_HUMAN
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YAFVRPVIL	Q96S16	JMJD8_HUMAN
PDEVIKKW	P14735	IDE_HUMAN
NIPGAIPHW	P17405	ASM_HUMAN
TTIEISELPVRTW	P11388	TOP2A_HUMAN
NVIETISSL	Q92616	GCN1_HUMAN
AASPFYRGY	P48506	GSH1_HUMAN
EVPPEEFSTF	Q96AY3	FKB10_HUMAN
SITDFHPDTW	Q8N2K1	UB2J2_HUMAN
EVANGRSLVW	Q9BSV6	SEN34_HUMAN
DVVKEDAFYSW	Q04637	IF4G1_HUMAN
EVIKELAQI	O15355	PPM1G_HUMAN
VQSIRPPY	Q9Y6Q9	NCOA3_HUMAN
EVYDPTTNAW	O95198	KLHL2_HUMAN
SAFPKEVKV	Q5TH69	BIG3_HUMAN
ETTEFLSKL	Q9UKK3	PARP4_HUMAN
EVIDFSHGL	Q96GS6	AB17A_HUMAN
SVIEQILHY	Q15386	UBE3C_HUMAN
DVSRSIGLF	P38435	VKGC_HUMAN
ETFGFRGEAL	A4D2B8	PM2P1_HUMAN
DIADNFEAF	Q99832	TCPH_HUMAN
IAFSRPVKY	Q99759	M3K3_HUMAN
EAIGAVIHY	Q9UBB6	NCDN_HUMAN
EVFTEILNY	Q8NAP3	ZBT38_HUMAN
DTISPTLGF	P36404	ARL2_HUMAN
EVAPSFRTL	Q5SRE5	NU188_HUMAN
STIQDYLGF	P35869	AHR_HUMAN
DTKEGILQY	P05067	A4_HUMAN
DIYGGDYERF	Q8TE04	PANK1_HUMAN
EAYNIRTDSW	Q53G59	KLH12_HUMAN
DVIGQTITI	Q6UN15	FIP1_HUMAN
ETFHFVFGSF	Q8N140	EID3_HUMAN
LSKGPGLEV	Q9Y613	FHOD1_HUMAN
EVSSISSKF	Q9Y5K6	CD2AP_HUMAN
SAAEIYNEV	Q9BVG8	KIFC3_HUMAN
EIIAQINTL	Q96PE3	INP4A_HUMAN
YIQDRIPSW	P07942	LAMB1_HUMAN
EIAPGLTGSEW	Q9C0C7	AMRA1_HUMAN
DTSIFNQTW	Q9NZD8	SPG21_HUMAN
YVQDRVPSY	Q9H992	MARH7_HUMAN
YVAGLSGSTW	P47712	PA24A_HUMAN
EVIPLVQTF	Q8WVB3	HEXD_HUMAN
FTVPHTHVF	Q8NFZ0	FBH1_HUMAN
LGAPAKPPL	P42226	STAT6_HUMAN
SATSLRVL	Q4L235	ACSF4_HUMAN
YAKLIAEL	Q8NI27	THOC2_HUMAN
DTIGYLLTRY	Q14CX7	NAA25_HUMAN

SLPPQLPPP	O00411	RPOM_HUMAN
EVYTEEDAASY	P10644	KAPO_HUMAN
AASALIRTL	Q13535	ATR_HUMAN
ALIEFIRSEY	P26639	SYTC_HUMAN
RKGGSYTQAASSDSAQGSVDLSLTA CKV	P04439	HLLA_HUMAN
DTNADKQLSF	P06702	S10A9_HUMAN
LSLLGDIATDY	P31151	S10A7_HUMAN
EINENNREF	Q9NS73	MBIP1_HUMAN
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DLDTNADKQL	P06702	S10A9_HUMAN
SVKLGHPDTLNQGEFKEL	P06702	S10A9_HUMAN
NSSIRPIF	O43663	PRC1_HUMAN
MKENFPNF	P31151	S10A7_HUMAN
YAKDDPLEF	P06756	ITAV_HUMAN
ETLDFPRSW	Q5JTH9	RRP12_HUMAN
SIPPLFWR	P28221	5HT1D_HUMAN
YTTVPRVAF	O75973	C1QRF_HUMAN
GKVLGRKHTLL	Q9NRM0	GTR9_HUMAN
LGHDPDTLNQGEFKEL	P06702	S10A9_HUMAN
IINTFHQY	P06702	S10A9_HUMAN
DTFPGPYAVL	Q14774	HLX_HUMAN
VAPEEHPVLLTEAPLNPK	P60709	ACTB_HUMAN
LDTNADKQLSF	P06702	S10A9_HUMAN
ETYIRSGTY	Q08257	QOR_HUMAN
DIYNFPIHAF	Q9BXY0	MAK16_HUMAN
PRLLKFW	Q9H0A0	NAT10_HUMAN
DVINSRTQGF	Q9Y230	RUVB2_HUMAN
DLFNGRYHVI	Q96SB4	SRPK1_HUMAN
KATNVVRL	Q9NYU1	UGGG2_HUMAN
SAVADVRLY	Q92521	PIGB_HUMAN
EVIKNFIQY	Q9Y262	EIF3L_HUMAN
FVLDAVKGT	Q8NBS3	S4A11_HUMAN
EIITSTTSNY	Q6P2Q9	PRP8_HUMAN
RIKAIQLEY	O43242	PSMD3_HUMAN
KENFPNF	P31151	S10A7_HUMAN
AETPDIKLF	P46782	RS5_HUMAN
EVVGYFGRF	Q9P2L0	WDR35_HUMAN
FTPPIVKRL	P84022	SMAD3_HUMAN
GVYPGHRPGL	Q63HR2	TNS2_HUMAN
SAIDFYRK	Q9GZZ1	NAA50_HUMAN
ESINHVVVF	Q53FT3	HIKES_HUMAN
TASPLVKS	Q6P4F7	RHGBA_HUMAN
LGHDPDTLNQGEF	P06702	S10A9_HUMAN
ELAKQITSY	P50990	TCPO_HUMAN
ETIESINQL	Q92925	SMRD2_HUMAN
STYFEGKSF	Q9BZJ4	S2539_HUMAN
SELDLTYGNRY	P11413	G6PD_HUMAN
EVVDFSSHY	Q9UKA2	FBXL4_HUMAN
PPGVLKIFG	Q5U651	RAIN_HUMAN

ETIAKLIK	O94808	GFPT2_HUMAN
ELRPGLIGW	Q14739	LBR_HUMAN
GVIEKLLT	O75534	CSDE1_HUMAN
DENSVIKSF	Q9H8H0	NOL11_HUMAN
ETIPDGIGKL	Q9BTT6	LRRC1_HUMAN
AQVPFEQIL	Q99828	CIB1_HUMAN
MSADRVVAF	P24468	COT2_HUMAN
DTPGHTLSW	P06865	HEXA_HUMAN
EVATHYLEI	O95436	NPT2B_HUMAN
IETIINTFHQY	P06702	S10A9_HUMAN
DINTDGAVNFQEF	P05109	S10A8_HUMAN
DLDTNADKQLSF	P06702	S10A9_HUMAN
EVTLLARY	P19388	RPAB1_HUMAN
LGHPDTLNQGEFKE	P06702	S10A9_HUMAN
DTNADKQLSFEEF	P06702	S10A9_HUMAN
RAYPAATI	O95071	UBR5_HUMAN
EVNASPLKHF	O95140	MFN2_HUMAN
DAASGEVVGKF	P52888	THOP1_HUMAN
DLYPSNPVSW	Q13042	CDC16_HUMAN
EVITGIRII	Q15439	MRP4_HUMAN
DVISSIRQL	O60343	TBCD4_HUMAN
GVIDVITK	Q9H2D1	MFTC_HUMAN
RLKDIGPEVVK	P51659	DHB4_HUMAN
KAEGHSSGSW	Q5VY80	ULBP6_HUMAN
DAWEGKGVSY	Q6PI47	KCD18_HUMAN
RLFVGSIPK	O60506	HNRPQ_HUMAN
LDTNADKQLSFEEF	P06702	S10A9_HUMAN
EVLRGAIETY	Q12797	ASPH_HUMAN
ETPLHISGF	Q9ULX3	NOB1_HUMAN
GLPPPLAAVPV	Q8TBN0	R3GEF_HUMAN
FTAGPDEVRAW	Q9NTK5	OLA1_HUMAN
HTVPIYEGY	P60709	ACTB_HUMAN
KVKDILSKV	Q52LJ0	FA98B_HUMAN
AVKAIYQY	P37268	FDFT_HUMAN
AAYPEIVAV	Q17RS7	GEN_HUMAN
LFRASPATL	P12273	PIP_HUMAN
ETIASVRS	O15514	RPB4_HUMAN
DTYPEESRSY	Q5T200	ZC3HD_HUMAN
EVKLGEPSW	P56134	ATPK_HUMAN
LIYPNSIQEY	Q86VI4	LAP4B_HUMAN
TTPSAVFRVW	Q9NRG9	AAAS_HUMAN
APPPPLPGL	Q27J81	INF2_HUMAN
AATTVLRQL	Q9UKL0	RCOR1_HUMAN
DIINSFQSI	P32780	TF2H1_HUMAN
EVIQAYETL	Q92797	SYMPK_HUMAN
EKALNSIIDV	P05109	S10A8_HUMAN
HSAPFSWET	Q9H425	CA198_HUMAN
YTADPYHAL	O43251	RFOX2_HUMAN
SFFVRGQEF	Q6IQ16	SPOPL_HUMAN
NAIEHVIIP	Q9Y5K8	VATD_HUMAN

SAHILSAAPI	Q9NZM4	BICRA_HUMAN
EVITKLDGL	Q4AC94	C2CD3_HUMAN
EVVDKKIEEF	O43847	NRDC_HUMAN
SAAGFPIRV	Q96H55	MYO19_HUMAN
EVVCIRSTW	Q5VW36	FOCAD_HUMAN
AAFEKALEV	Q13325	IFIT5_HUMAN
KHLICTR	Q13972	RGRF1_HUMAN
ISSVDRILT	Q9NYV8	T2R14_HUMAN
DINTDGAVNF	P05109	S10A8_HUMAN
AEINNIKI	P11388	TOP2A_HUMAN
VELHVHLDGS	P00813	ADA_HUMAN
SVKSVPENLLK	Q13155	AIMP2_HUMAN
EIVTTIPTI	P84085	ARF5_HUMAN
EVVESIEKI	Q12934	BFSP1_HUMAN
RWVELEKPLK	NA	NA
VYKNVILQV	NA	NA
DSIIAEVKAQY	NA	NA
DIPELEHGW	NA	NA
LSSSVIREL	NA	NA
ISGGKPLEV	Q8N9N2	ASCC1_HUMAN
VGMGHKPPIP	NA	NA
ISHIGKL	Q9P2W9	STX18_HUMAN
YITSVSRLY	NA	NA
TAAPGRFSF	NA	NA
NVIDKLAQF	NA	NA
AVRPASLNL	NA	NA
LMASNGVAVDG	NA	NA
KSVDWLLVF	Q96J42	TXD15_HUMAN
EVIGLLGGRY	NA	NA
SVKLGHPDTLNQGEF	P06702	S10A9_HUMAN
DVVSGSEVLHW	NA	NA
AAIDHQIEV	NA	NA
EIFDGNVAHI	NA	NA
TSLDFLFHF	NA	NA
FGVDRAILY	P06756	ITAV_HUMAN
DVTQTVSSF	NA	NA
ATKSSYLNI	NA	NA
SLKEIVINV	NA	NA
GLPPPLAAVPVP	Q8TBN0	R3GEF_HUMAN
RSYPYAFSV	NA	NA
EVLTSKGDW	NA	NA
SLHAVITFK	NA	NA
KGTTKPVNW	Q9NV96	CC50A_HUMAN
TTIAKYAQY	NA	NA
RLLYKLSTVRV	NA	NA
EVIVGVNKY	NA	NA
FAFEHSEY	NA	NA
PGGLTLPPV	Q96Q05	TPPC9_HUMAN
EVNEVIQKVSG	NA	NA
NSDTHSSTFDAGAGIALNDH	NA	NA

EVIKSQEVF	NA	NA
NASPINRIV	NA	NA
EVPKKLTEW	Q92616	GCN1_HUMAN
VLVGGSTRIPKVQK	P0DMV8	HS71A_HUMAN
TSSSFGKFSW	NA	NA
VLRVCSGVYF	NA	NA
YASDVQLIL	NA	NA
IAAGVPVVP	NA	NA
GPEELGAGP	NA	NA
SAFPEVRSL	NA	NA
HTVEDYQAI	Q99832	TCPH_HUMAN
LVKDQVILK	NA	NA
EVIINTEIW	NA	NA
KATAYILSV	NA	NA
DLPDHLLSY	NA	NA
RVYPQAVYF	NA	NA
EVFIHKDKGF	Q15233	NONO_HUMAN
DAISAGKNW	Q8IWX8	CHERP_HUMAN
DVFHGPYGNF	Q5T7M9	DIK1A_HUMAN
VFQYRLVEY	Q8TAD8	SNIP1_HUMAN
AVIIPRYR	Q9UPY3	DICER_HUMAN
AVFTTGQHW	Q92482	AQP3_HUMAN
ETIDSRVQEY	Q5VYV7	SLX4I_HUMAN
DTKDKVLVF	Q8NCM8	DYHC2_HUMAN
DVTQVSSAY	Q14247	SRC8_HUMAN
DTCDFLTHGF	Q9P2D0	IBTK_HUMAN
EISNIFSNY	P78545	ELF3_HUMAN
ELAENILKW	Q9NVX0	HAUS2_HUMAN
DVIFHPTQPW	Q14137	BOP1_HUMAN
EIAESVQAF	Q6PD74	AAGAB_HUMAN
SVQDPGLHVW	P40121	CAPG_HUMAN
DSRDGTPLSW	Q96NU0	CNT3B_HUMAN
DTIPYLKKF	Q96PC5	MIA2_HUMAN
EVTEVKVSSW	O95190	OAZ2_HUMAN
EVVEKYEIY	Q9BZD4	NUF2_HUMAN
ELITKFLQY	Q00537	CDK17_HUMAN
SPASFKYAEY	O00410	IPO5_HUMAN
EVTTHILSQF	Q9BR11	ZSWM1_HUMAN
CTYGKPVTF	Q9BRN9	TM2D3_HUMAN
RVPPPPPIA	B2RXH8	HNRC2_HUMAN
EVYVSRPSHF	P52630	STAT2_HUMAN
DLNTRVAYW	Q9Y3B3	TMED7_HUMAN
HLKDAQIFIQK	P04040	CATA_HUMAN
AYKNVKFVLK	Q9UNL2	SSRG_HUMAN
ILVVFMK	Q9NRD9	DUOX1_HUMAN
LFKPPQPPA	Q15372	EIF3H_HUMAN
VSSVRWISY	Q8TF05	PP4R1_HUMAN
EVISGYEEL	Q7L576	CYFP1_HUMAN
YSSPEILRV	Q2MV58	TECT1_HUMAN
EVIPALPRL	Q96Q05	TPPC9_HUMAN

GTQPWFISK	Q15746	MYLK_HUMAN
EVTEFISKL	Q8WYQ9	ZCH14_HUMAN
LVLSTLSGRPVK	Q9Y2P8	RCL1_HUMAN
NASPVISV	Q96T58	MINT_HUMAN
TFGERVVA	Q7LG56	RIR2B_HUMAN
HIAENILSY	Q9UKB1	FBW1B_HUMAN
VGVLPGVP	P15502	ELN_HUMAN
ELAGKILSTW	Q53EU6	GPAT3_HUMAN
GTFERAVVY	Q96AY4	TTC28_HUMAN
PTVLAPRLP	O00268	TAF4_HUMAN
YCSNLVRTL	Q9Y5B9	SP16H_HUMAN
EVVPEPVARW	P27707	DCK_HUMAN
DVIGDEICCW	Q9H3F6	BACD3_HUMAN
DVLGDEICCW	Q8WZ19	BACD1_HUMAN
YDGKIKVW	Q9UKB1	FBW1B_HUMAN
EVYDPATETW	Q8IXQ5	KLHL7_HUMAN
EIIHEIAVL	Q9UEE5	ST17A_HUMAN
EILHEIAVL	NA	NA
YAFPKAVSVF	O15427	MOT4_HUMAN
SASEVLKEW	Q86XZ4	SPAS2_HUMAN
GEPRFIAVGYYDD	P04439	HLLA_HUMAN
KTHLPPPAL	Q14159	SPIDR_HUMAN
HVADFAPEVAW	P07814	SYEP_HUMAN
LGEHNIDVLEGNEQFINAAK	NA	NA
IAFFTTASV	Q7RTX1	TS1R1_HUMAN
DVLGSAKGW	O15067	PUR4_HUMAN
SEFTGVWKY	O75340	PDCD6_HUMAN
EVKDSLGVY	Q9Y4C2	TCAF1_HUMAN
AVKGLPLPA	Q9H765	ASB8_HUMAN
DVIADIQTI	Q5THK1	PR14L_HUMAN
KLKDLAFLK	L0R6Q1	S35U4_HUMAN
SIFPTIPK	Q9NWH2	TM242_HUMAN
VLRDGLF	Q8WZ64	ARAP2_HUMAN
DVAPTQPRW	Q96RT7	GCP6_HUMAN
TLTDVAHEY	O94864	ST65G_HUMAN
EILEKSFSEF	O43390	HNRPR_HUMAN
KSRKPKKGA	Q13428	TCOF_HUMAN
KTTLIN	Q9UBZ4	APEX2_HUMAN
YAQIRTAI	P53396	ACLY_HUMAN
ETIKDGVSRF	Q8NFU5	IPMK_HUMAN
YIIQNIPGF	Q9H0U9	TSYL1_HUMAN
TGVSSSTNPFPRQK	P63218	GBG5_HUMAN
HTIGCNAVSW	P55735	SEC13_HUMAN
FFLRKFRN	P48751	B3A3_HUMAN
YAYTGRLEL	Q96PQ7	KLHL5_HUMAN
DVIGTSLGF	Q8N8Q9	NIPA2_HUMAN
EVVTTIPTI	P40616	ARL1_HUMAN
KYKDIYTEL	NA	NA
EIVEKILSV	NA	NA
DVIHEVAHSW	NA	NA

EIIPTLGQF	NA	NA
HTVGLIVQY	NA	NA
YTFPGILKW	NA	NA
EVVGEQVTSY	NA	NA
SANTRFAL	NA	NA
AVIAHDFLAF	NA	NA
EVVPAAVSGRW	NA	NA
EVAPALSVF	NA	NA
AAAEPKLF	NA	NA
YGSEGRFTF	NA	NA
SVIDGRFEGF	NA	NA
FTINGITNW	NA	NA
HVITGLLEHY	NA	NA
KDHVKFW	NA	NA
SGLIHRV	Q8N6L1	KTAP2_HUMAN
ETIARLQAL	NA	NA
ATAGPRLGW	NA	NA
ETFYNEKEESF	NA	NA
EVVSNVQEY	NA	NA

Appendix Table 12: Peptides observed in the immunopeptidome for A549 cells exposed to phthalic anhydride – individual peptide sequences are presented alongside the associated Uniprot protein accessions and IDs (where available).

Peptide	Accession	ID
YAFVRPVIL	Q96S16	JMJD8_HUMAN
AAFLKAIGY	O75533	SF3B1_HUMAN
RNLDIRPTY	P68366	TBA4A_HUMAN
EVIGHYPGSSF	Q969W9	PMEPA_HUMAN
GVIEKLLTSY	O75534	CSDE1_HUMAN
ESFSDYPPLGRF	P68104	EF1A1_HUMAN
GTYENLIHVW	Q6Q0C0	TRAF7_HUMAN
GVIDVITKTW	Q9H2D1	MFTC_HUMAN
DVRPPYAEY	Q7Z4N8	P4HA3_HUMAN
DTVVFVNQW	Q16678	CP1B1_HUMAN
DVVEVAGLTSF	O75391	SPAG7_HUMAN
DPVDIYKSW	P46940	IQGA1_HUMAN
DTAPRILFW	Q15904	VAS1_HUMAN
AANPHSFVF	Q9NQ55	SSF1_HUMAN
EVFHPTHEW	Q9H173	SIL1_HUMAN
FASGLIHRV	Q8N6L1	KTAP2_HUMAN
EVNTEKLTA	A2A3N6	PIPSL_HUMAN
VATTRDYYF	P06737	PYGL_HUMAN
DSFSDLYSSY	Q9BTX1	NDC1_HUMAN
AAFAYTVKY	Q8N2K1	UB2J2_HUMAN
YGYDNVKEY	Q96GN5	CDA7L_HUMAN
EVPSEPGRLAF	P16144	ITB4_HUMAN
TAFPKPLLT	Q9BZG8	DPH1_HUMAN

VALLRVTPF	Q8N4H5	TOM5_HUMAN
DLIEHFSQF	Q13151	ROA0_HUMAN
TVIEEHLGKF	Q6DKI1	RL7L_HUMAN
EAFDLEARTW	Q8IXV7	KLD8B_HUMAN
EVAEVKISHF	Q8IZT6	ASPM_HUMAN
EIVKEVSTY	P68104	EF1A1_HUMAN
EIYGSDSRFAGY	O75533	SF3B1_HUMAN
STIPPELVKQK	Q9BVS4	RIOK2_HUMAN
DVKDYIQEY	Q63HN8	RN213_HUMAN
VATEKAVEL	P29401	TKT_HUMAN
EVISQHLVSY	P12270	TPR_HUMAN
DTVTKELVSW	Q96DN5	TBC31_HUMAN
AAANAIRVY	Q9NRK6	ABCBA_HUMAN
TAADIFKQY	Q8N3U4	STAG2_HUMAN
GWRPPPPPL	O95302	FKBP9_HUMAN
GTADELVLHSW	Q5VWZ2	LYPL1_HUMAN
AAAVPRAAF	P30040	ERP29_HUMAN
DTFGPRAQGW	Q9ULX6	AKP8L_HUMAN
SAYGGPVGAGIREV	P08729	K2C7_HUMAN
AQGPTPRYF	O60427	FADS1_HUMAN
DVQRPTGSF	Q722K6	ERMP1_HUMAN
TTFPRPVTV	Q15233	NONO_HUMAN
FGTIRTIDY	Q96T37	RBM15_HUMAN
HVADENLKAF	Q5BKU9	OXLD1_HUMAN
FASHVSPEV	Q9NP61	ARFG3_HUMAN
DTSDIVHIW	Q71F23	CENPU_HUMAN
HASDRIIAL	P29401	TKT_HUMAN
ASFDGRISVY	O94979	SC31A_HUMAN
AAFDKIQL	Q9P2I0	CPSF2_HUMAN
EVVAGIKEY	Q9UBU8	MO4L1_HUMAN
SAYGSVKAY	P07355	ANXA2_HUMAN
SAFADRPAP	Q16678	CP1B1_HUMAN
TVAGLALIKKY	P43490	NAMPT_HUMAN
GIYEGVFKTY	Q99700	ATX2_HUMAN
AVIGDVIRVY	Q9NR30	DDX21_HUMAN
YAAPHPLQSY	Q9ULL5	PRR12_HUMAN
DVVRVVGAY	Q8N2G8	GHDC_HUMAN
DVASGQVVRKF	Q9BRX9	WDR83_HUMAN
DTADQVIASF	O43707	ACTN4_HUMAN
DTVKKIESF	P49792	RBP2_HUMAN
DAVGRVQGW	Q8IZY2	ABCA7_HUMAN
NVFGDGPYSTF	Q5BJF6	ODFP2_HUMAN
DVISTIGQAF	P29353	SHC1_HUMAN
EAIPDEVIKKW	P14735	IDE_HUMAN
NAYYEEVVY	P30838	AL3A1_HUMAN
DSISKFLQF	Q01814	AT2B2_HUMAN
LANGEVRIY	Q8NFJ9	BBS1_HUMAN
EVIASYNQL	Q13219	PAPP1_HUMAN
EVVSEPFERSF	Q13200	PSMD2_HUMAN
KQFPEVIKY	Q9UIF9	BAZ2A_HUMAN

SAIDRIFTL	Q86TU7	SETD3_HUMAN
ETVDSGYRSF	Q9Y2T1	AXIN2_HUMAN
DVIAQGIGKL	P05387	RLA2_HUMAN
YAI DNPLHY	A5YKK6	CNOT1_HUMAN
DTYNVAIRNY	Q6PGP7	TTC37_HUMAN
ILTERGYSF	P60709	ACTB_HUMAN
DTIPYLKKF	Q96PC5	MIA2_HUMAN
ELIRYISEL	Q93008	USP9X_HUMAN
ETPSWTGSGF	P55268	LAMB2_HUMAN
YDAEISQIHQ	P35908	K22E_HUMAN
EIYPPKLHQF	P24864	CCNE1_HUMAN
EVIKEVQEF	P21926	CD9_HUMAN
ETFSGVYKKL	P62081	RS7_HUMAN
EVISALKQTW	Q96HC4	PDL15_HUMAN
AAYGYGIRY	P06737	PYGL_HUMAN
AAALRDLSF	Q32P28	P3H1_HUMAN
DVISSIRNF	Q8N4H5	TOM5_HUMAN
SVYSIVPQSW	Q71RC2	LARP4_HUMAN
DVFSEKSLSY	Q13368	MPP3_HUMAN
VAINHIVDF	P78346	RPP30_HUMAN
DVAEIQTGKF	Q55007	LRRK2_HUMAN
EIPEGYVPEHW	Q43674	NDUB5_HUMAN
GAYEQVIKY	P98194	AT2C1_HUMAN
SVPRDLPSW	P78527	PRKDC_HUMAN
QVADVVVSRW	P49327	FAS_HUMAN
FATPFLVVR	P15954	COX7C_HUMAN
SAYPQRLEI	Q07973	CP24A_HUMAN
EVEVGDRTSW	Q96F44	TRI11_HUMAN
RLKDIGPEVVK	P51659	DHB4_HUMAN
SVKSVPENLLK	Q13155	AIMP2_HUMAN
SVVKELSSF	P38398	BRCA1_HUMAN
ELIAKIPNF	Q01105	SET_HUMAN
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